ESCMID

Abstract Book 2020

European Congress of Clinical Microbiology and Infectious Diseases

ECCMID

30th

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Winfried V. Kern ECCMID Programme Director says Goodbye

ECCMID 2014
Deputy Programme Director

ECCMID 2015 – 2020
Programme Director

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Introduction

Welcome Address

Dear colleagues and friends,

It is our pleasure to present in this volume the scientific abstracts which were selected to appear at the 30th European Congress on Clinical Microbiology and Infectious Diseases (ECCMID).

While the on-site congress in Paris did not occur in April of 2020 as a consequence of COVID-19 pandemic, we would like to acknowledge the hard work that went into the planning of ECCMID, and the messages of support that have been received since the announcement of the on-site cancellation.

It was again another record-breaking year for the submission of ECCMID abstracts, with 6,980 pieces of scientific work being submitted in late 2019 for inclusion , as well as 181 abstracts that were received in February 2020 as latebreaker submissions. A big thank you to all submitters for being part of this record-breaking year!

The scientific abstracts are subject to a stringent review process, with each submission being viewed and rated by at least three ECCMID abstract reviewers. These reviewers represent the pre-eminent experts in various specialties from the fields of Clinical Microbiology and Infectious Diseases. As with every year, we thank them all for their outstanding and essential work in the abstract rating process.

Once the ratings were finalised, the ECCMID Programme Committee decided on the accepted abstracts by specific topic, and allocated them into abstract sessions, as presented herein.

The ECCMID Abstract Programme represents the latest studies and findings from the last year of Clinical Microbiology and Infectious Diseases, and we congratulate all of the authors who had their work included. We hope that the works included herein spark conversations and collaborations between scientists across disciplines and across the world.

We are also looking forward to receiving abstract submissions later this year for inclusion in the ECCMID 2021 abstract programme.

We hope that you enjoy reading the ECCMID 2020 abstracts, and we are looking forward to seeing you in person in Vienna for ECCMID 2021!

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Acknowledgements

The ECCMID Programme Committee is proud to acknowledge the scientific input from the following organizations in setting up the scientific programme and/or organizing joint workshops and symposia:

ASM – American Society for Microbiology

EACS – European AIDS Clinical Society

EANM – European Association of Nuclear Medicine

ECDC – European Centre for Disease Prevention and Control

EF-CLIF – European Foundation For the Study of Chronic Liver Failure

EITaF – ESCMID Emerging Infections Task Force

ERS – European Respiratory Society

ESDPPP – European Society for Developmental, Paediatric and Perinatal Pharmacology

ESPID – European Society for Paediatric Infectious Diseases

EU Commission's Directorate-General for Research and Innovation

EUCAST – European Committee on Antimicrobial Susceptibility Testing

EUCIC – European Committee on Infection Control

EU-JAV – European Joint Action on Vaccination

FEMS – Federation of European Microbiological Societies

GARDP – Global Antibiotic Research and Development Partnership

ISF – International Sepsis Forum

ISIRV – International Society for Influenza and other Respiratory Virus Diseases

MSF – Médecins Sans Frontières

WHO – World Health Organization

Future Congresses

31st ECCMID

VIENNA, AUSTRIA
10 – 13 April 2021

Reed Messe Vienna

32nd ECCMID

LISBON, PORTUGAL
23 – 26 April 2022

Altice Arena Lisbon / FIL Lisbon

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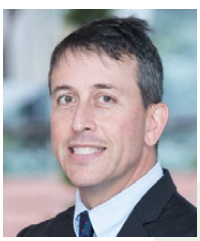

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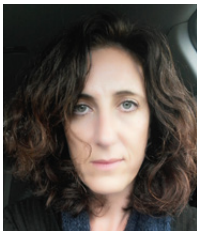

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How it all began. Learn this and more in the brochure „the first 35 years“

Brochure available at

https://www.escmid.org/fileadmin/src/media/pictures/contentpictures/Yearbook/ESCMID_TheFirst35Years_300dpi.pdf

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MANAGING INFECTIONS
PROMOTING SCIENCE

ESCMID-ECDC Observerships

Visit ECDC and find out about the organization!

A group of 15 observers (ESCMID members) will participate in a five-day programme at the European Centre for Disease Prevention and Control (ECDC) in Solna, Sweden.

The application period for this five-day visit will be announced via the ESCMID website as well as the ESCMID social media channels.

www.escmid.org/ECDC_Observer
www.ecdc.europa.eu

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Abstract Programme

1. Viral infection & disease

- HIV/AIDS (incl diagnostics & epidemiology, anti-retroviral drugs, treatment & susceptibility/resistance)
- Viral hepatitis (incl diagnostics & epidemiology, antiviral drugs, treatment & susceptibility/resistance)
- Influenza and respiratory viruses (incl diagnostics & epidemiology, antiviral drugs, treatment, excl vaccination)
- Herpesviruses (incl diagnostics & epidemiology, antiviral drugs, treatment & susceptibility/resistance, excl clinical studies in immunocompromised hosts)
- Emerging/re-emerging, vector-borne and zoonotic viral diseases (all aspects)
- Diagnostic virology (other than respiratory viruses, herpesviruses, hepatitis & HIV)
- Viral epidemiology – general, prevalence studies, molecular and genomic epidemiology (other than respiratory viruses, herpesviruses, hepatitis & HIV)
- Antiviral drugs, treatment, susceptibility/resistance (other than respiratory viruses, herpesviruses, hepatitis & HIV)
- Other

Session accepted as Paper Poster Session

Clinical aspects of non-flu respiratory viruses

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2886 **Respiratory syncytial virus, an underestimated disease in the elderly population**
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3060 **Non-invasive ventilation in patients with acute respiratory failure secondary to viral respiratory infection: a nested case-control study**
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3640 **Antimicrobial stewardship intervention in FLU/ respiratory syncytial virus adult hospitalisations: major impact on antimicrobial management of a systematic epidemiological surveillance process including training and feed-back**
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4169 **Antiviral efficacy of released-active antibodies to interferon gamma against MERS Coronavirus**
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7219 **Positive respiratory viral panel results moderately shorten antibiotic duration in patients with presumed respiratory tract infections**
J. Von Bulow (Wall, United States), L. Rodriguez, S. Lee, K. Ota Sullivan, J. Gallagher*

7730 **In-hospital and midterm out-hospital complications of hospitalised respiratory syncytial virus-positive adults in France**
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Session accepted as Mini-oral ePoster Session

Constant threat of emerging infections

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4903 **Decision tree algorithm that differentiates dengue from other febrile illnesses at the early stage of the disease: a health centre-based prospective observational cohort study**
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Session accepted as Paper Poster Session

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2374 **Detection of dengue virus antibodies in febrile patients suspected of malaria attending a health centre in Jos, Nigeria**
N. Miri (Jos, Nigeria), J. Mawak, N. Chuwang, T. Ezekiel, S. Acheng, C. Chukwu*

2587 **Evaluation the impact of dengue infection in gestation and conception: an ecological study using time series analysis**
O. Lupi (Rio de Janeiro, Brazil), F. Meque, D. Villela, P. Brasil*

3103 **High-resolution mapping reveals emergence and autochthonous transmission of dengue fever outbreak in a previously low-epidemic region in south-east China, 2019**
Y. Zhang (Shanghai, China), J. Ai, W. Zhang*

4561 **Evaluation of the diagnostic accuracy of a rapid dengue NS1 antigen lateral flow immunochromatography test in UK returned travellers**
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4853 **Clinical dilemma in patients presenting with dengue viral infection**
M. Irshad (Karachi, Pakistan), S. Sethi, K. Habib, M. Mushtaq, F. Mahmood, B. Jamil*

6292 **Dealing with the current dengue viral fever outbreak: an experience from a tertiary care hospital in Karachi**
S. Sarfaraz (Karachi, Pakistan), F. Herekar, S. Iftikhar*

7244 **Dengue virus infects HBMEC cell model and regulates proteins related to the blood-brain barrier function**
J. Yu (Guangzhou, China), X. He, X. Liu, W. Zhao*

8305 **Dengue awareness in patients with acute febrile illness in Sindh province of Pakistan**
J. Farooqi (Karachi, Pakistan), M. Long, K. Barr, K. Imtiaz, E. Khan*

Session accepted as Paper Poster Session

Diagnostic aspects of non-flu respiratory viruses

1239 **The clinical application of FILMARRAY respiratory panel in children with acute respiratory tract infections**
F. Pan (Shanghai, China), H. Zhang*

3030 **Acceptability and usefulness of self-collected mid-turbinate swabs to diagnose and measure viral shedding in a pilot randomised controlled trial of hypertonic saline nasal irrigation and gargling in adults with a common cold**
S. Ramalingam (Edinburgh, United Kingdom), C. Graham, J. Dove, L. Morrice, A. Sheikh*

3263 **Clinical evaluation of a multiplex real-time PCR-based Neoplex RV-Panel A kit for the simultaneous detection of respiratory viral pathogens**
A. Cho, J. Kim, J. Gu, S. Hong, W. Cho, K. Lee (Gyeonggi-Do, South Korea), S. Hong, S. Kim*

4170 **Detection of influenza and non-influenza respiratory viruses detected in lower respiratory tract specimens of hospitalised adult patients and analysis of the clinical outcome**
C. Hsu (Taipei, Taiwan), H. Chen*

4628 **Meta-analysis of accuracy of rapid influenza antigen detection tests in community-care settings accounting for antigen type, setting, population and manufacturer**
E. Gentilotti (Verona, Italy), E. Cremonini, P. De Nardo, A. Gorska, F. Mazzaferri, M. Paul, H. Goossens, E. Tacconelli*

4857 **Reduction of laboratory turnaround time is not the only answer for shorten length of stay at the emergency department**
L. Lind (Gävle, Sweden), K. Gullsby, D. Scholder, E. Röjerås*

6411 **Usefulness of sputum for the identification of the viral aetiology in adults with community-acquired pneumonia**
J. Berastegui Cabrera (Seville, Spain), M. Aguilar-Guisado, J. Crespo Rivas, M. López Verdugo, L. Merino, A. Escoresca Ortega, C. Calero, L. Carrasco Hernandez, J. Toral Marín, M. Abad Arranz, N. Ramírez Duque, B. Barón Franco, J. Sánchez Céspedes, J. Pachon-Diaz*

8960 **Multiplex respiratory pathogen PCR and parental work absenteeism**
S. Mattila, N. Paalanne (Oulu, Finland), M. Honkila, T. Pokka, T. Tapiainen*

9511 **Adenovirus types associated with severe respiratory diseases in intensive care unit-admitted patients during the 2017-2019 period**
A. Piralla (Pavia, Italy), F. Novazzi, F. Giardina, A. Fratini, G. Salve, S. Pregnolato, F. Baldanti, F. Mojoli*

Session accepted as 2-Hour Oral Session

Emerging viral infections: a great concern

1143 **Phylogenetic analysis of complete genomes reveals the circulation of multiple lineages of rabies lyssavirus in India**
H. Pulleri Kandi Anuraj (Bengaluru, India), C. Pattabiraman, G. Yale, A. Mahadevan, R. Mani*

1817 **Epidemiological investigation of newly detected highly lethal Borna disease virus 1 cases reinforcing indirect shrew contact as possible source of infection: results from in-depth interviews, Germany, 2019**
P. Kirsten (Berlin, Germany), C. Frank, H. Wilking, D. Rubbenstroth, M. Böhmer*

2155 **Viral and immunologic factors associated with fatal outcome of patients with severe fever with thrombocytopenia syndrome in Korea**
J. Kwon (Seoul, South Korea), J. Kim, S. Ra, T. Kim, S. Park, M. Kim, S. Park, D. Kim, H. Cha, H. Lee, N. Jeon, M. Kim, Y. Chong, S. Lee, S. Choi, Y. Kim, J. Woo, K. Lee, S. Kim, S. Kee*

2525 **Disease course, management and predictors of fatality in hospitalised patients with real-time PCR confirmed Lassa fever in Nigeria: a prospective cohort study**
A. Duvignaud (Bordeaux, France), M. Jaspard, I. Etafo, D. Gabillard, B. Serra, C. Abejegah, C. Le Gal, A. Abidoye, S. Owhin, A. Augier, A. Salam, L. Ahmed, J. De Bruyne Mushenvula, E. Ogbaini-Emovon, S. Günther, P. Horby, A. Adedosu, X. Anglaret, O. Ayodeji, D. Malvy*

2675 **Predictors of worse outcome in patients with West Nile virus infection: a multi-centre study**
G. Virgili (Bologna, Italy), L. Attard, M. Bartoletti, L. Raumer, G. Rossini, R. D'Angelo, L. Spinardi, V. Geatti, L. Massoli, M. Di Nuzzo, E. Biagi, C. Contini, M. Libanore, E. Fallica, V. Tugnoli, E. Franceschini, C. Mussini, M. Lancellotti, G. Martelli, F. Cristini, S. Venturini, M. Crapis, K. Kaveh Moghadam, P. Viale*

2747 **Rift Valley fever in pregnancy: a systematic review and meta-analysis of foetal outcomes**
N. Kayem (Oxford, United Kingdom), C. Benson, C. Aye, S. Baker, M. Tome, S. Kennedy, P. Ariana, P. Horby*

5194 **Neurodevelopment outcomes at 24 months of age in ZIKV-exposed and ZIKV-unexposed infants in French territories in the Americas: preliminary results from the ZIKA-DFA-BB cohort study**
R. Grant (Paris, France), O. Flechelles, B. Tressières, M. Dialo, N. Elenga, N. Mediamolle, A. Mallard, J. Hebert, N. Lachaume, E. Couchy, B. Hoen, A. Fontanet*

6399 **Post-exposure prophylaxis for high risk contacts of Ebola virus using immunotherapies with monoclonal antibodies in the eastern DRC: a compassionate use program**
M. Jaspard (Paris, France), S. Juchet, B. Serra, B. Baweye, I. Malam Kanta, M. Camara, K. Ntondi, E. Toguyadji Adidjingar, B. Efoloko, R. Kojan, D. Malvy*

6929 Toscana virus: clinical and biological studies based on 864 cases
N. Ayhan (Marseille, France), R. Charrel*

Session accepted as Paper Poster Session

Epidemiology of non-flu respiratory viruses

689 **Enterovirus D68 subclade B3 in children with acute flaccid paralysis in west Africa: evidence of spread of outbreaks reported in US and Europe, 2016**
A. Fall (Dakar, Senegal), K. Ndiaye, N. Ndiaye, O. Kebe, M. Jallow, D. Kiori, S. Sy, D. Goudiaby, M. Dia, M. Niang, N. Dia*

1115 **Incidence of hospitalisation for respiratory syncytial virus in children aged 0-5 years in Ontario, Canada**
S. Buchan (Toronto, Canada), H. Chung, N. Daneman, A. Guttmann, J. Kwong, M. Murti, A. Campigotto, J. Gubbay, T. Karnauchow, K. Katz, A. Mcgeer, J. Mcnally, S. Mubareka, D. Richardson, S. Richardson, M. Smieja, G. Zahariadis, T. To, S. Deeks*

1437 **Multi-centre study of common pathogen epidemiology in hospitalised children with acute respiratory tract infection in winter from 2017 to 2018, China**
L. Meng (Shanghai, China), H. Zhang, X. Shao, J. Zhou*

1710 **Replication of MERS and SARS Coronaviruses in bat cells offers insights to their ancestral origins**
J. Fung (Hong Kong, Hong Kong), S. Lau, H. Luk, U. Wernery, P. Woo*

2333 **Proposing the spike gene of Coronavirus OC43 as a target for nosocomial outbreak investigation in long-term care facilities**
H. Mistry (Toronto, Canada), L. Yip, K. Bozek, H. Mbareche, A. Linkenheld-Sturk, R. Kozak, V. Williams, D. Pajak, J. Leis, S. Mubareka*

2451 **Impact of Point-of-Care testing on the surveillance of respiratory viral infections in West Midlands, England**
D. Ironmonger (Birmingham, United Kingdom), A. Bains, T. Hong, D. Todkill, J. Hawker, O. Edeghere*

3369 **Morbidity burden of different viral and bacterial pathogens in acutely ill children**
H. Pöyry (Oulu, Finland), M. Kiviniemi, A. Raappana, N. Paalanne, T. Pokka, P. Valmari, T. Tapiainen*

3985 **Assessing Pharyngeal Respiratory virus Carriage in healthcare workers Over Time (APRICOT): a feasibility study**
A. Melhuish, J. Minton (Leeds, United Kingdom)*

3986 **Comparative virulence of respiratory viruses on the winter seasons from 2017 to 2019: a southern European multi-centre cohort study**
A. Almeida (Lisbon, Portugal), M. Boattini, E. Christaki, T. Marques, I. Moreira, L. Cruz, V. Tosatto, D. Antao, G. Bianco, M. Iannaccone, C. Costa, G. Tsiolakkis, E. Khattab, D. Kasapi, R. Cavallo, R. Corte Real*

4046 **Burden of viral pneumonia among patients with lung infiltrates undergoing bronchoalveolar lavage: a retrospective one-year study**
C. Maurel (Trieste, Italy), E. Gibbin, L. Segat, R. Luzzati*

4278 **Respiratory syncytial virus bronchiolitis and recurrent wheezing: a 1-year follow-up study**
P. Venkat Ramanan (Chennai, India), K. Subbiah*

4691 **Respiratory pathogens detected in children with community-acquired sepsis-like syndrome in 6 European countries**
V. Matheeussen (Edegem, Belgium), K. Loens, K. Jacobs, P. Horby, H. Goossens, M. Kohns Vasconcelos, M. Sharland, M. De Jong, M. Koopmans, P. Fraaij, M. Ieven*

5169 **Building a predictive score for local risk of respiratory syncytial virus hospitalisation: Normative Outcome Hospitalisation Assessment for Newborns (NOHAN)**
C. Jean-Sebastien (Lyon, France), M. Jourdain, R. Kramer, S. Couray-Targe, A. Myard-Dury, D. Ploin, Y. Gillet, E. Javouhey, B. Lina, M. Benchaib*

5391 **Comprehensive analysis of evolutionary dynamics of circulating strains and immunopathogenesis of respiratory syncytial virus-associated acute lower respiratory tract infections in children**
S. Sarkar (Chandigarh, India), R. Ratho, M. Singh, A. Singh, M. Singh*

6025 **Aetiology and outcome of children hospitalised for acute respiratory tract infections in Europe: findings from a multi-country combined case-control and cohort study**
M. Kohns Vasconcelos (London, United Kingdom)*

6120 **Comprehensive analysis of evolutionary dynamics of circulating strains and immunopathogenesis and co-infections of human metapneumovirus associated acute lower respiratory tract infections in children**
R. Ratho (Chandigarh, India), S. Sarkar, M. Singh, A. Singh, M. Singh*

6569 **Nanopore metagenomic sequencing to investigate nosocomial transmission of human metapneumovirus from a unique genetic group among haematology patients in the United Kingdom**
Y. Xu, K. Lewandowski, K. Jeffery, L. Downs, D. Foster, N. Sanderson, J. Kavanagh, A. Vaughan, C. Salvagno, R. Vipond, M. Carroll, R. Danby, T. Peto, D. Crook, A. Walker, P. Matthews, S. Pullan (Salisbury, United Kingdom)*

6779 **Clinical characteristics and outcomes of respiratory syncytial virus infection among hospitalised adult patients: risk factors of intensive care unit hospitalisation and 30-day mortality**
C. Youngeun (Seoul, South Korea), J. Kim, S. Kim, Y. Yoon, J. Sohn, M. Kim*

6910 **Viral respiratory tract infections in children: epidemiology and impact of the implementation of a multiplex PCR**
A. Amine Khodja, D. Boufedji, B. Mesples, L. Landraud, M. Cotillon, R. Basmaci, F. Joannes (Colombes, France)*

7191 **Epidemiology and outcomes of respiratory syncytial virus Infection in haematopoietic cell transplant recipients: findings from a multinational respiratory viral infection consortium (RVIC)**
D. Shah (San Antonio, United States), M. Salvatore, K. Patel, M. Satlin, J. Lum, S. Mossad, J. Horan, C. Wolfe, M. Morris, J. Camargo, M. Abidi, P. Chong, D. Vinh, J. Papenburg, B. Zoghi, L. Kannikanan, C. Silva, N. Hamerschlak, S. Shete*

7289 **Comparison of humoral response against both haemagglutinin and neuraminidase after seasonal influenza vaccination**
J. Mendez Legaza, I. Sanz, R. Ortiz De Lejarazu, L. Sanchez De Prada (Valladolid, Spain)*

7926 **Nosocomial respiratory syncytial virus infections: a two-season European multi-centre cohort study**
T. Moreira Marques (Lisbon, Portugal), A. Almeida, M. Boattini, E. Christaki, R. Corte Real, M. Moreira, V. Tosatto, D. Antao, L. Cruz, G. Bianco, C. Costa, R. Cavallo, M. Iannaccone, G. Tsiolakkis, D. Kasapi, E. Khattab*

7932 **Severe viral respiratory infections in paediatric intensive care unit: a 4-year experience in an Italian paediatric hospital**
M. De Luca, C. D'Amore, L. Gargiullo, V. Clemente, C. Tripiciano, S. Mercadante, D. Perrotta, J. Nunziata, R. Bianchi, E. Rossetti, C. Concato, A. Vittucci, P. Zangari, L. Romani (Rome, Italy), F. Calò Carducci, M. Ciofi Degli Atti, P. D'Argenio*

8010 **A retrospective study of rhinoviruses molecular diversity in three Paris hospitals: differential behaviours of HRV groups?**
O. Haddad, M. Bertine, N. Fidouh, D. Bouzid, X. Duval, V. Bunel, R. Borie, J. Lucet, D. Descamps, B. Visseaux (Paris, France)*

8295 **A majority of adult hospitalised patients with community-acquired lower respiratory tract infections had viral infections**
N. Sundell, L. Gustavsson, M. Lindh, L. Andersson, J. Westin (Gothenburg, Sweden)*

8919 **Different expression of CD26 and CD66 receptors on PBMCs from MERS Coronavirus infected patients**
A. Alhetheel (Riyadh, Saudi Arabia), A. Albarrag, Z. Shakoor, A. Somily, M. Barry, M. Bakhrebah, M. Nassar, Z. Memish, A. Asiri*

9028 **Medical software approach for French ILI sentinel surveillance**
L. Vaillant (Paris, France), R. Pons, T. Launay, D. Simon, C. Goupillon, C. Hervé, V. Roussel, C. Turbelin, T. Blanchon*

Session accepted as Paper Poster Session

Herpesvirus and CMV infections

792 **Feasible alternatives to dried blood spot in the retrospective diagnosis of congenital cytomegalovirus infection**
C. Reyes Ruiz (Madrid, Spain), I. Taravillo, N. Moral, C. Moraleda, D. Blázquez-Gamero, L. Folgueira*

1015 **Association of single nucleotide polymorphisms in *IL1B* and *IL28B* genes with the outcome of congenital cytomegalovirus infection**
B. Kasztelewicz (Warsaw, Poland), D. Jedlińska-Pijanowska, J. Czech-Kowalska, A. Dobrzańska, K. Dzierzanowska-Fangrat*

1559 **Pooled saliva cytomegalovirus-PCR: a viable laboratory technique for universal cytomegalovirus screening of healthy newborns**
Y. Shlonsky, O. Golan-Shany (Haifa, Israel), N. Shehade, R. Mubariki, I. Srugo, M. Hemo, A. Riskin, D. Bader, E. Bamberger*

3080 **Validity of International Classification of Diseases (ICD) for the identification of herpes zoster virus infection requiring hospitalisation**
E. Capistran (Sherbrooke, Canada), V. Morin, D. Marcoux, S. Proulx, M. Gagné, C. Abou Chakra, N. Gagnon, A. Carignan*

4293 **Universal neonatal screening for congenital cytomegalovirus, the time is now?**
J. Van Acker (Gent, Belgium), E. Vanlaere, A. Van Den Abeele, V. Staelens, I. Dierickx, C. Verfaillie*

4659 **CRISPR/Cas9 targeting of essential herpes simplex virus type 1 genes impairs virus replication in the mammalian cell**
N. Demidova (Moscow, Russian Federation), R. Klimova, D. Karpov, A. Kushch*

6168 **HHV-6A infection and systemic sclerosis: clues of a possible association**
E. Caselli, I. Soffritti (Ferrara, Italy), M. D'Accolti, D. Bortolotti, R. Rizzo, D. Giuggioli, C. Ferri*

7248 **Etiological structure of exanthema subitum in children of younger age**
O. Silveystrova (Moscow, Russian Federation), E. Domonova, O. Shipulina, E. Samitova, I. Khegai*

7955 **Varicella zoster: a complicated primoinfection in an elderly patient**
S. Brandão Lopes (Vila Nova de Famalicão, Portugal), G. Cruz, F. Santos, C. Ventura, E. Rabadão, J. Cunha*

8671 **MDM2 expression in Epstein-Barr virus-associated gastric cancers**
M. Timóteo (Porto, Portugal), L. Afonso, R. Henrique, R. Medeiros, H. Sousa*

9595 **Evolution of awareness and knowledge of congenital cytomegalovirus infection among healthcare providers in France between 2011 and 2018**
T. Fellah, J. Sibiude, C. Vauloup-Fellous, A. Cordier, L. Grangeot-Keros, A. Benachi, L. Mandelbrot, S. Guitton, O. Picone (Colombes, France)*

Session accepted as 2-Hour Oral Session

Herpesviruses: old foes, new problems

1063 **Diagnostics value of Epstein-Barr virus DNA load in whole blood and plasma from paediatric transplant recipients**
B. Kasztelewicz (Warsaw, Poland), J. Teisseyre, K. Janiszewska, I. Jankowska, P. Kaliciński, K. Dzierzanowska-Fangrat*

1919 **Anti-apoptotic role of human cytomegalovirus miRNAs, miR UL-70-3p and UL-148D on hydrogen peroxide-induced apoptosis in HEK 293T cells**
S. Gosipatala (Lucknow, India), A. Pandeya, S. Saxena*

2660 **Metagenomics next-generation sequencing for the identification of undiagnosed DNA and RNA viruses in adult allogeneic haematopoietic cell transplant recipients with steroid refractory graft-versus-host disease**
M. Zanella, S. Cordey, F. Laubscher, M. Docquier, G. Vieille, C. Van Delden, D. Neofytos, V. Braunersreuther, T. Mckee, J. Lobrinus, S. Masouridi Levrat, Y. Chalandon, L. Kaiser (Geneva, Switzerland), D. Vu Cantero*

3540 **Clinical validation of an ELISpot-based *in vitro* diagnostic assay to monitor cytomegalovirus-specific cellular immunity in immunocompromised transplant recipients**
D. Wolff, B. Banas, E. Wagner, D. Teschner, B. Krämer, B. Krüger, C. Wolschke, D. Janson, K. Schaefer-Eckart, J. Gärtner, S. Mielke, M. Schreder, G. Kobbe, M. Kondakci, I. Hilgendorf, M. Von Lilienfeld-Toal, S. Klein, D. Heidenreich, S. Kreil, M. Verbeek, S. Grass, M. Ditschkowski, T. Gromke, D. Steubl, L. Renders, D. Chittka, M. Banas, T. Wekerle, M. Koch, O. Witzke, M. Lindemann, A. Mühlfeld, C. Sommerer, A. Habicht, C. Hugo, T. Huenig, T. Schmidt, A. Rascle (Regensburg, Germany), H. Guldan, S. Barabas, R. Wagner, L. Deml*

3768 **Neonatal screening for congenital cytomegalovirus infection: identification of a viral DNA diagnostic cut-off value in saliva samples**
M. De Paschale, G. Turello, A. Chiereghin, D. Gibertoni, S. Santandrea, F. Baiesi, M. Borghi, C. Pavia, M. Manco, M. Capretti, C. Marsico, A. Ruscitto, M. Bellini, A. Porta, L. Pogliani, L. Parola, P. Clerici, T. Lazzarotto (Bologna, Italy)*

4954 **Herpes simplex virus resistance testing: an automated interpretation platform linking genotype to phenotype**
E. Gallagher (London, United Kingdom), D. Bibby, D. Williams, J. Mbisa*

7714 **Central nervous system infections caused by herpes simplex virus and varicella zoster virus in France, 2014-2018: a nationwide retrospective study**
D. Boutolleau (Paris, France), S. Burrel*

8268 **Novel mutations found in UL56 terminase subunit and UL54 DNA polymerase after human cytomegalovirus infection treatment with letermovir**
M. Santos Bravo (Barcelona, Spain), S. Sanchez-Palomino, M. Mosquera Gutiérrez, C. Martin Gandul, M. Rodríguez Hernandez, N. Plault, V. Gonzalo, E. Cordero Matias, S. Alain, M. Marcos*

Session accepted as Paper Poster Session

HIV clinical aspects

646 **Investigating the sexual protective behaviour among HIV-positive women in Tehran, Iran**
Z. Talebi Tamajani (Ghazvin, Iran), R. Lotfi, K. Kabir, Z. Bayat Jozani, M. Mohraz*

893 **Incidence of influenza-like illness among HIV-positive patients: an outpatient clinic survey-based study**
A. Almeida (Lisbon, Portugal), P. Barreto, T. Marques, T. Pacheco, M. Leal Dos Santos, S. Pinheiro, I. Germano, F. Maltez, M. Alves, E. Teofilo*

1185 **Epstein-Barr virus biomarkers in HIV-related non-Hodgkin lymphoma in the modern cART era**
J. Lupo (Grenoble, France), R. Germi, R. Lancar, M. Genin, D. Costagliola, P. Morand, C. Besson*

3047 **Prognostic factors in HIV-infected patients with lymphoma: a single-centre experience**
F. Volpato (Bologna, Italy), A. Cascavilla, M. Bartoletti, P. Viale*

3198 **Are neurological co-infections common in AIDS-related cerebral toxoplasmosis?: a prospective cohort study on late cART era in São Paulo, Brazil**
J. Telles (Sao Paulo, Brazil), R. Fernandes, A. Maestri Neto, T. Vitoriano, T. Dahrug Barros, R. Marcusso, L. Borges, R. Teixeira, M. Haziot, A. Penalva De Oliveira, J. Vidal Bermúdez*

4096 **Factors associated with in-hospital mortality in hospitalised patients with HIV/AIDS**
J. Hoyos Pulgarin (Medellin, Colombia), A. Alzate, O. Bolaños, J. Martinez*

5160 **A wide spread of sexually-transmitted infections among users of pre-exposure prophylaxis attending the dedicated outpatient clinic in Modena, Italy**
G. Cuomo, A. Raimondi (Modena, Italy), C. Rogati, M. Tutone, B. Beghetto, G. Nardini, E. Roncaglia, V. Borghi, G. Guaraldi, M. Coppini, C. Mussini*

5552 **Missed opportunities for an early HIV diagnosis**
D. Bassoulis (Athens, Greece), E. Kostaki, C. Gialouri, E. Iliadi, D. Paraskevis, M. Psichogiou*

5644 **Audit on HIV quality of care to new patients in a level 4 teaching Hospital**
N. Nurdin (Dublin, Ireland), C. Kerr, C. Bergin*

5915 **Detection of high rates of HIV-seropositivity in urban university hospital emergency department**
L. May (Sacramento, United States), T. Chechi, S. Voong, N. Tran*

6446 **Squamous cell carcinoma of the anus screening in people living with HIV: HPV genotyping is as important as cytology in anal cancer early diagnosis**
M. Digaetano, C. Rogati, M. Menozzi (Modena, Italy), A. Bonazza, F. Spatafora, A. Farinetti, R. Gelmini, M. Pecorari, S. Tagliazucchi, L. Reggiani Bonetti, R. Iachetta, R. Villani, C. Mussini*

6551 **Sexual behaviour and incidence of sexually-transmitted infections in high-risk men who have sex with men following pre-exposure prophylaxis commencement Sophocles-P4G demonstration study**
M. Psichogiou (Athens, Greece), M. Papadopoulou, V. Sypsa, S. Roussos, S. Chanos, N. Dedes, G. Daikos, J. Schneider, A. Hatzakis*

8319 **Beta-D-glucan to aid the diagnosis of *Pneumocystis* pneumonia in HIV-positive patients**
T. Juniper (London, United Kingdom), C. Eades, E. Gil, E. Wey, S. Morris-Jones, K. Quinn, F. Post, R. Miller*

8436 **Late presentation of HIV infection in a hospital in the community of Madrid**
S. Mendoza Lizardo (Madrid, Spain), R. Escudero Sánchez, E. Perez Fernandez, L. Moreno, M. Velasco Arribas, R. Hervas Gomez, O. Martin Segarra, N. Mayoral Canalejas, S. Bellón Vallinot, A. Vegas Serrano, J. Losa García*

8476 **Progressive multifocal leukoencephalopathy, still a challenge in the combined antiretroviral therapy era**
I. Ianache, A. Olaru, R. Radoi, M. Nica, G. Tardei, L. Ene, A. Oprea (Bucharest, Romania)*

Session accepted as Paper Poster Session

HIV epidemiology and diagnosis

917 **Achieving the third 95: Keeping adolescents living with HIV virally suppressed in rural Nigeria in test and treat era using continuous quality improvement model of peer counseling & support group**
S. Usman (Abuja, Nigeria)*

922 **Assessment of viral load suppression rates among paediatric patients living with HIV in South-Western Nigeria**
S. Usman (Abuja, Nigeria)*

942 **Accelerated HIV case finding and bridging the gap in antiretroviral therapy enrolment among prison inmates: a break-even in achieving the 95-95-95 UNAIDS targets among key populations in Western Nigeria**
S. Usman (Abuja, Nigeria)*

943 **HIV-related stigma and discrimination in Western Nigeria: experiences of people living with HIV and rights issues**
S. Usman, I. Usman (Osogbo, Nigeria)*

1234 **Factors associated with low uptake of HIV testing among middle aged 15-17 adolescent girls in Uganda**
M. Lwetabe (Kampala, Uganda), A. Lutaya*

2532 **Cascade of HIV care in three different settings in Morrumbene, Mozambique**
P. Magro, C. Cerini, A. Da Gloria, S. Tembe, F. Castelli (Brescia, Italy), L. Tomasoni*

3900 **Would HIV infections and AIDS cases decrease in Japan? Time series analysis using Bayesian inference**
K. Iwata (Kobe, Japan), C. Miyakoshi*

4216 **Checkpoint Plus Freiburg: performance of an on-site integrated, low-threshold sexual transmitted diseases/HIV counselling and treatment service in Germany**
M. Müller (Freiburg, Germany), S. Usadel, S. Zimmermann, U. Hoffmeister, A. Fahrhöfer, W. Kern, S. Rieg*

4813 **Characteristics and trends of recently HIV infected individuals in Estonia in 2013-2017**
E. Jõgeda (Tartu, Estonia), R. Avi, P. Merit, P. Soodla, T. Päll, E. Kallas, H. Rajasaar, K. Rüütel, I. Lutsar, K. Huik*

5305 **Performance of the new random access molecular diagnostics analyser Alinity m**
R. Ehret (Berlin, Germany), J. Dhein, S. Breuer, M. Obermeier*

5486 **End-to-end Workflow for HIV-1 drug resistance genotyping of protease and reverse transcriptase in major group-M subtypes**
K. Clyde, C. Hinahon, X. Fang, E. Zeringer, L. He, A. Cheng, J. Fonseca, J. Trotta, E. Schreiber (San Francisco, United States)*

5791 **Implementation of a smartphone application intervention to increase linkage to and engagement with HIV care among people with tuberculosis and substance use in Irkutsk, Siberia**
J. Hodges (Charlottesville, United States), A. Waldman, O. Koshkina, A. Suzdalnitsky, E. Moiseeva, M. Koshcheev, J. Schwendinger, S. Vitko, O. Ogarkov, S. Zhdanova, R. Dillingham, S. Heysell*

7381 **Performance evaluation of a new screening and viral load monitoring HIV-1 assay on the NeuMoDx molecular system**
A. Narwold, C. Couture (Ann Arbor, United States), H. Lee, J. Bezenah, C. Nguyen, C. Butcher, M. Mastronardi, B. Wu, S. Brahmasandra*

7721 **Non-B subtypes are a major driver of clustered HIV-1 transmission in north Italy in recent years**
L. Colagrossi (Milan, Italy), M. Moioli, A. Nava, S. Carta, S. Chiappetta, V. Costabile, D. Motta, L. Chianura, R. Rossotti, D. Fanti, P. Carlo Federico, M. Puoti, C. Alteri*

8037 **Potential use of data from a national HIV testing surveillance system to improve community-based testing strategies, Ireland**
M. Brady (Dublin, Ireland), K. O'Donnell, A. Shanley, E. Nugent, C. Hurley, M. O'Tuathail, M. Fitzgerald, C. Flynn, R. Carson, D. Igoe*

8151 **Prevalence of non-B HIV-1 subtypes in north Italy and analysis of transmission clusters based on sequence data analysis**
G. Lorenzin (Brescia, Italy), F. Gargiulo, A. Caruso, F. Caccuri, E. Focà, A. Celotti, M. Quiros Roland, I. Izzo, F. Castelli, S. Corbellini, F. Gurrieri, G. Piccinelli, M. De Francesco*

8667 **Performances of a new random access system for human immunodeficiency virus RNA quantification**
A. Maillard, C. Pronier (Rennes, France), G. Lagathu, P. Comacle, C. Grolhier, V. Thibault*

8773 **Implementation of a full-length HIV-1 NGS assay into clinical diagnostics**
J. Heaney (London, United Kingdom), R. Ferns, M. Byott, P. Grant, A. Garcia, S. Kirk, C. Booth, J. Raffle, M. Paraskevopoulou, T. Mahungu, Z. Kozlakidis, D. Frampton, D. Pillay, E. Nastouli*

8857 **Epidemiological profile, mortality and causes of death in the first year of newly HIV-diagnosed patients of a national referral centre in Costa Rica from January 2015 to December 2017**
M. Brenes Madrigal (San Josè, Costa Rica), M. Villalobos Zúñiga*

8941 **Evaluation of HIV-1 and hepatitis B ad C viruses quantification by a new molecular system in comparison to established routine methods**
L. Martínez García (Madrid, Spain), B. Romero, A. Sanchez Diaz, M. Rodriguez, R. Canton Moreno, J. Galán*

Session accepted as 1-Hour Oral Session

HIV in 2020

4521 **Evaluation of a dual therapy and a simplified, patient-centred monitoring strategy for the long-term management of HIV infection: a non-inferiority, randomised, controlled, open-label clinical trial (SIMPL'HIV)**
D. Sculier, M. Annalisa (Genève, Switzerland), G. Wandeler, M. Stöckle, E. Bernasconi, D. Braun, P. Vernazza, M. Cavassini, K. Metzner, L. Decosterd, M. Buzzi, H. Gunthard, P. Schmid, S. Yerly, A. Limacher, M. Egger, A. Calmy*

5290 **Risk of failure in dual vs. triple therapy in naïve HIV patients: a meta-analysis**
A. Russo (Naples, Italy), M. Pisaturo, L. Onorato, S. Martini, S. Signoriello, P. Maggi, N. Coppola*

6541 **Unravelling HIV proviral latency by comparing HIV-1 and HIV-2 expression and reactivation with single round, double reporter constructs**
A. Bruggemans (Leuven, Belgium), G. Vansant, Z. Debyser*

8804 **Exposure to maternal antiretroviral therapy *in utero* frequently differs between twins**
M. Louchet, H. Didelot, G. Peytavin, M. Le, A. Bourgeois-Moine, L. Carbillon, D. Luton, I. Matheron, L. Rigonnot, L. Mandelbrot (Bagnolet, France)*

Session accepted as Paper Poster Session

HIV therapeutics

901 **The progress towards achieving the UNAIDS ambitious 95% viral suppression target among adults living with HIV in South-Western Nigeria**
S. Usman (Abuja, Nigeria)*

1945 **Alterations in the gut microbiome of HIV-infected patients under antiretroviral therapy**
S. Ray (Stockholm, Sweden), A. Narayanan, C. Giske, U. Neogi, A. Sönnerborg, P. Nowak*

2041 **Real-world experience of bictegravir/emtricitabine/tenofovir alafenamide in a diverse Dublin cohort**
M. Moriarty (Dublin, Ireland), G. Melanophy, E. Devitt*

2492 **Effectiveness and safety of a dual therapy with boosted darunavir and dolutegravir in patients with an advanced HIV infection**
J. Pasquau (Granada, Spain), C. García-Vallecillos, S. Sequera, L. Muñoz-Medina, M. Galido, T. Brieva, J. Santos, G. Verdejo, S. Ferra Murcia, F. Téllez Pérez, J. Garcia, D. Rial, J. Iribarren Loyarte, C. Hidalgo Tenorio*

2879 **Rapid antiretroviral therapy initiation in the era before universal treatment, Croatia, 2005 to 2014**
N. Bogdanic (Zagreb, Croatia), L. Bendig, L. Davorka, Š. Zekan, J. Begovac*

3095 **Darunavir/cobicistat monotherapy as simplification strategy for HIV patients: a retrospective Multi-centre Spanish Study (DRV-simply)**
A. Inciarte Portillo (Barcelona, Spain), J. Bernardino, Á. Mena De Cea, R. Mican Rivera, D. Carlos, C. García-Vallecillos, P. Callau, M. Castro Iglesias, J. Pasquau, E. Martinez, J. Blanco*

3601 **Systemic inflammation and activation of immunity in HIV-positive patients receiving antiretroviral therapy**
A. Matuzkova, N. Pshenichnaia (Moscow, Russian Federation), A. Suladze, L. Dosyagaeva, T. Tverdokhlebova*

4175 **Lipid profile change in HIV naïve patients treated with therapy tenofovir alafenamide-based**
L. Alessio (Caserta, Italy), S. Martini, P. Maggi, L. Onorato, S. Ferrara, V. Esposito, G. Di Filippo, A. Masiello, R. Santoro, V. Rizzo, C. Bellacosa, A. Iodice, N. Coppola*

4771 **HIV-1 transmitted drug resistance is slowly rising in Estonia in 2017**
A. Šablinskaja (Tartu, Estonia), P. Merit, E. Jõgeda, H. Rajasaar, P. Soodla, E. Kallas, T. Päll, K. Rüütel, I. Lutsar, K. Huik, R. Avi*

4815 **Analysis of the evolution of the rate and the associated factors of antiretroviral treatment switch due to intolerance symptom on children in France**
L. Cohen (Paris 19, France), J. Warszawski, J. Le Chenadec, P. Frange, V. Avettand-Fenoel, J. Sibiude, C. Dollfus, M. Caseris, A. Faye*

5282 **Evaluation of integrase strand transfer inhibitors on weight gain and body mass index**
M. Badowski (Chicago, United States), R. Goldberg, A. Kania, T. Chiampas, M. Patel, S. Michienzi*

6006 **Adherence to routine monitoring guidelines for people living with HIV is poorer in higher-volume outpatient settings: when more is not better!**
D. Ng (Singapore, Singapore), I. Wee, E. Sng, S. Lee, Z. Ling, L. Wijaya, Y. Teh*

6241 **Application of logistic regression model in the identification of potential HIV-1 drug resistance-associated mutations**
T. Wang (Taipei, Taiwan), J. Chang, P. Lin, C. Hung, S. Chang*

6531 **Improvements in HIV-1 transmitted drug resistance surveillance in Ireland**
M. Neary (Dublin, Ireland), M. Brady, J. Moran, J. Connell, S. Coughlan, S. Doyle, O. Ennis, F. Cooney, N. Eichler, S. Keating, C. Hurley, E. Nugent, S. O'Dea, L. Preston, H. Tuite, F. Lyons, K. O'Donnell, D. Igoe, C. Degascun*

6552 **Bone density, microarchitecture and tissue quality after 1 year of treatment with dolutegravir-abacavir-lamivudine**
J. Soldado, E. Lerma-Chipirraz, I. Arrieta, A. Gonzalez-Mena, I. Domingo, H. Knobel, R. Güerri Fernandez (Barcelona, Spain)*

8020 **A review of the resistance to integrase inhibitors in HIV-1 patients in a third level hospital: a four-year experience**
L. Haces Pinto, D. Ampuero, A. Candela (Madrid, Spain), P. García Morales, M. Jodar Checa, R. Alonso, P. Muñoz*

8455 **Immunotherapy in patients with relapsed/refractory HIV-related lymphomas**
M. Popova, Y. Rogacheva (Saint Petersburg, Russian Federation), I. Tsygankov, K. Lepik, A. Nekrasova, L. Stelmah, I. Moiseev, S. Bondarenko, N. Mikhaylova, V. Baykov, B. Afanasyev*

8722 **Cabotegravir and bictegravir placental transfers in *ex vivo* human cotyledon perfusion**
L. Pencolé (Colombes, France), M. Le, F. Bouchet Crivat, D. Duro, G. Peytavin, L. Mandelbrot*

Session accepted as Paper Poster Session

Influenza epidemiology and clinical aspects

244 **Hospital-acquired influenza characteristics and its correlation with the population-based surveillance in a tertiary care centre in Istanbul**
H. Bilgin (Istanbul, Turkey), E. Avci, G. Culha, N. Pazar, S. Guneytepe, I. Sagir, R. Can Sarınoğlu, E. Baran, U. Sili, V. Korten*

607 **Flu isolation wards: does medical specialty matter? Comparison of three specialties on outcome and antibiotic usage in hospitalised influenza A infected patients in Vienna during the season 2018/19**
M. Karolyi (Vienna, Austria), E. Pawelka, H. Kelani, G. Funk, B. Lindner, C. Porpaczy, S. Publig, T. Seitz, M. Traugott, A. Zoufaly, C. Wenisch*

2114 **Incidence of medically-attended influenza and influenza-related hospitalisations by co-morbidities among a commercially insured population in the United States**
A. Near, J. Tse, Y. Young-Xu, L. Connolly, C. Reyes (San Francisco, United States)*

2610 **The difference in mortality between adult patients with laboratory-confirmed influenza A and B, a single centre observational study**
D. Mabayoje (London, United Kingdom), T. Cutino-Moguel, J. Haigh, M. Wilks, C. Welch, M. Melzer*

3666 **Estimating the burden of influenza on hospitals using severe acute respiratory infections in metropolitan France, 2012-2018**
A. Bernadou (Bordeaux, France), N. Fortin, B. Hubert*

4416 **Triaging influenza in patients attending fever clinical scoring system for a modified influenza case definition**
W. Liyuan (Beijing, China), J. Zhao, Q. Zhou, X. Lu*

4427 **Prevalence and clinical outcomes associated with viral and atypical bacterial co-infections in a large global study of adults hospitalised with influenza (INSIGHT FLU003 Plus)**
D. Dwyer (Westmead, Australia), D. Wentworth, N. Gerry, M. Hoover, J. Neaton, R. Davey, M. Polizzotto, T. Clark, A. Paez, J. Paño Pardo, J. Lundgren, A. Babiker, S. Pett*

4461 **Hospital-based surveillance of influenza in Switzerland: a pilot study, season 2018/19**
A. Iten, A. Thiabaud (Geneva, Switzerland), N. Troillet, L. Senn, D. Flury, S. Kuster, C. Balmelli, C. Gardiol, A. Goncalves Cabecinhas, L. Kaiser, O. Keiser*

4466 **Epidemiology of influenza in Thailand: findings from near real-time laboratory-based influenza system, a network of 40 hospital in Thailand, 2010-2019**
T. Eamchotchawalit (Bangkok, Thailand), P. Piyaraj, P. Narongdej, S. Charoensakulchai*

4643 **Laboratory-confirmed influenza infection and acute myocardial infarction**
Y. Young-Xu, J. Smith (White River Junction, United States), S. Mahmud, E. Russo, R. Van Aalst, E. Thommes, J. Lee, A. Chit*

4651 **Different age distribution of influenza B virus infection by lineage**
Y. Kim, S. Han (Seoul, South Korea), K. Lee*

5894 **Delayed diagnosis and increased length of stay in patients requiring hospitalisation with influenza who present without fever**
B. Smith, M. Putland, B. Garbutt, D. Johnson, L. Irving, S. Tong (Melbourne, Australia)*

7769 **Bacterial and fungal infections associated with influenza virus in hospitalised patients**
F. Arnáiz De Las Revillas (Santander, Spain), L. Gibert Hernandez, J. García Palacios, P. Gonzalez García, N. Puente Ruiz, M. Gozalo Margüello, C. Armiñanzas Castillo, M. Gutierrez-Cuadra, M. Fariñas*

8102 **Analysis of patients with severe complicated influenza in a hospital, 2015-2019**
Y. Huang (Taichung, Taiwan)*

8516 **Multidisciplinary interventions to reduce nosocomial transmission of influenza**
B. Warne (Cambridge, United Kingdom), M. Reacher, M. Zambon, H. Jalal*

8702 **Aspergillosis complicating severe influenza in intensive care unit patients: a retrospective case-control study**
C. Visek (Chicago, United States), H. Nam, M. Ison*

9125 **Nosocomial influenza**
E. Rothman (Lund, Sweden), B. Bottiger, U. Karlsson*

9288 **Descriptive analysis of patients with influenza virus admitted to intensive care unit from 2010 to 2019**
M. Vallverdú, S. Carvalho Brugger (Lleida, Spain), M. Miralbés, S. Iglesias, B. Balsera, J. Caballero*

9399 **Burden of influenza C in a paediatric population with severe respiratory disease**
A. Wong, A. Presbitero, K. Pabbaraju, K. Fonseca, N. Zelyas, B. Berenger (Calgary, Canada)*

Session accepted as Paper Poster Session

Influenza vaccination

334 **Prevalence of the suggestion of the influenza vaccine to pregnant women among gynaecologists and obstetricians**
I. Akdemir (Ankara, Turkey), A. Usturalı Mut, G. Aydin, F. Keskin, K. Memikoglu, A. Azap*

616 **Immunogenicity and safety of a quadrivalent influenza vaccine (GC GLU) versus quadrivalent seasonal influenza vaccine (Fluarix Tetra) in Asian adults aged 20 to 50: a phase III prospective, open labeled, multi-centre study**
S. Pan (Taipei, Taiwan), H. Chuang, W. Lee, N. Wang, S. Hsieh*

971 **Increasing influenza vaccination rates among healthcare workers and residents of long term care facilities for the elderly in Graz, Austria**
I. Zollner-Schwetz (Graz, Austria), A. Gurde T, C. Pux, K. Prisching, W. Schippinger, E. Stoiser, R. Krause, E. König*

1172 **Influenza vaccine effectiveness against laboratory-confirmed influenza in Europe: results from DRIVE network 2018/19**
A. Stuurman, K. Bollaerts, J. Biccler, M. Alexandridou, R. Auvinen, U. Baum, A. Bella, S. Bellino, J. Diez-Domingo, M. Levi, S. De Lusignan, S. Mosca, H. Nohynek, E. Pandolfi, O. Punzo, M. Redlberger-Fritz, C. Rizzo, J. Rodrigo Pendas, O. Sandulescu, R. Syrjänen, T. Turunen, M. Riera Montes (Biniamar, Spain)*

2403 **Examining factors impacting influenza vaccination amongst healthcare workers in Asia and the Pacific**
H. Seale (Sydney, Australia), A. Thomson, R. Kaur*

2748 **Can adjuvanted influenza vaccine given as standard of care reduce the risk for influenza outbreaks in nursing homes: evidence from a cluster-randomized trial of 823 nursing homes**
K. Mcconeghy (Providence, United States), H. Davidson, L. Han, E. Saade, D. Canaday, V. Mor, S. Gravenstein*

2751 **EUCIC survey on influenza vaccination among infection control team: Action speaks louder than words**
Ş. Keske, N. Mutters (Heidelberg, Germany), C. Tsioutis, Ö. Ergönül*

3493 **A quality improvement project to increase influenza vaccination uptake amongst inpatients in a tertiary care centre supported by Electronic Healthcare Records (EHR)**
A. Orourke (Dublin, Ireland), M. Kelly, C. Cunningham, G. Courtney, U. Geary, S. Moores, G. Melanophy, A. Mcgreal-Bellone, K. Murray, C. O'Broin, C. Bergin*

4092 **Influenza vaccine in chronic obstructive pulmonary disease**
Y. Young-Xu, J. Smith (White River Junction, United States), N. Neupane, S. Mahmud, E. Russo, R. Van Aalst, E. Thommes, J. Lee, A. Chit*

4498 **Effectiveness of influenza vaccine in preventing medically attended influenza virus infection among healthcare personnel: a test-negative case-control study in Bangkok, Thailand, 2018/19 season**
T. Eamchotchawalit (Bangkok, Thailand), P. Piyaraj, P. Narongdej, S. Charoensakulchai*

4832 **A multi-centre analysis of the value of systematic screening of influenza virus and vaccination on emergent admissions to a cardiac intensive care unit**
A. Galar Recalde (Madrid, Spain), M. Juárez, I. Sousa Casasnovas, M. Valerio Minero, P. Catalán, P. Antunez, G. Barbeito Castiñeiras, S. Blanco, L. Folgueira, J. García-Acuña, A. Lalueza, F. Lázaro, E. López De Sá, L. Martin, E. Muñez Rubio, F. Portillo, A. Ramos Martínez, S. Rosillo, M. Martinez-Selles, F. Fernandez-Aviles, E. Bouza, P. Muñoz*

6039 **Coverage of influenza vaccination in patients over 64 years hospitalised for severe acute respiratory infection according to their chronic diseases**
L. Miriam (Zaragoza, Spain), A. Larrauri, A. Gherasim, C. Mazagatos, N. Martínez Cameo, M. Hernández, Y. Gracia, S. Pina, V. Guerrero, A. Rezusta, A. Milagro Beamonte*

6157 **Chronic pluripathological patients in over 64 years old with flu or serious acute respiratory infection, according to flu vaccination status**
L. Miriam (Zaragoza, Spain), A. Larrauri, A. Gherasim, C. Mazagatos, N. Martínez Cameo, M. Hernández, Y. Gracia, S. Pina, A. Martínez-Sapiña, A. Rezusta, A. Milagro Beamonte*

6193 **Severity of chronic diseases in patients over 64 years old with flu or serious acute respiratory infection, according to flu vaccination status**
L. Miriam (Zaragoza, Spain), A. Larrauri, A. Gherasim, C. Mazagatos, N. Martínez Cameo, M. Hernández, Y. Gracia, V. Guerrero, A. Martínez-Sapiña, A. Rezusta, A. Milagro Beamonte*

6492 **Study of the humoral response against adjuvanted and non-adjuvanted influenza vaccine in the elderly by age groups**
L. Sanchez De Prada (Valladolid, Spain), I. Sanz, S. Tamames, A. Lopez, J. Méndez-Legaza, S. Rojo, R. Ortiz De Lejarazu, J. Eiros*

6586 **Study of the serological efficacy of influenza vaccine along 28 consecutive seasons**
L. Sanchez De Prada (Valladolid, Spain), I. Sanz, S. Tamames, A. Lopez, J. Méndez-Legaza, S. Rojo, R. Ortiz De Lejarazu, J. Eiros*

6625 **Does vaccines needs a gender perspective? Influenza says yes!**
L. Sanchez De Prada (Valladolid, Spain), I. Sanz, S. Tamames, A. Lopez, S. Rojo, R. Ortiz De Lejarazu, J. Eiros*

7072 **Public health impact of the introduction of a high dose quadrivalent inactivated influenza vaccine in France**
M. Costa, F. Bianic, N. Largeron, F. Alvarez, M. Levant, M. Uhart (Lyon, France)*

7189 **Neuraminidase antibody response in a population vaccinated with split and adjuvant influenza vaccines**
J. Mendez Legaza, I. Sanz, R. Ortiz De Lejarazu, L. Sanchez De Prada (Valladolid, Spain)*

8352 **Immunodominance Hierarchy after seasonal Influenza vaccination**
L. Sanchez De Prada (Valladolid, Spain), I. Sanz, R. Ortiz De Lejarazu, J. Eiros, A. Garcia-Sastre, T. Aydillo*

9170 **Cascade of care for influenza vaccination among inpatients in a US academic medical centre: Oct 2018 - Mar 2019**
J. Kubes, J. Jacob (Atlanta, United States)*

Session accepted as Paper Poster Session

Influenza: diagnostics

603 **Nasopharyngeal viral load determinants among influenza-infected patients receiving primary care in France: 2010-2018**
R. Gueneau (La Tronche, France), S. Behillil, E. Vincent, M. Yoann, S. Van Der Werf*

666 **Cost-benefit analysis of rapid influenza testing in German emergency rooms**
R. Diel, A. Nienhaus, J. Becker (Kornwestheim, Germany)*

797 **Impact of a routine molecular Point-of-Care test-and-treat strategy for influenza in adults hospitalised with acute respiratory illness: a pragmatic, multi-centre, randomised controlled trial (FluPOC)**
T. Clark (Southampton, United Kingdom), K. Beard, N. Brendish, A. Malachira, S. Mills, C. Chan, S. Poole, S. Ewings, N. Cortes*

805 **Evaluation of the FebriDx host response Point-of-Care test to differentiate viral from bacterial aetiology in adults hospitalised with acute respiratory illness during influenza season**
K. Beard (Southampton, United Kingdom), N. Brendish, S. Poole, C. Chan, S. Mills, T. Clark*

2431 **Performance of two rapid influenza diagnostic testing compared to real-time PCR**
Y. Oh (Yongin, South Korea), S. Jin, S. Yoon, S. Park, H. Bae*

2900 **Can a combination of several biological markers help to diagnose influenza co-infections?**
N. Delettre (Rouen, France), A. Schrapp, A. Baron, L. Joly, V. Brunel*

2961 **Serum IFI27 mRNA as a novel host response biomarker of monitoring the influenza A virus infection**
W. Dong (Shanghai, China), D. Yu, D. Zhang, G. Shi, X. Zhang*

2972 **Performance evaluation of the STANDARD F Influenza A/B FIA for detection of influenza A/B virus infection**
K. Choi (Daejeon, South Korea), H. Kim, M. Koo, J. Kim, S. Koo*

3192 **Hemagglutinin sequence-derived phylogenetic and genetic characterisation of A(H3N2) influenza viruses circulating during 2013-2019 winter seasons in Southern Greece**
A. Kossyvakis, A. Kontou, A. Flountzi (Athens, Greece), M. Euagelidou, V. Pogka, A. Kalliaropoulos, I. Karagiannis, E. Antalis, T. Lytras, D. Sgouras, S. Tsiodras, A. Mentis*

3859 **Assessment of the performances of the second generation of the ID NOW influenza A&B and comparison with the GeneXpert**
E. Farfour (Suresnes, France), A. Roux, M. Ballester, M. Vasse*

4316 **Influenza and respiratory syncytial virus antigen diagnostic tests: do they still have a place in a routine diagnostic laboratory?**
B. Vanmassenhove (Ostend, Belgium), A. Hervent, L. Persijn, L. Vynckier, G. Alliet*

4386 **Suspected reverse zoonosis of influenza A(H1N1) pdm09 virus infection found in *Ailuropoda melanoleuca* in Hong Kong Oceanarium**
C. Chang (Hong Kong, Hong Kong), Y. Fong, J. Teng, S. Lau, P. Woo*

4890 **Laboratory-confirmed seasonal influenza virus infection in Qatar: 2016-2018 national surveillance data**
J. Daghfal Nader (doha, Qatar), A. Omrani, M. Al-Maslamani, P. Coyle, M. Shebash, S. A. Hashim*

5458 **Rapid diagnosis of seasonal influenza virus and cohorting of hospitalized patients on a 'flu ward': a prospective analysis of outcomes**
B. O'Kelly (Dublin, Ireland), A. Kelly, A. Conway, S. Mcconkey, C. Mcnally, E. De Barra*

6326 **Evaluation of Genomera CDX system for influenza and respiratory syncytial virus infections**
E. Choquet, C. Chessa, M. Prat, A. Larivière, A. Beby Defaux, N. Lévêque, M. Pichon (Poitiers, France)*

6360 **Clinical benefits of Point-of-Care rapid molecular influenza test at a hospital emergency service**
J. Nordh (Växjö, Sweden), H. Janson*

6936 **Comparison of Illumina and nanopore sequencing methodologies for whole genome sequencing of influenza A virus from clinical isolates**
J. Heaney (London, United Kingdom), D. Frampton, H. Gliddon, M. Byott, P. Grant, R. Mckendry, E. Nastouli*

7933 **Next generation sequencing of influenza A virus from environmental samples at the human-animal interface**
N. Bell (Toronto, Canada), B. Kwok, L. Yip, C. Bekking, Y. Berhane, K. Prost, M. Qadir, S. Mubareka*

9036 **Cost analysis of a Point-of-Care diagnostic test for detecting influenza A/B and respiratory syncytial virus in the ER setting in Norway**
J. Mewes, A. Voermans, T. Ofstad (Oslo, Norway), T. Halvorsen, K. Ersek, L. Steuten*

9134 **Laboratory diagnosis and circulation of respiratory syncytial virus (A and B subgroups) and influenza virus A (H1 and H3 subtypes) and B in a three-winter season (2016-17 to 2018-19) hospital-based survey in northern Italy**
M. Arcangeletti, C. Maccari (Parma, Italy), F. De Conto, F. Ferraglia, F. Pinardi, P. Montagna, C. Chezzi, A. Calderaro*

9145 **Impact of influenza Point-of-Care testing in the emergency department on clinical care of adult patients at three hospitals in Lanarkshire, Scotland: an observational study**
A. Ho, P. Anstey, H. Black, E. Kerr, J. Mcallister, C. Mullen, M. Tate (Glasgow, United Kingdom), D. Cromie, I. Mccormick, S. Whitehead*

Session accepted as Paper Poster Session

Influenza: therapeutics

492 **Treatment of influenza and influenza-like illnesses with antiviral having anti-inflammatory efficacy**
N. Pshenichnaia (Moscow, Russian Federation), V. Bulgakova, E. Volchkova, E. Kareva, V. Gorodin, A. Grekova*

710 **Five-day versus ten-day oseltamivir chemoprophylaxis to prevent hospital influenza transmission: a non-inferiority randomised open-label study**
L. Lepen, M. Velušček, R. Blagus, A. Hodžić, M. Mavrič, R. Saletinger, D. Stupica (Ljubljana, Slovenia)*

3433 **Nucleoside analogue for the treatment of influenza**
N. Lvov (St. Petersburg, Russian Federation)*

4000 **Template RNA loops determine aberrant RNA synthesis and innate immune activation during influenza virus infection**
H. French (Cambridge, United Kingdom), A. King, A. Te Velthuis*

4819 **Protection against H9N2 Influenza A(H9N2) virus induced by recombinant M2e-HA2 fusion protein**
M. Moghadaszadeh (Tabriz, Iran), M. Zeinolabedin, M. Golchin, R. Ghanbarpour, H. Tavakkoli*

5126 **Preclinical efficacy, pharmacokinetics and safety of CD377, a novel antiviral Fc-conjugate against influenza**
V. Ong, J. Levin, A. Borchardt, T. Lam, W. Jiang, Z. Chen, Q. Do, T. Brady, A. Noncovich, J. Fortier, M. Nakamura, K. Amundson, J. Locke, A. Almaguer, N. Dedeic, G. Hough, J. Cole, S. Döhrmann, R. Grewal, E. Abelovski, J. Balkovec, M. Schlosser, K. Bartizal, L. Tari (San Diego, United States)*

5707 **CD377, a novel antiviral Fc-conjugate, demonstrates a lower resistance potential than baloxavir and oseltamivir against pandemic influenza A(H1N1)**
A. Almaguer (San Diego, United States), A. Borchardt, W. Jiang, Z. Chen, T. Brady, J. Locke, L. Tari*

5788 **Antiviral treatment in severe influenza pneumonitis**
Y. Pai, Y. Huang (Taipei City, Taiwan), C. Su, K. Tsao, C. Hung, Y. Hsieh, K. Kao, C. Huang, A. Dutta, C. Huang*

5793 **Efficacy of CD377, a novel antiviral Fc-conjugate against seasonal influenza in lethal mouse models**
J. Levin (San Diego, United States), K. Amundson, K. Shathia, A. Borchardt, T. Lam, W. Jiang, Z. Chen, T. Brady, S. Döhrmann, V. Ong, L. Tari*

6009 **Efficacy of CD377, a novel antiviral Fc-conjugate, against influenza A(H1N1) in a lethal mouse model of Severe Combined Immunodeficiency (SCID)**
J. Levin, K. Amundson, K. Shathia, A. Borchardt, T. Lam, W. Jiang, Z. Chen, T. Brady, S. Döhrmann, V. Ong, L. Tari (San Diego, United States)*

7868 **Adjuvants that contain saponin may be an important component of influenza peptide vaccines to induce broadly reactive functional antibodies**
C. Sei (Gaithersburg, United States), N. Rikhi, R. Schuman, K. Muema, L. Daum, G. Fischer*

8820 **Fc-mediated FcγR receptor engagement of CD377, a novel antiviral Fc-conjugate, translates into potent antibody-dependent cellular phagocytosis and antibody-dependent cellular cytotoxicity activity**
S. Döhrmann (San Diego, United States), R. Grewal, E. Abelovski, T. Brady, W. Jiang, Z. Chen, A. Borchardt, J. Cole, L. Tari*

8832 **CD377, a novel antiviral Fc-conjugate, demonstrates potent broad-spectrum activity in multiple *in vitro* assays against influenza A and B**
S. Döhrmann (San Diego, United States), A. Almaguer, N. Dedeic, T. Brady, W. Jiang, Z. Chen, A. Borchardt, J. Cole, J. Locke, L. Tari*

Session accepted as 1-Hour Oral Session

Innovative therapeutic approaches against influenza

2693 **Baloxavir treatment of ferrets infected with influenza A virus reduces transmission**
L. Lee (Melbourne, Australia), J. Zhou, R. Frise, D. Goldhill, P. Kozsalka, E. Mifsud, K. Baba, T. Noda, Y. Ando, K. Satou, Y. Ishikawa-Aoe, T. Shishido, T. Uehara, S. Wildum, E. Zwanziger, N. Collinson, K. Kuhlbusch, B. Clinch, A. Hurt, W. Barclay*

7514 **Comparative effectiveness of combined favipiravir and oseltamivir therapy versus oseltamivir monotherapy in critically-ill patients with influenza virus infection**
Y. Wang (Beijing, China)*

8045 **Influenza immunoglobulin in hospitalised patients with serious influenza A**
A. Dahl (Winnipeg, Canada), M. Ison, T. Babinchak, C. Hall, D. Anderson*

8839 **CD377, a novel antiviral Fc-conjugate, demonstrates superior reduction of viral burden and cytokine levels compared to oseltamivir in a lethal mouse model of influenza A(H1N1) infection**
S. Döhrmann (San Diego, United States), A. Almaguer, N. Dedeic, K. Amundson, K. Shathia, T. Brady, W. Jiang, Z. Chen, J. Locke, A. Borchardt, J. Cole, J. Levin, L. Tari*

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Neurotropic flaviviruses

856 **Treatment of flaviviruses in solid organ transplant recipients with intravenous immunoglobulin and interferon alpha-2b: a Mayo Clinic Arizona experience**
S. Kasule (Phoenix, United States), R. Patron, M. Grill*

2380 **An imported case of West Nile virus neuroinvasive disease in the UK**
N. Khan (London, United Kingdom), R. Lewis, P. Papineni, W. Lynn, G. Sandhu*

3650 **Clinical characteristics and outcomes in patients with severe West Nile neuroinvasive disease in Croatia**
M. Santini (Zagreb, Croatia), S. Haberle, V. Savic, I. Tabain, K. Viskovic, M. Kutlesa, V. Krajinovic, L. Barbic, T. Vilibic-Cavlek*

3953 ***In vitro* modeling of patient-specific susceptibility to neurotropic flavivirus infection by using induced pluripotent stem cells**
S. Riccetti (Padova, Italy), A. Sinigaglia, G. Desole, M. Pacenti, T. Smura, R. Kant, O. Vapalahti, M. Trevisan, L. Barzon*

5019 **West Nile virus 2018 season in Italy: rapid spreading of West Nile neuroinvasive disease in northwest Italy.**
E. Burdino (Turin, Italy), T. Allice, M. Milia, G. Gregori, G. Morleo, R. Cipriani, C. Pasqualini, P. Ferrero, V. Ghisetti*

7233 **Characteristics of the initial phase of tick-borne encephalitis**
P. Bogovic (Ljubljana, Slovenia), S. Lotric-Furlan, K. Ogrinc, T. Avsic, F. Strle*

7342 **10 years surveillance of West Nile virus neuroinvasive disease**
C. Popescu (Bucharest, Romania), S. Florescu, M. Zaharia, D. Stanciu, M. Violeta, V. Simion, C. Cristea, B. Voinescu, E. Nedu, F. Cojanu Banicioiu, O. Burcos, A. Dogaru, A. Kosa, D. Codreanu, G. Tardei, M. Nica, E. Ceausu, S. Ruta*

9540 **Monitoring mosquito populations and detection of West Nile virus and Usutu virus in mosquito pools collected in Attica regional units, Greece, 2017-2018**
E. Patsoula (Athens, Greece), S. Beleri, G. Balatsos, V. Karras, N. Tegos, F. Sereti, D. Papachristos, A. Michaelakis*

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Paediatric and perinatal infections

861 **Comparison of immune function between T, B lymphocytes, Th17, Th22 and Treg cells in children with hand, foot and mouth disease caused by EV71 and other enterovirus infections**
W. Song (Hangzhou, China), S. Zhao, Y. Wei*

3291 **Mother-to-child transmission of curable sexually-transmitted infections in HIV-infected women in South Africa**
R. Peters (East London, South Africa), U. Feucht, D. Olivier, L. De Vos, P. Ngwepe, J. Klausner, A. Medina-Marino*

3729 **Congenital toxoplasmosis: outcomes of newborns from mothers with documented seroconversion out of a multi-centre cohort in two tertiary referral hospitals**
V. Meroni (Pavia, Italy), A. Bonetti, A. Comelli, L. Tomasoni, F. Genco, A. Chiesa, F. Prefumo, V. Spinoni, S. Caligaris, C. Bonfanti*

3754 **Challenges in setting-up and conducting a global multi-centre prospective observational cohort of sepsis in hospitalised neonates: the NeoOBS study**
A. Riddell (London, United Kingdom)*

4500 **Uncovering the role of airborne transmission and asymptomatic contact shedding in outbreaks of scarlet fever**
R. Cordery (London, United Kingdom), A. Purba, L. Begum, E. Mills, M. Mosavie, E. Jauneikaite, P. Hoffman, T. Lamagni, S. Sriskandan*

4576 **A comparison of GenomEra GBS PCR and GeneXpert GBS PCR assays with culture of group B *Streptococcus* with and without broth enrichment**
S. Nielsen (Aarhus, Denmark), J. Kjølseth Møller, M. Khalil*

5196 **Vaccination uptake in sickle cell disease: results from a London teaching hospital**
K. Isitt (London, United Kingdom), A. Calvert, M. Haq, P. Heath, C. Cosgrove*

5275 **Modulation of the immune status in pyelonephritis caused by *Pseudomonas aeruginosa* in children with hydronephrosis**
M. Svitlana (Kharkiv, Ukraine), M. Maryna, I. Marchenko, V. Davydenko, Y. Mozgova*

6306 **Global multi-centre prospective observational cohort of sepsis in hospitalised neonates highlights complex case mix: the NeoOBS Study**
A. Cook (London, United Kingdom)*

6481 **Phylogenetic groups and virulence factors of uropathogenic *Escherichia coli* in pregnant and non-pregnant women in St. Petersburg, Russia**
M. Razinkova (St. Petersburg, Russian Federation), T. Khusnutdinova, E. Shipitsyna, O. Budilovskaya, A. Krysanova, K. Shalepo, A. Savitcheva*

6497 **Innovative diagnosis strategy for pneumococcal infections in children using an immunochromatographic test in respiratory specimens**
C. Haddar (Saint-Priest-En-Jarez, France), J. Joly, A. Carricajo, P. Verhoeven, G. Florence, O. Mory, E. Begaud, Y. Germani, A. Cantais, P. Bruno*

7115 **Global assessment of neonatal sepsis incidence and case fatality**
C. Fleischmann-Struzek (Jena, Germany), F. Reichert, A. Cassini, T. Harder, N. Kissoon, K. Reinhart, B. Allegranzi, T. Eckmanns*

7145 **Invasive pneumococcal disease in children: the risk of a moving target**
M. Corcoran (Dublin, Ireland), J. Mereckiene, S. Murchan, S. Cotter, R. Cunney, H. Humphreys*

8276 **Investigation of hypervirulent Group B *Streptococcus* ST17 clone by MALDI-TOF MS**
E. Aktas, E. Karacan (Istanbul, Turkey), N. Kina, M. Bulut, G. Malkoçoglu*

8634 **Fast and reliable detection of group B *Streptococcus* during antepartum screening: evaluation of the PCR-based Simplexa GBS Direct assay in comparison to routine culture after Lim Broth enrichment and from ESwabs without enrichment**
T. Alcaro, S. Nisticò, M. Colosimo, G. Panduri, G. Caruso, M. De Fazio, A. Surace, D. Talarico, P. Minchella (Catanzaro, Italy)*

8767 **Outcome of a screening programme for the prevention of neonatal invasive early-onset Group B *Streptococcus* infection in a maternity unit of the University Hospital "Dr Dragisa Misovic" (Belgrade, Serbia)**
M. Lacković, M. Gostimirović (Belgrade, Serbia), S. Mihajlović*

8936 **Vaginal carriage of *Enterobacter cloacae* and *Klebsiella pneumoniae* among pregnant women in Bukavu, Democratic Republic of Congo: prevalence, risk factors and adverse pregnancy outcomes**
K. De Keyser (Ghent, Belgium), G. Mulinganya, S. Balole, J. Boelens, G. Claeys, D. De Vos, A. De Vulder, E. Hendwa, R. Kambale, F. Kampara, I. Mubalama, J. Mongane, I. Nianci, S. Zigabe, S. Callens, M. Vaneechoutte, P. Cools*

8956 **Re-evaluating and refining predictors of bacterial infection in children with cancer and febrile neutropenia**
G. Haeusler (Melbourne, Australia), K. Thursky, M. Slavin, F. Babl, R. De Abreu Lourenco, F. Mechinaud, B. Phillips*

8975 **Role of epitopes of four immunogenic Group B streptococci (GBS) proteins and their derivatives indifferentiation between pregnant GBS carriers and non-carriers**
A. Dobrut, A. Malska-Wozniak, E. Brzozowska, S. Gorska, A. Gamian, M. Brzychczy-Wloch (Krakow, Poland)*

9505 **Diagnosing neonatal sepsis: question under discussion**
B. Mkhitaryan (Yerevan, Armenia), M. Grigoryan, H. Ghazaryan, D. Badalyan, G. Mazmanyan, G. Baklachyan, V. Manukyan, S. Brutyan, H. Hakobyan, L. Martirosyan, V. Asoyan, H. Apresyan*

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Recent advances in diagnosis of herpesviruses

3587 **Characterisation of the human cytomegalovirus genome diversity in longitudinally collected breast milk samples**
J. Götting, K. Lazar, N. Suárez, L. Steinbrueck, T. Rabe, T. Schulz, A. Davison, K. Hamprecht, T. Ganzenmueller (Tübingen, Germany)*

3727 **Clinical diagnostic evaluation of a real-time PCR assay for the quantitative detection of cytomegalovirus from EDTA-plasma and urine samples**
U. Eigner (Heidelberg, Germany), N. Hefner, M. Kolb, U. Betz*

4242 **Validation of Simplexa HSV 1 & 2 Direct and Simplexa VZV Direct kits for herpes simplex virus and varicella zoster virus detection from low-volume cerebrospinal fluid samples**
S. Burrel, O. Bomme, O. Roger, J. Piot, B. Le Labousse, N. Hamm, E. Chaicaud, D. Boutolleau (Paris, France)*

4793 **Transforming a multiplex laboratory developed real-time PCR for herpes simplex virus type 1 and 2 & varicella zoster virus into a sample-to-answer, cassette-based format**
M. Dierckx, R. Cartuyvels, M. Raymaekers (Hasselt, Belgium)*

5091 **Design of a varicella zoster virus PCR combined with a herpes simplex virus PCR in a multiplex assay: a diagnostic evaluation study**
B. Schmid (Zurich, Switzerland), M. Affolter, A. Buttafuoco, M. Glatz, P. Bosshard*

6298 **Quantitative detection of human cytomegalovirus and Epstein-Barr virus using the real-time PCR STAT-NAT CMV and STAT-NAT EBV assays**
D. Rigamonti, A. Mancon, G. Ferri, A. Di Cosimo, L. Spinelli, G. Torini, L. Bavagnoli, I. Merli, M. Incandela, M. Gismondo, M. Gramegna (Milan, Italy), V. Micheli*

6407 **Molecular detection of cytomegalovirus in intestinal tissue**
N. Bastón Paz (Las Palmas de Gran Canaria, Spain), M. Hernández-Betancor, M. peñate bolaños, P. Hernandez Cabrera, T. Tosco-Núñez*

7113 **A new approach for the quantification of clinical samples viral load based on virtual qPCR standard curves**
A. Gani (Padova, Italy), N. Paccagnella, D. Corradini, C. Savio, A. Polacchini, D. Paladin, R. Costacurta*

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Recent advances in HPV

664 **Anal human papilloma virus infection and disease in HIV-positive and -negative men and woman**
G. Capra (Palermo, Italy), P. Di Carlo, N. Serra, L. Pipito, D. Cabibi, C. Mascarella, D. Pistoia, M. Micciulla, T. Fasciana, A. Giammanco*

1106 **Human papilloma virus-testing in extragenital samples: usefulness and importance of complete genotyping**
A. García Caballero (Madrid, Spain), M. Rodriguez, R. Canton Moreno, J. Galán, B. Romero*

1164 **Persistent human papilloma virus type 16 infections in an established cohort of Slovenian women**
T. Triglav (Ljubljana, Slovenia), L. Hošnjak, A. Oštrbenk, M. Poljak*

1636 **HPV OncoPredict: analytical performance of a novel diagnostic tool allowing accurate determination of sample cellularity and normalised high-risk human papilloma virus genotype-specific viral load**
I. Vallini (Brescia, Italy), M. Raimondi, S. Paganoni, I. Sechi, M. Martinelli, P. Romano, A. Piana, C. Cocuzza*

2723 **Human papilloma virus and other sexually-transmitted infection prevalence among HIV-infected and HIV-uninfected women in Sikasso, Mali**
A. Jary (Paris, France), I. Teguete, Y. Sidibé, A. Kodio, O. Dolo, S. Burrel, D. Boutolleau, B. Bercot, C. Bébéar, L. Beauvais-Remigereau, S. Sayon, M. Kampo, F. Traoré, M. Sylla, C. Achenbach, R. Murphy, V. Calvez, A. Marcelin, A. Maiga*

3178 **Prevalence of high- and low-risk human papilloma virus in the anus and rectum, vagina and pharynx of asymptomatic men and women attending a sexually-transmitted diseases clinic**
O. Yosseppowitch, O. Schwartz, Y. Goor, K. Landsman, R. Sheffer, Y. Maor (Holon, Israel)*

3774 **Automation in full genotyping of human papilloma viruses: evaluation of the analytical performance of Anyplex HPV28 assay**
B. Vanmassenhove (Ostend, Belgium), A. Hervent, L. Persijn, L. Vynckier, G. Alliet*

4013 **Prevalence of high-risk human papilloma virus genotypes responsible for cervical cancer in Blida, Algeria**
S. Oukid (Blida, Algeria), M. Dhakya, M. Boudjella, N. Sadouki, R. Belouni*

5295 **Evaluation of the NeuMoDx HPV assay**
B. Hesselink (Amsterdam, Netherlands), S. Doorn, C. Meijer, D. Heideman, E. Craig, J. Zhu, S. Brahmasandra*

6810 **Diagnosis and sampling of human papilloma virus in men**
J. Muehlberger (Vienna, Austria), A. Stary, K. Schwarz*

7268 **Novel taxonomic and functional cervical microbiome biomarkers of persistency and histological progression to CIN2+ in women infected with high risk human papilloma virus**
T. Iftner, F. Stubenrauch, A. Iftner, M. Willmann (Tübingen, Germany)*

7746 **Human papilloma virus 16 viral load quantification using droplet digital PCR and correlation with cervical lesion**
M. Martinelli (Monza, Italy), C. Giubbi, R. Musumeci, F. Perdoni, F. Sina, R. Fruscio, F. Landoni, C. Cocuzza*

8198 **Cost-effectiveness analysis for human papilloma virus mitigation strategies implemented since 2019 in the Republic of Moldova based on infectious disease modelling**
A. Jarynowski (Kishinev, Moldova)*

8657 **Identification of a clinically relevant anal HPV infection in HIV-positive men having sex with men: data from Czech anal cancer screening programme**
J. Nemcova (Pilsen, Czech Republic), K. Cerna*

9054 **Prevalance of human papilloma virus 16, 18 and other high-risk genotypes in Baku, Azerbaijan**
A. Gumral (Baku, Azerbaijan), A. Agayev, L. Veliyeva, A. Mammadova, V. Narimanov, R. Bayramli, V. Huseynov*

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Recent findings in diagnosis of viral infections

2299 **Characterisation of the vaginal DNA virome in health and dysbiosis: an opening study in patients with non-female factor infertility**
T. Haahr, R. Riemer, D. Nielsen, T. Leser, W. Kot, J. Castro, P. Humaidan, J. Jensen (Copenhagen, Denmark)*

2319 **The impact of consolidating molecular sexually transmitted infections screening and viral load testing on a new fully automated platform**
E. Goldstein (Glasgow, United Kingdom), E. Campbell, J. Stewart, M. Johnson, R. Gunson*

2426 **Detection of norovirus major capsid protein using M-class UPLC/MSE**
P. Chu (Kaohsiung, Taiwan), M. Boonchan, H. Huang, K. Motomura, L. Ke*

4445 **Quantitative detection and impact of 5' terminally deleted Group B enterovirus populations on type I IFN response in peripheral blood or heart tissue samples from acute myocarditis paediatric patients**
M. Glenet, Y. N'Guyen, A. Mirand, C. Henquell, A. Lebreil, F. Berri, F. Bani Sadr, B. Lina, I. Schuffenecker, L. Andreoletti (Reims, France)*

5284 **Perspective of the phage mini-antibodies for virus detection by using electro-acoustic sensor**
O. Karavaeva (Saratov, Russian Federation), O. Guliy, B. Zaitsev, I. Borodina*

6373 **Performance evaluation of a novel BKV Quant Assay in plasma and urine specimens**
M. Gramegna (Milan, Italy), G. Ferri, A. Di Cosimo, G. Torini, L. Gong, D. Krause, C. Butcher, M. Mastronardi, B. Wu, S. Brahmasandra*

6509 **Clinical application of polyomavirus detection by metagenomic next-generation sequencing in urinary tract infection**
N. Li (Shanghai, China), B. Hu*

7050 **Effect of brincidofovir on adenovirus and cellular transcriptome profile**
M. Salmona (Paris, France), L. Feghoul, S. Mercier-Delarue, E. Diaz, A. Armero, J. Dutrieux, J. Le Goff*

7562 **Study on the diagnostic value of serum amyloid A(SAA) in pathogen classification and clinical stage identification of hand, foot and mouth disease**
W. Yidong (Hangzhou, China), W. Yi*

7795 **Identification of DNA virus in conventional culture by MALDI-TOF MS**
G. Martin (Oviedo, Spain), S. Rojo, R. Campo Ramos, I. Costales, Z. Pérez, X. García, M. Alavarez-Argüelles, S. Melón-García*

8308 **Diagnostic value of IgG avidity and/or Western blot test for the diagnosis of *Rubella virus* infection during pregnancy**
G. Olfa, A. Chtourou, S. Gargouri, H. Triki, B. Feiza, L. Feki-Berrajah, A. Hammami (Sfax, Tunisia), H. Karray-Hakim*

9440 **Comparison of different nucleic acid extraction methods for viral metagenomic analysis**
M. Sabatier (Lyon, France), A. Bal, G. Destras, F. Morfin, B. Lina, V. Navratil, L. Josset*

9497 **Characterisation of the host lipidome in Enterovirus-infected cells: implications on pathogenesis and potential antiviral strategies**
J. Chan (Hong Kong, Hong Kong), B. Yan, Z. Zou, H. Chu, J. Tsang, S. Yuan, C. Yip, R. Kao, K. Sze, S. Lau, K. Yuen*

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Viral epidemiology

1724 **Emergence of novel recombinant Coxsackievirus A6 in Hong Kong**
K. Aw Yong (Hong Kong, Hong Kong), S. Lau, P. Zhao, S. Sridhar, C. Yip, K. To, P. Woo, K. Yuen*

2445 **Molecular epidemiology and clinical features of human adenovirus: a 20-year retrospective observational study in Bern, Switzerland**
J. Akello (Bern, Switzerland), R. Kamgang, M. Barbani, F. Suter-Riniker, S. Leib, A. Ramette*

2801 **Human parechoviruses infections in northern of Spain, 2016-2019**
A. Navascués Ortega, A. Aguinaga Perez, M. Cabrerizo, M. Portillo (Pamplona, Spain), C. Ezpeleta Baquedano*

3434 **Seroprevalence of Coxsackievirus B1-6: retrospective study in an Italian population**
I. Sciandra, F. Falasca, P. Maida, G. Tranquilli, D. Di Carlo, L. Mazzuti, T. Melengu, G. Giannelli, G. Antonelli, O. Turriziani (Rome, Italy)*

3644 **Seroprevalences of ten ToRCH infectious pathogens in women residing in Europe, Latin America and China**
M. Pollmann (Lübeck, Germany), V. Borchardt-Lohölter, A. Moreira-Soto, S. Kaya, A. Gamze Sener, E. Gómez-Gusmán, L. Figueroa-Hernández, W. Li, F. Li, K. Buska, K. Zakaszewska, K. Ziolkowska, J. Janz, A. Ott, T. Scheper, W. Meyer*

3826 **National outbreak of norovirus genogroup II in a sushi restaurant chain associated with an internationally distributed seaweed product**
T. Misra, D. Jindal, C. Sawyer, J. Armitage, A. Patmore, A. Pahwa, R. Pateman, A. Charlett, R. Mearkle, S. Lock, D. Fenelon, W. Jemmott, A. Waters, C. Willis, C. Handford, S. Balasingam, M. d'agostino, R. Manuel (London, United Kingdom), J. Sedgwick, H. Bolt*

4147 **Subtyping of adenovirus strains isolated from pre-diagnosed patients with keratoconjunctivitis**
A. Güner (Pendik, Turkey), A. Karahasan, R. Can Sarınoğlu, F. Aydin, E. Toker, S. Akkaya Turhan*

4220 **Molecular epidemiology of varicella zoster virus in Pitié-Salpêtrière University Hospital, Paris, France**
M. Cheminet, S. Burrel, D. Boutolleau (Paris, France)*

4504 **Viral aetiology and epidemiology of acute paediatric gastroenteritis in southern region of Saudi Arabia with Yemen borders**
A. Babiker (Abha, Saudi Arabia), M. Hassan, A. Al-Hakami, A. Algahtani*

5010 **Enterovirus surveillance in an Italian paediatric hospital**
L. Piccioni, S. Ranno, L. Coltella, C. Auriti, G. Pizzichemi, S. Chiavelli, L. Lancella, L. Cursi, C. Concato (Rome, Italy)*

5215 **Genetic diversity and possible recombination of *Rs*-BatCoV HKU32 related viruses in southern China**
C. Wong (Hong Kong, Hong Kong), S. Lau, H. Luk, S. Ahmed, J. Cai, P. Zhao, J. Teng, K. Yuen, P. Woo*

5495 **Enterovirus-C99 associated with cases of acute flaccid paralysis in the south-eastern region of Brazil**
R. Carmona (São Paulo, Brazil), B. Machado, J. Dias, A. Chirelli, L. Louzado, A. Luchs, C. Sousa, M. Timenetsky, M. Eduardo*

5995 **Metagenomics analysis of novel viruses in dromedaries from the Middle East**
H. Lee (Hong Kong, Hong Kong), J. Teng, J. Fung, K. Yeong, K. Chan, S. Lau, P. Woo*

6412 **Phylogenetic and geographical analyses of bat Coronaviruses**
T. Chan (Hong Kong, Hong Kong), C. Wong, H. Luk, S. Lau, P. Woo*

6501 **Impact of enteric viral co-infections on gastroenteritis among hospitalised children in Palermo, Italy, during a 10-year surveillance**
S. De Grazia (Palermo, Italy), F. Bonura, L. Mangiaracina, C. Filizzolo, C. Bonura, V. Martella, G. Giammanco*

6641 **Varicella zoster virus seroepidemiology in Caribbean Netherlands: implications for vaccine policy**
R. Vos (Bilthoven, Netherlands), L. Mollema, M. Van Boven, A. Van Lier, G. Smits, A. Janga-Jansen, S. Baboe-Kalpoe, K. Hulshof, Y. Stienstra, V. Fiona, H. De Melker*

6793 **Prevalence and quantity of parvovirus B19 DNA among blood donors**
A. Uskudar Guclu (Ankara, Turkey), S. Yilmaz, M. Baysallar, I. Avci*

6916 **Epidemiological and molecular characteristics of human parechovirus infection in children <6 months hospitalised with symptoms of sepsis-like illness: Milan 2015-2018**
L. Pellegrinelli, S. Uceda Renteria (Milan, Italy), C. Galli, A. Orlandi, S. Binda, E. Pariani*

7042 **Introduction and spread of the novel GII.P16 pandemic recombinant norovirus in Italy detected by a newly designed PCR primer pair**
G. Giammanco (Palermo, Italy), N. Urone, F. Bonura, C. Filizzolo, L. Mangiaracina, C. Bonura, V. Martella, S. De Grazia*

8210 **Molecular investigation of a 4-year outbreak of human adenovirus A31 (HAdV-A31) infection on a paediatric haematopoietic stem cell transplantation ward**
R. Fattouh, P. Stapleton, A. Eshaghi, A. Thomas, M. Science, T. Schechter-Finkelstein, L. Streitenberger, J. Gubbay, A. Kajon, B. Fisher, J. Dean, P. Hubacek, M. Brown, A. Campigotto, S. Patel, M. Graham, S. Richardson (Toronto, Canada)*

8711 **Changing seroprevalance of viral diseases among young adults in a tertiary care educational university hospital? Experience with 1993 cases**
M. Isikgöz Tasbakan, D. Akyol (Izmir, Turkey), A. Zeytinoglu, H. Pullukcu*

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Viral hepatitis A and E

2526 **New freeze-dried multiplex one-step real-time qPCR assay with room temperature storage for hepatitis A virus and and norovirus detection in clinical and food/environmental samples**
C. Pilotti (Lodi, Italy), C. Casali, M. Savoldi Boles*

3138 **Presence and persistance of hepatitis E virus PCR in patients with specific IgM positivity**
C. Mendoza Lopez (Zaragoza, Spain), J. Gil, A. Rivero-Juarez, A. Leyva, R. Benito*

4664 **An outbreak of hepatitis A among young adult men in Cyprus**
P. Dimitriou, C. Flourou, G. Nikolopoulos, M. Koliou, E. Constantinou, C. Azina, M. Panagiotou, E. Christaki (Thessaloniki, Greece)*

4741 **Hepatitis E virus infection is a risk for liver transplant recipients in Sweden**
M. Karlsson (Göteborg, Sweden), C. Skoglund, M. Karlsson, M. Lagging, M. Castedal, H. Norder*

5642 **Seroprevalence of hepatitis E virus among blood donors in the Qassim Region, Saudi Arabia**
B. Alhatlani (Unayzah, Saudi Arabia), W. Aljabr, M. Almarzuqi, S. Alhatlani, A. Almusallam*

8642 **Development of a methodology for reverse transcription and amplification of small RNA amounts in serum for whole genome sequencing of hepatitis A virus**
P. Bardon, S. Tapia, L. Mora, E. Martínez, E. Clavijo (Malga, Spain)*

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Viral hepatitis B

1070 **Performance evaluation of the Xpert HBV Viral Load assay for the quantification of hepatitis B virus DNA in plasma samples**
H. Lam (Hong Kong, Hong Kong), B. Tang*

1071 **Performance evaluation of the Alinity m HBV assay for the quantification of hepatitis B virus DNA in plasma samples**
H. Lam (Hong Kong, Hong Kong), M. Ng, B. Tang*

1629 **Cardiovascular Disease risk in liver transplant recipients for hepatitis B,C and delta virus-associated cirrhosis**
P. Cirillo (Caserta, Italy), F. Calò, G. Stornaiuolo, G. Gaeta, P. Maggi*

3721 **HBV RNA and HBcrAg: two new biomarkers for monitoring chronic hepatitis B virus infection**
G. Roncarati (Bologna, Italy), S. Galli, A. Moroni, G. Furlini*

4047 **Use of chemiluminescence and electrochemiluminescence in the diagnosis and monitoring of hepatitis B viral infection**
D. Velcheva, A. Gotseva (Sofia, Bulgaria), Y. Slaveykova*

5897 **Hepatitis B virus epidemiology among chronic kidney disease patients under haemodialysis**
L. Villar (Rio de Janeiro, Brazil), K. Fraga, J. Miguel, E. Da Silva, B. Marques, A. Da Fonseca Mendonça, L. Lewis-Ximenez*

6145 **Hepatitis B and hepatitis D virus infection in immigrants living in south Italy: epidemiological and virological characteristics**
M. Pisaturo (Naples, Italy), L. Onorato, L. Alessio, C. Monari, L. Gualdieri, C. Minichini, G. Di Caprio, M. Starace, M. Caroprese, L. Occhiello, G. Scotto, M. Macera, E. Sagnelli, N. Coppola*

6153 **Effects of mutations in the hepatitis B virus genome on viral loads testing**
A. Keren Naus, D. Yardeni, H. Ben Zvi, O. Etzion, M. Cohen-Naftaly, S. Rozenberg, Y. Shemer-Avni (Beer Sheva, Israel)*

7262 **Evaluation of the whole blood spot on plasma separation card as a sample type for serological screening for hepatitis B and hepatitis D infection**
F. Velasquez (Barcelona, Spain), A. Rando Segura, P. Salmerón, U. Aldama, A. Najarro, A. Esteban, G. Ruiz, M. Riveiro-Barciela, M. Buti, E. Marins, F. Rodriguez_Frias*

7401 **Evaluation of the whole blood spot on plasma separation card as a sample type for hepatitis B virus viral load quantification on the COBAS 6800 system**
F. Velasquez (Barcelona, Spain), A. Rando Segura, P. Salmerón, U. Aldama, A. Esteban, A. Najarro, G. Ruiz, M. Riveiro-Barciela, M. Buti, E. Marins, F. Rodriguez_Frias*

7760 **MALDI-TOF MS as new tool for the identification of serological biomarkers for diagnosis of hepatitis B and C viruses infections**
A. Calderaro, M. Buttrini (Parma, Italy), S. Montecchini, F. Ferraglia, F. Pinardi, M. Arcangeletti, F. De Conto, C. Chezzi*

8141 **Construction and investigation of lncRNA-associated ceRNA network in chronic hepatitis B infection**
S. Wang (Chengdu, China), Y. Wei, J. Chen*

8563 **Performances of a new random access system for hepatitis B and C viral load quantification**
J. Besombes, C. Pronier (Rennes, France), A. Maillard, G. Lagathu, P. Comacle, C. Grolhier, V. Thibault*

8712 **Detection of hepatitis B virus reactivation and near complete sequencing of the viral genome by high-throughput sequencing in a kidney transplant**
M. Etoundi, S. Aherfi, A. Motte, V. Moal, P. Colson (Marseille, France)*

9491 **Longitudinal assessment of liver fibrosis rates using non-invasive APRI and Fib-4 scores in HIV, HBV and HIV-HBV co-infected patients**
D. Iacob (Bucharest, Romania), M. Luminos, B. Otilia, A. Tudor, S. Iacob, C. Olariu, M. Raus, L. Benea, C. Marin, S. Ruta*

Session accepted as Paper Poster Session

Viral hepatitis C

503 **Dried blood spots tested with the Abbott m2000 sp/rt system perform well to identify patients with active HCV infection in Vietnam**
T. Tran, B. Nguyen, T. Nguyen, T. Pham, T. Nguyen, T. Mai, B. Pham, T. Nguyen, H. Phan, N. Do, M. Ait Ahmed, F. Taieb, M. Yoann (Paris, France)*

2744 **Serorpevalence of anti-HCV antibodies in the Bulgarian population**
D. Velcheva, A. Gotseva (Sofia, Bulgaria), G. Popov*

2789 **Detection and quantification of hepatitis C Virus in cadaveric tissue donors' blood using different molecular kits**
V. Stadler Tasca Ribeiro, S. Raboni, P. Suss, J. Cieslinski, L. Kraft, J. Santos, L. Pereira, J. Telles, L. Arend (Curitiba, Brazil), F. Tuon*

3087 **Treatment of hepatitis C with direct-acting antiviral (DAA) agents: sustained virological response rate in a real care setting in the state of Ceará, north-eastern Brazil**
R. Pires Neto (Fortaleza, Brazil), E. Bomfim Hyppolito, J. Milton De Castro Lima, É. Antonio Gomes De Arruda, F. Sérgio Rangel De Paula Pessoa*

3227 **Applicability of dried blood spot for molecular epidemiology of HCV in coagulopathy patients**
L. Villar (Rio de Janeiro, Brazil), A. Da Fonseca Mendonça, B. Marques, J. Barbosa, J. Colares, D. Lima*

3852 **Extreme short course therapy for chronic hepatitis C infection**
G. Stroffolini (Turin, Italy), L. Boglione, T. Lupia, G. Cariti, G. Di Perri*

3992 **The Caserta Model: an hepatitis C virus way out in persons who use drugs in Italy**
G. Di Caprio (Caserta, Italy), V. Messina, A. Russo, E. Parente, G. Russo, T. Raimondo, A. Salzillo, F. Simeone, M. Pisaturo, N. Coppola*

4244 **Direct acting antiviral failure in hepatitis C virus genotype not 1: virological features and efficacy of re-treatment**
L. Occhiello (Naples, Italy), M. Pisaturo, M. Starace, C. Minichini, A. Di Fraia, S. De Pascalis, M. Macera, V. Messina, V. Sangiovanni, E. Claar, D. Precone, G. Stornaiuolo, M. Stanzione, I. Gentile, S. Martini, A. Masiello, A. Salomone Megna, C. Coppola, A. Federico, M. Persico, A. Galeota Lanza, A. Marrone, G. Gaeta, N. Coppola*

4509 **Effect of antiviral therapy against hepatitis C virus on gut microbiota**
B. Pinchera (Naples, Italy), R. Scotto, E. Zappulo, A. Buonomo, A. Maraolo, N. Schiano Moriello, F. Gison, F. De Filippis, D. Ercolini, I. Gentile*

4763 **The future of hepatitis C virus nucleic acid amplification techniques standardization?**
J. Fryer (Potters Bar, United Kingdom), P. Rigsby, J. Hockley, C. Morris*

6062 **Direct-acting antivirals failure in HCV genotype 3: virological features and efficacy of re-treatment**
M. Pisaturo (Naples, Italy), L. Occhiello, M. Starace, C. Minichini, A. Di Fraia, S. De Pascalis, M. Macera, V. Messina, V. Sangiovanni, E. Claar, D. Precone, G. Stornaiuolo, M. Stanzione, I. Gentile, S. Martini, A. Masiello, A. Salomone Megna, A. Federico, C. Coppola, E. Sagnelli, M. Persico, A. Galeota Lanza, A. Marrone, G. Gaeta, N. Coppola*

6288 **Using dried blood spots in drug dependency treatment centres to diagnose active hepatitis C infection**
M. Lara, D. García Martínez De Artola (Santa Cruz de Tenerife, Spain), J. Alcoba Flores*

7028 **Reliable HCV genotyping and resistance associated substitutions identification by a new next-generation sequencing approach**
J. Antonello, D. Corradini, M. Simonato, A. Polacchini, S. Tiozzo, A. Renesto, A. Gani (Padova, Italy), D. Paladin, M. Favarato*

7155 **Real-world drug resistance profile of hepatitis C patients who failed direct-acting antivirals: SHARED**
A. Howe, V. Di Maio, J. Dietz, A. De Salazar (Granada, Spain), S. Popping, S. Fourati, E. Tay, C. Rodrigo, E. Cunningham, M. Kjellin, F. Fay, J. Sfalcin, P. Gomes, C. Boucher, R. De Knegt, M. Poljak, M. Lunar, D. Salmon-Ceron, R. Usubillaga, M. Sayan, O. Mor, C. Devaux, A. Lloyd, J. Pawlotsky, J. Grebely, J. Lennerstrand, E. Knops, R. Kaiser, V. Chulanov, J. Alados Arboledas, M. Lara, J. Cabezas Gonzalez, M. Douglas, C. Sarrazin, F. Ceccherini Silberstein, F. Garcia Garcia, N. Janjua, R. Harrigan*

7169 **Detection of antibodies to hepatitis C virus using the Ortho VITROS: evaluation of the signal-to-cutoff ratio**
G. Colomba, N. Urone, C. Mascarella, D. Ferraro (Palermo, Italy)*

7971 **Patients related barriers for delay in seeking confirmatory test and treatment of hepatitis C in treatment naïve patients visiting a tertiary care hospital in Karachi, Pakistan**
H. Ashraf (Karachi, Pakistan), N. Mahmood, U. Shujat, N. Baig-Ansari, S. Iftikhar, R. Ansari*

8375 **Goal achieved! Elimination of hepatitis C in three penitentiary centres**
S. García Martín (Puerto Real, Spain), C. Freyre, F. Téllez Pérez, I. Virto, M. Martinez Rubio*

9243 **Hepatitis C reflex testing in Spain in 2019: a story of success**
F. Garcia Garcia (Granada, Spain), A. Aguilera, J. Calleja Panero, J. Eiros, A. Blasco Bravo, P. Lazaro, F. Garcia-Samaniego Rey, J. Crespo*

9389 **An optimised strategy for linkage to care of patients newly diagnosed of active hepatitis C infection**
A. Fuentes (Granada, Spain), F. García García, E. Ruiz, F. Sousa, F. Garcia Garcia*

Session accepted as Mini-oral Flash Session

Viral hepatitis in the real world

2897 **Changes in the characteristic of the population with chronic hepatitis C receiving treatment with direct acting antivirals in a referral centre during the post-interferon era**
A. Lombardi (Pavia, Italy), K. Vijayagopal, M. Sambo, P. Legnazzi, P. Sacchi, V. Zuccaro, R. Maserati, R. Gulminetti, L. Pagnucco, G. Michelone, D. Zananaboni, S. Ludovisi, R. Bruno*

4403 **Virological patterns of HCV-patients with failure to second-generation direct-acting antivirals**
L. Occhiello (naples, Italy), M. Starace, M. Pisaturo, C. Minichini, A. Di Fraia, S. De Pascalis, M. Macera, V. Messina, E. Claar, I. Gentile, V. Iovinella, L. Fontanella, G. D'Adamo, R. Santoro, A. Marrone, G. Gaeta, N. Coppola, L. Alessio*

4408 **Identification of mutations in hepatitis B virus reverse transcriptase associated with a tenofovir-resistant phenotype in South African adults**
J. Mokaya (Oxford, United Kingdom), T. Maponga, M. Van Schalkwyk, S. Hugo, J. Taljaard, C. Nwankwo, J. Singer, M. De Cesare, D. Bonsall, A. Ansari, W. Preiser, M. Andersson, C. Van Rensburg, E. Barnes, A. Mcnaughton, P. Matthews*

5266 **Whole genome sequencing to investigate genetic diversity in HBeAg-positive and HBeAg-negative hepatitis B virus infection**
A. Mcnaughton (Oxford, United Kingdom), M. De Cesare, L. Downs, J. Mokaya, J. Singer, S. Vattipally, D. Bonsall, M. Ansari, O. Amin, M. Maini, P. Matthews*

5286 **Progress towards the targets for the elimination of viral hepatitis in the European Union**
E. Duffell (Stockholm, Sweden), A. Mozalevskis, T. Noori*

5655 **Direct-acting antiviral based treatment for HCV-infected persons who inject drugs: a multi-centre real-life study**
L. Onorato (Naples, Italy), G. Di Caprio, A. Russo, C. Caruso, V. Rosato, E. Claar, V. Iovinella, V. Messina, N. Coppola*

5705 **Direct-acting antivirals-based treatment for HIV/hepatitis C virus co-infected patients: analysis of factors of virological sustained response in a real-life study**
L. Onorato (Naples, Italy), L. Alessio, V. Sangiovanni, F. Borrelli, E. Manzillo, V. Esposito, F. Simeone, S. Martini, N. Capoluongo, S. Leone, G. Di Filippo, M. D'Abbraccio, A. Salomone Megna, E. Milano, A. Saracino, N. Coppola*

7803 **HEV infection as an emergent public health issue: is it a concern for Italian blood donors?**
L. Colagrossi (Milan, Italy), M. Mercuri, A. Nava, E. Matarazzo, D. Campisi, P. Carlo Federico, D. Fanti*

8397 **Prevalence of Hepatitis E Virus in allogeneic-haematopoietic stem cell transplant recipients from Portugal**
S. Cruz (Rebordosa, Portugal), N. Santos-Ferreira, M. Nascimento, C. Pinho Vaz, F. Campilho, L. Leite, R. Branca, A. Campos Jr, R. Medeiros, H. Sousa*

9001 **Micro-elimination of hepatitis C in HIV co-infected persons in Slovenia: analysis of HCV infection in a national HIV cohort**
J. Cernosa (Smarje pri Jelsah, Slovenia), J. Tomažic, T. Vovko, B. Pecavar, G. Turel, M. Kordiš, M. Pleško, B. Ulčar, J. Meglič, M. Poljak, J. Lazarus, M. Maticic*

Session accepted as Mini-oral ePoster Session

Viral respiratory infections

1420 **High-resolution influenza mapping of a city reveals socioeconomic determinants of transmission within and between urban quarters**
A. Egli (Basel, Switzerland), N. Goldman, N. Mueller, M. Brunner, D. Wüthrich, S. Tschudin-Sutter, E. Hodcroft, C. Saalfrank, R. Neher, J. Hadfield, T. Bedford, M. Syedbasha, T. Vogel, N. Augustin, J. Bauer, N. Sailer, N. Amar-Sliwa, D. Lang, H. Seth-Smith, A. Blaich, Y. Hollenstein, O. Dubuis, M. Naegele, A. Buser, C. Nickel, N. Ritz, A. Zeller, T. Stadler, M. Battegay, R. Schneider-Sliwa*

2298 **Too much of a good thing? Evaluation of respiratory viral panel usage in paediatric bone marrow transplant patients**
M. Precit (Los Angeles, United States), M. Glucoft, K. Mongkolrattanothai, J. Dien Bard*

2471 **Predictors of mortality of influenza virus infections in a Swiss hospital during four influenza seasons: role of quick sequential organ failure assessment**
M. Papadimitriou Olivgeris (Lausanne, Switzerland), N. Gkikopoulos, M. Wust, A. Ballif, V. Simonin, M. Maulini, C. Nusbaumer, L. Bertaiola Monnerat, J. Tschopp, E. Kampouri, P. Wilson, H. Duplain*

3902 **Enterovirus D68: biennial circulation and molecular epidemiology in New York, USA, 2014-2018**
G. Wang (Valhalla, United States), V. Gilrane, J. Zhuge, W. Huang, C. Yin, C. Salib, S. Nolan, A. Dhand, J. Fallon*

4399 **Effect of rapid influenza detection tests on antibiotic prescriptions**
A. Berwa (Meylan, France), M. Gallouche, S. Larrat, J. Fauconnier, J. Bosson, C. Landelle*

5740 **Measurement of influenza antibodies in a cohort of vaccinated patients admitted to a cardiac intensive care unit: are they clinically relevant?**
A. Galar Recalde (Madrid, Spain), I. Sousa Casasnovas, A. Cobos, R. Alonso, P. Catalán, M. Valerio Minero, M. Juárez, P. Antunez, G. Barbeito Castiñeiras, S. Blanco, L. Folgueira, J. García-Acuña, A. Lalueza, F. Lázaro, E. López De Sá, L. Martin, E. Muñez Rubio, F. Portillo, A. Ramos Martínez, S. Rosillo, M. Martinez-Selles, F. Fernandez-Aviles, P. Muñoz*

6474 **Nanopore metagenomic sequencing of influenza virus directly from respiratory samples: diagnosis, drug resistance and nosocomial transmission**
Y. Xu (Oxford, United Kingdom), K. Lewandowski, L. Downs, J. Kavanagh, T. Hender, S. Lumley, K. Jeffery, D. Foster, N. Sanderson, A. Vaughan, M. Morgan, R. Vipond, M. Carroll, T. Peto, D. Crook, A. Walker, P. Matthews, S. Pullan*

7752 **Burden of severe influenza disease in France: epidemiological analysis from 2010/2011 to 2017/2018 based on the French national hospital administrative database**
F. Fouad, M. Lemaitre, A. Bessou, F. Carrat, P. Crépey, J. Gaillat (Pringy, France), G. Gavazzi, O. Launay, A. Mosnier, M. Levant, M. Uhart*

8890 **Evaluating the performance of a host-protein signature for distinguishing between bacterial and viral disease in adults with Lower Respiratory Tract Infection (LRTI): results from the OBSERVER clinical study**
M. Paz (Tirat Carmel, Israel), M. Stein, E. Moscoviz, S. Halabi, S. Shiber, S. Yanai, Y. Lishtzinsky, D. Kirshner, Y. Maor, T. Gottlieb, E. Simon, Y. Israeli, N. Avni, G. Kronenfeld, N. Sitry, M. Smith, A. Boukin, A. Angel, Y. Orr, N. Mastboim, T. Ilan-Ber, R. Gidron Budovsky, E. Eden, L. Shani*

Session accepted as Paper Poster Session

Viruses and transplantation

615 **Survival outcome in allogeneic haematopoietic stem cell transplant recipients with multiple, sequential cytomegalovirus, Epstein-Barr virus, BK virus and respiratory viral infections**
S. Tio (Parkville, Australia), M. Slavin, D. Ritchie, L. Chee, A. Bajel, J. Sasadeusz, C. Malpas, M. Yong*

824 **International survey on diagnosis and management of human herpes virus-8 infection in solid organ transplant recipients**
A. Mularoni (Palermo, Italy), L. Adamoli, M. Mikulska, M. Giannella, P. Grossi*

1006 ***In vitro* evaluation of the influence of immunosuppressive agents on human polyomavirus BK replication**
S. Lucia (Milan, Italy), E. Favi, M. Ferraresso, M. Dolci, R. Ticozzi, P. Ferrante, S. Delbue*

1522 **Do cytomegalovirus infection and valgancyclovir exposure increase the risk of BK viraemia and associated nephropathy after kidney transplantation?**
I. Rodriguez Goncer, L. Corbella Vazquez, F. Lopez-Medrano, R. San Juan Garrido, T. Ruiz Merlo, P. Parra, N. Polanco, E. Gonzalez, A. Andres, J. Aguado Garcia, M. Fernandez Ruiz (Madrid, Spain)*

1990 **Optimisation of a series of salicylamide derivatives of niclosamide as potent antiviral agents against human adenovirus**
J. Xu, J. Berastegui-Cabrera, H. Chen, J. Pachon-Diaz, J. Zhou, J. Sánchez Céspedes (Seville, Spain)*

2382 **Cidofovir-associated nephrotoxicity in adult allogeneic haematopoietic cell transplant recipients**
A. Stern, G. Papanicolaou, C. Garcia Vidal, C. Cardozo, C. Alonso, P. Köhler, C. Scheid, O. Cornely, D. Epstein, S. Masouridi Levrat, Y. Abi Aad, Y. Chalandon, C. Van Delden, D. Neofytos (Geneva, Switzerland)*

5029 **Impact of letermovir (LTV) on utilisation of pre-emptive therapy for cytomegalovirus after allogeneic haematopoietic cell transplantation: a single-centre experience**
J. Fang (New York, United States), P. Zavras, Y. Su, A. Stern, T. Nawar, M. Perales, G. Papanicolaou*

5402 **Retrospective study of cytomegalovirus infection in orthotopic liver transplantation recipients receiving low dose valganciclovir prophylaxis**
M. Lucey (Dublin, Ireland), S. Fitzgerald, S. Mcdermott*

5685 **Kaposi sarcoma herpes virus infection in solid organ transplant recipients**
L. Adamoli, F. Todaro, E. Conoscenti, D. Di Carlo, M. Miele, M. Di Bella, A. Gallo, P. Grossi, P. Conaldi, A. Mularoni (Palermo, Italy)*

5830 **Cytomegalovirus in intensive care unit immunocompetent patients: mortality and clinical aspects**
A. Lazo, C. Ramírez (San Jose, Costa Rica), J. Castro, T. Somogyi, J. Villalobos, L. Montero, R. Arguedas*

7069 **Impact of letermovir and associations of antivirals *in vitro* and in *ex vivo* first-trimester placenta model**
D. Andouard (Limoges, France), B. Gastineau, C. El Hamel Bellili, S. Hantz, S. Alain*

7767 **Letermovir reduces rehospitalisations among cytomegalovirus-seropositive allogeneic haematogenous stem-cell transplant recipients**
Y. Golan (Boston, United States), Y. Tang, S. Mt-Isa, H. Wan, V. Teal, C. Badshah, S. Dadwal*

7794 **Evaluation of association between immune modulation and incidence of cytomegalovirus reactivation in sepsis-induced immunosuppression**
G. Lambe (Maharashtra, India), F. Kapadia, C. Rodrigues, A. Shetty, S. Khodaiji, D. Mansukhani*

7948 **Cytomegalovirus reactivation as a diagnostic and prognostic indicator of increased risk of cardiovascular diseases**
V. Cento, L. Colagrossi (Milan, Italy), A. Nava, E. Matarazzo, M. Mercuri, F. Pansera, E. Piccinelli, I. Bossi, D. Armenia, P. Paba, F. Marcuccilli, D. Campisi, D. Fanti, F. Oliva, F. Ceccherini Silberstein, C. Giannattasio, P. Carlo Federico*

8039 **Letermovir pre-existent mutations in human cytomegalovirus UL56 terminase in solid organ and haematopoietic stem cell transplant recipients**
M. Santos Bravo (Barcelona, Spain), S. Sanchez-Palomino, N. Plault, M. Mosquera Gutiérrez, V. Gonzalo, F. Fernández, M. Suárez-Lledó, M. Rovira, F. Cofan, M. Moreno Camacho, L. Linares, M. Bodro Marimont, S. Alain, M. Marcos*

8079 **Evaluation of clinical safety and efficacy of letermovir for cytomegalovirus infection prevention in allogenic haematopoietic cell transplant recipients**
M. Korostelev (Paris, France), D. Michonneau, I. Madelaine, T. Sophie*

8298 **Relevance of EBV load monitoring in renal transplant recipients: a retrospective cohort study**
L. Gard (Groningen, Netherlands), C. Oliveira Dos Santos, W. Van Doesum, H. Niesters, W. Van Son, A. Diepstra, C. Stegeman, H. Groen, J. Sanders, A. Riezebos-Brilman*

Session accepted as Paper Poster Session

Viruses causing haemorrhagic syndromes

16 **Crimean-Congo haemorrhagic fever in an emergency department in Spain**
L. Monsalve-Arteaga (Salamanca, Spain), M. Belhassen García, J. Munoz-Bellido, M. Alonso Sardón, A. Negredo, M. Sanchez-Seco, F. De Ory Manchón, N. Leralta, I. Bas García, J. Sánchez Serrano, J. García Criado, A. Muro Alvarez, A. López Bernús*

514 **Seroprevalence of anti-CCHF IgG in population in different districts of endemic region and Crimean-Congo haemorrhagic fever morbidity**
N. Pshenichnaia (Moscow, Russian Federation), N. Golovchenko, L. Ermakova, E. Volchkova, A. Zhuravlev, A. Grekova*

785 **Forecasting of Crimean-Congo haemorrhagic fever outcome**
N. Pshenichnaia (Moscow, Russian Federation), G. Abuova, F. Berdalieva, B. Khodzhabekov, L. Ermakova, A. Zhuravlev*

913 **Lassa fever infection and prevention control availability and use at healthcare facilities in South-Western Nigeria**
I. Usman (Osogbo, Nigeria), S. Usman*

1384 **The ultrastructural visualisation of Severe Fever with Thrombocytopenia Syndrome (SFTS) virus in human PBMC sample**
Y. Lee, H. Lee, E. Park, H. Kim, S. Kim, C. Lee, S. Jun (Daejeon, South Korea)*

1488 **Geographical clustering of hantavirus isolates from *Apodemus agrarius* identified in the Republic of Korea indicates the emergence of a new hantavirus genotype**
D. Kim (Gwangju, South Korea), J. Sehrish, C. Kim, S. Jun-Won*

1906 **Hantavirus registry (HantaReg): a novel worldwide platform for epidemiological and clinical studies of hantavirus diseases**
F. Köhler (Cologne, Germany), M. Späth, J. Hoyer-Allo, M. Wanken, O. Cornely, V. Di Cristanziano, F. Schaefer, R. Müller, V. Burst*

2714 **Crimean–Congo haemorrhagic fever in pregnancy: a systematic review and meta-analysis of clinical presentation and maternal and foetal outcomes**
N. Kayem (Oxford, United Kingdom), C. Aye, C. Benson, S. Baker, M. Tome, S. Kennedy, P. Ariana, P. Horby*

3294 **Safe and high-throughput screening of natural compounds using pseudo-virus expressing SFTSV glycoprotein**
H. Cha (Seoul, South Korea), J. Kim, S. Park, I. Kim, S. Kim*

6175 **Renal manifestations of severe fever with thrombocytopenia syndrome**
S. Bae (Seoul, South Korea), J. Park, M. Bae, J. Jung, M. Kim, Y. Chong, S. Lee, S. Choi, Y. Kim, J. Woo, S. Kim*

6308 **Optimised standard of care for Ebola virus disease patients in eastern Congo: a mandatory effort associated with specific therapies**
M. Jaspard (Paris, France), S. Juchet, B. Serra, B. Baweye, I. Malam Kanta, I. Dicko, K. Ntondi, E. Toguyadji Adidjingar, R. Kojan, D. Malvy*

6358 **Usefulness of reverse transcriptase nested polymerase chain reaction in clinical specimens for the diagnosis of haemorrhagic fever with renal syndrome**
J. Seo (Gwangju, South Korea), C. Kim, N. Yoon, Y. Lee, M. Lawrence Panchali, D. Kim*

6517 **Clinical and epidemiological features of patients presenting with Crimean-Congo haemorrhagic fever at a tertiary care hospital in Karachi**
K. Habib (Karachi, Pakistan), I. Khanum, S. Awan, B. Jamil*

7402 **Increasing importance of reservoir hosts in viral infections: Hantavirus infection in rodents in East Anatolia of Turkey**
M. Timurkan (Erzurum, Turkey), H. Aydin*

7703 **The case for pharmacokinetic/pharmacodynamic studies during epidemics of high consequence pathogens: Tekmira for Ebola virus disease in Sierra Leone**
J. Scott (Glasgow, United Kingdom), R. Sharma, L. Meredith, J. Dunning, C. Moore, F. Sahr, S. Ward, I. Goodfellow, P. Horby*

Session accepted as Mini-oral ePoster Session

What's new in HIV?

446 **Haemophagocytic lymphohistiocytosis in human immunodeficiency virus: a systematic review of literature**
F. Fazal, A. Mittal, A. Ray, N. Gupta (Manipal, India)*

1986 **Testing EEG-LORETA and CSF Biomarkers in patients with HIV-associated neurocognitive disorders**
A. Lazzaro, V. Pirriatore, G. Stroffolini, A. Barco (Torino, Italy), G. Noce, D. Vai, G. Di Perri, S. Bonora, A. Calcagno*

1994 **Prevalence, correlates and outcomes of plasma cryptococcal antigen postivity among HIV-infected patients with a CD4+ T-cell count under 100/mm^3, diagnosed in Spain**
M. Pérez-Jacoiste Asín (Madrid, Spain), O. Bisbal, J. Iribarren Loyarte, S. Moreno Guillén, R. Rubio*

2091 **Which HIV-positive men who have sex with men patients benefit of anal cancer screening?**
C. Hidalgo Tenorio (Granada, Spain), C. Gil-Anguita, M. López-Ruz, J. Lopez Hidalgo, J. Pasquau*

2730 **A marked decrease in HIV-1 acquired drug resistance in Itlay over the last decade**
M. Franzetti, A. Lai, F. Saladini, B. Bruzzone, S. Di Giambenedetto, A. Di Biagio, S. Lo Caputo, M. Santoro, F. Maggiolo, S. Parisi (Padova, Italy), S. Rusconi, N. Gianotti, C. Balotta*

4724 **Evaluation of analytical and clinical performances of four commercial HIV-1 viral load assays on a wide panel of HIV-1/M and HIV-1/O**
M. Gueudin (Rouen, France), P. Cappy, E. Alessandri-Gradt, F. Damond, J. Moriceau, D. Descamps, A. Vabret, S. Laperche, J. Plantier*

7150 **Early, potent and sustained virus-specific antibody-dependent complement-mediated inactivation activity in HIV-2 infection**
G. Ozkaya Sahin (Lund, Sweden), S. Karlson, F. Mansson, J. Esbjornsson, M. Sallam, P. Medstrand, H. Norrgren, M. Jansson*

8101 **The N-terminus of APOBEC3C regulates the antiviral activity against HIV-1**
K. Balakrishnan (Düsseldorf, Germany), A. Jaguva Vasudevan, A. Sangwiman, S. Banerjee, C. Münk*

9109 **Conservation in p24 capsid protein regions in HIV-1 groups M, O, P and N**
P. Troyano Hernáez (Alcalá de Henares, Spain), R. Reinosa, Á. Holguín*

Session accepted as 2-Hour Oral Session

What's new in viral hepatitis?

1032 **Prospective evaluation of serological and virological response in chronic hepatitis B genotype E treated with tenofovir or entecavir**
I. De Benedetto (Turin, Italy), L. Boglione, T. Lupia, G. Cariti, G. Di Perri*

4164 **Eliminating mother-to-child transmission of hepatitis B virus in Namibia: a cost-effectiveness analysis**
C. Tamandjou Tchuem (Cape Town, South Africa), M. Andersson, J. Mufenda, C. Wiysonge, D. Diergaardt, W. Preiser, S. Cleary*

4340 **Virological features and efficacy of re-treatment in hepatitis C virus patients: a real experience in southern Italy**
A. Di Fraia (Naples, Italy), C. Minichini, M. Pisaturo, M. Starace, S. De Pascalis, M. Macera, V. Messina, V. Sangiovanni, E. Claar, D. Precone, G. Stornaiuolo, M. Stanzione, I. Gentile, S. Martini, A. Masiello, A. Salomone Megna, C. Coppola, A. Federico, M. Persico, A. Galeota Lanza, A. Marrone, G. Gaeta, N. Coppola*

4884 **Chronic hepatitis C care cascade in France: substantial impact of direct-acting antivirals but the path to elimination is still long**
C. Brouard (Saint-Maurice, France), J. Pillonel, M. Boussac, V. De Ledinghen, A. Rachas, C. Silvain, N. Lydié, S. Chevaliez, C. Pioche, J. Durand, F. Lot, E. Delarocque-Astagneau*

4922 **Characteristics of Resistance Associated Substitutions (RASs) in "unusual" HCV subtypes: a worldwide network of HCV resistance database**
S. Fourati (Creteil, France), S. Popping, A. Howe, A. De Salazar, V. Di Maio, E. Tay, C. Rodrigo, E. Cunningham, M. Kjellin, P. Gomes, M. Sayan, O. Mor, J. Sfalcin, D. Salmon-Ceron, R. Usubillaga, C. Seguin Devaux, A. Lloyd, R. Kaiser, V. Chulanov, M. Douglas, F. Ceccherini-Silberstein, R. Harrigan, F. Garcia Garcia, C. Boucher, J. Pawlotsky*

5068 **HCV resistance patterns in a large international cohort of DAA-naïve and -experienced patients with GT3a infection**
S. Fourati (Creteil, France), F. Ceccherini-Silberstein, A. Howe, V. Di Maio, A. De Salazar, S. Popping, E. Tay, C. Rodrigo, E. Cunningham, M. Kjellin, P. Gomes, M. Sayan, M. Poljak, O. Mor, D. Salmon-Ceron, R. Usubillaga, C. Boucher, L. Poiteau, A. Soulier, J. Grebely, J. Lennerstrand, R. Kaiser, V. Chulanov, J. Cabezas, J. Alados Arboledas, M. Douglas, F. Garcia Garcia, R. Harrigan, J. Pawlotsky*

5141 **Hepatitis E virus genotype 3 subtype-dependent clinical outcomes in Belgium 2010-2018**
P. Michael (Brussels, Belgium), T. De Somer, S. Klamer, F. Nevens, J. Delwaide, P. Stärkel, P. Willems, S. De Maeght, C. Moreno, M. Van Hoof, I. Colle, F. Sermon, C. Van Steenkiste, F. Janssens, J. Van Acker, A. Marot, E. Bottieau, M. Reynders, C. De Galocsy, L. Lasser, M. Steverlynck, J. Maus, W. Verlinden, A. Geerts, M. Gallant, S. Van Outryve, H. Reynaert, J. Mulkay, J. Decaestecker, V. Suin, S. Negrin-Dastis, S. Van Gucht, T. Vanwolleghem*

5592 **Innovative procedures for micro-elimination of hepatitis C virus infection in a high-risk population of undocumented migrants and low-income refugees**
L. Onorato (Naples, Italy), L. Alessio, S. De Pascalis, V. Messina, C. Sagnelli, E. Sagnelli, G. Di Caprio, M. Macera, M. Pisaturo, N. Coppola*

Session accepted as Paper Poster Session

Yellow fever, Zika, and Chikungunya

672 **Clinical manifestations of hospitalised chikungunya fever cases during epidemic in the state of Ceará, Brazil, from 2017 to 2019**
R. Pires Neto (Fortaleza, Brazil), F. Lillyan Christyan Nunes Beserra, J. D'arc Rocha Damasceno, D. Mendes De Melo, E. Girão*

2950 **Clinical outcomes of 3-day course of adjunctive oral ivermectin for the patients with chikungunya viral infection: a preliminary study**
S. Chusri (Songkhla, Thailand), T. Hortivakul, P. Surasombatpattana, K. Silpapojakul*

3210 **Clinical evaluation of the mosquito-borne virus panels of Genematrix based on multiplex real-time PCR**
J. Ju, S. Cho, S. Yang, K. Lee (Gyeonggi-Do, South Korea), S. Hong, S. Kim*

3280 **Malaria outbreak investigations reveal high seroprevalence of arbovirus infections among febrile cases in Baringo County, Kenya**
T. Nzomo (Nairobi, Kenya), R. Abdi*

4646 **Chikungunya positive reference material based on lentiviral vector system for RT-qPCR assays**
C. Escolar (Zaragoza, Spain), S. Valledor, E. De Tomas Mateo*

6276 **Epidemiology of dengue, chikungunya, Zika and West Nile diseases from 2012 to 2019: data from an Italian regional reference centre**
N. Zanchetta, A. Rizzo, C. Bossi, C. Pontoriero, R. Grande (Milan, Italy), G. Venturi, M. Gismondo*

6396 **Epidemiology and differential diagnosis of chikungunya and O'nyong-nyong virus: many gaps of knowledge to be filled**
L. Pezzi (Marseille, France), I. Diarra*

6857 **Results of a Zika virus screening programme in asymptomatic pregnant women in Spain**
C. Castelló-Abietar, I. Costales (Oviedo, Spain), S. Rojo, M. Alavarez-Argüelles, S. Melón-García, M. Rodriguez-Perez*

6979 **Zika virus: a global health threat and current situation in Pakistan**
K. Imtiaz, J. Farooqi, D. Prakoso, K. Barr, M. Long, E. Khan (Karachi, Pakistan)*

7043 **First vector-borne cases of Zika virus diseases in Europe: a seroprevalence survey**
H. Noël (Saint-Maurice Cedex, France), F. Franke, G. Durand, J. Paireau, S. Giron, G. Grard, P. Chaud, A. Decoppet, S. Cauchemez, M. Paty, H. De Valk*

7081 **Characterisation of ZIKV NS1 protein and development of ZIKV-specific monoclonal antibodies for rapid diagnosis**
H. Kim (Cheongju-Si, South Korea), S. Jun, E. Park, S. Kim*

7212 **Detection of Zika and Chikungunya viruses circulation in Pointe Noire district (Republic of Congo) during the 2019 Chikungunya outbreak**
C. Fortuna (Rome, Italy), F. Severini, M. Menegon, M. Di Luca, G. Venturi, A. Kimpamboudi Matondo, J. Imboua, M. Saint Gauhy, C. Boungou, A. Suardi, A. Chacon, F. Uberti, G. Rezza*

7513 **Chikungunya virus: neuromotor evaluation of infants born to infected mothers**
R. Freire, C. Gaspari (Rio de Janeiro, Brazil), L. Albuquerque*

7646 **A new menace emerges in South America: yellow fever outbreak looms in Venezuela**
A. Tami (Groningen, Netherlands), A. Paniz-Mondolf, M. Grillet, M. Vincenti-Gonzalez, E. Lizarazo, D. Forero-Peña, J. Castro, J. Oletta*

8527 **Can HLA type I and II alleles presence be associated with the clinical spectrum of chikungunya virus infection**
J. Arias Correal (Tabio, Colombia), J. Rueda Sanchez, A. Santos, J. Angarita, E. Saldarriaga, D. Martin Arsanios, V. Reyes, D. Padilla Ortiz, S. Bernal Macias, S. Arias Correal, N. Muñoz, I. Peláez Ballestas, M. Cardiel, J. Londoño*

8628 **The impact of Zika virus epidemic on maternal mental health in Brazil**
T. Araujo, T. De Araujo, D. Neves, S. Ferrite, L. Marques, I. Lua, G. Werneck (Rio de Janeiro, Brazil)*

8756 **Zika, dengue and chikungunya viruses seroprevalence among adolescents in Brazil**
T. Melo, M. Dantas Junior, V. Almeida, T. Silva, T. Nascimento, L. Pôrto, K. Bloch, G. Werneck (Rio de Janeiro, Brazil), G. Gibson*

8812 **Accuracy of chikungunya case definition in patients with arbovirus illness seeking care in an urban emergency department in Rio de Janeiro, Brazil**
H. De Paula, C. Lamas (Rio de Janeiro, Brazil), J. Moreira, R. Santana De Aguiar, S. Cardozo*

9073 **Who should we test for arboviral infection? Rational diagnostic testing in an era of increased global prevalence**
R. Ryan (London, United Kingdom), I. Milligan, S. Logan, E. Nastouli, A. Checkley, T. Rampling*

9345 **What does the space-time dynamics of arboviral diseases epidemic in Curaçao tell us? Unravelling potential factors of disease persistence and spread**
M. Vincenti-Gonzalez (Groningen, Netherlands), Y. Halabi, I. Gerstenbluth, A. Duits, A. Friedrich, M. Grillet, A. Tami*

9367 **"Tell me and I forget, involve me and I learn": citizen science for mosquito management in a Dutch Caribbean island**
M. Vincenti-Gonzalez (Groningen, Netherlands), D. De Kort, D. Haarsma, R. Haan, Q. Van Der Leest, B. Sagel, A. Duits, E. Schoop, M. Kelie, Y. Halabi, M. Braks, L. Tromp, A. Friedrich, M. Grillet, A. Tami*

9646 **Clinical evolution of yellow fever patients in the 2017-2018 outbreaks in Minas Gerais, Brazil: preliminary analysis of risk factors for death**
C. Rodrigues (Belo Horizonte, Brazil), W. Clemente, C. Bonis, P. Mourão*

Abstract Programme

2. Bacterial infection & disease

- Tuberculosis and other mycobacterial infections (incl antimycobacterial drugs, treatment & susceptibility/resistance, diagnostics & epidemiology)
- Severe sepsis, bacteraemia & endocarditis (incl host bio-markers)
- Community-acquired respiratory infections
- Community-acquired abdominal/gastrointestinal, urinary tract & genital infections
- Skin, soft tissue, bone & joint (excl prostheses) & central nervous system infections
- Zoonotic bacterial diseases (incl foodborne and waterborne pathogens and One Health aspects)
- Other intracellular or rare bacteria
- Other

Session accepted as Paper Poster Session

Antimicrobial prescribing and allergy

2393 **Back to the future: Comparison of beta-lactam days of therapy before and after negative penicillin skin testing**
C. Bland, A. Asbell, E. Heil (Baltimore, United States), S. Smith, B. Jones*

3020 **β-lactam allergy and risk of multidrug-resistant bacteria acquisition in an intensive care unit: a cohort study**
A. Strazzulla (Melun, France), L. Iordache, A. De Pontfarcy, A. Pitsch, N. Belfeki, S. Jochmans, G. Lezmi, M. Monchi, S. Diamantis*

3197 **Non-beta-lactam antibiotic hypersensitivity reactions in children**
L. Grinlington, S. Choo, N. Cranswick, A. Gwee (Melbourne, Australia)*

3742 **Variables associated with higher readmission frequency in an OPAT program**
L. Lopez-Cortes (Seville, Spain), E. Fraile-Ramos, J. Carmona-Caballero, M. Gutierrez, L. Navarro, B. Gutiérrez-Gutiérrez, P. Retamar Gentil, J. Praena, J. Pazod, M. Gil-Navarro, L. Rafael, J. Cisneros Herreros*

3743 **Considerations in the design and analysis of antibiotic duration trials in the presence of non-adherence**
Y. Mo (Singapore, Singapore), C. Lim, M. Mukaka, B. Cooper*

4656 **Paving the way for the implementation of a decision support system for antimicrobial prescribing in primary care in West Africa: a workshop with healthcare professionals**
N. Peiffer-Smadja (Paris, France), A. Poda, A. Ouedraogo, J. Guiard-Schmid, T. Delory, J. Le Bel, P. Jeanmougin, E. Bouvet, S. Lariven, R. Ahmad, X. Lescure*

4735 **Examining the long-term adoption of a clinical decision support system for antimicrobial prescribing in primary care**
N. Peiffer-Smadja (Paris, France), T. Delory, P. Jeanmougin, J. Le Bel, E. Bouvet, A. Holmes, Y. Yazdanpanah, S. Lariven, R. Ahmad, X. Lescure*

5556 **Appropriateness of antibiotic recommendations within infectious diseases guidelines for patients with a penicillin allergy: a systematic review**
M. Bianchini, E. Atchley, J. Markus, M. Jeffres (Aurora, United States)*

5756 **Independent risk factors associated to inappropriate antibiotic prescription in the emergency department**
M. Nuñez Orantos, F. Candel, E. Orviz, J. Gonzalez Del Castillo (Collado Villalba, Spain)*

8077 **Hospitalised patients with a label of penicillin allergy: which antibiotic therapy do they receive?**
M. Lehericey (Caen, France), C. Morice, H. Roger, R. Verdon*

9321 **Exploring barriers to penicillin allergy de-labelling in a UK teaching hospital**
C. Jones (Exeter, United Kingdom), S. Wade, E. Marshall, C. Jones, F. Canney, R. Lazarus*

Session accepted as Paper Poster Session

Bloodstream infections: be "positive"

7 **Bacteraemia with anaerobic bacteria and association with colorectal cancer**
U. Justesen (Odense, Denmark), S. Nielsen, T. Jensen, R. Dessau, J. Kjølseth Møller, J. Coia, S. Andersen, C. Pedersen, K. Gradel*

292 **Risk of invasive pneumococcal infection in patients with asplenia/hyposplenism: a nationwide population-based study compared to the general population**
J. Kang (Seoul, South Korea), E. Kim, M. Han, I. Jung, K. Ihn, J. Ahn*

379 ***Staphylococcus aureus* bloodstream infection: can the practice of the VIRSTA score replace the infectious disease consultation in case management?**
C. Saint-Pastou Terrier, N. Zemali, A. Bertolotti, R. Manaquin, A. Foucher, P. Poubeau, P. Gerardin, Y. Koumar (Saint Pierre, France)*

693 **Comparing clinical outcomes in Gram-negative bloodstream infections with desirability of outcomes ranking: focus on non-fermenting organisms**
K. Claeys (Baltimore, United States), E. Heil, J. Johnson, S. Leekha*

1245 **Risk factors and clinical manifestations of Group B streptococcal invasive infection in adult population**
I. Arregui, A. Aguinaga Perez, A. Navascués Ortega, J. Torroba Alvarez, C. Martín, M. Adelantado Lacasa, E. Erviti, C. Ezpeleta Baquedano (Pamplona, Spain)*

2232 ***In vitro* virulence of *Staphylococcus schweitzeri***
A. Grossmann, N. Froböse, A. Mellmann, S. Niemann, F. Schaumburg (Münster, Germany)*

2233 **Impact of immunosuppressive agents on clinical manifestations and outcome of *Staphylococcus aureus* bloodstream infection: a propensity-score matched analysis in two large, prospectively evaluated cohorts**
J. Camp (Freiburg, Germany), L. Glaubitz, T. Filla, A. Kaasch, F. Fuchs, M. Scarborough, K. Song, R. Tilley, C. Liao, J. Edgeworth, E. Nsutebu, L. Lopez-Cortes, L. Morata, M. Llewelyn, V. Fowler, G. Thwaites, H. Seifert, W. Kern, O. Kuss, S. Rieg*

2479 **Impact of universal infectious diseases consultation on the management of *Staphylococcus aureus* bloodstream infection in a Swiss community hospital**
M. Papadimitriou Olivgeris (Lausanne, Switzerland), V. Portillo Tunon, C. Nusbaumer, L. Bertaiola Monnerat, E. Kampouri, H. Duplain*

2680 **Evaluation of the expanded-coverage *Staphylococcus* species assays and improved methicillin resistance detection algorithms of the BioFire FilmArray Blood Culture Identification 2 (BCID2) panel**
T. Robinson, J. Antosch, K. Koch, I. Kavetska, J. Stone, B. Flaherty, M. Buccambuso, K. Holmberg, Y. Lu, B. Pons, M. Rogatcheva (Salt Lake City, United States), U. Spaulding*

4560 **The prevalence of puerperal sepsis causing *emm28 Streptococcus pyogenes* in four Nordic countries**
K. Gröndahl-Yli-Hannuksela (Turku, Finland), B. Henriques-Normark, D. Caugant, K. Kristinsson, J. Darenberg, H. Hyyrylainen, D. Vestrheim, M. Gottfredsson, J. Vuopio*

4674 **Mortality in patients with *Staphylococcus aureus* bacteraemia and the implications of *Staphylococcus aureus* bacteriuria for in-hospital: results of a monocentric retrospective cohort study**
T. Kramer (Berlin, Germany), B. Schlosser, F. Schwab, D. Gruhl, M. Behnke, P. Gastmeier, R. Leistner*

4766 **Evaluation of quality indicators in *Staphylococcus aureus* bacteraemia in a university hospital**
S. De La Villa Martinez (Madrid, Spain), P. Muñoz, A. Arias, A. Rojas, C. Sanchez Carrillo, M. Valerio Minero, A. Galar Recalde, A. Alvarez-Uria, E. Bouza Santiago*

5105 **Immunochemical detection of quorum-sensing autoinducers, an innovative strategy to diagnose infections by identifying *Staphylococcus aureus* strains**
E. Montagut Cañete (Barcelona, Spain), G. Godoy, J. Salvador, A. Lacoma, C. Prat, M. Marco*

5107 **Distribution of *mecA* in *Staphylococcus aureus* isolates in a multi-centre clinical study**
A. Thornberg (Carlsbad, United States), N. Whitfield, D. Trainor, J. Reid*

5222 **Clinical characteristics and prognosis of *Staphylococcus aureus* Bloodstream Infections in a French General Hospital**
S. Nguyen (Béthune, France), P. Wallard, O. Oddoux, M. Anastay, D. Descamps*

5249 **Distinguishing clinical characteristics and outcomes in patients with polymicrobial *Staphylococcus aureus* bacteraemia**
C. Kelsom (Pasadena, United States), E. Minejima, K. Tan, P. Nieberg, A. Wong-Beringer*

5417 **Healthcare-associated *Staphylococcus aureus* bloodstream infection (HA-SABSI): clinical practice variation in its management**
M. Garcia-Gasalla (Palma de Mallorca, Spain), C. Collado Giner, A. Villoslada Gelabert, L. Ventayol-Aguiló, M. Perez-Seco, M. Arrizabalaga Asenjo, M. Gallegos Alvarez*

5840 **Septic shock and age are risk factors for mortality in bacteraemia by multidrug-resistant pathogens in a Brazilian cohort of critical patients**
L. Campos, C. Rizek, M. Farrel Côrtes, S. Santos, A. Marchi, K. Gonçalves, S. Figueiredo Costa (São Paulo, Brazil)*

5878 **Characterising the incidence and outcomes of endogenous endophthalmitis in hospitalised patients with *Staphylococcus aureus* bacteraemia**
L. Wardlow (Columbus, United States), M. Sobhanie*

6111 **Secular trends in the epidemiology and clinical characteristics of *Enterococcus faecalis* infective endocarditis in a referral centre (2007-2018)**
L. Escolà-Vergé, N. Fernandez-Hidalgo (Barcelona, Spain), N. Larrosa, B. Almirante*

6262 **Development of a predictive score for *Enterococcus* spp. in biliary tract-related bloodstream infections: Results from the PROBAC study**
M. Mussa (Pavia, Italy), P. Pérez-Crespo, J. Lanz, L. Lopez-Cortes, P. Retamar Gentil, I. Fernandez Natal, J. Fernandez-Suarez, E. Calbo Sebastian, L. Boix-Palop, J. Sanchez Calvo, J. Sevilla Blanco, J. Cuquet Pedragosa, A. Jóver-Sainz, C. Natera, A. Sousa-Dominguez, J. Goikoetxea, J. Reguera Iglesias, E. Leon, C. Armiñanzas Castillo, C. Labayru Echeverría, F. Galan-Sanchez, A. Del Arco, A. Bahamonde, A. Smithson Amat, D. Vinuesa García, C. Herrero, A. Reyes Bertos, I. Perez-Camacho, A. Sánchez-Porto, M. Guzman, B. Becerril Carral, E. Merino De Lucas, J. Rodríguez-Baño*

6510 **Impact of infectious diseases consultation and appropriate empirical antibiotic therapy on mortality in patients with *Staphylococcus aureus* bloodstream infection: a two-year retrospective analysis**
A. Cona (Milan, Italy), L. Gazzola, O. Viganò, R. Castoldi, A. Renzelli, T. Bini, G. Marchetti, A. D'Arminio Monforte*

7675 **Recurrent bacteraemia with *Enterococcus faecalis* is predominantly caused by the same clone**
C. Tellapragada (Stockholm, Sweden), H. Östlund, P. Naucler, M. Rasmussen, C. Giske, A. Berge*

8603 **Bloodstream infections caused by *Enterococcus* spp.: incidence, clinical features, and outcomes**
T. Lupia, L. Scaglione, A. Curtoni, R. Cavallo, F. De Rosa, S. Corcione (Turin, Italy)*

8662 **Delayed diagnosis and increase mortality in native vs prosthetic/device-related coagulase-negative staphylococci infective endocarditis**
L. Prunonosa (Badolona, Spain) N. Vallejo, R. Núñez Aragón, M. Quesada, A. Vivero Larraza, E. Berastegui, C. Llibre, N. Sopena, E. Reynaga Sosa, B. Ruiz, A. Steinherr Zazo, L. Delgado, C. Munoz, G. Lladós, M. Pedro-Botet*

8880 **Clinical practice variation in the management of *Staphylococcus aureus* bacteraemia among infectious disease specialists in Latin America: an international study**
I. Perez (Santiago, Chile), A. Peters, R. Araos, M. Pinto, B. Cabieses, R. Rosales, S. Solar, E. Nannini, M. Villegas, T. Appel, J. Alave, E. Angles, C. Seas, A. Gales, J. Munita*

Session accepted as Paper Poster Session

Bone and joint infections

1122 **Evaluation of the BIOFIRE FILMARRAY Bone and Joint Infection (BJI) panel for the detection of microorganisms and resistance markers in synovial fluid specimens**
B. Kensinger (Salt Lake City, United States), B. Schmitt, A. Waggoner, F. Laurent, L. Abad, J. Balada-Llasat, J. Horn, T. Bauer, I. Mazariegos, D. Wolk, A. Jefferis, M. Hermans, I. Verhoofstad, C. Murphy, B. Cabrera, J. Esteban-Moreno, A. Macias-Valcayo, S. Butler-Wu, M. Umali-Wilcox, D. Craft, B. Von Bredow, A. Leber, K. Everhart, J. Dien Bard, J. Mestas, J. Daly, R. Barr, C. Graue, B. Pons, C. Jay, K. Bourzac*

Abstract Categories 2020

1409 **Usefulness of the 16S rRNA gene PCR and sequencing in the diagnosis of prosthetic joint infections**
G. Traglia, C. Tosello (Buenos Aires, Argentina), C. Barberis, G. Arevalo Calderon, L. Zubeldia Brenner, S. Repetto, F. Ivalde, A. Ferrero, M. Melo, H. Pueyrredon, J. Ottolenghi, D. Stecher, C. Vay*

1457 **Necrotising external otitis (NEO): analysis of risk factor for relapse in 66 patients managed during a 12 year period in a reference centre**
W. Danjou (Lyon, France), S. Chabbert, C. Fuchsmann, T. Perpoint, A. Pierrefeu, P. Miailhes, A. Becker, F. Laurent, A. Boibieux, P. Pradat, S. Roux, C. Triffault-Fillit, F. Valour, T. Ferry*

1680 **Total knee and hip arthoplasty after septic arthritis: retrospective analysis of 53 cases managed in a reference centre for bone and joint infections**
E. Portier, V. Zeller (Paris, France), S. Godot, Y. Kerroumi, B. Heym, V. Meyssonnier, S. Marmor, P. Chazerain*

2100 **Particularities of brucellar spondylodiscitis**
F. Hammami, K. Makram, A. Zayni, K. Rekik, F. Smaoui, E. Elleuch, C. Marrakchi, M. Ben Jemaa (Sfax, Tunisia)*

2209 **Necrotising otitis externa- a retrospective cohort study and treatment protocol proposal**
J. Frost (Colchester, United Kingdom), A. Samson*

2295 **Epidemiological, clinical and prognostic comparison of Gram-positive cocci (GPC) and Gram-negative bacilli (GNB) in native bone and joint infections (BJI): a multi-centre retrospective study of 538 patients**
M. Beaufrere (Caen, France), G. Avenel, E. Fiaux, V. Rasoldier, O. Vittecoq, C. Marcelli, A. Baldolli, J. Michon*

3135 **Should serum D-dimer be added as a first-line screening test for prosthetic joint infection?**
M. Fernandez Sampedro (Santander, Spain), I. Sanlés González, C. Garcia Ibarbia, N. Fañanas Rodriguez, D. Pablo-Marcos, G. Menendez Solana, C. Fariñas*

3538 **Oral versus intravenous antibiotics in the treatment of osteomyelitis in adults: a systematic review and meta-analysis**
R. Larrazabal, H. Chiu, M. Arcegono (Manila, Philippines), C. Abad*

3927 **Metagenomic antimicrobial resistance prediction from nanopore sequencing of orthopaedic implant-related infections: can we do more than detect species from sonication fluids?**
T. Street (Oxford, United Kingdom), C. Kolenda, N. Sanderson, C. Taunt, S. Oakley, B. Atkins, M. Mcnally, J. O'Grady, D. Crook, D. Eyre*

3963 **Vertebral osteomyelitis in patients with *Staphylococcus aureus* bloodstream infection: evaluation of risk factors for failure**
N. Jung (Cologne, Germany), A. Ernst, I. Joost, A. Yagdiran, G. Peyerl-Hoffmann, M. Hellmich, H. Seifert, W. Kern, A. Kaasch, S. Rieg*

4037 **Diagnostic utility of a novel Point-of-Care test of calprotectin for periprosthetic joint infection in total knee arthroplasty patients**
A. Klika (Cleveland, United States), J. Warren, H. Anis, K. Bowers, S. Zhang, J. Colon-Franco, N. Piuzzi, C. Higuera*

4475 **Efficacy of extended duration use of dalbavancin in pyogenic spondylodiscitis: a preliminary report**
M. Libanore (Ferrara, Italy), R. Bicocchi, M. Borrelli, R. Pora, I. Rambaldi, G. Caruso, P. De Bonis, R. Cultrera*

4968 **The challenge of managing bone and joint infection in the OVIVA era: significant drug/drug interactions are much more common in patients managed with oral regimes**
R. Neil (Glasgow, United Kingdom), A. Brown, F. Robb, L. Stewart, P. Wright*

5173 **Dalbavancin treatment for prosthetic joint infections in real-life: a national cohort study**
M. Matt (Garches, France), C. Duran, P. Pavese, V. Le Moing, B. Bonnin, L. Khatchatourian, P. Chavanet, C. Lechiche, J. Courjon, R. Lotte, P. Tattevin, V. Cattoir, F. Lacassin-Beller, I. Gabriela, E. Senneville, A. Dinh*

5236 **Epidemiology and risk factors of CC398 *Staphylococcus aureus* bone and joint infections**
K. Bouillller (Besancon, France), D. Hocquet, M. Sauget, X. Bertrand, C. Chirouze*

5281 **Interest of follow-up imaging examinations in patients with pyogenic vertebral osteomyelitis: a retrospective study**
S. Hecquet, F. Verhoeven, C. Prati, D. Wendling, C. Chirouze, K. Bouillller (Besancon, France)*

5449 **Duration of antibiotic prescription in the management of prosthetic joints infection in France: a national audit**
M. Le Marechal (La Tronche, France), B. Cecile, J. Gonzalez, A. Ferreira, A. Belbachir, S. Lustig, T. Ferry, J. Courjon*

5661 **Linezolid treatment for methicllin-sensitive *Staphylococcus aureus* bacteraemia**
A. Asif (Kingston upon Hull, United Kingdom), A. Samson, O. Ogunfuye, L. Mclachlan*

6745 **Efficacy and safety of tedizolid in difficult-to-treat osteoarticular infections: results of a multi-centre experience**
E. Benavent Palomares (L'Hospitalet de Llobregat, Spain), F. Escrihuela-Vidal, L. Morata, E. Reynaga, A. Soriano, D. Garcia-Somoza, X. Cabo, L. Albiach, A. Padulles, O. Murillo*

6762 **Pyogenic spinal infections in a tertiary care centre: trends in the last decade**
O. Dzupova (Prague, Czech Republic), J. Benes*

7596 **The role of local high microbial load in predicting the outcome of diabetic foot ulcers**
L. Soldevila-Boixader (L'Hospitalet de Llobregat, Spain), I. Mur, A. Fernández, E. Benavent Palomares, Y. Sierra, A. Rivera, J. Bosch, S. Marti, A. Montero, A. Soriano, C. Ardanuy Tisaire, L. Morata, N. Benito, O. Murillo*

7820 **Risk factors for daptomycin-induced eosinophilic pneumonia: a matched case-control study in a population with osteoarticular infections**
L. Soldevila-Boixader (L'Hospitalet de Llobregat, Spain), A. Padullés Zamora, E. Benavent Palomares, J. Gomez Junyent, D. Garcia-Somoza, X. Cabo, J. Ariza, O. Murillo*

8001 **Efficacy and safety of intravenous fosfomycin in patients with periprosthetic joint infection: preliminary results from the PROOF study: a prospective multi-centre study**
S. Karbysheva (Berlin, Germany), P. Morovic, D. Margaryan, L. Johannsen, A. Trampuz*

8053 **Comparison between Bedside Blind Bone Biopsy (B4) and Basic Bone Biopsy (B3) in the management of diabetic foot osteomyelitis**
G. Pean De Ponfilly (Paris, France), F. Feron, L. Potier, D. Gauthier, A. Munier, H. Jacquier, E. Lecorche, N. Grall, M. Laloi-Michelin, M. Marre, J. Riveline, E. Cambau, J. Gautier, R. Roussel, J. Kevorkian*

8154 **Retrospective analysis of spinal infections over a 10-year period (2008-2018) in tertiary care hospital**
A. Kan, E. Vryonis (Coventry, United Kingdom), V. Cajic*

8261 **Comparison of the molecular-based test system hyborg Dx and culture for the diagnosis of prosthetic joint infections**
A. Boesl (Feldkirch, Austria), H. Dirschmid, C. Ohmayer, A. Neugebauer, A. Brachner, B. Ronacher, F. Offner*

8282 **Intra-osteoblastic activity of dalbavancin during treatment of *Staphyloccocus aureus* bone and joint infection**
C. Pierre, L. Abad, A. Souche, C. Dupieux, J. Josse, T. Ferry, F. Laurent, F. Valour (Lyon, France)*

8285 **Extended-spectrum ß-lactamase-producing/ carbapenemase-producing *Enterobacterales* prosthetic joint infection in patients with positive rectal screening**
M. De Carne (Le Chesnay, France), A. Henry, E. Pinet, S. Balavoine, N. Nebot, P. Boisrenoult, C. Neulier, M. Amara, A. Therby*

8379 **Risk factors for mortality in diabetic foot infections**
P. Sen, T. Demirdal (Izmir, Turkey)*

8487 ***Granulicatella* sp. and *Abiotrophia* sp. as a rare cause of osteoarticular infections**
D. Slama (Paris, France), P. Morand, J. Loubinoux, A. Roux, L. Eyrolle, G. Auberger, M. Enser, T. Bauer, R. Gauzit, V. Zeller, D. Salmon-Ceron*

8545 **Epidemiology, complications, and outcomes of vertebral diskitis/osteomyelitis among patients with *Staphylococcus aureus* bacteraemia**
H. Ishaq, R. Ramesh (Hradec Kralove, Czech Republic), L. Baddour, M. Sohail, B. Varatharaj Palraj*

8686 **Osteomyelitis in sickle cell adults: descriptive study in a high-income country**
C. Pierre-Louis (Saint-Mandé, France), O. Steichen, A. Santin, C. Bachmeyer, P. M Bappe, F. Lionnet, S. Mattioni*

8694 **Performance of EUCAST's rapid antibiotic susceptibility testing on sterile body fluids in blood culture bottles**
S. Zimmermann (Heidelberg, Germany), J. Jasuja, I. Burckhardt*

8715 **Perioperative administration of cefepime-daptomycin combination during prosthetic joint replacement is associated with high bone and synovial concentrations**
E. Senneville (Tourcoing, France), O. Robineau, B. Brunschweiler, Y. Herpe, B. Eric, A. Grillon, C. Joseph, B. Nicolas, F. Jehl*

8893 **Risk factors for amputation in diabetic foot infections**
T. Demirdal (Izmir, Turkey), P. Sen*

9021 ***Acinetobacter baumannii*-complex related osteomyelitis**
P. Oliveira (São Paulo, Brazil), E. Saconi, V. Carvalho, J. Silva, A. Munhoz*

9119 **Cotrimoxazole in bone and joint infections is the "old" antibiotic still relevant**
M. Bardou, P. Seng (Marseille, France), A. Stein*

9429 **Diabetic foot osteomyelitis: an epidemiological retrospective analysis in a Portuguese university hospital**
A. Cipriano (Loulé, Portugal), D. Guerra, M. Abreu, A. Carvalho, M. Matos Dias Reis*

Session accepted as Paper Poster Session

BSI: new spectrum, new data

229 **Misuse of tampons and menstrual toxic shock syndrome in France: a community-based case-control study**
A. Billon, M. Gustin, A. Tristan, C. Gustave, P. Vanhems, G. Lina (Lyon, France)*

638 **Daptomycin decreased mortality in methicillin-resistant *Staphylococcus aureus* bacteraemia compared to vancomycin: a monocentric retrospective study of 96 cases**
A. Froment, R. Guiheneuf, C. Mabille, J. Lanoix (Amiens, France)*

837 **Focus on nuclear imaging and other complementary exams for bacteraemia in early post-operative cardiac surgery**
M. Thy (Paris, France)*

985 **Efficacy and safety of ceftazidime-avibactam in adults with Gram-negative bacteraemia from five phase III randomised clinical trials**
J. Mazuski, F. Wagenlehner, A. Torres, Y. Carmeli, J. Chow, D. Wajsbrot, G. Stone, P. Irani, V. Mascasullo, K. Cheng, M. Tawadrous (Groton, United States)*

2847 **Can we use sepsis scores to predict bacteraemia in the elderly?**
S. Subbarao (London, United Kingdom), S. Subba Rao, M. Andrews, Y. Milner, C. Nicfhogartaigh*

3031 **Rising incidence and mortality of bloodstream infections in Finland: a nation-wide population-based study during 2004–2018**
K. Kontula (Helsinki, Finland), K. Skogberg, J. Ollgren, O. Lyytikainen, A. Järvinen*

3457 **Impact of positive blood culture occurring in early post-operative cardiac surgery: a retrospective study**
M. Thy (Paris, France), H. Chaussade, R. Raffoul, N. Grall, J. Lucet, S. Alkhoder, C. Verdonk, W. Ghodhbane, C. Cimadevilla, L. Armand-Lefevre, P. Nataf, Y. Yazdanpanah, X. Lescure*

3685 **Ceftaroline fosamil for the treatment of methicillin-resistant *Staphylococcus aureus* bacteraemia: a real-world comparative clinical outcomes study**
J. Hammond, M. Benigno, R. Chambers, N. Patino, W. Ansari (New York, United States), J. Nguyen*

3753 ***Escherichia coli* bloodstream infections: a multinational population-based perspective**
M. Mackinnon (Guelph, Canada), S. Mcewen, O. Lyytikainen, G. Jacobsson, P. Collignon, D. Gregson, K. Laupland*

3780 **Clinical features and outcomes of patients with *Staphylococcus aureus* bacteraemia of unknown origin**
E. Minejima, E. Chan (Los Angeles, United States), K. Tan, C. Kelsom, P. Nieberg, A. Wong-Beringer*

3783 **Early-onset of bloodstream infections in a burn unit**
S. Scabini (Turin, Italy), A. Pensa, S. Mornese Pinna, C. Filippini, A. Curtoni, M. Stella, F. De Rosa, S. Corcione*

4133 **Comparative effectiveness of empiric antistaphylococcal penicillins versus cefazolin in methicillin-susceptible *Staphylococcus aureus* bacteraemia**
J. Cusumano (Warwick, United States), H. Appaneal, V. Lopes, K. Laplante, A. Caffrey*

4348 **Outcomes of bacteraemic and non-bacteraemic patients presenting to the emergency department**
R. Sparks (Neutral Bay, Australia), R. Chavada, C. Trethewy, A. Harada*

4517 **Antibiotic combination versus monotherapy for the treatment of *Pseudomonas aeruginosa* bacteraemia: a multi-centre retrospective study**
T. Babich (Petah Tikva, Israel), P. Naucler, J. Karlsson Valik, C. Giske, N. Benito, R. Cardona Corrales, A. Rivera, C. Pulcini, M. Fattah, J. Haquin, A. Macgowan, S. Grier, J. Gibbs, B. Chazan, A. Yanovskay, R. Ben-Ami, M. Landes, L. Nesher, A. Zaidman-Shimshovitz, K. Mccarthy, D. Paterson, E. Tacconelli, M. Buhl, J. Rodríguez-Baño, I. Morales, A. Oliver, E. Ruiz, Á. Cano Yuste, I. Machuca Sanchez, M. Gozalo Margüello, L. Martinez-Martinez, E. González-Barberá, I. Gomez Alfaro, M. Salavert, B. Beovic, A. Saje, M. Mueller-Premru, L. Pagani, V. Vitrat, D. Kofteridis, M. Zacharioudaki, S. Maraki, Y. Weissman, M. Paul, Y. Dickstein, L. Leibovici, D. Yahav*

4798 **The relationship between clinical outcomes and empirical antibiotic therapy in patients with community-onset Gram-negative bloodstream infection: a cohort study from a large teaching hospital**
A. Aryee (London, United Kingdom), P. Rockenschaub, M. Gill, A. Hayward, L. Shallcross*

6786 **Predictors of 30-day mortality rate in patients with *Pseudomonas aeruginosa* bacteraemia**
W. Rose (Madison, United States), L. Bagnell, L. Puzniak, L. Schulz*

7068 **Short-term and long-term mortality rates among patients with bloodstream infections receiving appropriate antibiotic therapy: a multi-centre, prospective cohort study**
S. Goepel (Tübingen, Germany), P. Beryl, S. Eisenbeis, F. Hölzl, M. Buhl, C. Cattaneo, A. Rohde, J. Falgenhauer, N. Kaeding, E. Kramme, A. Mischnik, S. Proske, S. Peter, P. Gastmeier, T. Chakraborty, M. Vehreschild, H. Seifert, J. Rupp, W. Kern, E. Tacconelli*

7084 **Enterococcal bacteraemia: epidemiology, clinical characteristics and causes of inappropriate treatment**
G. Grau Gómez (Terrassa, Spain), L. Boix-Palop, M. Lopez, U. Masats, M. Xercavins Valls, B. Dietl Gómez-Luengo, E. Calbo Sebastian*

7152 **Sepsis-3: a prospective clinical study of the clinical diagnosis and blood culture performance**
D. Yu, D. Unger, Å. Parke, C. Unge, C. Henning, J. Sunden-Cullberg, K. Strålin, V. Özenci (Stockholm, Sweden)*

8225 **Risk factors for mortality, intensive care unit admission, and bacteraemia of patients admitted with suspected infection in the emergency department**
V. D'Onofrio (Genk, Belgium), A. Meersman, S. Vijgen, P. Messiaen, R. Cartuyvels, I. Gyssens*

9009 **Community-Acquired Bacteraemia (CAB) in senior adults: risk factors, outcomes and correlation with frailty**
S. Ahmed (Leeds, United Kingdom), D. Kehlenbeck, S. Yaseen, G. Saiyad, J. Minton*

Session accepted as Paper Poster Session

Central nervous system infections

812 **Determination of pentraxin 3 levels in cerebrospinal fluid during central nervous system infections**
M. Zatta (Trieste, Italy), S. Di Bella, B. Bottazzi, F. Rossi, L. Segat, P. D'Agaro, M. Fabbiani, A. Mantovani, R. Luzzati*

862 **Multiplex detection of meningitis and encephalitis pathogens: a study from laboratory to the clinical**
Y. Zhou (Chengdu, China), W. Min Jin, T. Wu, S. Guo, Z. Meng, T. Wu, B. Ying*

1681 **Clinical utility of syndromic meningitis/encephalitis testing in children**
R. Yee (Los Angeles, United States), U. Pandey, C. Holifield, J. Flores, M. Fahit, S. Naccache, J. Dien Bard*

1683 **Rapid molecular diagnosis of *Neisseria meningitidis, Streptococcus pneumoniae, Listeria monocytogenes*, Enterovirus and parechovirus from blood in patients of the paediatric emergency department of a tertiary hospital**
M. Urrutikoetxea-Gutierrez (Bilbao, Spain), D. Montero Vazquez, M. Imaz Perez, E. Ugalde Zarraga, E. Garrote Llanos, G. Andrés, J. Díaz De Tuesta*

1884 **Viral meningitis in adults: what are we missing? The use of viral capture sequencing to detect pathogens in the cerebrospinal fluid of adults with meningitis**
F. Mcgill (Liverpool, United Kingdom), R. Tokarz, E. Thomson, A. Da Silva Filipe, S. Sameroff, S. Ashraf, I. Lipkin, C. Corless, C. Pattabiraman, M. Griffiths, A. Geretti, B. Michael, N. Beeching, D. Mckee, I. Hart, K. Mutton, A. Jung, A. Miller, T. Solomon*

2484 **Encephalitis in elderly patients in France, 2016-2019**
A. Mailles (Saint-Maurice, France), M. Martinot, E. Piet, C. Biron, G. Amandin, G. Isabelle, X. Argemi, S. Patrat-Delon, J. Stahl*

2642 **Unexpectedly high false positive *Haemophilus influenzae* rates using a meningoencephalitis syndromic PCR panel in two tertiary centres**
M. Zanella (Geneva, Switzerland), V. Hinic, A. Cherkaoui, D. Goldenberger, G. Renzi, A. Egli, J. Schrenzel*

2842 **Cerebrospinal fluid metabolomics profile in herpes virus type 1 encephalitis**
A. Mastrangelo (Campobasso, Italy), D. Franciotta, G. Scotti, L. Gorelik, R. Price, C. Roberta, T. Filippo, M. Morelli, A. Lazzarin, A. Castagna, P. Cinque*

3550 **Monitoring enterovirus human infections in Italy: molecular analysis of two recent outbreaks due to Echovirus 30**
S. Fontana (Rome, Italy), D. Cimini, K. Marinelli, G. Gori, V. Moroni, L. Collini, E. Pagani, E. Masi, G. Buttinelli, S. Fiore, C. Amato, V. Carraro, P. Stefanelli*

3586 **Which is the best progressive multifocal leukoencephalopathy risk stratification strategy in natalizumab-treated patients affected by multiple sclerosis?**
C. Prezioso (Rome, Italy), M. Zingaropoli, M. Iannetta, D. Rodio, M. Altieri, A. Conte, V. Vullo, M. Ciardi, A. Palamara, V. Pietropaolo*

3813 **Discrepancy results with meningitis/encephalitis panel FILMARRAY in cerebrospinal fluid**
C. Matovelle Ochoa (Zaragoza, Spain), J. Sahagún, S. Algarate, J. Gil, T. Khaliulina Ushakova, S. Salvo, R. Benito*

3883 **Detection of Enterovirus in cerebrospinal fluid 24 hours a day by a fully-automated PCR assay is associated with improved management of aseptic meningitis in adult patients**
M. Otto, C. Darles, J. Plantamura, S. Foucher, P. Benner, F. Janvier (Toulon, France)*

4081 **Opportunities to enhance empiric prescribing in community-acquired central nervous system infections among 187 US hospitals**
A. Babiker (atlanta, United States), S. Warner, M. Oshiro, S. Kadri*

4277 **Diagnostic accuracy of VIDISCA-NGS in patients with suspected central nervous system infections**
I. Van Zeggeren (Amsterdam, Netherlands), A. Edridge, D. Van De Beek, M. Deijs, S. Koekkoek, K. Wolthers, L. Van Der Hoek, M. Brouwer*

4743 **Comparison of three commercial sample-to-result platforms to an established real-time PCR assay for the detection of herpesviruses in cerebrospinal fluid**
R. Schuurman, E. Fries (Utrecht, Netherlands), S. Safak, N. Plantinga*

5015 **Human parechovirus 3 "outbreak" at a tertiary hospital**
M. Urrutikoetxea-Gutierrez (Bilbao, Spain), M. Imaz Perez, B. Elgoibar Álvarez, J. Rementeria Radigales, M. Cabrerizo, J. Díaz De Tuesta*

5527 **Do we really have to worry about acyclovir-induced nephrotoxicity?**
İ. Hasanoğlu (Ankara, Turkey), A. Kaya Kalem, B. Kayaaslan, Z. Atalay Altinkaynak, R. Guner*

5742 **Profile of neurological manifestations related to varicella zoster virus reactivation**
P. Girardie, J. Mansuy, C. Protin, F. Boneville, J. Pariente, P. Delobel, G. Martin-Blondel (Toulouse, France)*

6243 **The frequency and clinical implications of Epstein-Barr virus DNA in the cerebrospinal fluid of immunocompetent and immunodeficient patients diagnosed with meningoencephalitis**
N. Papic (Zagreb, Croatia), J. Begovac, A. Vince, S. Zidovec Lepej*

6861 **Characteristics and outcome of acute viral encephalitis in an infectious disease unit**
S. Hela (Kalaa Sghira, Tunisia), M. Wafa, I. Kooli, A. Toumi, A. Aouam, M. Chakroun*

7032 **Rapid syndromic panel for the diagnosis of infectious meningitis and encephalitis: a systematic review and meta-analysis of accuracy**
G. Menchinelli (Rome, Italy), B. Posteraro, M. Sanguinetti, T. Spanu, G. De Angelis*

7283 **Two-year experience of meningitis/encephalitis multiplex PCR assay on cerebrospinal fluids in comparison with conventional methods: advantages and disadvantages**
A. Calderaro, M. Buttrini, M. Martinelli (Parma, Italy), S. Montecchini, S. Covan, A. Ruggeri, M. Antonaci, F. Casula, M. Dell'Anna, S. Larini, F. Ferraglia, F. Pinardi, P. Montagna, M. Arcangeletti, F. De Conto, C. Chezzi*

7576 **Performance of the rapid molecular assay BioFire FilmArray Meningitis/Encephalitis for the diagnosis of CNS infections: a one-year evaluation in a tertiary care hospital**
O. Opota (Lausanne, Switzerland), Z. Naseri, R. Brouillet, L. Senn, G. Prod'Hom, G. Greub, K. Jaton*

7822 **Does tigecycline have a place in therapy for rickettsial infections of the central nervous system?**
A. Mastroianni (Cosenza, Italy), G. Guadagnino, S. Greco, V. Vangeli, S. De Santis, G. Apuzzo*

7911 **Procalcitonin serum concentration is higher in patients with meningococcal meningitis and/or invasive diseases: the MeningItaly study, preliminary results**
C. Pallotto (Perugia, Italy), A. Ripoli, F. Paciosi, C. Bolla, A. Parisini, C. Rescigno, M. Galli, S. Antinori, E. Nicastri, N. Bevilacqua, N. Capoluongo, D. Francisci, M. Pasticci, G. Palmiero, B. Cacopardo, M. Locatelli, N. Carannante, C. Malcontenti, C. Tiberio, F. Sbrana, S. Carbonara, D. Fiordelisi, P. Brambilla, A. Zoncada, G. Angioni, G. Bertolino, M. Bernardo, E. Sozio, C. Tascini*

7938 **Impact of a multiplex PCR in the management of viral meningitis**
G. Pean De Ponfilly (Paris, France), A. Chauvin, H. Benmansour, E. Lecorche, F. Mougari, A. Munier, S. Temim, J. Le Goff, E. Cambau, H. Jacquier*

7965 **Identification of central nervous system infection in children without cerebrospinal fluid pleocytosis using a syndromic meningitis/encephalitis panel**
L. Posnakoglou (Athens, Greece), T. Siahanidou, V. Syriopoulou, A. Michos*

7989 **Epidemiology of *Neisseria meningitidis* infections over a 17-year period in a tertiary hospital in Madrid, Spain**
D. Marcos Mencía (Madrid, Spain), A. García Caballero, R. Escudero Sánchez, P. Ruiz-Garbajosa, M. Moya, R. Canton Moreno, A. Sanchez Diaz*

8294 **Ceftaroline+rifampin versus vancomycin+rifampin in the treatment of methicillin-resistant *Staphylococcus aureus* meningitis in an experimental rabbit model**
D. Akdağ, T. Turhan, E. Bolat, G. Şanlıdağ, F. İşbilen, Ş. Aydemir, T. Yamazhan, H. Pullukcu, B. Arda (Izmir, Turkey), M. Isikgöz Tasbakan, B. Gokkilic, E. Kartal, H. Tipirdamaz Sipahi, S. Ulusoy, O. Sipahi*

8452 **Brain abscess in children: a retrospective single-centre experience**
D. Didovic (Zagreb, Croatia), I. Valenčak-Ignjatić, M. Vrdoljak, L. Stemberger Maric, S. Roglić, G. Tešović*

9135 **Modulation of toll-like receptors and interferons signalling pathways by sub lethal dose of scopolamine gives protection from Japanese encephalitis virus infection in embryonated chick model**
A. Bhattacharjee (Barrackpore, India), M. Saha*

9463 **Evaluation of on-site polymerase chain reaction technology for cerebrospinal fluid samples at Cork University Hospital versus referral to reference laboratories in suspected cases of meningitis or encephalitis**
R. Barry (Cork, Ireland), C. Dempsey, L. Barry, C. Hooton, C. Reynolds, M. Cremin, S. Felsenstein, D. Corcoran*

Session accepted as 1-Hour Oral Session

Challenges in the management of community-acquired pneumonia

1578 **Aspirin reduces cardiovascular events in patients with pneumonia: a prior events rate ratio analysis in a large primary care database**
F. Hamilton (Bristol, United Kingdom), D. Arnold, W. Henley, R. Payne*

1764 **Epidemiology of *Clostridioides difficile* infections among hospitalised community-acquired pneumonia patients who received empiric treatment with ceftriaxone plus a macrolide**
K. Lapensee, H. Le, S. Villano, T. Lodise (Watervliet, United States)*

3691 **Impact of positive microbiological testing on antimicrobial de-escalation and clinical outcomes in community-acquired pneumonia**
G. Abelenda Alonso (Madrid, Spain), A. Rombauts, C. Gudiol, C. Ardanuy Tisaire, Y. Meije Castillo, L. Ortega, M. Clemente, J. Niubò, J. Carratalà*

6817 **Evaluation of total and excess treatment duration for community-acquired pneumonia: experience from a tertiary centre in the UK**
L. Marvulli (Pavia, Italy), R. Santos, J. Lilley, C. Serra, N. Brown, T. Gouliouris*

7564 **Host- and pathogen-related factors for acute cardiac events in pneumococcal pneumonia**
A. Rombauts (Barcelona, Spain), G. Abelenda Alonso, J. Càmara, A. González Díaz, E. Sastre-Escolà, L. Lorenzo-Esteller, C. Gudiol, C. Ardanuy Tisaire, J. Carratalà*

Session accepted as Paper Poster Session

Community-acquired respiratory infections

174 **Primary care re-consultation after hospitalisation for community-acquired pneumonia in England: a large population-based cohort study**
V. Baskaran (Nottingham, United Kingdom), W. Lim, T. Mckeever*

193 **Antimicrobial susceptibility of *Streptococcus pneumoniae* strains, isolated from children carriers after PCV10 in Bulgaria**
M. Malcheva (Sofia, Bulgaria), I. Simeonovski, V. Levterova, N. Brankova, T. Kantardjiev*

235 **Effects of previous antibiotic exposure on the clinical course of pneumonia in the elderly: a single-centre prospective observational study**
S. Surme, I. Balkan, O. Bayramlar, R. Kara Ali, B. Mete, G. Can, F. Tabak, N. Saltoglu (Istanbul, Turkey)*

652 **Correlation between serum C-reactive protein levels and CURB-65 in elderly patients with community-acquired pneumonia**
W. Nseir (Poriya, Israel), A. Amara, R. Farah, T. Saidahmad*

937 **The optimal strategy of empirical antibiotic therapies for non-severe community-acquired pneumonia: a bayesian network meta-analysis of randomised controlled trials**
J. Lee, S. Moon (Jeju, South Korea)*

1564 ***Bordetella holmesii* in suspected cough: a frequent pathogen?**
S. Trombert Paolantoni (Saint Ouen L'aumone, France), S. Guillot, S. Brisse, J. Toubiana*

1936 **Comparison of clinical findings and risk factors of community-acquired and nosocomial *Legionella* pneumonia cases in Konya, Turkey**
H. Turan Özden (Konya, Turkey), K. Ucar Karabulut*

2005 **Single-shot azithromycin in treatment of *Legionella pneumophila*: 18-year experience at the Vienna General Hospital, Austria**
M. Karer (Vienna, Austria), M. Kussmann, M. Obermüller, H. Burgmann, H. Lagler*

2253 **Prevalence and clinical characteristics of *Mycoplasma pneumoniae* in Navarra (Spain), 2014-2018**
Á. Ana Isabel, A. Navascués Ortega, A. Aguinaga Perez, J. Castilla Catalan, C. Ezpeleta Baquedano (Pamplona, Spain)*

2342 **Comparative effectiveness of macrolides, fluoroquinolones or combination therapy for the treatment of Legionnaires' disease in the US Department of Veterans Affairs health system**
V. Stevens (Salt Lake City, United States), S. Gamage, A. Jasper, G. Roselle, N. Safdar*

2364 ***In vitro* activities of ceftaroline and comparator agents against bacterial pathogens frequently causing community-acquired respiratory tract infections in patients from Latin America: ATLAS surveillance programme 2016-2018**
J. Karlowsky, M. Hackel (Schaumburg, United States), S. Bouchillon, G. Stone, D. Sahm*

2392 **High burden and undetected clusters of pneumococcal disease in long term care in Ontario, Canada**
A. Mcgeer (Toronto, Canada), W. Rudnick, W. Demzcuk, W. Gold, I. Kitai, S. Krjaden, R. Lovinsky, I. Martin, M. Muller, J. Powis, N. Rau, G. Tyrrell, A. Simor, T. - Tibdn*

2395 **Shorter duration of antibiotherpy in super-infection pneumopathy occurring in viral infection**
S. Bessis (Paris, France), M. Trichet, A. Beresteanu, M. Matt, B. Davido, A. Dinh*

2517 **Surveillance for epidemic of *Mycoplasma pneumoniae* and macrolide resistance (A2063G and A2064G) using consecutive multiplex real-time PCR in Korea**
K. Roh (Goyang, South Korea), J. Park, Y. Yang, Y. Kim, H. Lee, S. Hong*

2551 **Ceftaroline for severe community-acquired pneumonia: a real-world two-centre experience in Italy and Spain**
M. Bassetti, A. Russo (Pisa, Italy), C. Cilloniz Campos, D. Giacobbe, A. Vena, R. Amaro, E. Graziano, A. Soriano, A. Torres*

2705 **Concordance of early and late endpoints for community-acquired bacterial pneumonia (CABP) trials**
S. Bart (Silver Spring, United States), S. Nambiar, R. Gopinath, D. Rubin, J. Farley*

2933 **Methicillin-susceptible *Staphylococcus aureus* in community-acquired pneumonia: risk factors and outcomes**
C. Cilloniz Campos (Barcelona, Spain), E. Moreno, C. Dominedò, C. Garcia Vidal, C. Vargas, A. Gabarrus, J. Becerril, C. Cardozo, D. Tovar, A. Torres*

2951 **Incidence and risk of hospitalised pneumococcal pneumonia among Catalonian adults with distinct underlying medical conditions**
O. Ochoa-Gondar (Tarragona, Spain), A. Vila-Córcoles, I. Hospital-Guardiola, A. Vila-Rovira, C. De Diego, E. Satue*

3306 **Antibiotic treatment for paediatric outpatients with community-acquired pneumonia: findings from 10 years of prescribing habits in Italy**
P. Costenaro (Marostica, Italy), A. Cantarutti, E. Barbieri, A. Scamarcia, A. Oletto, P. Sacerdoti, R. Lundin, L. Cantarutti, C. Giaquinto, D. Dona'*

3327 **Pneumococcal serotypes distribution in older adults hospitalised with CAP using the UAD Test (The CAPA study)**
P. España, R. Menendez (Valencia, Spain), A. Torres, J. Fernández Villar, J. Marimon, A. Martínez De La Fuente, J. López-Hontangas, F. Marco Reverte, F. Vasallo Vidal, M. Ercibengoa, I. Cifuentes, C. Méndez*

3328 **Beneficial impact of childhood pneumococcal vaccination on penicillin- and multidrug-resistance in adult invasive pneumococcal disease (1994-2018)**
J. Càmara (Barcelona, Spain), A. González Díaz, I. Grau, F. Tubau, L. Calatayud, M. Cubero, J. Yuste, R. Pallares, M. Domínguez Luzon, J. Linares, C. Ardanuy Tisaire*

3334 **Evolution of pneumococcal serotypes causing CAP in adults by co-morbidities in Spain using the UAD test (the CAPA study)**
P. España, R. Menendez, A. Torres (Barcelona, Spain), J. Fernández Villar, J. Marimon, A. Martínez De La Fuente, J. López-Hontangas, F. Marco Reverte, F. Vasallo Vidal, M. Ercibengoa, I. Cifuentes, C. Méndez*

3372 **Effectiveness of the 23-valent pneumococcal polysaccharide vaccine against vaccine serotype pneumococcal pneumonia in adults**
H. Lawrence (Nottingham, United Kingdom), T. Mckeever, C. Trotter, C. Rodrigo, P. Daniel, H. Pick, D. Ashton, V. Baskaran, C. Sheppard, S. Eletu, D. Litt, N. Fry, S. Rose, W. Lim*

3525 **Serotype, antimicrobial resistance and virulence profile of invasive *Streptococcus pneumoniae* isolates in a nation-wide surveillance study in Lebanon**
L. Reslan (Beirut, Lebanon), S. Khafaja, M. Moumneh, M. Finianos, M. Darwish, C. Boutros, G. Araj, G. Matar, G. Dbaibo*

3696 **Accuracy of emergency department diagnosis of community-acquired pneumonia**
A. Bloch (Brunswick, Australia), V. Sundarajan, O. Wawryk, A. Siddiqui, A. Attreya, K. Visvanathan*

3794 **If breaking a hip feels like a concern for the elderly, then getting pneumonia should be twice as concerning!**
L. Grammatico-Guillon (Tours, France), H. Coralie, C. Gaborit, J. Mizgerd, A. Guillon*

3874 **The effect of live attenuated influenza vaccine on pneumococcal colonisation densities among children aged 24-59 months in Gambia**
C. Peno (Edinburgh, United Kingdom), E. Armitage, M. Clerc, C. Balcazar, Y. Jagne, S. Drammeh, S. Jarju, H. Sallah, E. Senghore, D. Dockrell, E. Clarke, B. Kampmann, D. Bogaert, T. De Silva*

3995 ***Legionella pneumophila*** **sqPCR in serum and respiratory samples as a marker of Legionnaires' disease severity**
C. Allam (Lyon, France), N. Fessy, C. Ginevra, L. Beraud, J. Chastang, F. Ader, G. Descours, S. Jarraud*

4257 ***Burkholderia*** **spp. and Gram-negative non-fermenters in cystic fibrosis patients in Belgium: 2012-2018**
F. Echahidi, C. Peeters, E. De Canck, I. Wybo, D. Pierard (Brussels, Belgium), P. Vandamme*

4441 **Resistance trends among the common bacterial causes of community-acquired lower respiratory tract infection in the UK and Ireland, 2008-2018**
C. Horner (Birmingham, United Kingdom), S. Mushtaq, D. Livermore*

4505 **Invasive pneumococcal disease in the Comunidad Valenciana, Spain, 2011-2019**
M. Garrido Jareño (Valencia, Spain), A. Gil Brusola, N. Lozano Rodríguez, O. Sabalza, J. Frasquet, J. López-Hontangas*

4684 **Population-based incidence and mortality of community-acquired pneumonia in Germany**
R. Sprenger, F. Leverkus, J. Walker, D. Haeckl, C. Von Eiff (Berlin, Germany), C. Theilacker, J. Schiffner-Rohe*

5355 ***Nocardia*** **Infection over 10 years (2009-2019) in a Greek tertiary university hospital**
E. Kalogeropoulou, F. Kontos (Athens, Greece), S. Damianidou, P. Tsilikis, K. Orlandou, B. Basilopoulou, P. Varda, M. Kostoula, S. Pournaras*

5702 **An audit of community-acquired pneumonia antimicrobial compliance using a mobile audience response system (ARS) care bundle in an Irish hospital**
B. O'Kelly (Dublin, Ireland), M. Regan, A. Rueda Benito, K. Finan*

5836 **Evaluation of the clinical economic efficacy of the antibiotic therapy of inpatients with community-acquired pneumonia**
A. Demchuk (Vinnytsia, Ukraine), Y. Mostovoy*

5869 **Does herd immunity from conjugate vaccines alter the epidemiology of invasive pneumococcal disease in adults?**
A. Mcgeer (Toronto, Canada), A. Plevneshi, K. Hassan, W. Rudnick, S. Nayani, N. Farshait, W. Gold, K. Katz, K. Ostrowska, J. Powis, D. Ricciuto, D. Yamamura, G. Tyrrell*

6444 **Persistence of serotype 19F and the importance of non-vaccine serotypes in paediatric non-invasive pneumococcal pneumonia in Portugal: 2015-2018**
C. Silva-Costa, J. Gomes-Silva, M. Ramirez (Lisbon, Portugal), J. Melo-Cristino*

6450 **Impact of recent vaccine schedule changes on pertussis epidemiology in France**
J. Paireau, S. Guillot, F. Aït El Belghiti, S. Trombert Paolantoni, V. Jacomo, H. Salje, S. Brisse, D. Levy Bruhl, S. Cauchemez, J. Toubiana (Paris, France)*

6480 **Improving antibiotic prescribing for community-acquired pneumonia in resource-limited settings: pilot implementation of quality standards in a provincial hospital in northern Vietnam**
N. Do (Hanoi, Vietnam), R. Li, H. Dinh, H. Nguyen, M. Dao, T. Nghiêm, B. Nadjm, N. Luong, T. Cao, D. Le, F. Cluzeau, C. Ngo Quy, H. Chu, Q. Vu, C. Roberts, H. Rogier Van Doorn*

6577 **Epidemiology of serotypes of** ***Streptococcus pneumoniae*** **in patients older than 18-years in Russia**
R. Kozlov (Smolensk, Russian Federation), A. Muraviov, A. Chagaryan, A. Kurkova, N. Ivanchik*

6587 **Trends in invasive pneumococcal disease in Italy, 2010-2018**
R. Camilli (Rome, Italy), M. Del Grosso, F. D'Ambrosio, M. Monaco, F. Pimentel De Araujo, G. Errico, S. Boros, R. Urciuoli, M. Caporali, M. Del Manso, F. D'Ancona, S. Iannazzo, F. Riccardo, A. Pantosti*

6711 **Evaluation of plasma lipocalin-2 as a biomarker of community-acquired pneumonia**
A. Vergara (Barcelona, Spain), L. Boix-Palop, E. Padilla, E. Calbo, A. Blanco Suárez, P. Perez, J. Vila Estape, C. Casals-Pascual*

6728 **Predictors of mortality in invasive pneumococcal disease: a meta-analysis**
T. Demirdal (Izmir, Turkey), P. Sen, B. Emir*

6734 **Characterisation of** ***Staphylococcus aureus*** **isolates collected from children with respiratory tract infections in Tangier, Morocco**
N. Mourabit (Tangier, Morocco), A. Arakrak, M. Bakkali, M. Bes, F. Laurent, A. Laglaoui*

6870 **Study of the relationship of infections of** ***Chlamydophila pneumoniae*** **and** ***Mycoplasma pneumoniae*** **with recurrent course of respiratory sarcoidosis**
D. Antipushina, M. Smirnova, A. Zaytsev (Moscow, Russian Federation)*

6946 **Characterisation of** ***Mycoplasma pneumoniae*** **and** ***Chlamydophila pneumoniae*** **infections in Palestinian children older than 5 years of age**
J. Jeries (Bethlehem, Palestine), A. Neirokh, R. Bakri, N. Handal, H. Marzouqa, M. Hindiyeh*

7041 **Seroprevalence of** ***Bordetella pertussis*** **in Tunisian adults**
N. Habiba (Tunis, Tunisia), M. Osman, A. Mbarek, M. Ben Moussa*

7644 **An extreme chain reaction-based multiplex assay for detection of group A/C/G streptococci directly from throat swab specimens**
L. Gong (Ann Arbor, United States), B. Keusch, M. Olson, M. Carey, A. Ripley, B. Green, D. Kolk, M. Mastronardi, B. Wu, S. Brahmasandra*

7655 **Aging influences effector functions of neutrophil granulocytes in** ***Pseudomonas aeruginosa*** **lung infection**
S. Charline, N. Cramer, L. Müller, O. Danov (Hannover, Germany), B. Tümmler, A. Braun, K. Sewald, C. Brandenberger, S. Dehmel, S. Wronski*

8012 **Prevalence of *Mycoplasma pneumoniae* infections during six years (2014-2019) in two hospitals of Saint Petersburg**
O. Kameneva, S. Morozova, N. Kameneva, V. Zhukova, K. Kosyakova (Saint Petersburg, Russian Federation)*

8030 **The role of procalcitonin as a predictor of severity, prognosis and appropriate empirical antibiotic therapy in community-acquired pneumonia of bacterial aetiology**
A. Milia (Florence, Italy), L. Suardi, C. Nozzoli, F. Pieralli*

8393 **Impact of the use of C-reactive protein in micro-methods on the prescription of antibiotics in case of suspected respiratory infection in children and adults in ambulatory care in France**
R. Touitou, C. Levy, S. Béchet, E. Pinto, A. Laplante, J. Lion-Altmayer, B. Trincard, C. Jung, R. Cohen (Créteil, France)*

8506 **Excessive antibiotic use and costs in hospitalised adults with chronic heart failure**
O. Zorya, S. Rachina (Moscow, Russian Federation), A. Bobylev, G. Hewathanthirige*

8697 **Treatment outcome and clinical characteristics of patients with community-acquired pneumonia treated in an infectious disease intensive care unit**
M. Popović (Zagreb, Croatia), R. Novak, M. Kutlesa, M. Santini, B. Baršić, V. Krajinovic*

8875 **New trends in microbial aetiology of severe community-acquired pneumonia in intensive care unit**
A. Chlilek (Nîmes, France), C. Paris, R. Stephan, C. Roger, S. Barbar, J. Lefrant, H. Marchandin, J. Lavigne, L. Muller*

8990 **Severe community-acquired pneumonia in the Czech Republic**
H. Bartos (Usti nad Labem, Czech Republic), O. Dzupova*

9104 **Secretion of TNFα by human macrophages is dependent of the sequence type of clinical *Legionella pneumophila* isolates**
J. Guillemot (Villeurbanne, France), C. Ginevra, P. Doublet, A. Chapalain, S. Jarraud*

9681 **Levels of evidence supporting European and American community-acquired pneumonia guidelines**
J. Ferreira Freitas Coimbra (Porto, Portugal), S. Tejada Magraner, L. Campogiani, J. Rello*

Session accepted as Paper Poster Session

Diagnosis of tuberculosis and drug resistance

1699 **One day detection of live *Mycobacterium tuberculosis* from sputum by measuring heat-induced MPT64 secretion with ultra-sensitive ELISA**
R. Takeuchi (Izunokuni-shi, Japan), W. Wang, S. Jain, Y. Jiang, S. Watanuki, Y. Ohtaki, K. Nakaishi, S. Watabe, P. Lu, E. Ito*

1725 **Interim analysis: a large-scale clinical evaluation of QMAC-DST for rapid drug susceptibility testing of *Mycobacterium tuberculosis***
K. Seok, S. Kim (Seoul, South Korea), J. Na, S. Lee, E. Jo, H. Kim, D. Kim, S. Kwon*

1902 **Application of matrix-assisted laser desorption ionisation: time of flight mass spectrometry for *Mycobacterium tuberculosis* Beijing and Non-Beijing genotyping**
F. Yi (Chengdu, China)*

2125 **Evaluation of the cobas MTB and MTB RIF/INH assays on samples from Sierra Leone and Germany at a supranational reference laboratory for tuberculosis serving both low- incidence and high-burden settings**
D. Nadarajan (Sülfeld, Germany), D. Sievert, M. Kernbach, R. Kamara, L. Foray, M. Merker, A. Kuchta, J. Lau, M. Njoya, S. Krishnamurthy, A. Witt, K. Kranzer, F. Maurer*

2347 **Evaluating the effectiveness of current microbiological tools on time to diagnosis of pulmonary tuberculosis**
O. Umerah (Leicester, United Kingdom), H. Patel, R. Verma, N. Perera, M. Barer, G. Woltmann, P. Haldar*

2588 **A novel standardised artificial sputum for external quality control of the whole TB-diagnostic workflow**
M. Beutler (Gauting, Germany), U. Antonenka, F. Gerbl, M. Mihalic, S. Plesnik, E. Romancenco, S. Hofmann-Thiel, H. Hoffmann*

2589 **Multiplex detection of SNPs conferring rifampicin resistance in *Mycobacterium tuberculosis***
F. Nazé (Gembloux, Belgium), B. Gicquel, P. Mertens, L. Avrain*

2612 **Head-to-head comparison of analytical sensitivities of BD MAX MDR-TB, Xpert MTB/Rif Ultra and FluoroType MTB using human and artificial sputum**
M. Beutler (Gauting, Germany), S. Plesnik, M. Mihalic, L. Olbrich, N. Heinrich, S. Schumacher, M. Lindner, I. Koch, W. Grasse, C. Metzger-Boddien, S. Hofmann-Thiel, H. Hoffmann*

3111 **Contaminating microflora during examination for tuberculosis: saprophytes or potential pathogens?**
A. Lyamin (Samara, Russian Federation), D. Ismatullin, A. Zhestkov, A. Kovalyov, T. Persiyantseva, D. Davydova, A. Kozlov*

3335 **Clinical evaluation of a cartridge-based DNA extraction method for the whole molecular TB-diagnostic workflow**
M. Beutler (Gauting, Germany), M. Mihalic, S. Plesnik, A. Homann, N. Paust, M. Eckart, V. Allerheiligen, D. Czurratis, B. Maharjan, B. Shrestha, S. Hofmann-Thiel, H. Hoffmann*

3381 **DNA thermo-protection facilitates whole genome sequencing of mycobacteria direct from clinical samples by ONT MinION**
S. George, Y. Xu, G. Rodger, M. Morgan, N. Sanderson, S. Hoosdally, S. Thulborn, P. Rathod, G. Smith, S. Walker, T. Peto, D. Crook, K. Dingle (Oxford, United Kingdom)*

3630 **Analysis of analytical performances of the new MDR/MTB ELITe MGB kit for the detection of *Mycobacterium tuberculosis* complex and rifampicin- and isoniazid-associated mutations in comparison with the MTB ELITe MGB kit**
S. Svraka-Latifovic (Hilversum, Netherlands), L. Bakker, C. Timmerman, J. Dorigo-Zetsma*

3758 **CRISPR-based rapid and ultra-sensitive diagnostic test for smear-negative or sputum-scarce tuberculosis using bronchoalveolar lavage fluid: a prospective, multi-centre study in China**
X. Zhou (Shanghai, China), J. Ai, W. Zhang*

4208 **Two-hours direct detection of *Mycobacterium tuberculosis* complex in clinical samples by molecular method based on real-time PCR**
Cristina Escolar (Zaragoza, Spain), J. Comín, A. Picó, M. Strunk, H. Alonso, S. Samper*

4295 **Evaluation of BD MAX multidrug-resistant tuberculosis assay for detection of *Mycobacterium tuberculosis* complex in clinical specimens and identification of genetic resistance markers**
S. Hofmann-Thiel (Gauting, Germany), S. Plesnik, M. Mihalic, M. Beutler, H. Hoffmann*

4487 **Improved detection of acid-fast bacteria using an automated slide scanner with integrated deep learning analysis**
L. Horvath, S. Haenselmann (Altlussheim, Germany), H. Mannsperger, S. Degenhardt, K. Last, S. Zimmermann, I. Burckhardt*

4637 **Evaluation of the performance of CSF pyrosequencing in the diagnosis of TB meningitis- a single-centre retrospective diagnostic accuracy study**
K. Ajbani, M. Kazi, U. Agrawal (Mumbai, India), R. Soman, A. Shetty, A. Sunavala, C. Rodrigues*

5110 **MYCO-TB kit: rapid and efficient digestion and decontamination method for the detection of mycobacteria in extrapulmonary specimens**
F. Bisognin (Bologna, Italy), S. Felici, G. Lombardi, C. Vocale, G. Biundo, M. Re, P. Dal Monte*

5245 **Identification and discrimination of *Mycobacterium tuberculosis* and *Mycobacteroides abscessus* complex species directly from Mycobacteria Growth Indicator Tube (MGIT) culture media by Orbitrap ultra high-resolution mass spectrometry**
A. Bajaj, J. Freeke (Vantaa, Finland), M. Hutchins, B. Stielow, A. Barker*

5260 **From DNA to diagnosis: a rapid, next-generation sequencing pipeline for detecting multidrug-resistant *Mycobacterium tuberculosis* mutations**
L. Daum (San Antonio, United States), M. Agonafir, J. Eicher, I. Wright, N. Wood, S. Travers, J. Rodriguez, B. Fourie, G. Fischer*

5724 **Time to positivity for mycobacterial culture as a measurement of bacillary load in clinical practice**
M. Jonsson Nordvall (Linköping, Sweden), A. Bornefall, V. Kholod, B. Andersson, K. Niward, T. Schön*

6571 **Routine use of genotype Genotype MTBDR*sl* assay on clinical samples in a high TB burden setting in South Africa: a descriptive analysis**
K. Lutchminarain (Durban, South Africa), A. Kajee, N. Mvelase, K. Swe Swe Han*

6756 **Rapid simultaneous detection of TB and first line drugs gene mutations onto direct paediatric samples**
C. Russo (Rome, Italy), L. Gentile*

6932 **Xpert MTB/RIF Ultra: multi-centre evaluation of result "TRACE" in tuberculosis diagnosis**
S. Torri (Milan, Italy), C. Farina, P. Cichero, A. Lombardi, F. Morini, E. Sala, F. Gurrieri, V. Rognoni, C. Perno, E. Mazzola*

7205 **Evaluation of Myco-TBTM kit for decontamination of urine and stool specimens to detect *mycobacteria***
R. Grossi (Rome, Italy), A. Careddu, R. Nicotra, M. Sanguinetti, M. Sali*

7237 **One-year evaluation of Genelead VIII combined to Deeplex-MycTB to detect rapidly the genotype and the resistance profile of *Mycobacterium tuberculosis complex* directly from clinical samples**
I. Bonnet (Paris, France), S. Goumghar, G. Millot, J. Jaffré, A. Aubry, J. Robert, W. Sougakoff*

7836 **Evaluation of the MDR/MTB ELITe MGB assay for the detection of *Mycobacterium tuberculosis complex* and resistance to rifampicin and isoniazid**
V. Ok (Paris, France), L. Gandy, S. Goumghar, G. Millot, A. Aubry, J. Robert, W. Sougakoff*

7876 **Performance assessment of MDR/MTB ELITe MGB Kit for tuberculosis diagnosis**
E. Hodille (Lyon, France), Y. Benito, T. Delque, C. Genestet, I. Fredenucci, J. Rasigade, F. Laurent, G. Lina, O. Dumitrescu*

8278 **Xpert MTB/RIF assay useful for paediatric patient tuberculosis disease diagnosis**
V. Lora (Puebla, Mexico)*

8408 **Performance of XpertMTB/RIF Ultra assay on respiratory and extra-respiratory specimens in a high-resource setting with a low TB prevalence**
C. Martín Higuera (Madrid, Spain), M. Ruiz Serrano, C. Toro-Diez, M. Tato, M. Simon, D. Domingo, P. Lopez-Roa*

9392 **The concordances of genotypic and phenotypic drug susceptibility testing of *Mycobacterium tuberculosis* isolates from MDR TB patients**
C. Nelly (Chisinau, Moldova), S. Alexandru, A. Codreanu, N. Turcan, E. Noroc, V. Vilc, A. Donica, E. Chesov, D. Chesov, V. Crudu*

9515 **Direct detection of *Mycobacterium tuberculosis complex* in clinical specimens from patients in Norway by two different polymerase chain reaction tests**
I. Szpinda (Oslo, Norway), J. Kaur, M. Hagbø, S. Hamsund, O. Wold, T. Tonjum*

Session accepted as Mini-oral ePoster Session

Different aspects of UTI management

1136 **Effectiveness and safety of aminoglycosides for the empirical treatment of patients with upper urinary tract infection**
M. Elbaz (Hulon, Israel), H. Zadka, A. Weiss-Meilik, R. Ben-Ami*

1481 **Obstructive pyelonephritis associated with ureteral stones: microbiology, treatment and prognosis**
J. Won, J. Eom, Y. Cho, Y. Jang (Incheon, South Korea)*

1517 **Five versus seven days nitrofurantoin for urinary tract infections in women with diabetes: a non-inferiority study**
K. Hendriks-Spoor (Hilversum, Netherlands), T. Ten Doesschate, F. Wille, T. Verheij, M. Bonten, C. Van Werkhoven*

1717 **The effectiveness of nitrofurantoin, fosfomycin and trimethoprim for cystitis in relation to renal function**
T. Ten Doesschate (Utrecht, Netherlands), E. Van Haren, R. Wijma, B. Koch, M. Bonten, C. Van Werkhoven*

2049 **Antimicrobial treatment and treatment duration for urinary tract infections in adult males**
K. Farrell, A. Brænd, I. Gágyor, F. Jansåker, G. Hayward, M. Skow, V. Santiago, M. Tandan, I. Vik, A. Vellinga (Galway, Ireland)*

4678 **Clinical and bacteriological outcome in urinary tract infections caused by ESBL-producing *Enterobacterales* and characterisation of isolated pathogens: a prospective, multi-centre study**
H. Montelin (Uppsala, Sweden), A. Camporeale, A. Hallgren, M. Vading, C. Giske, T. Tängdén*

4693 **The urinary pharmacokinetics of nitrofurantoin in patients with uncomplicated urinary tract infections: interim analysis**
R. Wijma, B. Koch, T. Van Gelder, E. Van Haren, H. Karim, S. Croes, A. Muller (The Hague, Netherlands)*

7980 **Examining the urinary tract infection patient journey to identify opportunities to enhance the role of community pharmacists**
N. Peiffer-Smadja (Paris, France), R. Allison, L. Jones, D. Lecky, C. Mcnulty, R. Ahmad*

Session accepted as Paper Poster Session

Emerging Gram-negative infections: from A to S

3132 **Piperacillin-tazobactam versus carbapenem for the treatment of bloodstream infection caused by CTX-M-type ESBL-producing *Enterobacteriaceae***
L. Suardi (Florence, Italy), F. Lagi, E. Riccobono, T. Giani, A. Moggi Pignone, A. Morettini, C. Nozzoli, F. Pieralli, A. Berni, G. Rossolini, A. Bartoloni, F. Bartalesi*

3275 **Comparison of pneumonia and bacteraemia caused by *Stenotrophomonas maltophilia* : analysis of risk factors, clinical outcomes and impact on antibiotic resistance**
W. Lee (Taipei, Taiwan), F. Chen*

3516 **Non-carbapenem beta-lactams for the treatment of *Acinetobacter baumannii* bacteraemia: a multi-centre retrospective analysis**
G. La Martire (Paris, France), V. Fihman, A. Galy, D. Le Pluart, L. Noussair, A. Lecapitaine, E. Canoui, A. Munier, C. Richaud, C. Wemmert, R. Lepeule*

5232 **Use of N-acetylcysteine in critically ill patients with septic shock caused by carbapenem-resistant *Klebsiella pneumoniae* and *Acinetobacter baumannii*: a case-control study**
A. Oliva (Rome, Italy), A. Bianchi, A. Russo, G. Ceccarelli, F. Aloj, D. Alunni Fegatelli, C. Mastroianni, M. Venditti*

7214 **First case of osteomyelitis caused by hypervirulent *Klebsiella pneumoniae* spread within a family in Korea**
J. Chae (Seoul, South Korea), C. Lee, W. Choe, H. Lee, Y. Sohn*

7501 **Surveillance culture-guided empirical therapy for febrile neutropaenia: low prevalence of inappropriately treated Gram-negative bloodstream infections**
J. De La Court (Amsterdam, Netherlands), J. Heijmans, J. Janssen, K. Sigaloff, R. Schade*

8089 **Ceftazidime-avibactan monotherapy for 7 days as treatment of KPC carbapenemase-producing *Enterobacteriaceae* bacteraemia in severely immunosuppressed patients**
F. Herrera, E. Temporiti, M. Jorge, A. Rearte (Buenos Aires, Argentina), F. Nicola, S. Zerboni, F. Bues, R. Rojas, P. Bonvehi*

8729 **Differences in clinical characteristics and prognosis of patients with AmpC-producing *Enterobacteriaceae* versus *Escherichia coli* bloodstream infection**
A. Sousa (Vigo, Spain), M. Pérez-Rodríguez, M. Suárez, P. Diéguez, O. Lima, A. Cabaleiro, A. Otero, F. Vasallo Vidal, R. Longueira, A. López-Domínguez, A. Nodar, M. Crespo*

Session accepted as 2-Hour Oral Session

Endocarditis: what's new?

2898 **One-stage extraction and replacement of infected cardiac implantable electronic devices**
V. Attanasio, S. De Vivo, C. Rescigno, S. Severino, R. Pisapia, C. Sordelli, N. Capoluongo, M. Bernardo, G. Palmiero, M. Di Luca, C. Pallotto (Perugia, Italy), C. Tascini*

3049 **Does early de-escalation to anti-staphylococcal beta-lactams impact the duration of bacteraemia in patients with methicillin-susceptible *Staphylococcus aureus* endocarditis?**
M. Wungwattana (Portland, Maine, United States), M. Mangino, G. Ben, P. Stogsdill, A. Casapao*

3150 **Clinical and epidemiological characteristics of infective endocarditis with negative blood cultures: a multi-centre case-series in the south of Spain**
L. Suardi (Florence, Italy), L. Lopez-Cortes, L. Rafael, J. Ruiz Morales, A. Plata Ciezar, J. De La Torre Lima, C. Hidalgo Tenorio, D. Vinuesa García, F. Martinez-Marcos, A. De Alarcón, G. Ojeda, J. Reguera Iglesias, J. Gálvez-Acebal*

3293 **Six versus four weeks of intravenous antibiotic treatment for *Staphylococcus aureus* endocarditis**
S. Douiyeb (Amsterdam, Netherlands), A. Samson, N. Roescher, A. Meinders, T. Van Der Vaart, J. Van Der Meer, W. Baig, J. Wu, A. Prats, D. Harvey, R. Gillott, K. Sigaloff, J. Sandoe*

3833 **Comparative outcomes of cefazolin versus anti-staphylococcal penicillins for treatment of methicillin-susceptible *Staphylococcus aureus* endocarditis: a prospective multi-centre cohort study**
R. Lecomte (Nantes, France), A. Bourreau, D. Colin, N. Issa, P. Le Turnier, B. Gaborit, M. Chauveau, T. Le Tourneau, N. Asseray Madani, F. Raffi, F. Camou, D. Boutoille*

4837 **Anaemia is associated with mortality in patients with left-sided endocarditis: a POET sub-study**
M. Pries-Heje (Copenhagen, Denmark), N. Ihlemann, N. Bruun, E. Fosbøl, N. Tønder, C. Moser, K. Iversen, H. Bundgaard*

5386 **Mural endocarditis from a prospective national registry: the GAMES series**
A. Fernandez-Cruz (Madrid, Spain), P. Muñoz, M. Valerio Minero, A. Delgado, E. Gutiérrez, A. De Alarcón, M. Gutierrez-Cuadra, J. Miró Meda, M. Goenaga, G. Ojeda, M. Montejo, F. Martinez-Marcos, A. Ramos Martínez*

7045 **Analysis of the practices of the multidisciplinary consultation meeting on infectious endocarditis**
L. Sauvat (Clermont-Ferrand, France), M. Rosburger, A. Mulliez, F. Robin, M. Farhat, G. Clerfond, M. Vidal*

8150 **Contrast-enhanced ultrasound for the detection of abdominal complications in infective endocarditis**
G. Paul (Stuttgart, Germany), V. Priesner, G. Michels, C. Hohmann, R. Pfister, N. Mader, L. Blanke, M. Ohler, E. Piepenbrock, J. Rybniker, C. Lehmann, G. Fätkenheuer, N. Jaspers, N. Jung*

9207 **Early experience with percutaneous vegetation suction (Penumbra) versus valve replacement surgery for right-sided infective endocarditis in people who inject drugs**
M. Veve (Knoxville, United States), Y. Akhtar, P. Mckeown, M. Morelli, M. Shorman*

Session accepted as Paper Poster Session

Everything you always wanted to know about endocarditis

65 **Impact of referral bias on prognostic assessment in infective endocarditis: insights from a population-based cohort**
M. Collonnaz (Vandoeuvre Les Nancy, France), M. Erpelding, F. Alla, F. Goehringer, F. Delahaye, B. Iung, V. Le Moing, B. Hoen, C. Selton-Suty, N. Agrinier*

793 ***Kingella* endocarditis in children: a distinct entity or not ?**
A. Lowenthal, H. Weisblum-Neuman, E. Birk, I. Levy, H. Ben Zvi, G. Amir, G. Frenkel, E. Bruckheimer, G. Livni, D. Marom, L. Ashkenazi-Hoffnung, O. Schiller, E. Nahum, O. Scheuerman (Petach Tiqwa, Israel)*

2015 **External validation of the NOVA and DENOVA scores for clinical prediction of endocarditis in patients with *Enterococcus faecalis* bacteraemia**
P. Danneels (Angers, France), F. Chabrun, A. Beaudron, C. Rihet, C. Vannier, M. Kempf, V. Dubee*

2483 **Clinical and microbiologic factors associated with infective endocarditis among patients with *Staphylococcus aureus* bacteraemia**
M. Papadimitriou Olivgeris (Lausanne, Switzerland), P. Monney, C. Ting, C. Soldini, N. Ciocca, S. Giulieri, B. Guery*

2512 **Clinical and echocardiographic predictors of embolism in infective endocarditis**
M. Papadimitriou Olivgeris (Lausanne, Switzerland), C. Ting, C. Soldini, N. Ciocca, M. Kirsch, S. Giulieri, B. Guery, P. Monney*

3109 **Delayed diagnosis of infectious endocarditis: retrospective analysis conducted at an university hospital in the south of Italy**
A. Spera (Salerno, Italy), R. Benvenga, G. Galasso*

3156 **Clinical experience of dalbavancin in infectious endocarditis: stratifying its impact on treatment**
M. Valerio Minero (Madrid, Spain), M. Veintimilla Yanez, S. Mornese Pinna, M. Machado, A. Alvarez-Uria, A. Galar Recalde, M. Olmedo Samperio, C. Rincón, E. Bouza, P. Muñoz*

3175 **Infective endocarditis in older adults: distinguishing features**
L. Lemos, L. Ribeiro-Da-Silva, M. Correia, J. De Andrade, D. Menezes, R. Garrido, B. Zappa, G. Barbosa, C. Weksler, W. Golebiovski, C. Lamas (Rio de Janeiro, Brazil)*

3205 **Haemodialysis-associated infective endocarditis**
R. Garrido, M. Valle, L. Vasconcelos-Silva, M. Correia, B. Zappa, L. Lemos, L. Ribeiro-Da-Silva, J. De Andrade, D. Menezes, W. Golebiovski, C. Weksler, G. Barbosa, C. Lamas (Rio de Janeiro, Brazil)*

3894 **Challenges in infective endocarditis: valvular infective endocarditis in patients with cardiac implantable electronic devices: clinical characteristics and outcome: analysis on a national cohort**
L. Boix-Palop (Terrassa, Spain), M. Martinez-Selles, P. Muñoz, M. Marín, G. Cuerpo, M. Fariñas, M. Hernández-Meneses, K. Reviejo, A. De Alarcón, L. Lopez-Cortes, I. Antorrena, J. Porres, E. Calbo Sebastian*

4056 **Clinical features of late prosthetic valve endocarditis in a cardiac referral centre (2006-2019)**
L. Ribeiro-Da-Silva, L. Lemos, M. Correia, D. Menezes, J. De Andrade, R. Garrido, B. Zappa, G. Barbosa, C. Weksler, W. Golebiovski, C. Lamas (Rio de Janeiro, Brazil)*

4165 **A multi-national study for the treatment of enterococcal endocarditis with ampicillin-daptomycin combination therapy**
M. Sierra Hoffman, R. Deliz, A. Sekhon (Tomball, United States), A. Gollapalli, K. Saddler, M. Stevens, M. Castro-Lainez, J. Pericas*

4919 **Risk factors for in-hospital mortality in a prospective contemporary cohort of adult patients with infective endocarditis in a cardiac surgery hospital**
R. Garrido, G. Barbosa, M. Correia, L. Lemos, L. Ribeiro-Da-Silva, J. De Andrade, D. Menezes, B. Zappa, W. Golebiovski, C. Weksler, C. Lamas (Rio de Janeiro, Brazil)*

5491 **Cardiac 18F-fluorodeoxyglucose Positron Emission Tomography (18-F-FDG-PET/CT) use in infective endocarditis: a 10-year multi-centre cohort study**
M. Hernández-Meneses (Barcelona, Spain), S. Calzado, J. Llopis, A. Caresia-Aróztegui, A. Perissinotti, L. Boix-Palop, J. Diez De Los Rios, J. Cuquet Pedragosa, M. Andrés-Santamaria, C. Agustí, M. Ortiz, J. Tricás, J. Ambrosioni, D. Fuster, M. Moreno Camacho, O. Gasch Blasi, J. Miro*

6104 **Short- and long-term outcomes of infective endocarditis admission in adults: a population-based registry study in Finland**
E. Ahtela (Turku, Finland), J. Oksi, T. Vahlberg, P. Rautava, J. Sipilä, V. Kytö*

6613 **Definite prolonged antibiotic treatment in complicated prosthetic valve endocarditis with absolute contraindication to surgery: a single-centre retrospective analysis**
N. Cesta (Grottaferrata, Italy), T. Mulas, V. Malagnino, M. Iannetta, M. De Masi, G. Ruvolo, M. Andreoni, L. Sarmati*

6652 **Predictive value of sepsis scores for in-hospital mortality in patients with left-sided infective endocarditis**
B. Leal De Almeida (Sao Paulo, Brazil), T. Strabelli, M. Sommer Bittencourt, A. Mansur, M. Ribeiro Paixao, L. Zoboli Pocebon, D. M. Gualandro, F. Goldemberg, R. Focaccia Siciliano*

6733 **Examining the modified Duke criteria in infective endocarditis: a comparison of outcomes for 'typical' and 'atypical' bacteria**
R. Mehta (London, United Kingdom), P. Pabari, A. Hartley, Y. Razvi, B. Rana, A. Ghazy, M. Shehata, A. Abbara*

7251 **Epidemiology, characteristics and outcomes of bacteraemia and endocarditis caused by *Staphylococcus aureus* in cancer patients**
S. Grillo, G. Cuervo (Barcelona, Spain), J. Laporte Amargos, M. Tuells Morales, I. Grau, D. Berbel Palau, C. Gudiol, J. Carratalà, M. Pujol*

7511 **Impact of the anti-coagulant therapy before hospitalisation on cerebrovascular complications and mortality in infectious endocarditis**
J. Solera Rallo (Madrid, Spain), F. Galván Román, L. Domínguez Pérez, S. De Cossio Tejido, F. Lopez-Medrano*

7673 **Dalbavancin as a sequential treatment for Gram-positive infective endocarditis: 2-year experience at the University Hospital 12 de Octubre (Madrid)**
J. Solera Rallo (Madrid, Spain), M. Calderón Flores, I. Fernández Herrero, C. Vigil Martín, E. Aparicio Minguijón, M. Arrieta Loitegui, J. Caro Teller, S. De Cossio Tejido, L. Domínguez Pérez, F. Lopez-Medrano*

8072 **Daptomycin or vancomycin for methicillin-resistant *Staphylococcus aureus* infective endocarditis complicated by septic pulmonary emboli**
L. Vuong, T. Trinh (San Francisco, United States)*

8984 **Early-onset prosthetic valve endocarditis: features in a contemporary cohort**
R. Garrido, G. Barbosa, M. Correia, L. Ribeiro-Da-Silva, L. Lemos, B. Zappa, C. Weksler, W. Golebiovski, C. Lamas (Rio de Janeiro, Brazil)*

9219 **Outcomes of people who inject drugs with infectious endocarditis and valve replacement surgery**
M. Veve (Knoxville, United States), G. Cooksey, M. Shorman*

9533 **Endocarditis management and OPAT in the POET era**
G. Jennifer (London, United Kingdom), S. Burke, G. Pollara, S. Morris-Jones, S. Logan, J. Hatcher*

Session accepted as Paper Poster Session

Gastrointestinal infection

151 **A meta-analysis of the burden of non-typhoidal *Salmonella* in humans in the Middle East and North Africa**
R. Al Rifai (Al Ain, United Arab Emirates)*

262 **Epidemiological and clinical characteristics of patients with *Campylobacter* bloodstream infection: a retrospective case-control study**
L. Tau (Tel-Aviv, Israel), O. Shalom, A. Adler, Y. Paran, R. Cohen-Poradosu, D. Shasha, R. Ben-Ami*

513 **Evaluation of prevalence and risk factors of *Helicobacter pylori* infection in an urban population**
A. Oreh (Abuja, Nigeria), A. Onu, A. Moses*

525 **Characterisation of internalin genes in *Listeria monocytogenes* food strains, and their association with invasiveness *in vitro***
K. Roeske (Warsaw, Poland), I. Korycinski, A. Zasun, R. Stachowiak, D. Korsak, J. Bielecki*

1034 **Prevalence and antimicrobial susceptibility of *Campylobacter* species isolated from Greek diarrhoeal patients (2010-2018)**
S. Maraki (Heraklion, Greece), V. Mavromanolaki, D. Stafylaki, E. Nioti, G. Minadakis, A. Kassimati*

1038 **High prevalence of multi-stress tolerant *Campylobacter* species causing human infection**
S. Fekry (Alexandria, Egypt), M. Elhadidy*

1499 **Antibiotic resistance of 34,539 *Campylobacter* spp. isolated from human sources: National Surveillance Data of Switzerland from 2007 to 2018**
A. Egli (Basel, Switzerland), D. Vogt, P. Brodmann, H. Seth-Smith, J. Reist, A. Kronenberg, R. Stephan*

1608 **Identification of host-specific genetic elements of *Campylobacter jejuni* in Germany based on whole genome data**
L. Epping (Berlin, Germany), R. Piro, M. Knüver, M. Borowiak, C. Huber, A. Thürmer, B. Malorny, K. Stingl, A. Fruth, L. Wieler, T. Semmler*

1987 **Seroepidemiology of *Helicobacter pylori* infection in different regions of Croatia: new perspective after 20 years**
D. Varda Brkić (Zagreb, Croatia), M. Katičić, L. Zele-Starcevic, N. Beader, V. Tripkovic, B. Bedenic, I. Marekovic*

Abstract Categories 2020

2166 **Risk factors of severe dehydration among children under five**
A. Mkhoyan (Yerevan, Armenia), A. Demirchyan*

2513 **Role of enteroaggregative *Escherichia coli* in people with diarrhoea in Gipuzkoa**
M. Gómez Ruiz De Arbulo (Salvatierra, Spain), P. Vallejo Recuna, M. Arrastia Erviti, D. Grandioso Vas, T. Martín Peñaranda, M. Alkorta Gurrutxaga*

3126 **Heat wave-associated *Vibrio* infections in Germany 2018 and 2019**
T. Brehm (Hamburg, Germany), L. Berneking, H. Rohde, M. Christner, S. Schmiedel*

3276 **Characterisation of prevalence and resistance of *Aeromonas* isolated from patients with acute diarrhoea in Zhejiang province from 2010 to 2017**
X. Chen (Hangzhou, China), W. Ruonan, Z. Qiaoyun*

3473 **Prevalence and genetic characterisation of Shiga toxin-producing *Escherichia coli* isolates from cattle in Portugal**
H. Oliveira (Braga, Portugal), A. Balem, S. Gonçalves, I. García-Meniño, S. Flament-Simon, J. Blanco Alvarez, C. Pinto, J. Blanco, G. Almeida, C. Almeida*

3474 **A case of recurrent *Campylobacter* cured by faecal microbiota transplant in an immunosuppressed patient with common variable immune-deficiency**
A. Tamilarasan, R. Luber, P. Yong, K. Cheent, P. Irving, M. Meda, S. Goldenberg (London, United Kingdom)*

3949 **Cholera outbreak in Algeria, August-September 2018**
N. Benamrouche (Algiers, Algeria), C. Belkader, S. Zemam, S. Sadat, Y. Boutabba, R. Belhadj, F. Kias, H. Saoussene, K. Saighi, A. Meftah, M. Yousfi, F. Zmit, A. Zertal, F. Mechouet, S. Benadda, H. Letlout, S. Zouagui, A. Toua*

4173 **The frequency of diarrhoeagenic *Escherichia coli* isolates in children with acute diarrhoea under five years**
A. Koc, H. Turk Dagi (Konya, Turkey)*

4368 **Rapid increase of CTX-M-producing ST152 *Shigella sonnei* isolates in Switzerland**
E. Campos-Madueno, O. Bernasconi, C. Casanova, M. Elzi, C. Maffioli, T. Bodmer, A. Kronenberg, A. Endimiani (Bern, Switzerland)*

4512 **Evaluation of commercial multiplex real-time PCR panels to detect bacterial, parasite and viral gastrointestinal pathogens in clinical specimens**
P. Bird (Leicester, United Kingdom), C. Holmes*

4610 **Emergence of CTX-M-producing *Salmonella enterica* serotype Typhimurium in Greece**
E. Protonotariou, G. Meletis, G. Kagkalou, D. Papadopoulou, A. Tychala (Thessaloniki, Greece), F. Netsika, O. Vasilaki, P. Mantzana, M. Kachrimanidou, L. Skoura*

4969 **Treatment responses to azithromycin and ciprofloxacin in uncomplicated *Salmonella* Typhi infection: a comparison of clinical and microbiological data from a controlled human infection model**
M. Gibani (London, United Kingdom), C. Jin, S. Pennington, X. Liu, A. Ardrey, G. Aljayyoussi, M. Moore, B. Angus, C. Parry, G. Biagini, N. Feasey, A. Pollard*

5032 ***Escherichia coli* serotype O55:H9 as a new multidrug resistant hybrid pathotype producing Shiga toxin and carrying extra-intestinal virulence plasmid**
A. Cointe (Paris, France), P. Mariani, B. Philippe, A. Birgy, S. Lefevre, S. Delannoy, P. Fach, F. Weill, S. Bonacorsi*

5080 **Whole genome sequencing of *Salmonella enterica* from Spanish hospitals with resistance to third generation cephalosporins**
X. Vázquez (Oviedo, Spain), V. García Menéndez, M. De Toro, N. Rodríguez, M. Bances, M. Alkorta, J. Rodríguez-Lozano, J. Calvo-Montes, J. Fernández, M. Rodicio*

5211 **Epidemiology and comparative genomics of clinical isolates of *Salmonella enterica* serotype Typhimurium carrying the virulence-resistance plasmid pU0-StVR2**
N. Rodríguez, I. Montero, X. Vázquez, M. Bances, M. De Toro, J. Fernández, M. Rodicio, M. Rodicio (Oviedo, Spain)*

5280 **Genomic analysis of ciprofloxacin-resistant *Salmonella enterica* serovar Kentucky ST198 from Spanish hospitals**
X. Vázquez, N. Rodríguez, M. De Toro, M. Bances, M. Alkorta, S. Hernaez Crespo, E. Prieto, P. De La Iglesia, M. Rodicio, J. Fernández, M. Rodicio (Oviedo, Spain)*

5364 **Antimicrobial drug resistance, molecular typing and whole genome sequencing of *Salmonella enterica* serovar Derby from human clinical samples and pork products**
V. García Menéndez (Lugo, Spain), X. Vázquez, R. García-Fierro, P. Quirós, R. Granda, C. Cuervo, M. Bances, M. Rodicio, M. Rodicio*

5730 **Epidemiological study of main enteropathogens causing infectious gastroenteritis in a Madrid tertiary hospital**
A. Yarci Carrión, L. Fontan, S. Gómez De Frutos, E. Navarro Lara, A. García, T. Alarcon Cavero (Madrid, Spain)*

6069 **Comparison of clinical spectrum and outcomes of patients with extremely drug-resistant *Salmonella enterica* with multidrug-resistant strains**
F. Herekar (Karachi, Pakistan), S. Sarfaraz, S. Shahid, M. Mahesar, N. Ghouri*

6664 **Detection rates of the bacterial causes of gastroenteritis using a multiplex molecular assay in the South-African private sector**
C. Kingsburgh (Pretoria, South Africa), K. Strydom*

6669 ***Yersinia enterocolitica*-associated diarrhoea: descriptive epidemiology in a low-prevalence setting (Barcelona, Spain) from January 2016 to October 2019**
L. Goterris Bonet (Barcelona, Spain), C. Crespo, S. Mota, S. Gomez Calvo-Parra, J. Virto, A. Sáiz, T. Cornejo Sanchez, R. Rubio Leal, V. Rodríguez*

7653 **Enteroaggregative *Escherichia coli* in mid-Norway**
I. Haugan (Trondheim, Norway), M. Husby, D. Aamnes Mostue, A. Brun, H. Lange, R. White, L. Vold, J. Afset*

7689 **The burden of enteric fever from three urban centres: a multi-centre, multi-component prospective epidemiological study with 626,219 person years of observation**
J. Meiring (Oxford, United Kingdom), M. Shakya, F. Khanam, M. Voysey, M. Phillips, S. Tonks, T. Darton, S. Baker, C. Dolecek, S. Dunstan, G. Dougan, K. Holt, R. Heyderman, F. Qadri, V. Pitzer, B. Basnyat, M. Gordon, J. Clemens, A. Pollard*

8174 **Slovenian national outbreak of *Salmonella* Paratyphi B variant Java between 2014 and 2016**
Š. Klemen, M. Trkov, A. Storman, Z. Petrovic, A. Juricevic Dodic, I. Berce, M. Ravnik, M. Pirs (Ljubljana, Slovenia)*

8548 **Epidemiology of bloody diarrhoea in Georgia and haemolytic-uraemic syndrome associated with it**
M. Atskvereli (Tbilisi, Georgia), K. Gvantsa, N. Shulaia*

8588 **Diagnostic impact of molecular detection of enteropathogenic bacteria compared to stool culture**
S. Rodríguez-Pallarés (Cádiz, Spain), A. Ruiz-Castillo, P. Panes-Ortega, F. Arroyo Navarro, F. Galan-Sanchez, M. Rodriguez-Iglesias*

8608 **Rise in *Campylobacter jejuni* antimicrobial resistance in Split-Dalmatia County, Croatia: 2013 - 2018**
M. Carev (Split, Croatia), A. Novak, M. Tonkic*

8775 **Should we change our diagnostic strategy for the detection of verotoxigenic *Escherichia coli* infection?**
S. Illescas (Ciudad Real, Spain), S. Sanchez, V. Carmona, J. Martinez-Alarcon, M. Vidal*

9114 **Therapeutic response of meropenem and azithromycin in the treatment of extensively drug-resistant (XDR) typhoid fever in a lower-middle income country**
S. Qureshi (Karachi, Pakistan), F. Naz, A. Naveed, T. Yousafzai*

9185 **Etiology of viral and bacterial gastroenteritis in a third-level hospital in Spain in relation to age**
E. León, M. Gasca Santiyan, B. Palop (Málaga, Spain)*

9589 **Listeriosis in Ávila, Spain: a real warn amongst immunocompromised hosts**
M. Pedromingo Kus (Madrid, Spain), T. Meiras Arriaga, A. San Pedro Garrido, O. Fraile Santos, N. Iglesias Nuñez, R. Sanchez Arroyo, J. Barragan Casas, A. Antoli Royo*

Session accepted as 1-Hour Oral Session

Hot topics in central nervous system infection

2766 **Treatment of community-acquired bacterial brain abscess: an international multi-centre survey**
J. Bodilsen (Aalborg, Denmark), P. Tattevin, S. Tong, M. Brouwer, D. Van De Beek, P. Naucler, H. Nielsen*

3274 **Normocellular bacterial meningitis in adults: a prospective nationwide cohort study**
H. Vestergaard (Aalborg, Denmark), J. Bodilsen, H. Nielsen*

6754 **Recurrent community-acquired bacterial meningitis in adults**
L. Ter Horst (Amsterdam, Netherlands), M. Brouwer, A. Van Der Ende, D. Van De Beek*

6769 **Clinical features and prognostic factors in adults with community-acquired pneumococcal meningitis**
D. Koelman (Amsterdam, Netherlands), M. Brouwer, L. Ter Horst, M. Bijlsma, A. Van Der Ende, D. Van De Beek*

Session accepted as Paper Poster Session

Implications of Gram-negative infections

634 **The potential benefit of a second C-reactive protein measurement in patients with Gram-negative bacteraemia presenting to the emergency medicine department**
T. Levinson (Tel Aviv, Israel), N. Tamir, S. Shenhar-Tsarfaty, Y. Paran, D. Zeltzer, I. Shapira, D. Trotzky, P. Halpern, A. Weiss-Meilik, E. Raykhshtat, I. Goldiner, A. Adler, S. Berliner, O. Rogowski, A. Wasserman*

715 **Excluded versus included patients in a randomised controlled trial of infections caused by carbapenem-resistant Gram-negative bacteria: relevance to external validity**
V. Daitch (Petah Tikva, Israel), M. Paul, G. Daikos, E. Durante Mangoni, D. Yahav, Y. Carmeli, Y. Dishon, A. Skiada, N. Eliakim - Raz, A. Nutman, A. Antoniadou, A. Adler, Y. Dickstein, J. Pavleas, R. Zampino, R. Bitterman, H. Abu-Zayyad, F. Koppel, Y. Zak-Doron, T. Babich, A. Turjeman, H. Ben Zvi, L. Friberg, U. Theuretzbacher, L. Leibovici*

2057 **Comparative efficacy of piperacillin-tazobactam versus third-generation cephalosporins or carbapenems against susceptible ampC-bearing *Enterobacteriaceae***
V. Rico Caballero (Barcelona, Spain), D. Agüero González, L. Morata, M. Bodro Marimont, C. Garcia Vidal, P. Puerta, J. Ambrosioni, M. Hernández-Meneses, C. Cardozo, L. Linares, L. Albiach, E. Moreno, M. Chumbita, C. Pitart, C. Casals, A. Soriano, J. Martínez Martínez*

2210 **Relation of risk factors and mortality in carbapenem-resistant *Klebsiella pneumoniae* ST11 bloodstream infections**
T. Xiao (Zhejiang, China), X. Yonghong*

2628 **Risk factors for functional decline among survivors of Gram-negative bloodstream infection**
A. Turjeman (Petah Tikva, Israel), F. Koppel, E. Franceschini, D. Yahav, G. Dolci, T. Babich, R. Bitterman, A. Neuberger, N. Ghanem-Zoubi, A. Santoro, N. Eliakim-Raz, B. Pertzov, A. Stern, Y. Dickstein, E. Maroun, H. Zayyad, M. Meschiari, J. Bishara, E. Goldberg, C. Venturelli, C. Mussini, M. Paul, L. Leibovici*

2827 **No negative conversion at follow-up blood culture (FUBC) is significant predictors of early (1-week) mortality in carbapenem-resistant *Enterobacteriaceae* or vancomycin-resistant enterococci bacteraemia patient: univariate and multivariate analysis**
S. Hyejin (Seoul, South Korea), H. Choi, Y. Cho, J. Eom*

2828 **Accuracy of predicting early mortality of severity indicators among carbapenem-resistant *Enterobacteriaceae* or vancomycin-resistant enterococci bacteraemia patient: univariate and multivariate analysis**
S. Hyejin (Seoul, South Korea), H. Choi, Y. Cho, J. Eom*

2936 **Combination empiric treatment is equivalent to monotherapy in 317 sepsis episodes due to carbapenemase-producing *Klebsiella pneumoniae* in critically ill patients**
M. Papadimitriou Olivgeris (Lausanne, Switzerland), C. Bartzavali, A. Lambropoulou, V. Karamouzos, A. Georgakopoulou, F. Kolonitsiou, F. Fligou, M. Christofidou, M. Marangos*

3488 **Carbapenem-resistant *Escherichia coli* causing neonatal sepsis: NDM-5 gains prominence**
A. Bhattacharya, S. Mitra, S. Naha, B. Saha, S. Dutta, S. Basu (Kolkata , India)*

3607 ***Escherichia coli* bloodstream infections in a university hospital of northern Italy: resistance pattern and prognostic factors**
G. Volpato (Milan, Italy), D. Pocaterra, G. De Nadai, F. Tordato, B. Varisco, L. Canziani, F. De Fazio, M. Casana, P. Morelli*

4139 **Risk factors and mortality for patients with bloodstream infections of *Klebsiella pneumoniae* during 2014-2018: clinical impact of carbapenem resistance in a large tertiary hospital of China**
J. Wei, C. Haiyan, Y. Chen, C. Wu (Nanjing, China)*

4268 **Clinical profile of patients with bacteraemia caused by *Enterobacter cloacae* and *Klebsiella aerogenes*: more similarities than differences**
R. Alvarez-Marin, C. Martin Gandul, O. Gasch Blasi, J. Rodriguez Martinez, J. Calvo-Montes, R. Lara-Contreras, J. Lepe, F. Tubau, M. Cano, F. Rodríguez-López, J. Rodríguez-Baño, M. Pujol, J. De La Torre Cisneros, L. Martinez-Martinez, A. Pascual Hernandez, M. Jiménez-Mejías (Seville, Spain)*

5013 **Melioidosis in an Indian intensive care unit: the enigma of a 'Silent Killer'**
T. Shaw (Manipal, India), V. Kalwaje Eshwara, C. Mukhopadhyay*

5508 **Outcome of community-onset extended-spectrum β-lactamase-producing *Escherichia coli* bacteraemia and urinary tract infection: a historical population-based cohort study**
R. Richelsen (Aalborg, Denmark), P. Mariadas, J. Smit, H. Schønheyder, J. Rodríguez-Baño, H. Nielsen*

5987 **C-reactive protein patterns by age, sex and pathogen in patients with Gram-negative bacteraemia**
V. Prendki (Geneva, Switzerland), E. Von Dach, W. Albrich, A. Brunel, C. Cuvelier, D. Flury, A. Gayet-Ageron, B. Huttner, P. Kohler, E. Lemmenmeier, S. Harbarth, L. Kaiser, P. Bochud, A. Huttner*

6342 **Evaluation of carbapenem-resistant *Enterobacteriaceae* treatment outcomes in a quaternary hospital in the United Arab Emirates**
A. Ali (Abu Dhabi, United Arab Emirates), R. El Lababidi, M. Balkis, R. Ismail, F. Kablaoui*

6397 **Ceftolozane-tazobactam for the treatment of bloodstream infection due to *Pseudomonas aeruginosa* in neutropenic cancer patients: a real-life experience (ZENITH study)**
C. Gudiol (Barcelona, Spain), A. Albasanz, A. Fernandez-Cruz, P. Puerta, M. Hakki, I. Ruiz, C. Oltolini, C. Devoe, L. Drgona, O. Gasch Blasi, P. Martín-Dávila, M. Peghin, L. Vázquez, J. Laporte, M. Machado, C. Garcia Vidal, R. Duarte, I. Los Arcos, D. Clerici, S. Doernberg, J. Duran, J. Fortun Abete, N. Castaldo, F. Peña, P. Muñoz, E. González-Barca, N. Pallarès, J. Carratalà*

6776 **Clinical characteristics, aetiology and risk factors for mortality of neutropenic patients with bloodstream infection presenting with septic shock**
M. Chumbita (Barcelona, Spain), P. Puerta, C. Gudiol, J. Laporte-Amargós, A. Ladino, A. Albasanz, C. Helguera, N. Garcia-Pouton, A. Bergas, E. Moreno, F. Escrihuela, F. Marco Reverte, M. Condom, J. Martínez Martínez, A. Soriano, J. Carratalà, C. Garcia Vidal*

7107 **Clinical management of serious infections attributable to carbapenem-resistant Gram-negative pathogens in Spanish hospitals**
R. Ferrer, J. Calvo-Montes, E. Maseda, M. Salavert, G. Bou Arevalo, J. Diaz-Regañon, D. Lopez, V. Lozano, D. Gómez-Ulloa, R. Fenoll, E. Sánchez, E. Mccann (Rahway, United States)*

7309 **Amikacin or colistin monotherapy for complicated urinary tract infections by extensively drug-resistant *Pseudomonas aeruginosa***
I. López Montesinos (Barcelona, Spain), S. Gómez-Zorrilla, N. Prim, D. Echeverría-Esnal, M. Gracia-Arnillas, M. Montero, L. Sorlí, E. Padilla, S. Grau, J. Horcajada*

8659 **Are carbapenems a choice in OXA-163 carbapenemase-producing *Enterobacterales* infections? Clinical outcomes of 29 OXA-163 infections in a general hospital in Argentina**
M. Jaume, M. Flor Montero, M. Amaya, A. Sisto, L. Abusamra, L. Errecalde, F. Pasteran (Buenos Aires, Argentina), L. Guelfand, M. Rolón*

9290 **Delayed treatment response in healthcare-associated infections by OXA-48 carbapenemase-producing *Enterobacteriaceae***
M. Amer, O. Helmy (Cairo, Egypt), H. El-Mahallawy, M. Amin*

Session accepted as Paper Poster Session

Increasing knowledge on NTMs

1218 **The non-tuberculous mycobacteria experience: a single-centre study in Ireland**
T. Teoh (Dublin, Ireland), M. Casey, J. Tormey, B. Lynch, D. Brady, E. Muldoon, M. Lynch, B. Mc Cullagh*

1408 **Long-term suppressive treatment of cardiac surgery-related *Mycobacterium chimaera* disseminated infection**
V. Manfrin, M. Mascarello (Vicenza, Italy), M. Rassu, L. Fallico, L. Salvador, S. Mondino, R. Cazzaro*

1480 **A novel celecoxib-derivative kinase inhibitor, AR-12 (OSU-03012), is active against *Mycobacterium abscessus* complex *in vitro***
B. Li (Shanghai, China), Y. Zou, S. Zhang, H. Chu*

1774 **Contact effect of a *Methylobacterium* sp. extract on biofilm of a *Mycobacterium chimaera* strain isolated from a 3T heater-cooler system**
I. Pradal, J. Esteban-Moreno (Madrid, Spain), J. Aguilera-Correa*

1805 **Prevalence of non-tuberculous mycobacteria in a tertiary hospital in Beijing, China, January 2013 to December 2018**
J. Huang (Beijing, China), M. Xiao, T. Kudinha*

1940 **Pattern of osteoarticular infections caused by non-tuberculous mycobacteria: 9 years' experience**
A. Bleibtreu (Paris, France), I. Bonnet, S. Jauréguiberry, B. Fautrel, E. Caumes, J. Robert, E. Fourniols, A. Aubry*

2047 **Performances comparison between rapidly growing mycobacteria medium for direct-isolation of non-tuberculous mycobacteria, and its industrial version**
M. Vrignaud (La Balme les Grottes, France), E. Déléage, S. Orenga, D. Stephenson, J. Perry*

2080 **Differential drug susceptibility patterns of *Mycobacterium avium complex* isolates recovered in Greek university hospitals**
F. Kontos (Athens, Greece), G. Mavromanolakis, S. Pournaras*

2089 ***In vitro* antimicrobial susceptibility testing of rapidly growing mycobacteria isolated in a university hospital, Athens, Greece**
F. Kontos (Athens, Greece), S. Pournaras*

2188 **Decontamination strategies used for AFB culture significantly reduce the viability of *Mycobacterium abscessus* in sputum samples from patients with cystic fibrosis**
D. Stephenson, A. Perry, A. Nelson, A. Robb, M. Thomas, S. Bourke, J. Perry (Newcastle upon Tyne, United Kingdom), A. Jones*

2261 **Genomic analysis of cardiac surgery-associated *Mycobacterium chimaera* Infections in Italy**
A. Ghodousi (Pessano con Bornago, Italy), M. Peracchi, E. Borroni, G. Palu, L. Fallico, V. Quaresima, V. Manfrin, M. Rassu, V. Monzillo, R. Manganell, E. Tortoli, D. Cirillo*

2627 **Antimicrobial susceptibility of non-pigmented rapidly growing mycobacteria**
L. Salar Vidal, A. Broncano, C. Minea, M. Martin-Garcia, J. Aguilera-Correa, J. Esteban-Moreno (Madrid, Spain), A. Macias-Valcayo*

2646 **Compatibility of the new NTM Elite agar with MALDI-TOF for direct isolation and identification of non-tuberculous mycobacteria**
M. Vrignaud (La Balme les Grottes, France), E. Déléage, L. Devigne*

2727 **Identification and clinical significance of *Mycobacterium avium complex* isolates in a university hospital in a 13-year period**
F. Kontos (Athens, Greece), G. Skyllas, I. Kouva, I. Korbila, E. Manali, A. Antoniadou, S. Papiris, S. Pournaras*

3225 **Efflux pumps contribute to intrinsic clarithromycin resistance in clinical *Mycobacterium abscessus* isolates**
Q. Guo (Shanghai, China), B. Li, H. Chu*

4167 **New lean preparation method for identification of mycobacteria by MALDI Biotyper**
M. Timke, A. Pranada (Dortmund, Germany), M. Kostrzewa*

4731 **A novel deep sequencing platform for genotyping and drug resistance detection of *Mycobacterium leprae***
S. Braet (Antwerp, Belgium), P. Suffys, S. Ezidio Gonçalves Vasconcellos, G. Bisch, A. Ferre, E. Hasker, Y. Assoumani, A. Mzembaba, P. Supply, B. De Jong*

4806 **A new high-resolution melting PCR assay for a rapid detection of linezolid-resistance-associated mutations in *Mycobacterium avium complex***
R. Musumeci (Monza, Italy), L. Molteni, E. Mazzola, S. Torri, D. Fanti, A. Nava, M. Martinelli, F. Perdoni, C. Villa, P. Carlo Federico, C. Cocuzza*

4833 **Optimization of *Mycobacterium avium complex* therapy with synergistic and bactericidal drug combinations**
V. Sonawane (Nijmegen, Netherlands), M. Ruth, L. Pennings, J. Van Ingen*

4840 **Next-generation microscopically-observed drug susceptibility assay (NG-MODS) allows more rapid and precise phenotypic drug-susceptibility testing: preliminary results for *Mycobacteroides abscessus***
W. Chiu (Leuven, Belgium), C. Foo, P. Leyssen, E. Andre*

4898 **Genomic identification of clinically relevant *Mycobacterium* species by target sequencing**
V. Collin (La Balme les Grottes, France), F. Allard, M. Rumigny, F. Javerliat*

5128 **A radiologic score for pulmonary non-tuberculous mycobacterial infection: preliminary results**
M. Colaneri (Pavia, Italy), A. Lombardi, A. Di Matteo, M. Fabbiani, S. Vancheri, A. Valentini, V. Monzillo, R. Bruno*

5142 **Intact bacteria species-specific lipid profiling using the MALDI Biotyper Sirius can identify mycobacteria in one step**
B. Agnieszka, X. Gonzalo, M. Kostrzewa, F. Drobniewski, G. Larrouy-Maumus (London, United Kingdom)*

5150 **Cluster of invasive *Mycobacterium chimaera* infection in a single cardiac surgery unit: clinical features and management**
N. Riva (Reggio Emilia, Italy), L. Cavazzuti, L. Pescarolo, G. Marini, G. Magnani, M. Massari*

5191 **Detection of antimicrobial resistance in *Mycobacterium abscessus* complex by MALDI-TOF MS**
A. Godmer (Paris, France), N. Veziris, C. Eckert, S. Gallah, A. Aubry, L. Benzerara*

5584 **Routine use of MALDI-TOF MS for identification of non-tuberculous mycobacteria species in the clinical laboratory**
D. Rodriguez-Temporal (Barcelona, Spain), N. Vila, E. García, M. Mas, F. Alcaide*

5675 **Is *Mycobacterium lentiflavum* "the new" *Mycobacterium avium*?**
S. Gómez De Frutos (Madrid, Spain), A. Fraile Torres, A. Yarci Carrión, T. Soler Maniega, L. Cardeñoso, R. Girón, D. Domingo*

6392 **Identification of *Mycobacterium* species with MALDI-TOF mass spectrometry**
Z. Saribas, O. Koksalan, H. Gur (Ankara, Turkey), S. Demirci, A. Alp*

6563 ***Mycobacterium mucogenicum* in hospital water: a potential source for human infection**
J. Ory (Nîmes, France), C. Aumeran, O. Traore, E. Lecorche, C. Enault, E. Cambau, J. Lavigne, A. Pantel*

7001 **Identification by proteomic (MALDI-TOF MS) of non-tuberculous mycobacteria from liquid medium in clinical practice**
R. Sainz Rodriguez, M. Mediavilla Gradolph, F. Ana María, B. Palop (Málaga, Spain), A. Correa, M. Bermúdez Ruiz*

7440 **Long lasting outbreak of severe *Mycobacterium chimaera* infection among cardiac surgery patients operated with contaminated heater-cooler devices: Italy, 2010 to 2019**
M. Sabbatucci (Rome, Italy), A. Campanale, R. Cagarelli, A. Di Caro, S. Ditommaso, L. Lispi, V. Manfrin, F. Maraglino, M. Mazzolani, M. Moro, G. Napoletano, E. Narne, P. Ragni, R. Raso, F. Russo, C. Silvestre, C. Zotti, S. Iannazzo*

7481 **Monitoring and control of the heater-cooler unit colonisation by *Mycobacterium chimaera* and other NTMs used during open-heart surgery**
B. Casini (Pisa, Italy), B. Tuvo, G. Privitera*

7491 **Evaluation of the MGIT 960/EpiCenter TB eXiST system for drug susceptibility testing for *Mycobacterium abscessus* group**
N. Carvalho, S. Bombarda, S. Leão, R. Arbeit, E. Chimara (Sao Paulo, Brazil)*

7580 **Epidemiology of non-tuberculous mycobacteria in bronchiectasis and non-bronchiectasis patients in a university teaching hospital in Madrid**
S. Gómez De Frutos (Madrid, Spain), L. Fontan, E. Navarro Lara, N. Zurita Cruz, L. Cardeñoso, J. García Pérez, D. Domingo*

7745 **Prevalence of non-tuberculous mycobacteria in patients with cystic fibrosis in a tertiary hospital**
D. Ortega Larrea (Zaragoza, Spain), E. López, M. Moreno Hijazo, S. Mormeneo Bayo, S. Nabal Díaz, E. Valverde, M. Arias, B. Fortuño, M. Elu, J. Viñuelas*

7916 **Evaluation of the FluoroType mycobacteria assay for the detection and differentiation of clinically relevant mycobacteria**
C. Niccolai (Florence, Italy), A. Bartolesi, F. Marcelli, A. Andreini, R. Mannino, A. Antonelli, E. Tortoli, G. Rossolini*

8346 **Non-tuberculous lymphadenitis in children: epidemiology and management strategy in France during the last decade**
C. Le Brun (Tours, France), H. Guet-Revillet, O. Peuchant, A. Gaudart, C. Koebel, C. Piau, J. Bador, F. Canis, A. Vachée, C. Brehin, L. Ricco, P. Bemer, P. Lanotte, C. Carvalho Schneider, Z. Maakaroun Vermesse, A. Guillouzouic*

8619 **Characterisation of the unique contributions of bedaquiline and rifabutin against actively-growing and nutrient-starved populations of *Mycobacterium abscessus***
J. Lee, N. Ammerman (Baltimore, United States), E. Nuermberger*

8792 **Rapid detection of *Mycobacterium abscessus* complex and associated antibiotic resistance directly in cystic fibrosis samples**
A. Bordin (Brisbane, Australia), C. Coulter, J. Clark, S. Pandey, S. Bell, C. Wainwright, G. Nimmo, A. Jennison, M. Syrmis, C. Pardo, H. Hackett, D. Whiley*

9046 **Using whole genome sequencing to assess *M. leprae* transmission in French overseas Territories**
E. Lecorche (Paris, France), B. Violaine, M. Dalila, A. Charlotte, K. Elise, F. Mougari, H. Benmansour, V. Jarlier, E. Cambau*

9182 **Surveillance of *Mycobacterium leprae* in Analamanga region of Madagascar**
D. Randriarimanana (Antananarivo, Madagascar), M. Andrinarison, T. Rasamoelina, F. Rakotomalala, A. Charlotte, L. Ramarozatovo, B. Cauchoix, J. Berland, F. Rapelanoro Rabenja*

9328 **Complete genome sequencing and identification of *Mycobacterium chimaera* by MALDI-TOF MS: a modified approach to discriminate *Mycobacterium chimaera* and *Mycobacterium intracellulare***
J. Bagnarino, V. Monzillo, D. Barbarini, A. Piralla (Pavia, Italy), A. Ghodousi, E. Tortoli, P. Marone*

Session accepted as Paper Poster Session

Infections in the prism of One Health

1131 **Comparison of multidrug-resistant *Salmonella enterica* serovar I 4,[5],12:i:- and *Salmonella enterica* serovar Typhimurium isolated from swine in the USA**
S. Gonzalez (College Station, United States), K. Norman, R. Harvey, H. Scott, S. Lawhon, J. Vinasco*

1229 **Comprehensive proteomics and active immunisation reveals that extracellular vesicles derived from *Streptococcus equi* subspecies *equi* as an effective candidate for vaccine platform**
H. Lee (Cheongju, South Korea), S. Kim, L. Sang-Yeop, S. Yun, S. Jun, H. Ro*

1955 **Healthy people in Zanzibar are frequently colonised at intestinal level with MDR *Enterobacterales* identical to those detected in poultry and retailed chicken meat**
T. Büdel, E. Kuenzli, O. Bernasconi, E. Campos-Madueno, J. Zinsstag, C. Hatz, A. Endimiani (Bern, Switzerland)*

2297 **Genetic diversity evident from comparative genome analysis of ESBL-producing *Escherichia coli* isolated from swine microbiomes in Cameroon and South Africa**
L. Njoungang Yontchoung Epse Founou (Yaounde, Cameroon), R. Founou Zangue, S. Essack*

2424 **Molecular evidence of bacteria with medical relevance in fleas parasitising cats and dogs**
G. Dougas (Athens, Greece), A. Tsakris, A. Mageropoulou, A. Priftis, T. Lytras, S. Beleri, E. Patsoula, M. Linou, C. Billinis, J. Papaparaskevas*

2556 **Antibiotic and biocide resistance among staphylococci causing skin and soft tissue infections in companion animals in Portugal**
S. Santos Costa (Lisbon, Portugal), R. Ribeiro, V. Oliveira, M. Serrano, C. Ferreira, C. Morais, M. Pomba, I. Couto*

2991 **Detection and antibiogram of *Escherichia coli* O157 from *Oreochromis niloticus* (Tilapia) sold in Ibadan, Nigeria**
S. Ogunleye (Ibadan, Nigeria), O. Adedeji, O. Ishola, O. Okunlade*

4048 **First report of CC5-methicillin-resistant *Staphylococcus aureus*-IV-SCCfus "Maltese clone" in bat guano**
M. Assia, A. Touati, A. Pantel, A. Sotto, C. Dunyach-Remy, J. Lavigne (Nîmes, France)*

4128 **Analysis of resistance transmission among humans and livestock using microbiome profiling**
H. Pai (Seoul, South Korea), M. Rho, J. Kim, S. Lim, M. Seo, B. Kim*

4273 **Incidence rates of multidrug-resistant indicator pathogens increase in hospitalised horses during stay**
A. Kauter (Berlin, Germany), A. Lübke-Becker, D. Kannapin, S. Stöckle, L. Epping, R. Köck, T. Semmler, H. Gehlen, B. Walther*

4374 **Recreational waters: a reservoir for Shiga toxin-producing *Escherichia coli*?**
L. O'Connor, C. Brehony, B. Hooban, K. Fitzhenry, N. Cahill, L. Burke (Galway, Ireland), P. Hickey, S. Keane, A. Mcnamara, M. Cormican, D. Morris*

4524 **Fast Point-of-Care biomimetic receptor-based biosensor for detection and quantification of zoonotic *Campylobacter***
M. Heyndrickx (Melle, Belgium), S. Givanoudi, J. Robbens, P. Cornelis, G. Wackers, K. Hertogs, D. Yongabi, M. Schöning, P. Wagner*

5334 **Piglets as a potential reservoir of atypical enteropathogenic *Escherichia coli* (aEPEC) with serotypes of human enterohaemorrhagic *Escherichia coli* (EHEC), including the O80:H2-A-ST301 (CH27-54) eae-ξ clone**
I. García-Meniño (Lugo, Spain), A. Mora Gutiérrez, M. Blanco, J. Blanco Alvarez, V. García Menéndez, S. Flament-Simon, D. Díaz-Jiménez, P. Alonso, J. Blanco*

5555 ***Atelerix algirus* as host of *Salmonella* species in Tenerife, Spain**
E. Izquierdo Rodríguez, N. Martín Carrillo (San Cristobal de La Laguna, Spain), E. Baz-Gonzalez, P. Foronda Rodríguez*

6314 **Genomic investigation of *Klebsiella pneumoniae* complex isolates recovered from pigs and humans in Thailand**
T. Leangapichart (Oslo, Norway), K. Lunha, J. Jiwakanon, S. Angkititrakul, J. Järhult, U. Magnussen, M. Sunde*

6647 **First report of colistin resistance in *Salmonella* spp. isolated from fresh minced meats and poultry faeces from primary production phase in Bosnia and Herzegovina**
A. Ibrahimagic (Zenica, Bosnia and Herzegovina), M. Fetahagić, J. Dizdarević, E. Idrizović, S. Uzunovic, A. Kapidžić, A. Šanjta-Reis, M. Gladan*

6715 **Cefotaxime-resistance in *Escherichia coli* strains isolated from poultry faeces in primary production phase**
M. Fetahagić (Zenica, Bosnia and Herzegovina), A. Ibrahimagic, J. Dizdarević, S. Uzunovic, A. Šanjta-Reis, A. Kapidžić, M. Gladan*

6736 **Antibiotic resistance in *Staphylococcus pseudintermedius* associated with skin and soft tissue infections in dogs and cats**
C. Morais (Lisbon, Portugal), S. Santos Costa, P. Abrantes, M. Pomba, I. Couto*

7137 **Development of a ery-C recombinant protein-based ELISA approach for differentiating brucellosis infected cattle from vaccinated ones**
W. Abdelwahab (Cairo, Egypt), M. Salah El-Din Diab, A. Amin Samy, J. Abd Elhalim Eljaky*

7180 **One Health investigation of *Chlamydia psittaci* in Denmark in 2019**
R. Petersen (Copenhagen, Denmark), S. Uldum, O. Angen*

7340 **Genomic insights into the dynamic of OXA-48-producing *Enterobacterales* in a veterinary hospital**
M. Haenni (Lyon, France), H. Boulouis, C. Pierre, E. Hirchaud, J. Madec*

7566 **Microbiome ecology drives the epidemiology of antibiotic resistance and the efficacy of antibiotic stewardship interventions: a mathematical modelling study**
D. Smith (Paris, France), L. Temime, L. Opatowski*

7774 **Public health impact of similar ESBLs/pAmpC-producing *Escherichia coli* causing urinary tract infections in non-related companion animals and humans**
A. Belas (Lisbon, Portugal), J. Menezes, L. Telo Da Gama, J. Carriço, M. Pomba*

7906 **Development of bovine herpesvirus 4-based vaccines as an antibiotic-free strategy to control bacterial infection in livestock**
H. Nichols (Plymouth, United Kingdom), M. Jarvis, A. Murphy, T. Mauch, S. Henderson, Y. Wezel*

8882 **Resistance and virulence determinants of faecal *Salmonella* spp. isolated from slaughter animals in Benin**
V. Dougnon (Abomey-Calavi, Benin), E. Deguenon, L. Baba-Moussa*

9384 **Development of attenuated bovine herpesvirus 4 as a safe, inexpensive, single-dose vaccine to control *Streptococcus suis* infection in domestic pigs**
K. Sealey (Plymouth, United Kingdom)*

9395 **Global spread of poultry-associated *Campylobacter jejuni* genotypes to the Peruvian Amazon**
B. Pascoe (Bath, United Kingdom), M. Kosek, S. Sheppard*

9529 **Identification of methicillin resistance in *Staphylococcus* spp. of dogs with pyoderma**
L. Guimarães, I. Silva, M. Antunes, C. Fonseca, C. Pesset, I. Teixeira, A. Santos, B. Penna (Rio de Janeiro, Brazil)*

Session accepted as Paper Poster Session

Intra-abdominal infections

267 **Acute cholangitis secondary to choledocholithiasis in older population: subtle presentation and severe illness**
A. Hamdi (Rochester, United States), S. Khalil, M. Fida, E. Beam*

507 **Evaluation of efficacy of antibacterial prophylaxis in case of paraproctitis**
S. Zyryanov, G. Rodoman, M. Ivzhits (Moscow, Russian Federation), O. Romashov, M. Chenkurov, G. Putsman*

1377 **Pyogenic liver abscess: predictive factors of unfavorable course**
G. Rossi (Paris, France), Y. Nguyen, L. Gasperini, E. Lafont, B. Rossi, E. Canoui, O. Roux, S. Dokmak, F. Bert, B. Fantin, A. Lefort*

1458 **A retrospective cohort study investigating the clinical features, outcomes and risk factors leading to a poor outcome in pyogenic liver abscesses (2017-2019)**
J. Cheaveau (Middlesbrough, United Kingdom), B. Tomlinson, J. Williams, I. Kubelka, M. Kalra, J. Widdrington*

1684 **A retrospective study of pyogenic liver abscess caused by *Klebsiella pneumoniae* as a primary pathogen: computed tomography and clinical differentiation**
S. Hong, Y. Jang (Incheon, South Korea), J. Eom, Y. Cho*

2309 **Microbiology and molecular characterisation of *Enterobacterales* from children enrolled in global, prospective, controlled paediatric clinical trials for complicated intra-abdominal and urinary tract infections for ceftazidime-avibactam**
R. Mendes (North Liberty, United States), T. Doyle, G. Stone, A. Gardner, M. Castanheira, J. Bradley*

2940 **What is the optimal timing and technique for the source control in the subgroup of septic shock patients with intra-abdominal infections?**
U. Önal, D. Akyol (Izmir, Turkey), A. Uyan, C. Bulut, G. Guliyeva, S. Chousein Memetali, D. Baskol, G. Şanlıdağ, M. Demir, M. Mert, D. Akdağ, M. Isikgöz Tasbakan, S. Ulusoy, O. Sipahi*

3352 **Optimal antimicrobial therapy duration for patients with acute cholangitis after successful drainage by Endoscopic retrograde cholangiopancreatography (ERCP)**
S. Haal, B. Ten Böhmer, S. Balkema, A. Depla, P. Fockens, J. Jansen, S. Kuiken, B. Liberov, E. Van Soest, J. Van Hooft, E. Sieswerda (Amsterdam, Netherlands), R. Voermans*

6406 **Outbreak of *Arcobacter butzleri*? An emerging enteropathogen**
C. Ruiz De Alegria Puig (Santander, Spain), M. Fernández-Martínez, D. Pablo-Marcos, J. Aguero, J. Calvo-Montes*

Session accepted as 2-Hour Oral Session

JARMILA JELÍNKOVÁ MEMORIAL SESSION - Early life infections: what, when and how?

1044 **No benefit with empiric aminoglycosides in paediatric febrile neutropenia: analysis of a nationwide cohort study**
B. Mcmullan (Randwick, Australia), G. Haeusler, L. Hall, C. Blyth, C. Jones, P. Konecny, K. Thursky*

5352 **Feasible approach to reduce antibiotic overuse in preterm neonates**
J. Armann (Dresden, Germany), L. Mense, B. Seipolt, M. Rüdiger, R. Berner*

5453 **Impact of the FILMARRAY gastrointestinal polymerase chain reaction panel on the clinical management of children with suspected acute bacterial-diarrhoea**
J. Truong (Paris, France), E. Leroux, M. Michel, J. Boize, P. Mariani, A. Cointe, M. Desmarest, L. Titomanlio, A. Faye, S. Bonacorsi*

6264 **Preliminary data on initial antimicrobial regimen from a prospective cohort study of sepsis in hospitalised neonates: the NeoOBS study**
W. Stöhr (London, United Kingdom)*

6294 **Initial clinical features from preliminary analyses of a global multi-centre prospective observational cohort of sepsis in hospitalised neonates: the NeoOBS study**
N. Russell (London, United Kingdom)*

6968 **Epidemiology and mortality of neonatal Group B streptococcal meningitis and sepsis in the Netherlands: a 30-year nationwide surveillance study**
M. Van Kassel (Amsterdam, Netherlands), D. Jamrozy, S. Teeri, S. Bentley, M. Brouwer, A. Van Der Ende, D. Van De Beek, M. Bijlsma*

7231 **Evaluation of T2MR for the diagnosis of bloodstream infections in paediatric patients**
B. Lucignano, L. Mancinelli, M. Onori, M. Agosta (Rome, Italy), E. Masiello, L. Lancella, A. Onetti Muda, P. Bernaschi*

7319 **Type I interferon in viral and bacterial infections in children**
A. Ouziel, S. Viel, L. Boisselier, P. Rebaud, R. Basmaci, N. Droz, T. Ginhoux, B. Kassai-Koupai, A. Belot, F. Subtil, S. Pons, K. Brengel-Pesce, Y. Gillet, E. Javouhey, T. Sophie (Lyon, France)*

8507 **Impact of intra-partum azithromycin on carriage of group A *Streptococcus* in Gambia: an *ad hoc* analysis of a double-blind randomised trial**
I. Jagne (Fajara, Gambia), A. Bojang, E. Jallow, E. Senghore, B. Camara, C. Oluwalana, S. Bah, A. Keeley, C. Turner, A. Sesay, U. D'Alessandro, C. Bottomley, T. De Silva, A. Roca*

8783 **Contribution of vaginal culture to predict early-onset neonatal infection in case of preterm premature rupture of membrane before 34 weeks' gestation**
I. Ben M Barek (Colombes, France), K. Sallah, L. Landraud, M. Schneider, C. Couffignal, L. Desfrère, L. Mandelbrot*

Session accepted as Paper Poster Session

LTBI: epidemiology, diagnostic and treatment

583 **Treatment of latent tuberculosis infection based on the interferon-gamma releasing assay in allogeneic stem cell transplant recipients**
J. Park (Seoul, South Korea), M. Bae, S. Bae, E. Choi, H. Park, S. Choi, S. Lee, Y. Kim, J. Woo, J. Lee, J. Lee, K. Lee, T. Shim, S. Kim*

1475 **An audit of latent tuberculosis management at a tertiary referral centre in Ireland**
J. O'Connell (Dublin, Ireland), J. Oguntuase, S. Mcconkey, E. De Barra*

1745 **Associations of *HLA* genotypes with adverse events of hepatitis and skin rash during treatment of latent tuberculosis infection**
S. Lee, J. Feng, C. Shu, S. Lin, T. Wang, C. Chen, W. Huang, Y. Wei, H. Wu (Kaohsiung, Taiwan), S. Hung, W. Su*

1892 **Tuberculosis remains a threat in Portuguese patients treated with anti-TNFα**
A. Martins (Porto, Portugal), C. Silva, J. Caldas, S. Almeida Lacerda Pereira, A. Sarmento, C. Abreu*

2109 **Tuberculosis prevalence and latent tuberculosis infection management in solid organ transplantation recipients: a part of national snapshot**
A. Ozgen Alpaydin, T. Yeter Turunc, V. Avkan-Oguz (Izmir, Turkey), F. Oner-Eyuboglu, E. Tukenmez-Tigen, İ. Hasanoğlu, G. Aydin, Y. Tezer-Tekce, S. Senbayrak, F. Kizilates, A. Altunsoy Aypak, S. Altunisik-Toplu, P. Ergen, B. Kurtaran, M. Isikgöz Tasbakan, A. Yildirim, S. Yildiz, K. Caliskan, E. Ayvazoglu, E. Dulundu, E. Seref Parlak, I. Akdemir, M. Kara, S. Turkkan, K. Demir-Onder, E. Yenigun, A. Turgut, S. Alisir Ecder, S. Paydas, T. Yamazhan, T. Egeli, R. Ozelsancak, A. Velioglu, M. Kilic, A. Azap, E. Yekeler, T. Cakir, Y. Bayindir, A. Kanbay, F. Kuscu, K. Memikoglu, N. Sen, E. Kabasakal, G. Ersoz*

2186 **Evaluation of QuantiFERON-TB Gold Plus test in the diagnosis of *Mycobacterium tuberculosis* infection**
M. Yasar (Izmir, Turkey), C. Cavusoglu, T. Aydoğan*

2583 **Healthcare workers in Kyrgyzstan and QuantiFERON-TB Gold Plus testing for the detection of latent tuberculosis infection**
C. Corbett (Gauting, Germany), N. Umetalieva, M. Vogel, H. Hoffmann*

3994 **Moxifloxacin for the treatment of latent tuberculosis infection in liver transplant candidates and recipients: a single-centre experience**
J. Sequeira, M. Fernandez Ruiz (Madrid, Spain), M. Hernandez Jimenez, R. San Juan Garrido, A. Manrique-Municio, Ó. Caso-Maestro, C. Loinaz, J. Aguado Garcia*

4253 **Differentiate diagnosis active TB infection and latent T B infection by using Interferon-γ released from CD8+ T cell and HBHA antigen**
Y. Ma (Xi'an, China), J. Tang*

4685 **Quantiferon-TB Gold Plus: comparison of interferon-γ detection by ELISA and CLIA assay**
G. Lombardi, F. Bisognin, S. Felici, P. Monari, E. Gatti, M. Re, P. Dal Monte (Bologna, Italy)*

4767 **Low Interferon gamma release assay conversion rate in healthcare workers after exposure to laryngeal tuberculosis**
K. Wissel (St. Gallen, Switzerland), E. Lemmenmeier, B. Mani, M. Schlegel*

5410 **Identification of recently acquired tuberculosis infection using QuantiFERON-TB Gold Plus: an exploratory study**
S. Pérez (Barcelona, Spain), M. Grijota-Camino, A. Sánchez-Montalvá, L. Barcia, S. Campos, V. Pomar, R. Rabuñal-Rey, M. Balcells, D. Gazel, N. Montiel, D. Vicente-Anza, I. Goic Barisic, T. Schön, J. Paues, I. Mareković, J. Cacho, A. Barac, D. Goletti, M. García-Gasalla, J. Barcala, L. Anibarro, F. Alcaide, N. Pallarès, C. Tebe, M. Santin*

5662 **Reporting of interferon gamma release assay results close to cut-off value**
D. Folkvardsen, Y. Holicka, T. Lillebaek, V. Nikolayevskyy (London, United Kingdom)*

6329 **Latent tuberculosis infection among household contacts of pulmonary tuberculosis cases in Nairobi, Kenya**
S. Odera (Nairobi, Kenya), M. Mureithi, O. Anzala, J. Oyugi*

6755 **Evaluation of STANDARD E TB-Feron ELISA for the diagnosis of latent tuberculosis infection in healthcare workers**
M. Lee (Seoul, South Korea), O. Kweon, Y. Lim, H. Kim, T. Kim*

7033 **Evaluation of IP-10 as a potential biomarker for the diagnosis of latent tuberculosis infection in vulnerable populations at high risk of TB**
L. Petrone, A. Navarra, E. Petruccioli, V. Vanini, G. Cuzzi, T. Alonzi, C. Pinnetti, U. Massafra, G. Baldi, F. Cantini, F. Palmieri, A. Antinori, D. Goletti (Rome, Italy)*

7253 **Performance evaluation of the new automated chemiluminescent immunoanalyser-based interferon-gamma releasing assay in comparison with the QuantiFERON-TB Gold Plus to detect latent tuberculosis infection**
H. Benmansour (Paris, France), S. Boyer, E. Bernard, F. Mougari, E. Lecorche, J. Gehanno, S. Pramil, M. Pestel-Caron, E. Cambau*

7452 **Latent tuberculosis infection screening in persons with new diagnosis of HIV infection in Italy: a multi-centre study promoted by the Italian Society of Infectious and Tropical Diseases**
D. Goletti (Rome, Italy), A. Navarra, E. Petruccioli, C. Cimaglia, M. Compagno, G. Cuzzi, G. De Carli, L. Fondaco, F. Franzetti, A. Giannetti, A. Gori, G. Lapadula, M. Lichtner, C. Mastroianni, V. Mazzotta, N. Orchi, P. Pavone, D. Piacentini, V. Pirriatore, E. Pontali, L. Sarmati, A. Spolti, E. Tacconelli, M. Galli, A. Antinori, A. Calcagno, E. Girardi*

7682 **Screening, diagnosis and treatment of latent tuberculous infection in rheumatic patients candidate to biological therapy: experience of a tertiary tuberculous control unit**
X. Martinez Lacasa (Terrassa, Spain), S. Martinez, G. Salvador, M. Pujol, R. Font I Canals, G. Grau, E. Padilla, E. Cuchí Burgos, T. Pribic*

8288 ***Mycobacterium tuberculosis* serostatus in patients with multiple sclerosis treated with anti-CD20/52: effects of treatment and lymphocytic asset on QuantiFERON assay results**
E. Zappulo (Naples, Italy), A. Buonomo, R. Colicchio, G. Scalia, C. Russo, M. Petruzzo, M. De Angelis, B. Pinchera, R. Scotto, V. Bresciamorra, P. Salvatore, I. Gentile*

8871 **Prevalence of latent tuberculosis in the adult population of the National Institute of Respiratory Diseases in the period 2016-2019 through an interferon-gamma release assays**
E. Becerril Vargas, M. Mujica Sánchez, M. Segura Del Pilar (Mexico city, Mexico), L. Narváez Díaz, J. Martínez Orozco, A. Sanchez Tinajero, A. Delgado Cueva, I. Gallardo Reyes, E. Flores Perez*

9257 **Failure to complete treatment for latent tuberculosis infection in Portugal, 2013-2017: geographic, socio-demographic and medical associated factors**
A. Sentís Fuster (Badalona, Spain), P. Vasconcelos, R. Sá Machado, J. Caylà, M. Guxens, V. Ricoca Peixoto, R. Duarte, I. Carvalho, C. Carvalho*

9263 **Interferon gamma release assay and tuberculin skin test agreement in latent tuberculosis infection diagnosis among healthcare workers at a tertiary Hospital in western Saudi Arabia**
F. Farahat (Jeddah, Saudi Arabia), J. Ossenkopp, M. Abdalaziz, M. Alshamrani, A. Alsaedi*

9375 **Current management of latent tuberculosis in multiple sclerosis patients treated with disease-modifying therapies**
M. Zingaropoli (Rome, Italy), P. Pasculli, M. Iannetta, V. Perri, F. Pauri, M. Altieri, A. Conte, C. Mastroianni, M. Ciardi*

9448 **Inappropriate use of interferon gamma release assays in a UK teaching hospital**
R. Mills (Manchester, United Kingdom), R. Bazaz, J. Wingfield Digby*

Session accepted as Mini-oral ePoster Session

Lyme disease: epidemiology, detection, therapy

1205 **Lyme disease spirochete variants and human endothelial cells determinants for transendothelial migration: development of an *in vitro* system using primary human microvascular endothelial cells**
C. Kamaliddin (Calgary, Canada), M. Ho, X. Tan, M. Castellanos Escamilla, R. Devinney, G. Chaconas*

2365 **Treatment of Erythema migrans with doxycycline for 7 days versus 14 days: a non-inferiority randomised open-label study**
M. Velušček, A. Gomišček, R. Blagus, T. Cerar Kišek, K. Boršič, M. Nahtigal Klevišar, E. Ruzic-Sabljic, D. Stupica (Ljubljana, Slovenia)*

3185 **Risk of mood-affective disorders and use of psychoanaleptics in Lyme Neuroborreliosis patients**
M. Tetens (Copenhagen, Denmark), R. Haahr, R. Dessau, K. Krogfelt, J. Bodilsen, N. Skaarup Andersen, J. Kjølseth Møller, C. Roed, C. Christiansen, S. Ellermann-Eriksen, J. Bangsborg, K. Hansen, T. Benfield, C. Østergaard, N. Obel, A. Lebech, L. Omland*

3835 ***Borrelia burgdorferi* sensu lato in *Ixodes ricinus* in Slovenia**
T. Cerar Kišek (Ljubljana, Slovenia), J. Šušnjar, V. Cvitković-Špik, M. Kodre, A. Steyer, V. Ivović, E. Ruzic-Sabljic*

4299 **Increasing incidence of Lyme borreliosis in France: Surveillance results from 2005 to 2018**
J. Figoni (Saint Maurice, France), L. Fournier, E. Moutengou, A. Septfons, C. Bonnet, H. De Valk, B. Jaulhac, T. Blanchon*

4928 **Evaluation of *OspC* as marker for direct diagnostic of Lyme disease**
V. Dolange (Gif sur Yvette cédex, France), D. Marcé, E. Ferquel, S. Simon, V. Choumet, N. Morel*

5072 **Detection of *Borrelia burgdorferi* cell-free DNA in human plasma samples for improved diagnosis of early Lyme borreliosis**
J. Branda (Boston, United States), J. Lemieux, L. Blair, A. Ahmed, D. Hong, S. Bercovici, T. Blauwkamp, D. Hollemon, C. Ho, K. Strle, N. Damle, T. Lepore, N. Pollock*

8643 **Descriptive study of Lyme disease suspected patients with discordant serological tests: negative enzyme immunoassay and positive immunoblot**
Y. Hansmann (Strasbourg, France), C. Sauton, N. Lefebvre, D. Christmann, E. Talagrand-Reboul, P. Boyer, B. Jaulhac*

Session accepted as Paper Poster Session

Markers and scores for sepsis

159 **Plasma levels of hepcidin, a potential biomarker during septic shock**
J. Olinder (Helsingborg, Sweden), C. Rydén Rubin, H. Herwald*

1829 **Human endogenous retroviruses as markers of severity in sepsis**
M. Mommert, O. Tabone, K. Brengel-Pesce, E. Cerrato, V. Cheynet, M. Denizot, P. Fournier, A. Guichard, M. Naville, G. Oriol, A. Pachot, A. Lepape, G. Monneret, F. Venet, J. Volff, J. Textoris, F. Mallet (Marcy-L'Etoile, France)*

1947 **Characterisation of the kinetics and LPS dose-response profiles of presepsin, procalcitonin and sTREM-1 as potential biomarkers for severe infections and sepsis in a human endotoxemia model**
L. Aulin (Leiden, Netherlands), A. Kleijburg, P. Hameeteman, H. Hijma, P. Van Der Graaf, M. Moerland, C. Van Hasselt*

4009 **Is the modified quick SOFA scale superior to quick SOFA in patients with diagnosed septic shock?**
D. Akyol (Izmir, Turkey), C. Bulut, U. Onal, A. Uyan, D. Akdağ, M. Mert, G. Şanlıdağ, D. Başkol, S. Chousein Memetali, G. Guliyeva, S. Uysal, M. Demir, S. Mermer, H. Sipahi, S. Ulusoy, O. Sipahi*

4375 **Comparison of different sepsis scoring systems and pathways: qSOFA, SIRS, Shapiro Criteria and CEC SEPSIS KILLS pathway in bacteraemic and non-bacteraemic patients presenting to the emergency department**
R. Sparks (Neutral Bay, Australia), R. Chavada, C. Trethewy, A. Harada*

4507 **Endotoxin activity assay as a better predictor for septic shock in critically ill cirrhotic patients**
V. Khillan (New Delhi, India), P. Badhan, R. Maiwall, P. Kale*

6223 **The REAnimation Low Immune Status Markers study: phenotypic and functional alterations of adaptive immune response in critically ill patients**
V. Moucadel (Lyon, France), F. Venet, J. Textoris, S. Blein, M. Rol, B. Canard, P. Cortez, C. Tipple, M. Lazou, A. Griffiths, E. Peronnet, A. Pachot, G. Monneret, T. Rimmelé*

8043 **Host transcriptome analysis accurately diagnoses and prognoses acute infections and sepsis in emergency department patients**
W. Bauer, K. Kappert, D. Lehmann, N. Galtung (Berlin, Germany), O. Liesenfeld, J. Wacker, R. Tauber, R. Somasundaram*

8477 **Lower concentrations of immunoglobulins (IgM, IgG and IgA) in patients with septic shock compared with sepsis**
D. Lendak (Novi Sad, Serbia), D. Mihajlović, M. Ubavić, A. Novakov Mikic, J. Boban, I. Mitić, S. Brkic*

9433 **Superior discriminatory capacity of qSOFA over SIRS criteria for predicting mortality and extensiveness of organ failure in sepsis**
S. Adamovic (Novi Sad, Serbia), D. Becejac, S. Mitic, M. Drljača, A. Vukelic, D. Lendak*

Session accepted as Mini-oral Flash Session

Multi-resistance: a new hope

1093 **Effectiveness of IV fosfomycin in critically ill patients with CRE infection and analysing the impact of variables on mortality in Indian setting**
S. Patil (Mumbai, India), P. Sathe, A. Bulle, S. Shah, S. Bhagat, H. Barkate*

1824 **Influence of empirical piperacillin-tazobactam on 30-day mortality in bacteraemia due to ESBL-producing versus non-ESBL-producing non-AmpC *Enterobacteriaceae***
D. Agüero González (Barcelona, Spain), L. Morata, M. Bodro Marimont, C. Garcia Vidal, P. Puerta, C. Cardozo, J. Ambrosioni, M. Hernández-Meneses, L. Linares, L. Albiach, E. Moreno, M. Chumbita, V. Rico Caballero, C. Pitart, C. Casals, A. Soriano, J. Martínez Martínez*

2958 **Use and impact of aminoglycoside empirical combination therapy in intensive care unit patients with ESBL-producing *Enterobacteriaceae* bloodstream infections: a multi-centre retrospective observational cohort**
L. Benetazzo, P. Delannoy, M. Houard, F. Lambiotte, A. Vachée, C. Batt, N. Van Grunderbeeck, S. Nseir, O. Robineau, A. Meybeck (Tourcoing, France)*

5353 **A systematic literature review of the efficacy and tolerability of polymyxins in resistant Gram-negative infections**
R. Dillon, A. Colosia, S. Khan, C. Masaquel, E. Mccann (Rahway, United States)*

5963 **Phenotype or genotype: association between mortality and minimum inhibitory concentration or beta-lactamase genes for patients with ceftriaxone non-susceptible *Escherichia coli* or *Klebsiella* spp. treated with piperacillin/tazobactam compared with meropenem**
A. Henderson (Brisbane, Australia), D. Paterson, M. Chatfield, P. Tambyah, D. Lye, P. De, R. Tzer-Pin Lin, K. Chew, Y. Mo, T. Lee, M. Yilmaz, R. Cakmak, T. Alenazi, Y. Arabi, M. Falcone, M. Bassetti, E. Righi, B. Rogers, S. Kanj, H. Bhally, J. Iredell, M. Mendelson, T. Boyles, D. Looke, N. Runnegar, S. Miyakis, G. Walls, M. Al Khamis, A. Zikri, A. Crowe, P. Ingram, N. Daneman, P. Griffin, E. Athan, L. Roberts, S. Beatson, A. Peleg, K. Cottrell, M. Bauer, K. Chaw, G. Nimmo, T. Harris-Brown, P. Harris*

5975 **Meropenem versus piperacillin-tazobactam for definitive treatment of bloodstream infections caused by AmpC beta-lactamase-producing *Enterobacter* spp., *Citrobacter freundii*, *Morganella morganii*, *Providencia* spp, or *Serratia marcescens*: a pilot multi-centre randomised controlled trial (MERINO-2)**
A. Stewart (Brisbane, Australia), D. Paterson, B. Young, D. Lye, J. Davis, N. Runnegar, M. Yilmaz, S. Archuleta, S. Kalimuddin, T. Harris-Brown, P. Harris*

7141 **Real-world treatment patterns observed in patients with carbapenem-resistant Gram-negative infections in Italian hospitals**
E. Durante Mangoni, C. Mastroianni, P. Viale, M. Bassetti, R. Citton, R. Fenoll, M. Roset, E. Mccann (Rahway, United States)*

7148 **Real-world treatment of patients diagnosed with serious infections due to carbapenem-resistant Gram-negative pathogens in Greek hospitals**
D. Georgopoulos, A. Safarika, E. Ischaki, E. Filiou, K. Mantzarlis, D. Athanasopoulos, R. Fenoll, E. Sánchez, E. Mccann (Rahway, United States)*

8766 **Impact of imipenem MIC in the outcome of patients with OXA-48 carbapenem-resistant *Klebsiella pneumoniae* bacteraemia**
M. Pérez-Rodríguez (Vigo, Spain), O. Lima, F. Vasallo Vidal, A. Sousa, A. Pérez-Landeiro, P. Diéguez, M. Suárez, R. Longueira, A. López-Domínguez, A. Nodar, M. Crespo*

Session accepted as Paper Poster Session

Multi-resistance: burden and risk factors

667 **The clinical and molecular epidemiology of non-carbapenemase-producing carbapenem-resistant *Enterobacteriaceae*: a case-case-control matched analysis**
R. Bouganim (Tel Aviv, Israel), L. Dykman, O. Fakeh, Y. Motro, R. Oren, T. Lazarovitch, R. Zaidenstein, J. Moran-Gilad, D. Marchaim*

1265 **Determining the burden of infectious diseases caused by carbapenem-resistant Gram-negative bacteria in Spain**
L. Morata (Barcelona, Spain), R. Canton Moreno, R. Huarte, J. Trillo Mata, R. Muñoz Peñin, A. González Calvo, M. Tort, X. Badia*

1454 **What are the risk factors associated with development of infection by carbapenemase-producing *Klebsiella pneumoniae*? ANGEL-KpS study**
Á. Cano Yuste (Cordoba, Spain), M. García, M. Gallo-Marín, I. Machuca Sanchez, I. Gracia-Ahufinger, M. Causse, J. Torre-Giménez, A. Frutos, L. Kindelán-Segador, E. Perez-Nadales, A. M.Natera, J. Castón, J. Rodríguez-Baño, L. Martinez-Martinez, J. De La Torre Cisneros, B. Gutiérrez-Gutiérrez*

2110 **Characterising clinical and bacterial factors of community-associated carbapenem-resistant *Enterobacteriaceae* infections**
C. Luterbach (Chapel Hill, United States), L. Komarow, W. Dai, M. Earley, L. Chen, B. Hanson, E. Cober, R. Salata, L. Bartelt, A. Naziripour, L. Abbo, G. Weston, B. Fries, K. Baum, R. Arias, C. Hill, R. Bonomo, C. Arias, B. Kreiswirth, V. Fowler, D. Van Duin*

2541 **Risk factors for bacteraemia from urinary tract infections caused by carbapenem-resistant Gram-negative pathogens in US hospitals (2014–2018)**
R. Shields (Pittsburgh, United States), H. Kanakamedala, Y. Zhou, B. Cai*

2633 **Deaths from bloodstream infections caused by antibiotic-resistant bacteria in Japan between 2015 and 2017: a population-level estimation**
S. Tsuzuki (Shinjuku-ku, Japan), N. Matsunaga, K. Yahara, A. Hirabayashi, T. Kajihara, M. Sugai, K. Shibayama, N. Ohmagari*

2934 **Sepsis due to Gram-positive bloodstream infections in critically ill patients during a five-year period (2012-16): dissemination of linezolid-resistant *Staphylococcus epidermidis* ST22 and predictors of fatality**
M. Papadimitriou Olivgeris (Lausanne, Switzerland), F. Kolonitsiou, V. Karamouzos, K. Tsilipounidaki, M. Plota, A. Nikolopoulou, F. Fligou, M. Marangos, E. Petinaki, I. Spiliopoulou*

2964 **Comparison of clinical manifestations, antimicrobial susceptibility patterns, and carbapenem resistance determinants between *Acinetobacter seifertii* and *Acinetobacter nosocomialis* isolated in Taiwan**
Y. Lee (Taipei, Taiwan), Y. Yang, J. Sun, L. Li*

4115 **Treatment patterns and healthcare resource use among hospitalised adults with carbapenem non-susceptible Gram-negative infections in a large US electronic health record database**
R. Dillon, T. Burton, A. Anderson, J. Seare, E. Mccann (Rahway, United States)*

4745 **Factors associated with extended-spectrum β-lactamases and carbapenem-resistant *Klebsiella pneumoniae* bloodstream infections: a five-year retrospective study**
A. Tofarides, P. Dimitriou, G. Nikolopoulos, E. Khattab, D. Kasapi, E. Christou, M. Constanti, P. Maikanti, D. Pieridou, C. Flourou, G. Tsiolakkis, M. Panopoulou, E. Christaki (Thessaloniki, Greece)*

4870 **An antimicrobial stewardship program in emergency department: clinical and epidemiological study of sepsis due to multidrug-resistant organism**
G. Marini (Reggio Emilia, Italy), S. Mezzadri, R. Corsini, N. Riva, M. Massari, G. Riussello, P. Giorgi Rossi, M. Ottone, C. Bonilauri, D. Lucchesi, A. Ferrari*

5248 **Risk of infection in patients with carbapenem-resistant *Enterobacterales* (CRE) rectal carriage: a comparative study of KPC and NDM CRE (CHIMERA Study)**
M. Falcone (Pisa, Italy), G. Tiseo, V. Galfo, C. Giordano, A. Leonildi, L. Saccaro, E. Tagliaferri, S. Barnini, F. Menichetti*

5328 **Microbial epidemiology of acute graft pyelonephritis**
P. Martinet, S. Rezig (Brest, France), L. Lanfranco, D. Tandé, Y. Le Meur, S. Ansart*

5437 **Clinical features related to *bla*KPC versus *bla*NDM carbapenem-resistant *Enterobacteriaceae* bacteraemia: are we talking about the same?**
P. Favier (Buenos Aires, Argentina), E. Serio, J. Maresca, C. Muñoz Soto, F. Pinilla Huayta, C. Raffo, L. Kumar, J. Perez, M. Lovigne, I. Primost, C. Blanco, D. Torres, A. Macchi*

7254 **Genomic and phenotypic diversity of carbapenemase-producing *Enterobacteriaceae* isolates from bloodstream infections: a multi-centre epidemiological, microbiological and genetic study in China**
B. Zheng (Hangzhou, China), H. Xu, Y. Xiao*

8557 **Evaluation of obesity as a risk factor for drug-resistant *Enterobacteriaceae* among hospitalised adults**
N. Narayanan (Piscataway, United States), S. Chaudhry, D. Vinarov, T. Bucek, L. Johnson, C. Mathew, T. Lin, L. Brunetti*

8685 ***Enterobacter* spp. infections: epidemiology and risk factors for resistance to third generation cephalosporins**
M. Garcia (San Jose, Costa Rica)*

9200 **Risk factors for carbapenem-resistant *Enterobacteriaceae* infections among rectal carriers in carbapenemase co-circulation setting: data from SPACE-CP study**
P. Favier (Buenos Aires, Argentina), E. Serio, J. Maresca, F. Pinilla Huayta, C. Muñoz Soto, D. Torres, C. Raffo, J. Perez, M. Gallino, L. Kumar, C. Blanco, A. Macchi, S. Nuñez*

Session accepted as Paper Poster Session

Mycobacterial pathogenesis and population studies

414 **A descriptive study of tuberculosis hospital admissions in Ireland**
J. O'Connell (Dublin, Ireland), E. De Barra, S. Mcconkey*

428 **Doramapimod treatment inhibits granuloma formation and improves antibiotic activity in *Mycobacterium tuberculosis*-infected mice**
C. Hölscher, J. Gräb (Cologne, Germany), J. Rybniker*

494 **Tuberculous lymphadenitis: are Asians at greater risk?**
T. Billard-Pomares, F. Méchaï (Bobigny, France), F. El Alaoui, J. Figoni, V. Walewski, O. Bouchaud, E. Carbonnelle, H. Cordel*

772 ***Mycobacterium tuberculosis* drives expansion of low-density neutrophils equipped with regulatory activities**
M. La Manna, B. Tamburini, P. Di Carlo (Palermo, Italy), A. Cascio, V. Orlando, S. Lo Sauro, F. Amatuzzo, R. Asselta, E. Paraboschi, B. Romanin, F. Dieli, N. Caccamo*

969 **The dominant model analysis of *Sirt3* genetic variants is associated with susceptibility to tuberculosis in a Chinese Han population**
T. Wu (Chengdu, China), L. Jiao, H. Bai, M. Wang, X. Hu, Z. Zhao, B. Ying*

1370 **Features and outcomes of tuberculosis among internally displaced people in East Ukraine**
O. Konstantynovska (Kharkiv, Ukraine), T. Synenko, A. Kuznietsova*

1630 **Knowledge about transmission and determinants of tuberculosis among Pakistani adults: evidence from demographic and health survey**
A. Rahman (Norrköping, Sweden), Y. Jahan*

1772 **Dalbavancin provides a second-line option for patients who fail conventional on outpatient parenteral antimicrobial therapy (OPAT): a case series in Aberdeen**
S. Falconer (Aberdeen, United Kingdom), N. Chafer*

1918 **Tuberculosis in renal failure: clinical presentation and outcome from a TB endemic area**
S. Kumar (Karachi, Pakistan), A. Naseem, Z. Babar*

2009 **Tuberculosis screening among newly arrived asylum seekers in Denmark**
K. Kristensen (Copenhagen, Denmark), M. Norredam, S. Graff Jensen, N. Seersholm, M. Joergensen, B. Bakir, F. Huber, E. Andersen, P. Ravn, T. Lillebaek*

2105 **Tuberculous spondylodiscitis: diagnostic and therapeutic approach**
F. Hammami, K. Makram, A. Zayni, K. Rekik, F. Smaoui, E. Elleuch, C. Marrakchi, M. Ben Jemaa (Sfax, Tunisia)*

2507 **On non-tuberculous mycobacteria in human alveolar macrophages**
I. João, V. Borges, S. Sousa, J. Gomes, L. Jordao (Lisboa, Portugal)*

2635 **Evolution of tuberculosis in children under five in our healthcare area**
E. Lozano Mochón (Bilbao, Spain), J. Unzaga, M. Urrutikoetxea-Gutierrez, M. Larrauri, M. Amezua, E. Garrote Llanos, J. Díaz De Tuesta*

2952 **The genetic architecture of tuberculosis susceptibility: comprehensive research synopsis, meta-analysis, and epidemiological evidence**
L. Jiao (Chengdu, China), J. Song, B. Ying*

3086 **Active case-finding of tuberculosis using mass chest radiography among prisoners in Songkhla Province, Thailand**
S. Ruangchan (Muang Songkhla, Thailand)*

3344 **Clinical characteristics, disease management and treatment outcome of paediatric tuberculosis in Denmark**
A. Nordholm (Copenhagen, Denmark), I. Larsen Holden, U. Hartling, P. Andersen, T. Lillebaek, I. Johansen*

3437 **Global metabolism indicates novel mechanism of *GreA*-induced dormancy in *Mycobacterium tuberculosis***
Z. Zhao (Guangzhou, China), W. Liang, D. Lin, S. Feng, X. Wen, C. Shen, L. Liang, J. Li, G. Tian*

3638 **PD-L1 expressing CD4+ and CD8+ T cells as a biomarker of tuberculosis disease and treatment response**
I. Kontsevaya (Borstel, Germany), M. Reimann, J. Hofmeister, F. Daduna, S. Dox, D. Schaub, B. Kalsdorf, E. Tolosa, L. Glau, J. Heyckendorf, C. Lange, P. Sanchez-Carballo*

3739 **A diagnostic accuracy study of a novel blood-based assay for identification of tuberculosis in people living with HIV**
E. Södersten, A. Mantsoki, R. Wyss, D. Persing, S. Banderby, L. Stromqvist Meuzelaar, J. Prieto, D. Gnanashanmugam, P. Khatri, S. Ongarello, S. Schumacher, C. Denkinger (Heidelberg, Germany)*

3846 **Dissecting the single-cell heterogeneity and subpopulation dynamics of quiescence in *Mycobacterium tuberculosis***
L. Singh (Paris, France), C. Chica, N. Pietrosemoli, G. Manina*

3858 **Serum C-reactive protein: a useful tool in the diagnosis of tuberculosis?**
T. Sullivan (London, United Kingdom), A. Brown*

3935 **Tuberculosis in the elderly: a current challenge**
P. Gijón, B. Alvarez Romasanta (Madrid, Spain), A. Valera, M. Veintimilla Yanez, S. Rodriguez, M. Ruiz Serrano, D. Garcia De Viedma*

3984 **Culture-negative „tuberculosis": which patients are at risk of misdiagnosis?**
O. Collas (London, United Kingdom), I. Suchett-Kaye, J. Barrett, T. Corrah*

4191 **Neutrophil extracellular traps and matrix metalloproteinases are increased in TB meningitis patients with contrast enhancement, ventricular dilatation and poor neurological outcome: findings from a paediatric cohort**
X. Poh (Singapore, Singapore), J. Hong, Q. Miow, Y. Wang, P. Thong, S. Tiong, M. Fukushima, K. Wong, S. Fong, T. Lim, T. Yeo, C. Ong*

4692 **Gene expression pattern analysis using dual-color RT-MLPA and integrative genome-wide association studies of expression quantitative trait loci (eQTL) for tuberculosis susceptibility**
J. Ai (Shanghai, China), H. Zhang, W. Zhang*

5335 **Pathogenic determinants of the *Mycobacterium kansasii* complex: an unsuspected role for distributive conjugal transfer**
F. Tagini (Lausanne, Switzerland), T. Pillonel, C. Bertelli, K. Jaton, G. Greub*

5343 **The diagnostic impact of adding a molecular-based algorithm to routine mycobacterial testing for non-respiratory samples at a reference Saudi Arabian laboratory**
A. Binjomah (Riyadh, Saudi Arabia), A. Alnimr, S. Zareah, K. Alasmari, S. Alharbi, A. Aljubran, E. Alshammari, A. Alharbi, K. Aldosari*

5428 **Diabetes and tuberculosis: the new emerging problem in middle-low-income countries like Colombia**
J. Garcia-Goez (Cali, Colombia), N. Romero-Rosas, L. Parra-Lara, R. Rivera, M. Peña*

5709 **Analyzing the public health impact of human immunodeficiency virus and tuberculosis co-infections in Brazil**
H. Pai (London, United Kingdom), A. Suseanu, O. Butt*

6438 **Leukocytes apoptosis in pulmonary tuberculosis patients with different treatment schemes**
O. Hovardovska (Kharkiv, Ukraine)*

6565 **Inhibition of metabolic signalling pathways controls inflammatory tissue destruction in tuberculosis**
R. Asher (London, United Kingdom), J. Friedland*

7046 **T cell immunomonitoring of pulmonary tuberculosis treatment using mass cytometry: a multi-centre prospective study in high-burden countries**
C. Chedid (Lyon, France), E. Kokhreidze, N. Tukvadze, S. Banu, M. Uddin, S. Biswas, G. Russomando, C. Diaz, N. Rakotosamimanana, P. Ranaivomanana, C. Razafimahatratra, P. Herindrainy, M. Hamze, B. Ismail, R. Bayaa, J. Berland, G. Delogu, T. Andrieu, H. Endtz, F. Ader, D. Goletti, J. Hoffmann*

7432 **Genital tuberculosis in a low prevalence setting: an unsuspected cause of infertility and severe gynaecological disease**
M. Veintimilla Yanez (Madrid, Spain), C. Rodriguez Grande, M. Ruiz Serrano, A. Alvarez-Uria, B. Alvarez Romasanta, B. Padilla, P. Munoz, P. Gijón, D. Garcia De Viedma*

7958 **Tuberculosis in elderly patients**
P. Caraux Paz (Villeneuve Saint Georges, France), A. Belkacem, M. Fernanda, A. Raffetin, K. Diallo, D. Jaafar, J. Naturel, O. Patey*

8353 **Identification of risk factors for extrapulmonary tuberculosis**
G. Aydin (Afyonkarahisar, Turkey), I. Akdemir, A. Azap, K. Memikoglu*

8403 **Burden of tuberculosis in Nepal: where do we stand?**
P. Shrestha (Kathmandu, Nepal)*

8478 **Diabetes and obesity reduce weight gain on tuberculosis treatment**
R. Banerjee (Liverpool, United Kingdom), J. Barrett, A. Whittington*

9005 **Collaborative organised database for extrapulmonary tuberculosis (CODE TB): common protocol for collecting data for characterisation of extrapulmonary tuberculosis: prevalence, demographics and risk factors**
R. Po (Paranaque City, Philippines), P. Guevarra, M. Gler*

9442 **Tuberculosis (TB) and cancer: why a previous TB infection may not alert us in a near future**
M. Pedromingo Kus (Madrid, Spain), J. Barragan Casas, A. Antoli Royo, T. Meiras Arriaga*

9623 **Neutrophilia is associated with lung tissue damage in pulmonary tuberculosis**
M. Miranda De Melo (Rio de Janeiro, Brazil), A. Rezende Moreira, C. Da Silva Monteiro, C. Lalucha, A. Almeida Silveira, T. Dutra, E. Costa Da Silva, A. Kritski*

Session accepted as Paper Poster Session

Mycobacterium tuberculosis genomics and evolution

822 **Pinpointing the genetic intra-host diversity of *Mycobacterium tuberculosis* and its determinants**
C. Genestet (Lyon, France), E. Hodille, A. Barbry, J. Berland, L. Jacob, G. Lina, S. Dray, S. Venner, O. Dumitrescu*

1389 **Extreme levels of diversity of *Mycobacterium tuberculosis* across a large genomic dataset: a map to disease pathogenesis and stress survival**
D. Papakonstantinou (Birmingham, United Kingdom), S. Dunn, A. Cunningham, M. O'Shea, A. Mcnally*

2088 **Evaluating the usefulness of whole genome sequencing in tuberculosis treatment decisions in a low-incidence clinical setting**
M. Park (London, United Kingdom), G. Satta, O. Kon*

2770 **Classifying the *Mycobacerium tuberculosis* complex into the main phylogenetics lineages (Seville, Spain, 2015-2019): is something changing?**
V. Gonzalez Galan, M. Torres Sanchez, L. Rafael, N. Veronica, M. Juan Francisco, R. Valencia, B. Eduardo, J. Aznar (Seville, Spain)*

3524 **Costs and impact of whole genome sequencing on tuberculosis diagnostics in a high prevalence and high MDR-TB burden country**
M. Vogel (Gauting, Germany), A. Iskakova, C. Utpatel, C. Corbett, H. Hoffmann, S. Niemann*

4256 **Stopping exposing rifampicin-resistant *Mycobacterium tuberculosis* to further rifampicin may lead to reversion to wildtype, preventing the evolution of compensating mutations**
P. Fowler (Oxford, United Kingdom)*

4483 ***fabG1 L203L*: clinical and public health impact of detecting a synonymous mutation conferring isoniazid resistance in routine WGS**
A. Telford (London, United Kingdom), H. Farooq, V. Nikolayevskyy, D. Wyllie, R. Myers, T. Walker, G. Smith, E. Robinson, E. Alexander*

5424 **Epidemiology of pyrazinamide-resistant tuberculosis in a low-incidence setting**
C. Martín Higuera (Madrid, Spain), E. Prieto Ávalos, B. Velazquez-Gonzalez, M. Ramírez-Vela, I. Muñoz Gallego, P. Lopez-Roa*

5620 **Whole genome sequence-based country-wide study reveals a high ongoing transmission of multidrug-resistant M*ycobacterium tuberculosis* in southern Brazil**
R. Salvato (Porto Alegre, Brazil), A. Reis, S. Schiefelbein, S. Salvato, R. Barcellos, E. Dalla Costa, P. Almeida Da Silva, J. Perdigao, A. Kritski, M. Rosa Rossetti*

5669 **Molecular characterisation of multiresistant *Mycobacterium tuberculosis* strains circulating in the state of Santa Catarina, Brazil from 2013 to 2017**
L. Nunes, M. Valmorbida, D. Rovaris, L. Lima, M. Scheffer (Florianopolis, Brazil), M. Bazzo*

5907 **Standardization of a *pncA* gene complementation in *Mycobacterium tuberculosis pncA*-knockout: tool for the study of the relationship between mutations in *pncA* and phenotypic parameters**
Y. Cauna (Lima, Peru), M. Zimic, P. Sheen*

6494 **Discovery of convergent mutations associated with *Mycobacterium tuberculosis* clinical and microbiological characteristics**
O. Lebedenko (Saint Petersburg, Russian Federation), M. Rotkevich, V. Zhuravlev, E. Chernyaeva, P. Yablonsky*

6525 **Genomic and structural protein characterisation of mutations conferring bedaquiline resistance in *Mycobacterium tuberculosis* clinical strains**
A. Spitaleri, S. Battaglia, J. Carter, A. Ghodousi (Pessano con Bornago, Italy), A. Cabibbe, P. Fowler, S. Hoosdally, D. Cirillo*

6811 **Efficient long-term storage of mycobacteria using conventional laboratory reagents**
F. Schramm (Strasbourg, France), É. Talagrand-Reboul, P. Boyer, A. Chabaud, B. Jaulhac, C. Koebel*

7271 **Genetic mutations in drug-resistant paediatric tuberculosis: experience from a paediatric tertiary care centre in north India**
P. Khurana (Delhi, India), K. Saigal, A. Ghosh*

7480 **Genomic analysis of multi-resistant *Mycobacterium tuberculosis* strains in France: evolution from 2006 to 2018**
F. Morel (Paris, France), G. Millot, J. Jaffre, A. Aubry, N. Veziris, J. Robert, V. Jarlier, E. Tagliani, W. Sougakoff*

8103 **Assessment of the performances of the novel BioNumerics-7.6 MTBC plugin for phylogenomic analysis and drug resistance prediction from *Mycobacterium tuberculosis* whole genomes**
W. Sougakoff (Paris, France), F. Morel, G. Millot, A. Aubry, J. Robert*

8350 ***Mycobacterium tuberculosis* genotypes' landscape in HIV-negative and HIV-positive tuberculosis patients in Russia**
A. Panova (Moscow, Russian Federation), G. Kaminski, A. Vinokurov, A. Shemetova, M. Shulgina, I. Vasilyeva*

9066 **Evaluation of PrimeStore molecular transport medium for long-term preservation of mycobacterial RNA at ambient temperature and subsequent detection of *Mycobacterium tuberculosis* Ag85B**
S. Matukane, B. Fourie (Pretoria, South Africa)*

9626 **Structural study of new *KatG* mutations selected on isoniazid-resistant strains of *Mycobacterium tuberculosis in vivo***
A. Bostanaru (Iasi, Romania), M. Mares*

Session accepted as Mini-oral Flash Session

New interventions for NTMs: from diagnosis to treatment

1395 **Pathogen Box screening identifies novel antimicrobials that target *Mycobacterium chimaera***
D. Cantillon (Brighton, United Kingdom), A. Goff, S. Taylor, S. Stoneham, S. Waddell*

2453 **Benzimidazole SPR719/720 is a potent new candidate for treatment of non-tuberculous mycobacterial infections**
L. Pennings (Nijmegen, Netherlands), T. Lister, D. Melnick, N. Cotroneo, I. Critchley, M. Pucci, T. Parr, S. Stokes, J. Van Ingen*

4307 **Performance of RealAccurate Quadruplex Mycobacteria PCR for detection of non-tuberculous mycobacteria in clinical samples**
J. Coppens (Edegem, Belgium), S. Van Goethem, K. Bergs, M. Michiels, L. Rigouts, H. Goossens, H. Jansens, V. Matheeussen*

5775 **ECOFFs for non-tuberculous mycobacteria: towards a EUCAST reference method and clinical breakpoints for antimicrobial susceptibility testing**
T. Schön, E. Chryssanthou, F. Maurer, H. Benmansour, S. Boarbi, P. Keller, M. Viveiros, D. Machado, J. Werngren, D. Cirillo, C. Giske, G. Kahlmeter, E. Cambau, J. Van Ingen (Nijmegen, Netherlands)*

6506 **Transglutaminase 2 inhibitors as a future intervention against non-tuberculous mycobacteria**
I. Palucci (Rome, Italy), A. Salustri, M. Sali, F. De Maio, L. Petrone, G. Fimia, M. Sanguinetti, D. Goletti, M. Piacentini, G. Delogu*

7078 **Synergistic activity of a three-drug combination against clinical isolates of *Mycobacterium abscessus* complex**
M. Fernandez (Barcelona, Spain), M. Monte, A. Roman, E. Portell Buj, A. López, G. Tudó, J. Gonzalez*

7553 **Preclinical evaluation of liposomes carrying bioactive lipids as an immune therapeutic tool against *in vitro* and *in vivo* infection with *Mycobacterium abscessus***
C. Riva (Soresina, Italy), N. Poerio, M. Rossi, F. De Santis, E. Tortoli, M. Fraziano, D. Cirillo*

8909 **Amikacin resistance mechanisms in *Mycobacterium abscessus***
M. Søndermølle (Paris, France), G. Sbaa, E. Lecorche, H. Benmansour, F. Mougari, E. Cambau*

9430 **Blocking mycobacterial efflux pumps might potentiate efficacy of antimycobacterial drugs *in vitro***
M. Ruth (Nijmegen, Netherlands), L. Pennings, J. Schildkraut, V. Koeken, H. Wertheim, J. Van Ingen*

Session accepted as 2-Hour Oral Session

One Health: the bacterial perspective

716 **Investigation of the prevalence of Verocytotoxigenic *Escherichia coli* (VTEC) contamination of private groundwater wells in Ireland**
E. Brosnan, L. Olaore, L. O'Connor, B. Hooban, K. Fitzhenry, N. Cahill, C. Chique, M. Ryan, D. Morris, P. Hynds, J. O'Dwyer, L. Burke (Galway, Ireland)*

2878 **Characterisation of methicillin-resistant *Staphylococcus aureus* strains isolated from purulent subcutaneous lesions of food-producing rabbits**
V. Silva (Vila Real, Portugal), P. Gómez, T. Sousa, A. Oliveira Da Silva, J. Pereira, C. Sabença, M. Vieira-Pnto, C. Torres, J. Capelo, G. Igrejas, P. Poeta*

3430 **Emergence of multiple ESBL-producing *Salmonella enterica* serovars in hospitalised horses due to an epidemic spread of a CTX-M-3 plasmid pSIEL-3**
Z. Dor, A. Shnaiderman-Torban, K. Kondratyeva, M. Davodovich, A. Rokney, A. Steinman, S. Navon-Venezia (Ariel, Israel)*

4467 **Genomic evidence that the recurrence of *Salmonella enterica* serovar Weltevreden in human salmonelloses in Asia is triggered by the aquatic environment**
Y. Hounmanou (frederiksberg, Denmark), A. Dalsgaard, T. Sopacua, G. Uddin, P. Leekitcharoenphon, R. Hendriksen, M. Larsen*

4696 **The transmission risk of multidrug-resistant organisms between pets and humans: n exploratory case control study protocol**
C. Hackmann (Berlin, Germany), P. Gastmeier, D. Gruhl, B. Laos De Henner, A. Lübke-Becker, S. Schwarz, R. Leistner*

5079 **Presence and zoonotic potential of *Escherichia coli* ST131 recovered from wildlife and food-producing animals, with high prevalence of *mcr-1* within porcine isolates**
I. García-Meniño (Lugo, Spain), A. Herrera, V. Gómez, S. Viso González, V. García Menéndez, D. Díaz-Jiménez, S. Flament-Simon, J. Blanco, A. Mora Gutiérrez*

7052 **One Health in practice: longitudinal screening of antibiotic residues, antibiotic resistance genes and zoonotic bacteria in soils fertilised with pig manure**
M. Heyndrickx (Melle, Belgium), T. Van Den Meersche, E. Daeseleire, E. Van Coillie, G. Rasschaert*

9068 **Antimicrobial resistant and enteropathogenic bacteria in 'filth flies': a cross-sectional study from Nigeria**
F. Onwugamba (Münster, Germany), A. Mellmann, N. Oluohaegbulam, F. Schaumburg*

9436 **Detection of pathogenic *Vibrio* species in estuary water samples in southwest Spain**
T. Trujillo-Soto (Cádiz, Spain), J. Ruiz-Cayuso, I. Guerrero Lozano, F. Galan-Sanchez, S. Papaspyrou, M. Rodriguez-Iglesias*

Session accepted as Paper Poster Session

Rarities and difficult to pronounce names

959 **An ultrasensitive rapid single molecule counting method detects *Bacillus anthracis* lethal factor directly in blood samples**
D. Straus (Chelmsford, United States), A. Tempesta, S. Gite, S. Schulz, B. Walsh, J. Bowers*

1722 **A rocky road: lessons learned from a case of disseminated *Rhodococcus hoagii* infection**
R. Hoffmann (Bellville, South Africa), C. Van Der Westhuizen, M. Newton-Foot*

2038 ***Streptococcus pneumoniae*: the chameleon of ocular diseases**
C. Andre (Chatou, France), J. Rouhana, M. Gilmore, P. Bispo*

2117 ***Lawsonella clevelandensis*: an emerging cause of vascular graft infection**
R. Ramesh (Hradec Kralove, Czech Republic), Z. Esquer Garrigos, K. Rodino, B. Pritt, M. Sohail*

2227 ***Chlamydia psittaci /C. abortus* detection in respiratory samples (England and Wales, 2012-2018)**
S. Mayet (London, United Kingdom), J. Day, L. Vaghji, A. Peace, D. Ready, V. Chalker, M. Chand, B. Afshar*

2945 **A study of *Bartonella bacilliformis* bacteraemia in asymptomatic individuals during an inter-outbreak period in an endemic region**
H. Biasizzo (Postojna, Slovenia), P. Ventosilla, C. Augusto Ugarte Gil, D. Moore*

3079 ***Bacillus subtilis*** **as a causative of true bacteraemia in patients with peritonitis**
C. Sassa (Tokyo, Japan), K. Sonobe, N. Ichimura, Y. Hadano, S. Tohda*

3930 **Failure to perform a repeat ascitic tap at 48 hours is associated with poor outcome in patients with spontaneous bacterial peritonitis**
J. Tan (London, United Kingdom), J. King, J. Ryan, M. Morgan, R. Westbrook, E. Wey*

5753 **An eight years-long experience of *Nocardia* spp. infection in Italy: does immunosuppression matter?**
M. Colaneri (Pavia, Italy), V. Monzillo, B. Mariani, A. Lombardi, E. Brunetti, M. Sambo, E. Seminari*

6649 **Toxigenic *Corynebacterium ulcerans* isolated from an Italian hunter**
G. Zambolin (Brescia, Italy), B. Saccani, G. Tomasoni, N. Latronico, A. Spinetti, L. Signorini, F. Castelli, Z. Youliang, Z. Nicola*

6796 ***Moraxella keratitis:*** **investigating emerging pathogenicity through clinical and microbiological findings and whole genome sequencing for virulence determinants**
G. Connolly (Dublin, Ireland), A. Curry, D. Jaen Luchoro, C. Murphy, T. Mcswiney, S. Knowles*

7302 ***Streptococcus suis*** **infection: a series of 37 cases from a community-based hospital, Thailand**
S. Pinsai (Bangkok, Thailand)*

7390 **Clinical features and outcomes of patients with *Elizabethkingia meningoseptica* infection: an emerging pathogen**
N. Nasir (Karachi, Pakistan), A. Umair*

7472 **Clinical spectrum of infections by new members of the *Staphylococcus aureus* complex**
A. Ang (Singapore, Singapore), K. Chew*

7648 **Melioidosis in patients suspected with recurrent tuberculosis: a disease in disguise**
R. Garg (Manipal, India), T. Shaw, C. Mukhopadhyay*

7884 **Impact of early infectious diseases intervention and microbiologically led antimicrobial therapy in patients with idiopathic granulomatous mastitis**
R. Ryan, R. Lever (London, United Kingdom), S. Morris-Jones, J. Franks, V. Rathbone, U. Mahadeva, M. Brown*

8056 **Low incidence of Gram-negative infections in people who inject drugs in Tennessee**
M. Veve (Knoxville, United States), G. Cooksey, B. Nabors, Z. Smith, M. Shorman*

8356 **Comparison of clinical characteristics and mortality between patients with pulmonary nocardiosis and patients with pneumonia**
I. Margalit (Petah Tikva, Israel), E. Goldberg, K. Muhsen*

9565 **Severe respiratory diphtheria caused by *Corynebacterium ulcerans*: lessons learned from a rare emerging infection**
R. Huq (Manchester, United Kingdom), R. Shortern, A. Jha, A. Cardozo, I. Chaudry, L. White, A. Muir, G. Amirthalingam, M. Chand, P. Jumaa*

9662 **Outbreak of mixed cases of gastrointestinal and cutaneous anthrax in the rural village of northern Luzon, Philippines, March 2017**
K. Lonogan (Baguio City, Philippines), A. De Guzman, V. De Los Reyes, N. Sucaldito, F. Avelino*

Session accepted as Paper Poster Session

Sepsis: an ever evolving story

1341 **Community and nosocomial sepsis in older adults with bacteraemia: a retrospective study in a geriatric ward**
M. Saottini, G. Orlando (Modena, Italy), O. Moioli, C. Mussi, M. Menozzi, M. Meschiari, E. Franceschini, C. Puzzolante, A. Bedini, M. Digaetano, C. Mussini, M. Bertolotti*

1362 **Bloodstream infections caused by strong biofilm-producing bacteria increase the risk of end-organ disease and mortality in patients with haematologic malignancies**
E. Di Domenico, F. Marchesi, I. Cavallo (Rome, Italy), L. Toma, G. Prignano, F. Pimpinelli, E. Papa, I. Terrenato, F. Ensoli, A. Mengarelli*

1531 **Clinical and microbiological characteristics and outcomes for community-onset sepsis patients in a teaching hospital in Latvia: a retrospective, single-centre, cohort study**
L. Puceta (Riga, Latvia), A. Grāmatniece*

3096 **Clinical characteristics and outcome of bloodstream infections in HIV-infected patients with febrile neutropenia: A case-control study**
P. Puerta (Barcelona, Spain), J. Ambrosioni, M. Hernández-Meneses, C. Cardozo, M. Chumbita, E. Moreno, N. Garcia-Pouton, F. Marco Reverte, J. Mensa, M. Rovira, J. Martínez Martínez, J. Esteve, A. Soriano, C. Garcia Vidal, J. Miró Meda*

3860 **Characteristics of bloodstream infections in patients with liver cirrhosis in a general hospital**
S. Nguyen (Béthune, France), P. Wallard, O. Oddoux, M. Anastay, D. Descamps*

4847 **Assessing the contribution of sepsis to mortality in Oxfordshire**
E. Pritchard (Oxford, United Kingdom), A. Walker, T. Peto, D. Crook, L. Peto, N. Fawcett, A. Brent*

5504 **Analysis of causes of death and mortality risk factors in extreme elderly patients with sepsis**
J. Delgado Correal (Rio de Janeiro, Brazil), R. Rufino, M. Fornasari, C. Alburquerque, M. Martins, P. Damasco*

5544 **Analysis of *Escherichia coli* phylotypes and known sepsis-causing sequence types in UK sewage reveals a direct link between sepsis rates and carriage of pathogenic sequence types in the community**
M. Toleman (Cardiff, United Kingdom), J. Mathias, A. Almusallam, D. Babenko*

5751 **Prospective evaluation of septic shock patients in a tertiary care educational university hospital: a series of 739 cases**
D. Akyol (Izmir, Turkey), C. Bulut, U. Onal, A. Uyan, D. Akdağ, M. Mert, G. Şanlıdağ, D. Başkol, S. Chousein Memetali, G. Guliyeva, S. Uysal, M. Demir, S. Mermer, H. Sipahi, S. Ulusoy, O. Sipahi*

6107 **Epidemiological changes in bloodstream infection in southern Spain during the last ten years: results from the PROBAC study**
P. Pérez-Crespo (Seville, Spain), L. Lopez-Cortes, P. Retamar Gentil, J. Lanz, D. Vinuesa García, E. Leon, E. Torres Martos, F. Galan-Sanchez, C. Natera, A. Del Arco, A. Sánchez-Porto, I. Gea-Lázaro, B. Becerril Carral, A. Reyes Bertos, J. Reguera Iglesias, I. Perez-Camacho, M. Guzman, A. Sousa-Dominguez, J. Goikoetxea, C. Armiñanzas Castillo, M. Mantecón, T. Marrodán-Ciordia, J. Fernandez-Suarez, L. Boix-Palop, M. Bustamante, F. Barcenilla Gaite, A. Bahamonde, A. Smithson Amat, E. Merino De Lucas, J. Rodríguez-Baño*

7246 **Epidemiology, risk factors and treatment of anaerobic bloodstream infections: a 7-year study**
R. Figueroa-Cerón, M. Macho, A. Gonzalez Sarria (Bilbao, Spain), C. Aspichueta, M. Urrutikoetxea-Gutierrez, F. Calvo Muro, J. Diaz De Tuesta*

8238 **Hospital admission for sepsis and mortality in Brazil from 2009 to 2018: analyzing 10 years of government database (Datasus) information**
R. Fleury, W. Freitas (Rio de Janeiro, Brazil)*

8431 **Epidemiology and risk factors for mortality in patients with *Pseudomonas aeruginosa* bacteraemia**
I. Perez-Camacho (Malaga, Spain), J. Ruiz-Mesa, I. Márquez Gómez, L. Caballero Martinez, B. Sobrino, L. Valiente De Santis, A. Plata Ciézar, J. Reguera Iglesias*

8461 **Clinical characteristics and treatment outcome of patients with sepsis treated in an infectious disease intensive care unit**
R. Novak (Zagreb, Croatia), M. Popović, B. Baršić, M. Santini, M. Kutlesa, V. Krajinović*

8962 **Dynamics and distribution of attributable and non-attributable mortality in *Staphylococcus aureus* bacteraemia**
R. Kühl (Basel, Switzerland), L. Morata, H. Seifert, S. Rieg, H. Kim, E. Kim, C. Liao, R. Tilley, L. Lopez-Cortes, M. Llewelyn, V. Fowler, G. Thwaites, J. Cisneros, M. Scarborough, E. Nsutebu, M. Gurguí, J. Pérez, G. Barlow, S. Hopkins, H. Ternavasio De La Vega, E. Torok, P. Wilson, A. Kaasch, A. Soriano*

Session accepted as 1-Hour Oral Session

Sepsis: from burden to treatment

892 **The effect of mesenchymal stem cells on the mortality of severe sepsis and septic shock: a promising therapy**
E. Alp Mese, Z. Gonen, K. Gundogan, A. Esmaoglu, L. Kaynar, A. Cetin, M. Karakukcu, M. Cetin, G. Kalın Ünüvar (Kayseri, Turkey), M. Doganay*

3882 **A randomised prospective clinical trial to assess the role of procalcitonin-guided antimicrobial therapy to reduce long-term infections' sequelae (PROGRESS)**
E. Kyriazopoulou (Athens, Greece), L. Liaskou-Antoniou, G. Adamis, A. Panagaki, G. Chrysos, L. Sybardi, Z. Alexiou, G. Poulakou, M. Lada, E. Giamarellos-Bourboulis*

4636 **Impact of rapid molecular detection of sepsis on time to optimal antimicrobial therapy in paediatric cancer patients at the National Cancer Institute, Egypt**
H. El-Mahallawy, E. Ebeid, S. Hassan, F. Naguib, R. Khedr (Cairo, Egypt)*

6277 **The global burden of sepsis in adults: updated systematic review and meta-analysis**
C. Fleischmann-Struzek (Jena, Germany), L. Mellhammar, N. Rose, A. Cassini, K. Rudd, P. Schlattmann, B. Allegranzi, K. Reinhart*

Session accepted as Paper Poster Session

Skin and soft tissue infections

19 **Genetic characterisation of co-circulating community *Staphylococcus aureus* and *Streptococcus pyogenes* causing skin and soft tissue infections in Gambia**
A. Keeley (London, United Kingdom), S. Bah, E. Armitage, E. Senghore, J. Manneh, S. Darboe, A. Sesay, B. Pichon, U. Schaefer, C. Turner, T. De Silva*

780 **Effectiveness of implementing a locally developed antibiotic use guideline for community-acquired cellulitis at a large tertiary care university hospital in Thailand**
R. Sirijatuphat (Bangkok, Thailand), P. Nookeu, V. Thamlikitkul*

845 **Characterisation of *Staphylococcus aureus* in soft tissue infections: relevance of PVL producers**
N. Leal, G. Vieira, N. Osório, C. Antunes Chaves, F. Rodrigues, A. Rodrigues (Coimbra, Portugal)*

1008 **Impact of underlying comorbidities on outcomes of patients treated with ceftaroline fosamil for complicated skin and soft-tissue infections: pooled results from three phase III clinical trials**
M. Wilcox (West Yorkshire, United Kingdom), M. Kantecki, J. Yan, M. Dryden*

1839 ***Actinotignum schaalii* in breast abscesses, an emerging pathology? Report on five cases**
L. Deroche (Poitiers, France), C. Nadeau, V. Huguier, M. Pichon, L. Broutin, P. Chloé, C. Burucoa, A. Michaud*

2051 **Comparison of genetic diversity in *Streptococcus pyogenes* isolates from Gambia and United Kingdom causing skin and soft tissue infections**
S. Bah (Sheffield, United Kingdom), A. Keeley, E. Armitage, E. Senghore, J. Manneh, L. Tilley, S. Darboe, A. Sesay, T. De Silva, C. Turner*

2202 **Exclusive oral post-surgical antibiotherapy is effective for infectious flexor hand tenosynovitis: a study of 127 patients**
C. Dujeux, A. Fournier, M. Malherbe, F. Guérin, G. Rochcongar, A. Baldolli, R. Verdon, J. Michon (Caen, France)*

2481 **Self-reported health status in ambulatory acute bacterial skin and skin structure infection patients who inject drugs, who received oral therapy with omadacycline or linezolid**
K. Lapensee (King of Prussia, United States), S. Chitra*

5500 **Acute rheumatic fever in children in Morocco: a prospective study**
S. Himri (Fes, Morocco), B. Oumokhtar, S. El Fakir, S. Atmani*

6260 **An epidemiological description of Panton-Valentine-leukocidin-positive *Staphylococcus aureus* (PVL-SA) at ambulatory health units of the Rhine-Ruhr metropolitan region in North Rhine-Westphalia, Germany**
C. Tellez-Castillo (Bochum, Germany), M. Griego, P. Göcke, R. Rujbr, U. Scharmann, C. Scharmann*

6327 **Cutaneous lesions due to *Staphylococcus aureus* in inflammatory bowel disease patients undergoing anti-TNFα treatment: molecular characteristics and strains comparison in different niches**
S. Hoche, C. Dunyach-Remy (Nîmes, France), E. Schowb, O. Dereure, R. Altwegg, A. Du-Thanh, J. Lavigne*

6560 **MRSA from skin and soft tissue infections in Poland**
M. Orczykowska-Kotyna (Warsaw, Poland), D. Żabicka, A. Skoczyńska, J. Empel*

6994 **Dalbavancin use in the United Kingdom: a multi-centre, retrospective evaluation of real-world use of an extended dosing interval lipoglycopeptide**
R. Neil (Glasgow, United Kingdom), K. Cartwright, J. Cunniffe, S. Curtis, C. Durojaiye, D. Enoch, S. Falconer, A. Guleri, R. Laing, A. Seaton, H. Sharp, L. Sheridan, S. Tiberi, B. White*

8111 **Biomarker profiles in streptococcal skin and soft-tissue infections with or without necrosis or shock: a prospective multi-centre study**
E. Rath (Bergen, Norway), S. Skrede, L. Palma Medina, K. Mosevoll, E. Saccenti, S. Jahagirdar, A. Norrby-Teglund, T. Bruun*

8645 **Characteristics and management of skin and soft tissue infections caused by Panton-Valentine leukocidin-producing *Staphylococcus aureus* (PVL-SA): a retrospective study of 99 cases**
A. Assaf (Lille, France), C. Loiez, M. Chopin, S. Panaget, A. Dozier, E. Faure, K. Faure, F. Vuotto*

9238 **Clinical characteristics and treatment of 255 patients hospitalised with bacterial cellulitis**
L. Lukic (Zagreb, Croatia), M. Mudrovčić, M. Puljiz, I. Pulijiz*

9419 **Factors contributing to the duration of hospitalisation of patients with bacterial cellulitis**
M. Mudrovčić (Zagreb, Croatia), L. Lukic, M. Puljiz, I. Puljiz*

Session accepted as Paper Poster Session

STIs: epidemiology, diagnosis, treatment

146 **Sexually-transmitted infections in soldiers: a cross-sectional assessment and a review of literature**
C. Gottwald, N. Schwarz, H. Frickmann (Hamburg, Germany)*

1066 **Triple site versus urine *only N. gonorrhoea/C. trachomatis* testing among Israeli MSM in the condom fatigue era: a prospective study**
D. Zoker, D. Turner, R. Ben-Ami, A. Adler, I. Singer, Y. Dizitzer, T. Halperin (Tel Aviv, Israel)*

1267 ***Mycoplasma genitalium* infections in men who have sex with men: prevalence and macrolide resistance in north-east Italy**
L. Clemente (Monfalcone, Italy), M. Drabeni, G. Moise, F. Fontana*

2001 ***Streptococcus pneumoniae*: an uncommon possible cause of male urethritis?**
F. Menotti, S. Comini, C. Crocillà, R. Sparti, G. Amarù, C. Solimine, A. Cuffini, V. Allizond, G. Banche (Turin, Italy)*

2332 **Detection and genotyping Lymphogranuloma venereum in Tenerife, Spain**
B. Pino-Calm, D. García Martínez De Artola (Santa Cruz de Tenerife, Spain), J. Alcoba-Florez, Ó. Díez Gil*

2339 **Prevalence of *Mycoplasma genitalium* and frequency of resistance to macrolides and fluoroquinolones in Tenerife, Spain**
B. Pino-Calm, D. García Martínez De Artola (Santa Cruz de Tenerife, Spain), J. Alcoba-Florez, Ó. Díez Gil*

2345 **Opportunistic screening for sexually-transmitted infections in young men with leukocyturia and negative urine culture in primary care**
I. Angulo López, A. Gonzalez Sarria (Bilbao, Spain), J. Aragón-Díez, M. Imaz Perez, L. Hernandez Ragpa, J. Alava Menica, J. Díaz De Tuesta*

2632 **Rapid detection of ciprofloxacin susceptible strains of *Neisseria gonorrhoeae:* an important guide for treatment**
C. Cox (Belfast, United Kingdom), J. Mckenna*

2993 **Genetic relatedness of ceftriaxone-resistant multidrug-resistant *Neisseria gonorrhoeae* isolates in Singapore**
N. Abdul Rahman (Singapore, Singapore), M. Chio, S. Goh, A. Tan, T. Koh, K. Ko*

3039 **The rapid method for detecting *Neisseria gonorrhoeae* and antimicrobial susceptibility**
J. Sakai (Moroyama-cho, Japan), N. Tarumoto, K. Imai, T. Maeda, S. Maesaki*

3110 **Inflammatory changes on routinely-performed Papanicolaou smear are more frequently associated with bacterial vaginosis**
S. Baka (Athens, Greece), A. Chasiakou, S. Demeridou, G. Kaparos, E. Kouskouni, V. Gennimata, A. Tsakris*

3904 ***Trichomonas vaginalis* trends for women and men in a national reference laboratory database**
E. Marlowe (San Juan Capistrano, United States), R. Kagan*

Abstract Categories 2020

3916 **Prevalence of *Mycoplasma genitalium* and macrolide resistance in Israel**
O. Treigerman (Iod, Israel), G. Prajgrod, D. Shasha*

4229 **High prevalence of sexually-transmitted infections among at-risk HIV-positive patients**
K. Lin, H. Sun, Y. Chuang, U. Wu, W. Liu, T. Lee (Taipei, Taiwan), S. Chang, Y. Chen, C. Hung*

4262 **Reduced clinical improvement after treatment for urethritis in men with azithromycin resistant *Mycoplasma genitalium***
J. Braam (Amsterdam, Netherlands), A. Van Dam, S. Bruisten, M. Van Der Loeff, M. Van Rooijen, H. De Vries, C. Vergunst*

4314 **Experimental evolution of high-level azithromycin resistance in *Neisseria gonorrhoeae* during morbidostat culture**
J. Laumen (Antwerp, Belgium), S. Manoharan-Basil, E. Verhoeven, S. Abdellati, I. De Baetselier, T. Crucitti, B. Xavier, S. Chapelle, C. Lammens, C. Van Dijck, S. Malhotra-Kumar, C. Kenyon*

4597 **Active search through multiplex PCR method for sexually-transmitted infections in patients with sterile pyuria**
H. Gil Campesino, L. Sante (San Cristobal De La Laguna, Spain), M. Callejón Fernández, E. Callejas Castro, M. Lecuona*

4606 **Comparison of ResistancePlus MG and pyrosequencing for macrolide resistance detection in *Mycoplasma genitalium* and evaluation of macrolide and fluoroquinolone resistance in Badalona, Spain**
B. Rivaya Sanchez (Badalona, Spain), C. Le Roy, G. Fernández Rivas, C. Casan, V. González, L. Matas Andreu, C. Bébéar, S. Pereyre*

4667 **Characterisation of *Neisseria gonorrhoeae* isolates using a core-genome multilocus sequence typing scheme**
P. Higgins (Cologne, Germany), J. Wille, H. Seifert*

4962 ***Mycoplasma genitalium* resistance against antibiotics in a Berlin MSM cohort tested with the Allplex MG & AziR Assay and Allplex MG & MoxiR Assay**
M. Obermeier (Berlin, Germany), S. Breuer, R. Ehret*

4992 **Prevalence of *Chlamydia trachomatis* and *Neisseria gonorrhoeae* at extragenital sites in the north metropolitan area in Catalonia**
C. Casan, G. Fernández Rivas, À. Hernández Rodríguez, M. Carrasco, G. Linares, B. Rivaya Sanchez (Badalona, Spain), N. Romaní Rodés, A. Fernández Navarro, L. Matas Andreu*

5100 ***Haemophilus influenzae* as the causing pathogen of epididymo-orchitis: a case report**
T. Demuyser (Brussels, Belgium), K. Vandoorslaer, S. Jacobs, L. Van Dijck, D. Pierard*

5138 **Incidence and predictors of *Chlamydia trachomatis, Ureaplasma urealyticum, Mycoplasma hominis* and *Mycoplasma genitalium* in patients with sterile pyuria**
A. Aggarwal (New Delhi, India), B. Dhawan, N. Wig, N. Vikram, M. Soneja, R. Chaudhry, A. Kapil*

5441 **Microbiological features of vulvovaginitis in prepubescent girls**
M. Damala, A. Nikolakopoulou, C. Anthoulaki (Athens, Greece), I. Koumpi, E. Prifti, L. Michala, N. Loukopoulou*

5482 ***Neisseria gonorrhoeae* transcriptome analysis: profiling molecular determinants of resistance**
H. Machado, G. Toledo-Silva, J. Martins, M. Schörner, L. Golfetto, R. Mazzon, M. Bazzo (Florianópolis, Brazil)*

5616 ***Mycoplasma genitalium* infections can comprise mixtures of both quinolone-susceptible and quinolone-resistant strains**
E. Sweeney (Herston, Australia), K. Lowry, C. Bletchly, G. Nimmo, D. Whiley*

5863 **Associaton between the detection of human papilloma virus and pathogens causing sexually-transmitted infections in woman in reproductive period**
I. Hadji Petrusheva Meloska (Skopje, Macedonia), K. Icev, A. Hadji-Petrusheva Jankijevikj*

5918 **Epidemiology of *Neisseria gonorrhoeae* antimicrobial resistance and evaluation of alternative antibiotics**
J. Yan (Hangzhou, China), S. Van Der Veen*

6274 **Bacterial STI-testing in the private sector in France, 2006-2018**
D. Viriot (Saint-Maurice, France), N. Ndeikoundam, E. Lucas, N. Dupin, B. De Barbeyrac, A. Bertolotti, C. Cazanave, S. Fouere, C. Pioche, F. Lot*

6596 **Detection rates of bacterial vaginosis and sexually-transmitted pathogens associated with genital discharge syndrome in the South-African private sector**
C. Kingsburgh (Pretoria, South Africa), K. Strydom, M. Kock*

6602 **The natural history of gonorrhoea infection: an illustrative review**
J. Whelan (Amsterdam, Netherlands), E. Beck*

6696 **Epidemiology and treatment outcome of *Neisseria gonorrhoeae* infections**
J. Parkes-Smith, C. Palmer, A. Jennison, V. Hicks, L. Ariotti, S. Bell, D. Whiley, A. Walker, G. Playford, A. Henderson (Brisbane, Australia)*

6727 **Does trichomonas hurt? A five-year comprehensive full-region study**
M. Berends (Groningen, Netherlands), D. Scoop, J. Weel, T. Schuurs*

6875 **Is *Lactobacillus crispatus* a marker of cytolytic vaginosis in women under 45-years old?**
L. Fontan, A. Yarci Carrión, S. Gómez De Frutos, A. Fraile Torres, L. Cardeñoso (Madrid, Spain), A. García*

6878 **High prevalence of Lymphogranuloma venereum in men who have sex with men in Alicante, south-east Spain**
V. Ortiz-De La Tabla (Alicante, Spain), G. Gázquez, A. Infante*

6898 **Clinical performance of the novel multiplex real-time PCR ResistancePlus MG FleXible: a cartridge-based assay for simultaneous detection of *Mycoplasma genitalium* and macrolide resistance**
M. Fernández-Huerta (L' Hospitalet de Llobregat, Spain), P. Salmerón, A. Silgado Gimenez, T. Pumarola-Suñé, M. Espasa, Y. Hoyos-Mallecot, J. Serra Pladevall*

6982 **Determination of prevalence of *Chlamydia trachomatis* in pregnant women between 15 to 25 years old at Hospital Universitario La Paz, Madrid, Spain**
B. Gómez Arroyo (Madrid, Spain), P. González Donapetry, C. Fabra Garrido, M. Dorado Criado, C. González Arboleya, E. Merino San Martín, C. Calvo Rey, M. De La Calle Fernández-Miranda, I. Quiles, J. García Rodríguez*

7009 **The role of using the UBU (Urethritis Basic Unit) and the FVU (First-Void Urine) in the quick diagnosis and adjustment of treatment in urethritis**
T. Martín Peñaranda (Donostia/San Sebastian, Spain), I. De La Caba, D. Grandioso Vas, M. Gómez Ruiz De Arbulo, P. Idigoras*

7040 **Single-locus-sequence-based typing of the *mgpB* gene reveals transmission dynamics in *Mycoplasma genitalium***
M. Fernández-Huerta (L' Hospitalet de Llobregat, Spain), J. Serra Pladevall, J. Esperalba, A. Moreno-Mingorance, C. Fernández Naval, M. Barberá, D. Aparicio, O. Pich, T. Pumarola-Suñé, J. Jensen, M. Espasa*

7075 ***Haemophilus influenzae/parainfluenzae* as triggers of urethritis in men: risk factors and characteristics of this emerging problem**
L. Fontan, A. Yarci Carrión, E. Navarro Lara, N. Zurita Cruz, L. Cardeñoso (Madrid, Spain), A. García*

7425 **Evaluation of ResistancePlus GC assay for the detection of *Neisseria gonorrhoeae* and markers associated with ciprofloxacin-susceptibility and resistance**
P. Salmerón (Barcelona, Spain), P. García, M. Viñado, B. Romero, J. Colomina Rodríguez, O. Martinez, G. Martin-Saco, N. Sanchez Oliver, E. Alcoceba, L. Villa, A. Torreblanca, T. Pumarola-Suñé, Y. Hoyos-Mallecot, J. Serra Pladevall*

7450 **Resistance to azithromycin in *Mycoplasma genitalium* from patients of a tertiary hospital from Madrid, Spain**
P. García Clemente, V. Guedez López, S. Román Soto (Madrid, Spain), J. Bernardino, E. Sendagorta, I. Quiles*

7506 **Antimicrobial susceptibility of *Neisseria gonorrhoeae* in southern Spain and co-infection with other sexually-transmitted pathogens**
L. Rojas, C. Gómez-Camarasa, A. De Salazar (Granada, Spain), F. Ferrer, E. Serrano-Conde*

7786 **Fluoroquinolone and Macrolide resistance-associated mutations in *Mycoplasma genitalium***
M. Oggioni (Milan, Italy), S. Uceda Renteria, L. Tartaglione, C. Melchionna, M. Maddeo, A. Orlandi, M. Cusini, G. Lunghi*

7849 **Genomic epidemiology and antimicrobial resistance surveillance of gonococci in Spain**
C. Francés-Cuesta (Valencia, Spain), J. Serra, A. Fabregat-Bolufer, B. Romero, T. Pumarola-Suñé, J. Colomina Rodríguez, J. Galán, F. Gonzalez-Candelas*

7904 ***Mycoplasma genitalium*: evaluation of macrolide resistance in a very large setting of sexually-transmitted infections**
A. Nava, E. Matarazzo, L. Colagrossi (Milan, Italy), P. Carlo Federico, D. Fanti*

8003 **Distribution of minimum inhibitory concentration of ceftriaxone to gonococcal strains in a reference sexually-transmitted disease clinic in Madrid, Spain**
C. Lejarraga (Madrid, Spain), B. Menendez, E. Tello, F. Geriz, O. Ayerdi, T. Puerta, M. Garcia, J. Ballesteros, P. Clavo, G. d'Elia, C. Rodríguez, J. Del Romero*

8110 **Characterisation of multidrug resistant *Shigella sonnei* isolated from men who have sex with men in Zagreb, Croatia**
J. Vranes (Zagreb, Croatia), N. Prazic, B. Bedenic, B. Matica, G. Zarfel, I. Mareković*

8114 **Antimicrobial susceptibility of *Neisseria gonorrhoeae* in Málaga, Spain**
F. Ana María, M. Valverde Troya, I. De Toro Peinado, M. Rojo Martin, B. Palop (Málaga, Spain), M. Mediavilla Gradolph*

8271 **Epidemiology, management, and costs of syphilis in Germany: a public health analysis**
R. Smit (Frankfurt am Main, Germany), B. Lohr, K. Hunfeld*

8300 **Molecular epidemiology of *Neisseria gonorrhoeae* clinical isolates in Reunion and Mayotte: lessons from the study of island populations**
H. Jacquier (Paris, France), G. Miltgen, D. Hoarau, O. Rollot, S. Bruniquet, N. Ndeikoundam, S. Kumanski, G. Ly Pat Yuen, O. Belmonte Garcia, B. Bercot, B. Roquebert*

8505 **Prevalence of resistance-associated mutations for ciprofloxacin in *Neisseria gonorrhoeae* and azithromycin and moxifloxacin in *Mycoplasma genitalium***
R. Nijhuis (Amersfoort, Netherlands), R. Duinsbergen, P. Godschalk*

8523 **Clonality and molecular resistance to tetracyclines of *Neisseria gonorrhoeae* among men who have sex with men using post-exposure prophylaxis with doxycycline**
B. Bercot (Paris, France), A. Braille, D. Carrette, I. Charreau, N. Schnepf, C. Delaugerre, L. Cotte, C. Bébéar, P. Gilles, C. Capitant, F. Raffi, J. Molina*

8966 **Drug-resistant *Neisseria gonorrhoeae* and *Mycoplasma genitalium* identified in the private healthcare sector in South Africa**
L. Maduna, R. Peters, C. Kingsburgh, K. Strydom, M. Kock (Pretoria, South Africa)*

Session accepted as Mini-oral ePoster Session

STIs: risk factors, diagnosis and treatment across the globe

443 **Prevalence and antimicrobial susceptibility of *Ureaplasma* species and *Mycoplasma hominis* in female patients in Korea: increasing trend of pristinamycin-resistant isolates**
J. Lee (Seoul, South Korea)*

2858 **Global prevalence estimates of syphilis among men who have sex with men: a systematic review and meta-analysis**
M. Tsuboi (London, United Kingdom), J. Evans, E. Davies, J. Rowley, T. Clayton, M. Taylor, D. Mabey, R. Chico*

4178 **High prevalence of azithromycin-resistant *Mycoplasma genitalium* in both urogenital and anal samples in men and women**
J. Braam (Amsterdam, Netherlands), D. Hetem, J. Brand, M. Van Rooijen, C. Vergunst, S. Kuizenga-Wessel, A. Van Dam, S. Bruisten*

4347 **Risk factors for *Chlamydia* and gonorrhoea infections and STI testing uptake amongst youth in Harare, Zimbabwe**
K. Martin (Brighton, United Kingdom), M. Marks, N. Buwu, E. Dauya, J. Muzangwa, I. Olaru, K. Kranzer, R. Ferrand*

6004 **Co-infection with *Mycoplasma* or *Ureaplasma* spp. among HIV-positive men who have sex with men in Taiwan**
T. Lee (Taipei, Taiwan), K. Lin, W. Liu, Y. Chen, H. Sun, Y. Chuang, U. Wu, S. Chang, C. Hung, P. Hsueh*

6063 **How long do patients with undiagnosed *Chlamydia* infection remain test positive? A lesson from the Finnish new variant of *Chlamydia trachomatis***
K. Rantakokko-Jalava (Turku, Finland), N. Hieta, M. Havana, S. Jokiranta*

6270 **A retrospective analysis of ceftriaxone-resistant *Neisseria gonorrhoeae* isolated in Japan nation-wide surveillance in 2013**
H. Mami (Tokyo, Japan), K. Aoki, Y. Ishii, K. Tateda*

6853 **Microbiology of tubo-ovarian abscess in a tertiary hospital in Spain**
C. Aspichueta (Bilbao, Spain), E. Lozano, M. Imaz Perez, F. Calvo Muro, J. Unzaga, M. Caceres, J. Díaz De Tuesta, M. Vidal-García*

7458 **Alarmingly high occurrence of multidrug resistance of *Mycoplasma genitalium* in a cohort of men who have sex with men using pre-exposure prophylaxis in Belgium (Be-PrEP-ared study)**
I. De Baetselier (Antwerp, Belgium), C. Kenyon, H. Smet, V. Cuylaerts, K. Wouters, M. Laga, B. Vuylsteke, T. Crucitti*

Session accepted as Paper Poster Session

The multiresistance strikes back

430 **Multidrug resistant Gram-negative infections among critically ill patients: analysis of baseline characteristics and factors associated with mortality**
E. Altawil (Riyadh, Saudi Arabia), F. Aljamman, A. Almeman*

1074 **Mortality outcome in critically ill CRO infection patients treated with polymyxin-B and its prediction based on morbidity and mortality scores**
S. Patil (Mumbai, India), B. Jibhkate, K. Shah, K. Parikh, A. Bhattacharya, N. Shinde, S. Bhagat, H. Barkate*

1486 **Colistin resistance increases fatality in bloodstream infections due to carbapenem-resistant *Klebsiella pneumoniae***
I. Balkan (Istanbul, Turkey), M. Alkan, A. Gokhan, M. Kuskucu, H. Ankarali, A. Karagoz, S. Şen, H. Yaşar, M. Biçer, R. Kara Ali, B. Mete, N. Saltoglu, F. Tabak*

1685 **Comparing outcomes and clinical characteristics associated with carbapenemase-producing and non-carbapenemase-producing carbapenem-resistant *Enterobacteriaceae* bacteraemia**
M. Hovan (Piscataway, United States), N. Narayanan, V. Cedarbaum, T. Bhowmick, T. Kirn*

1782 **A mortality prediction model for adult intensive care unit patients infected with *Klebsiella pneumoniae* in a tertiary hospital: a retrospective cohort study**
T. Tran (Antwerp, Belgium), D. Vu, H. Nguyen, T. Nguyen, N. Tran, G. Nguyen, H. Pham, D. Hong Gam, T. Trinh, S. Abrams, R. Bruyndonckx, S. Coenen*

4633 **No attributable mortality due to third generation cephalosporin resistance but common risk factors for mortality in patients with infections due to *Enterobacteriaceae***
J. Wang (Geneva, Switzerland), M. Zhou, J. Sauser, W. Zingg*

5114 **Carbapenem resistance associated with outcomes of bloodstream infections caused by *Enterobacteriaceae* in Guangdong province, China**
Y. Yang (Guangzhou, China), G. Chen, Y. Yang, M. El-Sayed Ahmed, M. Lin, X. Wen, G. Tian*

5134 **Clinical outcomes with the use of telavancin for methicillin-resistant *Staphylococcus aureus* bacteraemia with minimum inhibitory concentration >1 mcg/mL for vancomycin**
B. Garcia, J. Gonzalez (Piscataway, United States), Y. Kuo, S. Chaudhry*

5183 **Predictors of mortality in patients with bloodstream infections caused by metallo-ß-lactamases *Enterobacterales***
M. Falcone (Pisa, Italy), G. Tiseo, S. Barnini, C. Giordano, A. Leonildi, E. Tagliaferri, S. Sani, D. Bassoulis, G. Daikos, F. Menichetti*

5484 **Real-world multi-centre experience of meropenem-vaborbactam in patients treated for serious Gram-negative bacterial infections**
S. Alosaimy, A. Lagnf, S. Jorgensen, T. Morrisette (Detroit, United States), T. Carslon, J. Jo, K. Garey, D. Allen, V. Venugopalan, S. Davis, M. Veve, K. Claeys, V. Athans, S. Saw, J. Ortwine, C. Yost, R. Mynatt, J. Pogue, M. Rybak*

6927 **Increasing rates of antimicrobial resistance in *Escherichia coli* and *Klebsiella* sp. bacteraemia are not associated with a proportional increase in mortality**
A. Crawford, A. Breathnach, P. Riley (London, United Kingdom)*

7154 **Outcomes and predictors of outcomes of serious infections attributable to carbapenem-resistant Gram-negative pathogens in southern European hospitals**
D. Georgopoulos, E. Durante Mangoni, C. Mastroianni, P. Viale, F. Arnáiz De Las Revillas, M. Bassetti, R. Ferrer, E. Giamarellos-Bourboulis, E. Maseda, M. Salavert, S. Malachias, G. Bou Arevalo, A. Kyriakoudi, V. Tsolaki, D. Lopez, D. Gómez-Ulloa, N. Lara, E. Mccann (Rahway, United States)*

7163 **Resource utilisation associated with infections attributable to carbapenem-resistant Gram-negative pathogens in southern European hospitals**
E. Durante Mangoni, D. Georgopoulos, M. Fernández-Martínez, C. Mastroianni, P. Viale, M. Bassetti, R. Ferrer, E. Giamarellos-Bourboulis, E. Maseda, M. Salavert, E. Perivoliotis, G. Bou Arevalo, A. Koutsoukou, K. Mantzarlis, V. Lozano, D. Gómez-Ulloa, M. Roset, E. Mccann (Rahway, United States)*

7170 **Clinical characteristics and outcome of patients with plasmid-borne AmpC β-lactamase-producing *Klebsiella pneumoniae* bacteraemia at a tertiary medical centre**
Y. Huang (Taipei, Taiwan), S. Chou, Y. Cheng, Y. Lin*

Session accepted as Paper Poster Session

The path to sepsis

2045 **Quality of care indicators in the management of bloodstream infections caused by *Enterobacteriaceae*: systematic review (MAMBOO-E study)**
P. Malosso (Bologna, Italy), L. Scudeller, S. Ianniruberto, L. Bussini, R. Pascale, L. Pancaldi, M. Bartoletti, M. Gatti, P. Viale, M. Paul, M. Giannella*

2363 **A single dose of gentamicin in patients with sepsis in the emergency department is safe with regard to renal function**
M. Cobussen (Maastricht, Netherlands), M. Haeseker, P. Savelkoul, P. Stassen*

2425 **Assessing the impact of using sepsis bundle to salvage critically sick patients admitted with sepsis in a tertiary care hospital in India**
M. Srivastava (Gurugram(Haryana), India), S. Kumari, R. Datta*

4030 **How we achieved improvement in diagnosis and management of sepsis at County Durham and Darlington Foundation Trust, UK**
J. Malkin (Durham, United Kingdom), A. Robinson, L. Ward, C. Stocks, P. Latimer*

4965 **The external validity of an investigator-initiated randomised controlled trial comparing 7 versus 14 days for Gram-negative bacteraemia**
F. Koppel (Haifa, Israel), E. Baum, E. Khazem, R. Nassar, A. Turjeman, D. Yahav, L. Leibovici, A. Neuberger, M. Paul*

6224 **The Red Flag Sepsis Screening tool and Sepsis Six. defining the New Zealand Red Flag Sepsis population and introducing the change**
K. Walland (Hamilton, New Zealand), P. Huggan, O. Paul, R. Morell, A. Gwynne, S. Munroe, M. Neville*

6417 **High rate of microbiological clearance using intravenous fosfomycin combined regimens in infections caused by multidrug-resistant non-fermenting Gram-negative bacilli: clinical experience in an intensive care unit in Rome**
A. D'Avino (Roma, Italy), S. Mazzocchetti, E. Paciacconi, D. Menghetti, A. Schiattarella, D. Grande, P. Dionisi, A. Mastromatteo*

7555 **Improved prediction of mortality in sepsis using peripheral capillary oxygen saturation to estimate the respiratory dysfunction score: a cohort study**
J. Karlsson Valik (Stockholm, Sweden), L. Ward, A. Henriksson, H. Dalianis, K. Stralin, P. Naucler*

9323 **Impact of out-of-hours results and infection specialist intervention on the time to the first appropriate antimicrobial therapy in patients with Gram-negative bacteraemia: the South London CLAHRC cohort experience**
C. Suarez (London, United Kingdom), E. Vitale, E. Galiza, S. Mathur, D. Jeyarathnam, S. Goldenberg, J. Edgeworth, T. Planche*

Session accepted as 2-Hour Oral Session

Tuberculosis detection and treatment 2020

1831 **Detection of rifampin and isoniazid resistance using molecular testing to initiate an ethambutol-free 3-drug regimen in pulmonary tuberculosis: a French non-inferiority multi-centre randomised clinical trial**
N. De Castro (Paris, France), F. Méchaï, D. Bachelet, A. Canestri, V. Joly, M. Vandenhende, D. Boutoille, M. Kerjouan, N. Veziris, J. Molina, N. Grall, P. Tattevin, C. Laouenan, Y. Yazdanpanah*

2027 **Systematic validation of blood transcriptional biomarkers for active pulmonary tuberculosis in a high-burden setting: a prospective diagnostic accuracy study**
C. Turner, R. Gupta, E. Tsaliki, J. Roe, P. Mondal, G. Nyawo, Z. Palmer, R. Miller, B. Reeve, G. Theron, M. Noursadeghi (London, United Kingdom)*

3692 **Predicting the effect of single nucleotide polymorphisms on fluoroquinolone resistance in *Mycobacterium tuberculosis* by computational methods**
A. Brankin (Oxford, United Kingdom), P. Fowler, A. Walker*

3955 **A systematic review and meta-analysis of the risk of latent tuberculosis acquired during travel**
T. Diefenbach-Elstob, B. Alabdulkarim (Montreal, Canada), P. Deb-Rinker, S. Schofield, C. Abou Chakra, G. Schwarzer, I. Shrier, J. Pernica, C. Greenaway*

3961 **Standard-dose vs higher-dose of rifampicin in patients with tuberculosis: a meta-analysis**
V. Gentile (Rieti, Italy), L. Onorato, A. Russo, G. Di Caprio, L. Alessio, N. Coppola*

3979 **Employing tongue swabs and urine as clinical alternatives to sputum for *Mycobacterium tuberculosis* testing on a solid state nanopore sensor platform**
T. Morin, D. Alexander (Santa Cruz, United States)*

4341 **Extrapulmonary tuberculosis among migrants in Europe**
S. Hayward (London, United Kingdom), T. Noori, L. Nellums, S. Hargreaves, J. Friedland*

6902 **Cure rate comparison between rifampicin mono-resistant and multidrug-resistant tuberculosis: a retrospective multi-centre study from 1990 to 2017**
N. Riccardi, S. Villa (Milan, Italy), M. Ferrarese, P. Castellotti, M. Saporiti, A. Torre, F. Franzetti, L. Saderi, M. Raviglione, G. Sotgiu, L. Codecasa, G. Besozzi*

7693 **Evaluation of MediScout for the planning, operationalisation and monitoring of community-based tuberculosis active-case finding interventions: a prospective study in the Democratic Republic of Congo**
M. Faccin, O. Rusumba, F. Boutachkourt, O. Smaoui, J. Vanvolsem, F. Birembano, J. Kabuayi, M. Kaswa, E. Andre (Leuven, Belgium)*

8291 **Omics approaches for detection of unique features of *Mycobacterium tuberculosis* Beijing B0/W148 cluster**
J. Bespyatykh (Moscow), E. Shitikov, D. Bespiatykh, K. Klimina, M. Dogonadze, V. Zhuravlev, E. Ilina*

Session accepted as Paper Poster Session

Tuberculosis management and treatment

303 **Management of tuberculosis: are the practices homogeneous in Europe?**
F. Méchaï (Bobigny, France), H. Cordel, L. Guglielmetti, A. Aubry, M. Jankovic Makek, M. Viveiros, M. Santin, D. Goletti, E. Cambau*

844 **Investigation of a nosocomial pulmonary tuberculosis in a French university hospital**
E. Christelle (Lyon, France), C. Dorado-Cortez, O. Dumitrescu, F. Ader, P. Ceruse, C. Pasquet-Volkmann, B. Grisi, P. Vanhems, C. Dananché*

1065 ***HLA-DPB1*05:01* is associated with adverse drug reactions to rifampin and isoniazid for treatment of latent tuberculosis infection in South Korea**
E. Joo (Seoul, South Korea), S. Park, J. Kim, H. Cheong, H. Kim, J. Yeom*

1533 **Anakinra for the treatment of protracted paradoxical inflammation in HIV-associated tuberculosis**
A. Keeley (London, United Kingdom), V. Parkash, A. Tunbridge, J. Greig, P. Collini, W. Mckane, R. Tattersall*

2211 **Monitoring of difficult-to-treat tuberculosis patients in Ghana identifies additional pre-XDR and XDR cases**
I. Otchere (Accra, Ghana), P. Morgan, P. Asare, A. Wiredu, S. Gagneux, S. Osei-Wusu, D. Yeboah-Manu*

2457 **Clinical impact of ceasing isolation procedure using a single molecular test for suspected pulmonary tuberculosis in The Royal Melbourne Hospital**
L. Guillem (Reus, Spain), N. Zaidan, B. Lin, J. Denholm, D. Williamson, C. Marshall*

2681 **Targeting membrane transporters and energy metabolism in *Mycobacterium tuberculosis* through *in silico* drug repurposing**
L. Rodrigues (Lisbon, Portugal), P. Cravo, M. Viveiros*

2800 **A prospective randomised controlled trial comparing the effectiveness of smartphone video directly-observed therapy (VDOT) versus in-person DOT in newly-diagnosed pulmonary tuberculosis patients**
T. Saewong (Hatyai, Thailand), W. Keeratichananont*

2923 **Analysis of adherence to treatment among rural patients with various behaviour and social characteristics**
L. Parolina, N. Pshenichnaia (Moscow, Russian Federation)*

3050 **Monitoring and drug resistance analysis of isolated bacteria from tuberculosis patients in west China hospital of Sichuan University from 2010 to 2019**
Z. Liu (Sichuan, China)*

3077 **Benzofuroxans: discovering new compounds to fight tuberculosis**
D. Leite Campos (Araraquara, Brazil), G. Fernandes, J. Santos, F. Pavan*

3166 **Tolerance of pyrazinamide for the treatment of tuberculosis in elderly patients over 75 years**
S. Rousset (Toulouse, France), H. Guet-Revillet, C. Protin, J. Le Grusse, H. Derumeaux, P. Delobel, G. Martin-Blondel*

3250 **Intracellular drug targets in *Mycobacterium tuberculosis* revealed by a chemogenetic approach**
K. Tsui (Doha, Qatar), F. Sorrentino, G. Narula, A. Bojang, A. Lopez, X. Zheng, M. Remuiñan, Y. Av-Gay*

3869 **Multidrug-resistant tuberculosis imported into high-income countries: a GeoSentinel analysis, 2008–2017**
J. Eimer (Paris, France), C. Patimeteeporn, E. Caumes, M. Jensenius, E. Gkrania-Klotsas, M. Grobusch, L. Chen, E. Barnett, N. Hochberg, A. Duvignaud, E. Trigo Esteban, C. Greenaway, M. Gertler, K. Angelo, D. Hamer, H. Ásgeirsson*

4394 **Delamanid in MDR/XDR pulmonary tuberculosis in Russia: first experience**
A. Maryandyshev, S. Lorsanov, Z. Khaidarkhanova, D. Perkhin, O. Sveshnikova, A. Gaida, E. Khimova, V. Privolnev (Moscow, Russian Federation)*

4496 **Contribution of new tuberculosis cases for multidrug-resistant tuberculosis cases notification in Ethiopia**
D. Negia (Addis Ababa, Ethiopia)*

5087 **Are large cities at higher risk for tuberculosis drug resistance? A French appraisal**
S. Chiesi (Brescia, Italy), L. Guglielmetti, M. Bachir, A. Aubry, N. Veziris, N. Lemaitre, J. Robert*

5147 **eHealth use in tuberculosis: results from a systematic review and focus group interviews in six countries worldwide**
M. Ioana (Groningen, Netherlands), O. Akkerman, C. Louka, Y. Stienstra, J. Alffenaar*

5233 **Therapy directly observed by video for the supervision of tuberculosis treatment: experience in a series of patients from Cali, Colombia, 2019**
M. Tello-Cajiao, J. Garcia-Goez, N. Romero-Rosas, S. Ardila-Giraldo (Cali, Colombia), J. Mosquera-Hernández, L. Parra-Lara*

5629 **Quality of life and its determinants among pulmonary tuberculosis patients taking direct observation therapy in Kabul, Afghanistan**
A. Azizi (Kabul, Afghanistan), K. Hashemi*

6597 **Drugs repurposing: *in vitro* testing of licensed drugs to assess role against MDR/XDR-TB**
X. Gonzalo (London, United Kingdom), F. Drobniewski*

6967 **A model-based analysis identifies differences in phenotypic resistance between *in vitro* and *in vivo*: implications for translational medicine within tuberculosis**
O. Clewe, A. Faraj (Uppsala, Sweden), Y. Hu, A. Coates, U. Simonsson*

7220 **Graphene oxide-linezolid combination as potential new anti-TB treatment**
F. De Maio (Rome, Italy), V. Palmieri, A. Salustri, G. Perini, I. Palucci, M. Sali, M. Sanguinetti, M. De Spirito, G. Delogu, M. Papi*

7278 **Management of MDR-TB cases: roadmap towards TB elimination in Italy**
V. Marchese (Brescia, Italy), B. Formenti, G. Sotgiu, G. Pinsi, A. Matteelli*

7723 **Pharmacokinetic/pharmacodynamic informed assessment of pyrazinamide phenotypic resistance testing and *pncA* sequencing in multidrug-resistant tuberculosis**
J. Millard (Liverpool, United Kingdom), C. Nimmo, N. Mthabela, K. Chetty, K. Brien, T. Naidoo, S. Moodley, F. Karim, A. Pym, G. Davies*

8145 **Evaluation of efflux pump inhibitor combination with fluoroquinolones and aminoglycosides in resistant clinical isolates of *Mycobacterium tuberculosis***
F. Pavan (Araraquara, Brazil), C. Maríngolo, J. Grecco, D. Bellato*

8230 **Development and validation of a questionnaire to explore tuberculosis knowledge, attitudes and practices in foreign-born subjects from high tuberculosis-incidence countries**
M. Di Nuzzo, G. Valpiani, C. Morotti, E. Biagi, L. Massoli, M. Maritati, A. Grilli, A. Gallerani, N. Barp, C. Contini (Ferrara, Italy)*

8404 **The real-life impact of the Xpert MTB/RIF Ultra assay on the diagnosis of tuberculosis in a hospital in central Israel**
O. Schwartz, O. Yosseppowitch, Y. Maor (Holon, Israel)*

9237 **A study to determine the frequency of QT interval prolongation in people treated with bedaquiline for drug-resistant tuberculosis**
S. Isralls (London, United Kingdom), J. Millard, K. Baisley, E. Ngam, J. Der, A. Grant*

9245 **Designing a feasible, locally-appropriate socioeconomic intervention for TB-affected households in Nepal: a mixed-methods study**
K. Dixit (Kathmandu, Nepal), B. Rai, T. Aryal, S. Gurung, R. Dhital, M. Caws, T. Wingfield*

Session accepted as Paper Poster Session

Uncommon pathogens: the ancient and contemporary

995 **Melioidosis in French Guiana? Cases with a clinical isolate of *Burkholderia* sp., Cayenne, 2012 – 2018**
Y. Lambert (Cayenne, French Guiana), V. Sainte-Rose, C. Leborgne, B. Moreau, M. Demar*

1513 **First case of *Gemmiger formicilis* bacteraemia identified using partial 16S rRNA gene sequencing**
S. Tan (Singapore, Singapore), I. Wee, Y. Cao, N. Abdul Rahman, A. Tan, K. Ko*

1529 **First report of *bla*NDM-1 and *bla*OXA-181 harbouring *P. vermicola* from Nepal**
K. Haque (Narita, Japan), T. Matsumoto, T. Sekizuka, M. Kuroda, R. Sah*

2618 **Genomic characterisation of *Kerstersia gyiorum*, an isolate from a patient with acute otitis media**
A. Kruglov, V. Gostev (Saint Petersburg, Russian Federation), D. Likholetova, O. Generalova, S. Sidorenko*

3413 **Understanding the molecular history of an ancient *Pseudomonas* species isolated from a pharaonic Egyptian mummy: a genomic tale from the 11th dynasty of the middle kingdom**
M. El-Sayed Ahmed (Guangzhou, China), Y. Yang, C. Shen, X. Wen, Y. Yang, G. Tian*

3584 **A novel pathogenic bacteria *Scardovia wiggsiae* involved in early childhood caries: ultrastructural characterisation of biofilm by an original scanning electron microscopy protocol**
G. Vrenna, R. Papa, M. Artini, G. Familiari, P. Spigaglia, F. Barbanti, A. Salucci, G. Di Giorgio, M. Bossu, M. Relucenti, A. Polimeni, L. Selan (Rome, Italy)*

4926 **Persistence of *Tropheryma whipplei* colonisation: a longitudinal study in Italy**
A. Beltrame, L. Moro, G. Zavarise, G. Castagna, C. Piubelli, A. Ragusa, F. Formenti, F. Perandin, R. Silva, Z. Bisoffi (Negrar, Italy)*

5866 **A case of sepsis from a novel pathogen: *Haematospirillum jordaniae***
P. Annamaraju, S. Wade, B. Varatharaj Palraj (Rochester, United States)*

8383 ***Actinotignum schaalii* bacteraemia: a ten-year retrospective analysis in a tertiary hospital in Madrid, Spain**
A. Rojas (Madrid, Spain), L. Arroyo Pedrero, C. Sanchez Carrillo, L. Alcala, P. Muñoz*

8931 **Actinomycosis: a case series of 10 patients from an infectious diseases department**
J. Caldas, R. Filipe, J. Nuak, C. Piñeiro, C. Abreu, N. Rocha Pereira (Porto, Portugal), A. Silva-Pinto, A. Sarmento*

Session accepted as Paper Poster Session

UTI Dx and Rx

954 **Individualised autovaccination is a promising strategy for managing recurrent urinary tract infections in women**
E. Esteve-Palau, E. Martinez Franco, A. Gonzalez-Cuevas, A. Capella, E. Moreno, M. Alvarez, M. Garro, M. Carreras, M. Cespedes, D. Cuadras, V. Diaz-Brito Fernandez (Sant Boi, Spain)*

1439 **Risk factors for hospital readmission following complicated urinary tract infection: a multinational, retrospective cohort study**
T. Babich (Petah Tikva, Israel), N. Eliakim - Raz, A. Turjeman, M. Pujol, J. Carratalà, E. Shaw, A. Gomila, C. Vuong, I. Addy, I. Wiegand, S. Grier, A. Macgowan, C. Vank, N. Cuperus, L. Van Den Heuvel, L. Leibovici*

1706 **Extended spectrum beta-lactamase producing *Enterobacteriaceae* urinary tract infections: is cefoxitin an effective therapy?**
W. El Nekidy (Abu Dhabi, United Arab Emirates), M. Abdelsalam, A. Nusair, R. Dajani, R. El Lababidi, I. Ghazi*

2167 **Sensitivity of C-reactive protein and procalcitonin to diagnose urinary tract infections in nursing home residents**
S. Kuil (Amsterdam, Netherlands), S. Hidad, J. Fischer, J. Harting, C. Hertogh, J. Prins, F. Van Leth, M. De Jong, C. Schneeberger*

2362 **Acute cystitis symptom score questionnaire for patient-reported outcome measure in female patients with acute uncomplicated cystitis: clinical validation as part of a phase III trial comparing antibiotic versus non-antibiotic therapy**
J. Alidjanov, A. Overesch, D. Abramov-Sommariva, M. Höller, H. Steindl, F. Wagenlehner, K. Naber (Straubing, Germany)*

3187 **Efficiency of antibiotic prophylaxis in recurrence of UTI among kidney transplant recipients**
F. Runyo (Paris, France), O. Aubert, P. Parize, H. Lecuyer, L. Amrouche, R. Sberro Soussan, C. Legendre, C. Charlier, A. Scemla*

3191 **Urinary tract infections in nursing homes in the era of multidrug resistance: a 4-year study**
E. Riquelme-Bravo (Albacete, Spain), L. Robles Fonseca, C. Sáinz De Baranda Camino, J. Parra Martinez, V. Solves Ferriz*

3617 **Presentation, treatment and natural course of severe symptoms of urinary tract infections measured by a smartphone app**
A. Vellinga, K. Farrell (Galway City, Ireland)*

3710 **French Urinary Tract Infections in Healthcare Facilities (FURTIHF): an historic cohort**
L. Grammatico-Guillon (Tours, France), S. De Lafforest, A. Magnier, F. Saint, F. Bruyere*

4171 **Usefulness of escalation therapy in urinary tract infection caused by extended beta-lactamase-producing *Escherichia coli* with bacteraemia**
T. Shindo (Kobe, Japan), H. Nishioka*

4230 **Acute bacterial prostatitis due to *Escherichia coli*: clinical characteristics and outcomes in patients treated with or without β-lactam antibiotics: a cohort study**
L. Gisbert (Barcelona, Spain), H. Monzon, B. Dietl, T. Moreno-López, L. Boix-Palop, M. Xercavins Valls, E. Calbo Sebastian*

4279 **Epidemiology and clinical characteristics of upper urinary tract infections in infectious diseases emergency department of a tertiary teaching hospital in Slovenia**
K. Nadrah (Ljubljana, Slovenia), M. Logar*

4437 **High utility of Gram-stain of urine specimens for guiding empiric clinical management of pyelonephritis**
K. Oh (Kobe, Japan), K. Egami, C. Nishio, H. Goshima, H. Konishi*

4474 **Urinary tract infection caused by *Enterococcus* spp.: risk factors and mortality**
E. Alvarez Artero (Palencia, Spain), A. Campo Núñez, I. García-García, M. García Bravo, O. Cores Calvo, I. Galindo Pérez, J. Pendones Ulerio, A. López Bernús, M. Belhassen-García, J. Pardo Lledias*

6441 **Phenotypic and genotypic comparison between *Escherichia coli* isolates causing recurrent and sporadic cystitis**
V. Nicolas (Rouen, France), S. Dahyot, M. Leoz, F. Caron, F. Gravey, S. Le Hello, R. Fabre, K. Alexandre, M. Pestel-Caron*

6594 **Methenamine: an audit of its use for recurrent UTIs in a large UK trust**
N. Mccann (London, United Kingdom), M. Arias, N. Sweeney, P. Panesar, M. Pakzad, S. Logan*

6683 ***In vitro* susceptibility of fosfomycin in *Aerococcus* spp. isolated from urine samples**
I. Angulo López (Durango, Spain), E. Ugalde Zarraga, J. Aragón-Díez, D. Fernández-Vecilla, L. Lasa Epelde, J. Díaz De Tuesta*

6760 **Differentiation of phenotypic and genotypic characteristics of uropathogenic *Escherichia coli* isolates in acute and recurrent phases of urinary tract infection**
M. Pooya (Tehran, Iran), M. Saleh, A. Abd, H. Mazaheri, E. Khosravi, A. Abdollahi, S. Bouzari, M. Mardani Dashti*

6829 **Heroes and villains: the dynamics of antibiotic-uropathogens interactions during recurrent urinary tract infections management**
M. Vallée (Poitiers, France), P. Aldridge, A. Mz Tan, C. Mowbray, C. Walton, C. Harding, J. Hall*

6975 **Prevalence of fosfomycin resistance among *Escherichia coli* and *Enterococcus faecalis* isolates causing urinary tract infection in 34 primary care units in Brazil**
I. Van Der Heijden (Sao Paulo, Brazil), A. Natario, C. Rodrigues, R. Beltrame, F. Fonseca, S. Figueiredo Costa*

7574 **Clinical effectiveness of temocillin in a French university hospital**
E. d'huart, F. Meyer, B. Demoré, A. Charmillon (Vandoeuvre lès Nancy, France)*

7616 **Prevalence of ST131 in community-acquired *Escherichia coli* urinary tract infections in Gauteng, South Africa**
K. Hoog, J. Pitout, E. Hoosien, M. Ehlers, M. Kock (Pretoria, South Africa)*

8739 **Bacteriological profile of urinary tract infection in a rural area in Uganda**
F. Carrasco (Madrid, Spain), J. Cuadros, D. Roca, M. Górgolas, R. Perez Tanoira*

Session accepted as Paper Poster Session

Zoonotic infections around the world

136 **Microscopic agglutination test in determining leptospirosis seroprevalence in Western Province, Sri Lanka**
T. Giguruwa Gamage (Galle, Sri Lanka), M. Weerasekera, N. Ranasinghe, C. Gamage, C. Marasinghe, N. Fernando, L. Karunanayake, C. Gunasekara*

453 **Value of the CXCL13 ELISA and a CXCL13 lateral flow immunoassay in the diagnosis of Lyme neuroborreliosis**
K. Ziegler (Nuremberg, Germany), A. Rath, C. Schoerner, R. Meyer, T. Bertsch, F. Erbguth, J. Steinmann, J. Held*

538 **Hepatosplenic bartonellosis in immunocompetent adults: a case series and literature review**
F. Berteau (Brest, France), R. Mahieu, P. Le Turnier, N. Jean Baptiste, L. Quaesaet, D. Tandé, B. Rouvière, D. Boutoille, S. Ansart, P. Tattevin*

711 **Association of statin use and microbiological and clinical characteristics of early Lyme borreliosis**
M. Velušček, R. Blagus, T. Cerar Kišek, E. Ruzic-Sabljic, F. Strle, D. Stupica (Ljubljana, Slovenia)*

758 **Increasing trend of leptospirosis in an area of northern Spain (1986-2019)**
M. Echeverria Irigoyen (San Sebastian, Spain), M. Montes, M. Salicio, L. Pineiro, T. Martín Peñaranda, G. Cilla*

1397 **Anaplasmosis in Poland: underestimated disease?**
A. Moniuszko (Bialystok, Poland), J. Dunaj, P. Czupryna, S. Grygorczuk, J. Zajkowska, M. Kondrusik, S. Pancewicz*

1873 **Spatiotemporal mapping of *Bartonella bacilliformis* in Peru and qualitative analysis of local perceptions and understanding of the disease**
N. Kokkinos (London, United Kingdom), D. Moore, C. Munayco Escate, C. Augusto Ugarte Gil*

1882 **Murine typhus, a step beyond the clinic: how does it affect us in the 21st century? Epidemiology in Spain (1997-2015)**
B. Rodríguez-Alonso, H. Almeida, M. Alonso Sardón, V. Velasco-Tirado, Á. Romero-Alegría, A. López Bernús (Salamanca, Spain), C. Carranza-Rodríguez, M. Del-Río-García, N. Casado-Espada, A. García-Pérez, J. Chelea, P. Colina-Azofra, J. Perez Arellano, M. Belhassen-García*

1920 **Leptospirosis registry: LeptoScope. A novel global registry for emerging leptospirosis infections**
F. Köhler (Cologne, Germany), M. Späth, J. Hoyer-Allo, O. Cornely, F. Schaefer, R. Müller, V. Burst*

2079 **Neurological manifestations of rickettsiosis**
F. Hammami, K. Makram, A. Zayni, K. Rekik, F. Smaoui, E. Elleuch, C. Marrakchi, M. Ben Jemaa (Sfax, Tunisia)*

2236 **Clinical features of acute Q fever in Réunion Island: a retrospective cohort study**
A. Aubin, C. Eldin (Marseille, France), E. Braunberger, J. Jaubert, Y. Koumar, M. Moiton, P. Poubeau, N. Zemali, P. Gerardin, A. Bertolotti*

2862 **Identification, genotyping and antimicrobial susceptibility testing of *Brucella* spp. isolated from livestock in Egypt**
W. Abdelwahab (Cairo, Egypt)*

2949 **Evaluation of effect of combination chemotherapy with tetracycline and fluoroquinolone for Japanese spotted fever**
S. Sakabe (Ise, Japan), Y. Nakanishi, H. Toyoshima, K. Azuma, T. Nakagawa, N. Yamazoe, H. Tanaka*

3058 **Validation of serum procalcitonin measurement for the diagnosis of rickettsial infections disease**
S. Sakabe, H. Tanaka (Ise, Japan), Y. Nakanishi, H. Toyoshima*

3184 **Lyme neuroborreliosis epidemiology in Denmark, 1996 to 2015**
M. Tetens (Copenhagen, Denmark), R. Haahr, R. Dessau, K. Krogfelt, J. Bodilsen, N. Skaarup Andersen, J. Kjølseth Møller, C. Roed, C. Christiansen, S. Ellermann-Eriksen, J. Bangsborg, K. Hansen, T. Benfield, C. Østergaard, N. Obel, L. Omland, A. Lebech*

3259 **Serum levels of neutrophil elatinase-associated lipocalin in acute brucellosis and brucellar spondylodiscitis**
S. Sumer, N. Aktug Demir, L. Demir, D. Findik, S. Kolgelier, O. Ural (Konya, Turkey)*

3478 ***Coxiella burnetii* DNA in cheeses and bulk milk samples of sheep and goats in Puglia and Basilicata, Italy**
M. Basanisi, D. Raele, M. Cafiero, G. La Bella, G. Nobili, R. Sottili, S. Tola, G. La Salandra (Foggia, Italy)*

3951 **Serodiagnostic testing for Lyme borreliosis: should we believe what we see?**
A. Zóka (Budapest, Hungary), M. Gönczi, V. Barbai, R. Nikolova, E. Ujhelyi, Z. Kienle, G. Bekő*

Abstract Categories 2020

4213 **Role of the *Ixodidae* (Acari: *Ixodidae*) ticks, mosquitoes, and horse-flies in the transmission of vector-borne diseases in Belarus**
V. Kniazeva (Minsk, Belarus), Y. Pogockaya, Y. Leshchanka, A. Krasko*

5000 **Molecular detection of Lyme disease and Q Fever agents in *Dermanyssus gallinae* (Acari: Mesostigmata) mites related to outbreaks of dermatitis in city-dwellers (southern Italy)**
D. Raele, D. Galante, N. Pugliese, G. La Salandra, M. Lomuto, M. Cafiero (Foggia, Italy)*

5052 **Effectiveness of single-dose of doxycycline for the prevention of tick-borne relapsing fever**
Y. Binenbaum, R. Ben-Ami, G. Baneth, D. Shasha, B. Langford, Y. Negev, L. Tau, Y. Paran (Tel Aviv, Israel)*

5392 ***Leptospira* spp. in rodents and environmental samples from Lisbon and Setubal districts (Portugal): what are the risks for public health?**
M. Oliveira Fernandes (Lisbon, Portugal), F. Delgado, T. Carreira, R. Teodósio, M. Vieira*

5419 **Clinical epidemiology of Lyme disease in Quebec, Canada and compliance with American and European guidelines**
J. Musonera (Sherbrooke, Canada), F. Milord, L. Valiquette, G. Baron, D. Marcoux, K. Thivierge, C. Abou Chakra, S. Bedard-Dallaire, R. Lachance, J. Bourget, C. Simard, E. Cantin, F. Abbasi, L. Haraoui, A. Carignan*

5452 **Regional lymphadenopathy caused by *Bartonella henselae* among children: a single-centre study**
I. Valenčak-Ignjatić, D. Didovic (Zagreb, Croatia), A. Šokota, L. Prtoric, V. Stevanovic, O. Dakovic Rode, M. Gužvinec, B. Miše*

5586 **Neuro-inflammation in patients with chronic and Q fever fatigue syndrome**
R. Raijmakers (Nijmegen, Netherlands), M. Roerink, S. Keijmel, L. Joosten, M. Netea, J. Van Der Meer, I. Sommer, H. Klein, C. Bleeker-Rovers, J. Doorduin*

5731 **Serodiagnosis of Lyme disease: cheese and chalk or peas in a pod?**
K. Macgregor, F. Hamilton, M. Albur (Bristol, United Kingdom)*

5741 **A cross-sectional survey of the perceived workload of UK infection specialists related to Lyme disease**
K. Macgregor (Porton, United Kingdom), M. Dryden*

6361 **Q fever endocarditis among patients with culture-negative infective endocarditis in South Korea**
M. Bae (Seoul, South Korea), C. Jin, J. Park, S. Bae, S. Lee, S. Choi, Y. Kim, J. Woo, Y. Shin, S. Kim*

6367 **Early Lyme borreliosis in patients with chronic inflammatory bowel disease**
V. Maraspin Carman (Ljubljana, Slovenia), P. Bogovic, K. Ogrinc, E. Ruzic-Sabljic, F. Strle*

6808 **Professional exposure to brucellosis and Q-fever in veterinarians in Bosnia and Herzegovina**
Z. Sulaver (Mostar, Bosnia and Herzegovina), J. Nikolic, S. Skocibusic, J. Arapovic*

7331 **Limited value of fluorescence in situ hybridization for the detection of *Coxiella burnetii* in tissue samples of patients with chronic Q fever**
S. Buijs (Utrecht, Netherlands), T. Jensen, M. Hermans, M. Boye, P. Nooijen, A. Hoepelman, C. Bleeker-Rovers, J. Oosterheert, P. Wever*

8413 **Sero-prevalence and risk factors of brucellosis among suspected febrile patients attending a referral hospital in southern Saudi Arabia (2014-2018)**
A. Alkahtani (Abha, Saudi Arabia), M. Assiry, H. Chandramoorthy, A. Al-Hakami, M. Hamid*

8587 **Rickettsiosis in southern Tunisia: serodiagnosis, epidemiology and severe cases**
G. Olfa, N. Ben Ayed, A. Chtourou, B. Mnif, S. Mezghani, F. Rhimi, H. Karray-Hakim, A. Hammami (Sfax, Tunisia)*

8638 **Childhood brucellosis: characteristics and outcomes in a sample from an endemic country**
R. Nahhas, Z. Nemer, W. Alzahrani, Z. Askar, A. Thabit (Jeddah, Saudi Arabia)*

9242 **Cat scratch disease in children and adults: what a difference?**
C. Le Brun (Tours, France), A. Lemaignen, A. Pastuszka, P. Lanotte, L. Mereghetti, Z. Maakaroun Vermesse*

9249 **Rickettsiosis: a series of 80 cases**
F. Larbi, M. Ben Azaiez (Monastir, Tunisia), J. Chelli, S. Arfa, O. Berriche, M. Sfar*

9424 **Study on *Bartonella* related to small mammals in the Canary Islands, Spain**
E. Abreu Yanes, A. Martin-Alonso, N. Martín Carrillo (San Cristobal de La Laguna, Spain), K. García Livia, E. Izquierdo Rodríguez, N. Abreu Acosta, J. Miquel, C. Feliu, P. Foronda Rodríguez*

9627 **Clinical profile and associated comorbidities to predict outcomes in patients with scrub typhus with acute kidney injury: a study from Central India**
D. Jeswani (Nagpur, India), D. Jeswani*

Abstract Programme

3. Bacterial susceptibility & resistance

- Resistance surveillance & epidemiology: MRSA, VRE & other Gram-positives
- Resistance surveillance & epidemiology: Gram-negatives
- Susceptibility testing methods (incl assay validation and comparative studies, excl TB)
- Resistance mechanisms (excl TB)
- Resistance detection / prediction approaches (rapid and/or molecular assays, resistome analysis, inference methods)
- Other

Session accepted as Paper Poster Session

Acinetobacter: epidemiology and mechanisms of resistance

656 **Genome-based epidemiology and antimicrobial susceptibility of a nation-representative collection of clinical isolates of *Acinetobacter baumannii* obtained from Saudi Arabia**
R. Bawazeer (Riyadh, Saudi Arabia), T. Abujamel, M. Alghoribi, L. Okdah, M. Alzayer, A. Alswaji, E. Alrashidi, R. Alarfaj, S. Alhassinah, H. Balkhy, S. Al-Johani, M. Doumith*

2240 **The novel resistance mechanism of tigecycline in *Acinetobacter baumannii***
X. Hua, J. He (Hangzhou, China), Y. Yu*

2420 **Carbapenem resistance development in an OXA-499-harbouring, non-resistant *Acinetobacter pittii* isolate under imipenem selective pressure**
L. Zhang (Hangzhou, China), Y. Chen, Y. Yu*

3238 **Amikacin resistance due to the *aphA6* gene in multiply antibiotic-resistant *Acinetobacter baumannii* isolates belonging to global clone 1 from Iran**
M. Douraghi (Tehran, Iran), P. Aris, S. Ghourchian, M. Boroumand*

3898 **Polyclonal New Delhi metallo-β-lactamase producers *Acinetobacter* sp. in Algerian hospital**
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4532 **Unravelling colistin resistance diversity in clinical *Acinetobacter baumannii:* in-depth analysis of COL-R strain-profiling and genomics**
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6567 **First outbreak of colistin-resistant OXA-23/NDM-1-producing *Acinetobacter baumannii* (France, 2019)**
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6642 **Investigating the contribution of the RND-type efflux pump AdeABC in tolerance to chlorhexidine digluconate in *Acinetobacter baumannii* ATCC 19606**
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4640 **Comparable resistance levels between regional networks in the Netherlands**
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8969 **Antibiotic resistance profile of ESKAPE pathogens in Limpopo, South Africa: A two-year retrospective analysis**
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4118 **Global dissemination of multidrug-resistant *E. coli* co-expressing ESBL/pAmpC and *mcr-1* genes in chicken farms in Lebanon**
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4503 **Comparative epidemiological study of MRSA in lactating animals, dairy products, environment and personnel of dairy processing facilities in Northern Greece**
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5444 **Emergence of *mcr-1* among diverse multidrug-resistant *Escherichia coli* in gulls from a coastal city uncovers potentially underestimated transmission routes**
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5758 **CREATE:Carbapenem-Resistant *Enterobacteriaceae*: Animal Testing and Epidemiology. A plan for veterinary medicine**
S. Cole, D. Oakley, S. Rankin (Philadelphia, United States)*

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6644 **Characterisation of a *cfr* gene variant in multidrug-resistant (MDR) livestock-associated methicillin-resistant *Staphylococcus aureus* (LA-MRSA), isolated from Italian pig herds**
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6751 **Manipulation of raw pig meat is a risk for transmission of carbapenem-resistant *Pseudomonas fluorescens* to humans in the community**
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6784 **Genome analysis of *mec*C-harbouring methicillin-resistant *Staphylococcus aureus* and methicillin-sensitive *Staphylococcus aureus* CC130 strains from different origins**
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7109 **Genomic characterisation of CTX-M-15/DHA-1/OXA-48-producing *Klebsiella pneumoniae* of ST15/ST11/ST307 lineages from companion animals in France**
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7557 **Co-existence of *bla*NDM- and *mcr-1*-producing *Escherichia coli* isolated from human, poultry and environment water from Pakistan: a One Health problem**
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7792 **CTX-M-1/14/15/27-producing *Escherichia coli* and CTX-M-15/OXA-48-producing *Klebsiella pneumoniae* from Mediterranean clams *Ruditapes decussatus* at retail in Tunisia**
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7899 **Genetic relatedness, antimicrobial resistance, virulence and biofilm-forming abilities of *Klebsiella pneumoniae* from healthy broilers and turkeys**
F. Franklin (Oslo, Norway), M. Hetland, R. Bakksjø, L. Nesse, I. Löhr, A. Telke, M. Sunde*

7900 ***bla*CTX-M-55/*mcr-1*/IncHI2 plasmids in *Escherichia coli* from foodstuffs in Tunisia**
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7919 **Extended-spectrum β-lactamase in *Escherichia coli* and *Klebsiella pneumoniae* of chicken meat in butchers in Algeria, with detection of ESBL-CTX-M-55 and *E. coli*-B2/ST131**
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8450 **Feedlot lambs, carcasses and nearby animals are implicated in the transmission of cephalosporin-resistant *Escherichia coli***
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8471 **Phenotypic and genomic diversity of bacterial isolates from humans and healthy pigs in Thailand**
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8631 **Antimicrobial resistance of *Escherichia coli* strains isolated from frugivorous (*Eidolon hervum*) and insectivorous (*Nycteris hispidia*) bats in Southeast Nigeria, with detection of CTX-M-15-producing isolates**
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9531 **Deciphering resistome and virulome of Gram-negative bacteria isolated from farmed fish and molluscs**
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9601 **Unexpected low antibiotic resistance of *Klebsiella* spp. isolated from childrens' faeces, water samples, soil and animals from Andean rural homes in Cajamarca, Peru**
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R. Cabrera (Barcelona, Spain), L. Fernandez Barat, N. Vázquez Burgos, R. López-Aladid, V. Alcaraz, L. Bueno, R. Amaro, P. Oscanoa, L. Muñoz, A. Torres*

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3053 **Analysis of resistance mechanism affecting ceftolozane/tazobactam in *Pseudomonas aeruginosa* isolates using whole genome sequencing (STEP Study)**
M. Hernández García (Madrid, Spain), M. García-Castillo, S. García-Fernández, J. Cristino, M. Feijo Pinto, E. Goncalves, V. Alves, A. Vieira, E. Ramalheira, L. Sancho, J. Diogo, R. Ferreira, D. Fonseca E Silva, C. Antunes Chaves, L. Pássaro, L. Paixao, R. Canton Moreno*

3337 **Predominant mechanisms of carbapenem resistance in *Pseudomonas aeruginosa* and *Klebsiella pneumoniae* and tools for their detection**
P. Irina (Moscow, Russian Federation), N. Bagirova, V. Aginova, I. Tereshchenko, Z. Grigoryevskaya, S. Dyakova, K. Elena, N. Dmitrieva*

4559 **Interspecific transfer of a *bla*VIM-2-containing plasmid between *Pseudomonas* spp. during a nosocomial outbreak**
J. Pirzadian (Rotterdam, Netherlands), N. Strepis, A. Heikema, W. Zandijk, H. Koene, W. Goessens, M. Vos, C. Klaassen, J. Severin*

4892 **CrpP-like fluoroquinolone-modifying enzymes among *Pseudomonas aeruginosa* clinical isolates in Europe**
J. Ortiz De La Rosa (Fribourg, Switzerland), P. Nordmann, L. Poirel*

5339 **Co-prodution of KPC and SPM carbapenemases by *Pseudomonas aeruginosa* in same hospital in northern Brazil**
A. Quaresma (Pará, Brazil), L. Guerra Dutra, M. Ferreira Ribeiro, R. Nazaré, D. Brasiliense*

5407 **Carbapenemase-producing *Pseudomonas* form Bulgarian hospitals: spread of ST233 with multiple virulence factors**
I. Ivanov (Sofia, Bulgaria), V. Dobrinov, K. Ivanova, E. Dobreva, M. Nedyalkov, R. Hristova, S. Sabtcheva, T. Kantardjiev*

5568 **Spread of metallo-β-lactamases among distinct species of *Pseudomonas putida* group in Brazil**
F. Lei, C. Silva Nodari, A. Streling, F. Ozorio, J. Paulino, R. Cayô Da Silva, A. Gales (São Paulo, Brazil)*

5762 **Contribution of high risk clones *Pseudomonas aeruginosa* ST111 and ST235 in the spread of VIM-2 carbapenemase in a Greek Hospital**
A. Verra, V. Galani, E. Malli, K. Tsilipounidaki, S. Xitsas, C. Papagiannitsis, E. Petinaki (Thessaloniki, Greece)*

5964 ***In vitro* susceptibility of multidrug-resistant *Pseudomonas aeruginosa* following treatment-emergent resistance to ceftolozane-tazobactam**
A. Rubio (Pittsburgh, United States), E. Kline, C. Jones, M. Nguyen, C. Clancy, R. Shields*

6183 **Characterisation of *Pseudomonas aeruginosa* isolates co-harbouring IMP18 and VIM-2 metallo-beta-lactamases from Peru**
K. Yauri (Lima, Peru), S. Oueslati, L. Dortet, E. Gonzales, T. Naas*

6275 **WGS-based characterisation of clinical *Pseudomonas aeruginosa* isolates obtained from teaching and specialist hospitals in Lagos, Nigeria**
A. Olalekan (Lagos, Nigeria), B. Iwalokun, B. Bader, S. Vogt, A. Dike, M. Mannie-Udoh, A. Lalremruata, M. Marschal, P. Oberhettinger, J. Liese, S. Peter*

6401 **The interplay of resistance mechanisms associated with reduced susceptibility and resistance to imipenem and ceftazidime-avibactam in clinical *Pseudomonas aeruginosa* isolates from Switzerland**
B. Babouee Flury (St. Gallen, Switzerland), A. Bösch, V. Gisler, M. Oberle, H. Fankhauser, V. Hinic, A. Egli, S. Seiffert, N. Oliver, J. Findlay*

7174 **Sub-inhibitory concentrations of beta-lactam, aminoglycoside and polymyxin antibiotics induce differential proteomic responses in *Pseudomonas aeruginosa***
B. S. Jongers (Wilrijk, Belgium), K. Bielen, A. Hotterbeekx, E. Timmerman, C. Lammens, H. Goossens, S. Malhotra-Kumar, S. Kumar-Singh*

7538 **Susceptibility profile of *Pseudomonas* species in a tertiary care hospital over a 9-year period and impact of antimicrobial stewardship**
S. Saliba (Beirut, Lebanon), O. Zmerli, A. Chamieh, Z. Daoud, E. Azar, C. Afif*

8064 **Identification of the extended-spectrum β-lactamase L2 in an extensively drug-resistant *Pseudomonas aeruginosa* isolate, United States**
R. Stanton (Atlanta, United States), G. Mcallister, W. Zhu, D. Campbell, J. Grass, M. Kainer, M. Walters, A. Laufer-Halpin*

8380 **Genomic characterisation of MBL-producing non-*aeruginosa Pseudomonas* spp. in Saint-Louis University hospital in Paris, France**
F. Caméléna (Paris, France), M. Merimèche, M. Rouveau, S. Delliere, M. Benyamina, T. Sophie, M. Lafaurie, B. Bercot*

8501 **Development of a combination antibiogram for empiric treatment of *Pseudomonas aeruginosa* in the intensive care unit**
B. Dionne (Boston, United States), S. Kanjilal, K. Brade*

8644 **Prominent role of *oprD* mutations in carbapenem-resistant *Pseudomonas aeruginosa* strains in a previous context of VIM-1 outbreaks**
H. Raqioui, A. Bertoncelli, A. Mazzariol (Verona, Italy)*

9093 **Characterisation of a new class 1 integron carrying *bla*VIM-1 and *bla*GES-7 in extensively and pandrug-resistant *Pseudomonas aeruginosa* ST155 isolates from patients with ventilator-associated pneumonia**
M. Hernandez (Valladolid, Spain), L. Alvarez-Montes, D. Abad, C. Díaz Ríos, A. Arribi, A. Ocampo-Sosa*

9339 **VIM-producing *Pseudomonas aeruginosa* isolated in Southern Tunisia, 2012-2018**
Y. Jellouli, N. Ben Ayed, B. Mnif, A. Hammami (Sfax, Tunisia)*

9469 **Integrons & antibiotic resistance: do integrons provide 'adaptation on demand' ?**
C. Souque (Oxford, United Kingdom), J. Escudero, C. Maclean*

9588 **Carbapenemase-producing *Pseudomonas aeruginosa* in south Brazil**
C. Sanches Ito, L. Bail (Ponta Grossa, Brazil), L. Arend, M. Pilonetto, G. Becker, K. Nogueira, F. Tuon*

Session accepted as Mini-oral Flash Session

Antimicrobial resistance in the community

3196 **Bacteriophage control the prevalence of *Escherichia coli* ST131 in different countries**
J. Mathias (Cardiff, Wales, United Kingdom), D. Babenko, A. Almusallam, R. Farzana, M. Toleman*

4075 **Fluoroquinolone resistance in *Escherichia coli* isolates after exposure to non-fluoroquinolone antibiotics: a retrospective case-control study**
L. Chaname Pinedo, R. Bruyndonckx, B. Catry (Brussels, Belgium), K. Latour, S. Abrams, H. Goossens, S. Coenen*

4146 **Optimised positioning of carbapenem-sparing options for treatment of UTIs by molecular antibiotic susceptibility testing**
N. Adomakoh, N. Mahfouz, P. Harris, F. Franceschi, A. Henderson, S. Beisken, E. Littringer, A. Posch (Wien, Austria)*

4185 **Clonal spread of *mcr*-3-carrying multidrug-resistant ST34 *Salmonella Typhimurium* and its monophasic from human globally**
L. Fang (Guangzhou, China), R. Sun, W. Guo, J. Sun, X. Liao, Y. Liu*

5341 **Population structure dynamics of *Escherichia coli* ST131 over time**
G. Peirano (Calgary, Canada), T. Lynch, R. Devinney, T. Finn, Y. Matsumura, J. Pitout*

6705 **Restriction modification systems affect the ability of *Escherichia coli* ST73 to acquire plasmids**
J. Alves Gama (Tromsø, Norway), J. Kloos, P. Johnsen, O. Samuelsen*

8075 **SNP-based phylogeny revealing establishment of ciprofloxacin-resistant *Shigella sonnei* lineage in India**
D. M.S. (Vellore, Tamil Nadu, India), A. Pragasam, K. Vasudevan, D. Murugan, S. Anandan, V. Balaji*

9632 **Measuring and mapping the burden of antimicrobial resistance in enteric infections**
C. Dolecek (Oxford, United Kingdom), A. Browne, B. Kashef, E. Kumaran, C. Moore, P. Rao, G. Robles-Aguilar, S. Dunachie, M. Chipeta, S. Baker, A. Lopez, N. Day, S. Hay*

Session accepted as Paper Poster Session

Antimicrobial resistance in urinary tract infections

911 **High prevalence of antimicrobial resistance in community-acquired urinary tract infections in Harare, Zimbabwe**
I. Olaru (London, United Kingdom), M. Chisenga, R. Ferrand, S. Yeung, H. Hopkins, R. Stabler, P. Chonzi, J. Bradley, K. Kranzer*

1278 **Antimicrobial resistance and genotypic markers of trimethoprim resistance in *Escherichia coli* and *Klebsiella* spp. isolated from patients with urinary tract infections**
Y. Somorin (Belfast, United Kingdom), N. Weir, M. Higgins, C. Hughes, D. Gilpin, M. Crockard, M. Tunney*

1548 **Comparison of antibiotic susceptibility of *Escherichia coli* between community-acquired and post-prostate biopsy acute bacterial prostatitis**
G. Song (Chuncheon, South Korea), J. Lee, M. Park, S. Kwon, H. Choi, K. Kim, S. Bae*

3173 **Prevalence of antibiotic resistance among *Enterobacterales* isolates recovered from urinary samples in France**
E. Farfour (Suresnes, France), A. Si Larbi, N. Chatelain, L. Dortet, A. Poisson, T. Guillard, A. Mizrahi, D. Fournier, N. Degand, P. Morand, F. Janvier, V. Fihman, S. Corvec, L. Broutin, C. Le Brun, N. Yin, G. Hery-Arnaud, A. Grillon, E. Bille, H. Jean-Pierre, M. Amara, F. Jaureguy, C. Isnard, V. Cattoir, T. Diedrich, E. Flevin, A. Mérens, H. Jacquier*

3319 **Antimicrobial resistance in urinary tract infection cases submitted to a computerised decision support system for antibiotic prescribing in primary care in France**
T. Delory (Paris, France), P. Jeanmougin, S. Lariven, F. Tubach, P. Boëlle, E. Bouvet, X. Lescure, J. Le Bel*

4061 **Urinary tract infections in children: antibiotic resistance of major pathogens in Western Attika, Greece (October 2014 to October 2019)**
P. Karakosta, E. Kalogeropoulou, A. Vasilakopoulou, E. Oikonomoula, P. Tsilikis, S. Damianidou, A. Tarpatzi, A. Spiliopoulou, K. Tsekouras, S. Pournaras (Athens, Greece)*

4823 **Resistance among urinary tract infection pathogens collected in Europe during 2018**
I. Critchley (Cambridge, United States), N. Cotroneo, M. Pucci, A. Jain, R. Mendes*

5684 **Increase of *Escherichia coli* with reduced susceptibility to cefepime and OXA-1 compatible phenotype in urinary tract infections along the years**
S. Nabal Díaz, J. Bueno, P. Pilar, S. Mormeneo Bayo, B. Sanz, C. Guerrero, J. Garcia-Lechuz Moya, A. Rezusta, A. López-Calleja (Zaragoza, Spain)*

6554 **Antimicrobial resistance among urinary *Enterobacteriaceae* from patient living in nursing homes**
S. Thibaut (Nantes, France), T. Coeffic, D. Boutoille, G. Birgand, J. Caillon, P. Network*

6871 ***In vitro* susceptibility of carbapenem-resistant *Enterobacterales* urinary isolates to nitroxoline and other oral urinary antibiotics**
A. Sonnevend (Pécs, Hungary), A. Ghazawi, T. Pal*

7433 **Antimicrobial resistance among bacteria causing asymptomatic bacteriuria in pregnant women, rural Burkina Faso**
I. Guiraud, M. Peeters, A. Bonko, G. Zakaria, K. Ibrahima, A. Post, P. Lompo (Ouagadougou, Burkina Faso), S. Ombelet, S. Diallo, J. Bognini, K. Berenger, Q. De Mast, A. Van Der Ven, H. Tinto, J. Jacobs*

9434 **Retrospective analysis of antibacterial resistance among uropathogen *Escherichia coli* in a veterinary teaching hospital (Italy, 2014-2019)**
P. Nebbia (Turin, Italy), A. Bellato, A. Attili, M. Stella, F. Canavesi, P. Robino*

Session accepted as Paper Poster Session

Antimicrobials against Gram-positive bacteria

1019 **Activity of omadacycline and comparator agents against bacterial pathogens from the United States by infection type (2019)**
M. Huband (North Liberty, United States), M. Pfaller, J. Streit, L. Duncan, R. Flamm*

1043 ***In vitro* surveillance of eravacycline against Gram-positive pathogens, including resistant isolates, collected from European hospitals in 2018**
S. Hwang, S. Hawser, I. Morrissey (Monthey, Switzerland), F. Monti, E. Efimova, M. Olesky*

1322 **Resistance mechanisms associated with pleuromutilins among Gram-positive clinical isolates from the worldwide surveillance programme for lefamulin in 2018**
R. Mendes (North Liberty, United States), T. Doyle, M. Castanheira, R. Flamm, S. Gelone, S. Paukner, H. Sader*

1650 **Distinct effectiveness of oritavancin against tolerance-induced *Staphylococcus aureus***
L. Harven, V. Bingley, P. Kulkarni, S. Khaire, S. dey, P. Smolenski, A. Berti (Detroit, United States)*

1886 **Longitudinal (2011-2018) activity of oritavancin against Gram-positive isolates causing bacteraemia and endocarditis in Europe, including enterococcal infections requiring adjusted daptomycin dosing**
C. Godoy Carvalhaes (North Liberty, United States), H. Sader, J. Streit, R. Flamm, R. Mendes*

1887 **Delafloxacin activity against drug-resistant *Streptococcus pneumoniae, Haemophilus influenzae, Haemophilus parainfluenzae*, and *Moraxella catarrhalis* from European medical centres (2014-2018)**
D. Shortridge (North Liberty, United States), J. Streit, M. Huband, R. Flamm*

2338 **Evaluation of tedizolid and comparators activity against Gram-positive bacterial isolates causing skin and skin structure infections from paediatric patients in Europe and surrounding countries (2015-2019)**
C. Godoy Carvalhaes (North Liberty, United States), H. Sader, J. Streit, R. Flamm, R. Mendes*

2359 **Tedizolid activity against a global collection of Gram-positive bacterial isolates causing bone and joint infections (2017-2019)**
C. Godoy Carvalhaes (North Liberty, United States), H. Sader, J. Streit, R. Flamm, R. Mendes*

2367 **European regional analysis of the *in vitro* activities of ceftaroline and comparator agents against bacterial pathogens frequently isolated from patients with community-acquired respiratory tract infections: ATLAS surveillance programme 2015-2018**
J. Karlowsky, M. Hackel (Schaumburg, United States), S. Bouchillon, G. Stone, D. Sahm*

2371 ***In vitro* activity of ceftaroline and comparator agents against bacterial pathogens collected from patients with skin and soft tissue infections in Europe: a regional analysis of results from the ATLAS surveillance programme 2015-2018**
J. Karlowsky, M. Hackel (Schaumburg, United States), S. Bouchillon, G. Stone, D. Sahm*

2735 **5-year surveillance of lefamulin against Gram-positive cocci collected from Acute Bacterial Skin and Skin-Structure Infections (ABSSSI) and Bloodstream Infections (BSI) in Europe (SENTRY 2015–2019)**
S. Paukner (Vienna, Austria), S. Gelone, S. Arends, H. Sader*

2774 **Ozenoxacin, a topical fluoroquinolone, demonstrates activity versus methicillin-susceptible and methicillin-resistant *Staphylococcus aureus*, and *Streptococcus pyogenes* wound isolates including fluoroquinolone-, fusidic acid- and mupirocin-resistant strains**
P. Lagacé-Wiens (Winnipeg, Canada), H. Adam, M. Baxter, J. Karlowsky, G. Zhanel*

3010 ***In vitro* activity of omadacycline against pathogens isolated from mainland China during 2017-2018**
Y. Guo, D. Dong, Q. Chen, Y. Zheng, Y. Yang, S. Wu, D. Zhu, J. Deng (Shanghai, China), P. Bradford, H. Reinhart, F. Hu*

3561 **Delafloxacin *in vitro* activity in skin and soft tissue infections by methicillin-resistant and levofloxacin-resistant *Staphylococcus aureus***
M. Liras Hernández (Madrid, Spain), J. García Rodríguez, R. Gomez*

3606 **Antimicrobial activity of XF-73 against clinically relevant Gram-positive bacteria**
I. Romeo-Melody (Birmingham, United Kingdom), D. Hynes, W. Rhys-Williams, B. Love, P. Lambert, T. Worthington*

3840 **Reporting antimicrobial susceptibilities and resistance phenotypes in *Staphylococcus* spp.: a nation-wide proficiency study**
F. Fernández-Cuenca (Seville, Spain), I. López-Hernández, M. Conejo, N. Tormo, C. Gimeno Cardona, E. Cercenado, A. Pascual Hernandez*

3921 **Ceftobiprole susceptibility of European Gram-positive and *Enterobacteriaceae* clinical isolates from different infection sources collected in 2018**
S. Hawser (Monthey, Switzerland), I. Morrissey, N. Kothari, N. Jemmely*

4060 **Comparison of susceptibility of rifabutin and rifampicin on *Staphylococcus* spp. isolated in bone and joint infections**
P. Thill, O. Robineau, E. Senneville (Tourcoing, France), B. Nicolas*

4292 ***In vitro* activity of ceftaroline and comparators against *Staphylococcus aureus* clinical isolates from a tertiary hospital in Greece**
A. Tychala (Thessaloniki, Greece), M. Arhonti, F. Netsika, G. Meletis, P. Mantzana, O. Vasilaki, G. Kagkalou, E. Protonotariou, L. Skoura*

4704 **Increased fusidic acid resistance among *Staphylococcus aureus* skin and soft tissue infections in Portugal**
T. Conceição (Oeiras, Portugal), C. Ferreira, R. Luzio, H. De Lencastre*

4715 **Antimicrobial activity of ceftobiprole against clinical *Staphylococcus aureus* isolates from Germany**
F. Layer (Wernigerode, Germany), B. Strommenger, I. Klare, G. Werner*

5472 **Therapeutic innovation in bone and joint infections: evaluation of the activity of exebacase (CF-301 lysin) on clinical strains belonging to *Staphylococcus epidermidis* species**
A. Souche (Lyon, France), C. Kolenda, C. Dupieux, R. Schuch, T. Ferry, F. Laurent, J. Josse*

5738 **Prevalence of antibiotic resistance in skin infections among migrants compared to Danish-born patients**
G. Köse (Norrebro, Denmark), L. Sloth, R. Nielsen, C. Østergaard, M. Nørredam*

6951 ***In vitro* activity of ceftaroline and ceftobiprole against *Enterococcus faecalis* recovered from infective endocarditis and/or bloodstream infections**
R. Rodríguez García, I. Costales, A. Rodríguez-Esteban, M. Telenti, E. Garcia, J. Fernández (Oviedo, Spain)*

6997 **Distinct augmenting contribution of hyperbaric oxygen therapy to neutrophil function and antibiotic efficacy against *Staphylococcus aureus***
F. Schwartz (Copenhagen, Denmark), L. Christophersen, P. Jensen, C. Johann Lerche, C. Moser*

7007 **Pleuromutilin resistance in methicillin-resistant *Staphylococcus aureus* at the human-animal interface, Denmark**
J. Larsen (Copenhagen, Denmark), A. Petersen, R. Sieber, A. Larsen, U. Sönksen*

7217 ***In vitro* activity of delafloxacin against highly-levofloxacin-resistant invasive isolates of *Streptococcus pneumoniae***
E. Cercenado (Madrid, Spain), C. Loras, A. Cobos, J. Sanz*

7328 **Mupirocin exposure in the preceding year is associated with mupirocin resistance among methicillin-resistant *Staphylococcus aureus* in a tertiary care hospital in the United States of America**
E. Drehs (Tampa, United States), L. Holt, S. Lakshmi, J. Kalter, A. Abraham, K. Atrubin, P. Thompson, S. Silbert, A. Kumar*

7377 **Evolution of teicoplanin susceptibility pattern of *Staphylococcus aureus* and coagulase-negative *Staphylococcus* spp. related to orthopaedic infections**
P. Oliveira, V. Carvalho, A. Anjos, J. Arauju (Sao Paulo, Brazil), C. Panico, T. Vitoriano, L. Silva Neto, I. Marinho, V. Amorim, F. Rossi, A. Munhoz*

8343 **Prevalence of *blaZ* gene types and the inoculum effect with cefazolin among bloodstream isolates of methicillin-susceptible *Staphylococcus aureus***
I. Guerrero Lozano, F. Galan-Sanchez (Cádiz, Spain), J. Peñate, V. Andrada-Brazo, M. De La Rubia, M. Rodriguez-Iglesias*

8944 **Antibiotic resistance patterns of *Staphylococcus aureus* isolated in blood cultures in primary care**
S. Thibaut (Nantes, France), T. Coeffic, D. Boutoille, G. Birgand, J. Caillon, P. Network*

9002 **Efficacy of teicoplanin-loaded targeted nanoparticles in a *Staphylococcus aureus* thigh infection model**
B. Borsa (Linköping, Sweden), M. Aldag, I. Baris, M. Sudagidan, I. Acuner, V. Ozalp*

Session accepted as Paper Poster Session

Bad news: carbapenem resistance

203 **Diffusion of KPC-carbapenemases among urinary tract isolates of *Klebsiella pneumoniae* in Croatia**
B. Bedenic (Zagreb, Croatia), S. Sardelic, N. Beader, S. Šuto, M. Bogdanić, G. Zarfel, J. Vranes*

1116 **Fitness cost of *mgrB* alterations in carbapenem-resistant *Klebsiella pneumoniae* isolates from Moscow**
O. Shamina (Moscow, Russian Federation), O. Kryzhanovskaya, A. Lazareva, N. Mayanskiy*

1180 **Costs and benefits of OXA-48 variants selected under sub-lethal concentrations of ceftazidime**
C. Fröhlich (Tromsø, Norway), J. Alves Gama, K. Harms, P. Johnsen, O. Samuelsen, H. Leiros*

1235 **Emergence of *bla*NDM and *mcr-1* positive pan- and extremely-drug resistant bacterial infections in patients with renal diseases**
U. Ghoshal (Lucknow, India), A. Pathak, S. Singh, C. Sahu, N. Prasad*

2242 **Prevalence of carbapenemase-producing Gram-negative bacilli in a health area of southern Spain**
F. Cobo (Granada, Spain), F. Fernández-Cuenca, L. Martín-Hita, I. López-Hernández, J. Gutiérrez Fernández, A. Pascual Hernandez, J. Navarro-Marí*

3397 **Qualitative detection of OXA-23-like, OXA-24-like and OXA-58-like carbapenemases from *Acinetobacter* species by real-time PCR**
M. Mentasti, K. Prime, K. Sands, S. Khan, M. Wootton (Cardiff, United Kingdom)*

3409 **Whole genome sequence analysis of *Klebsiella pneumoniae* isolates belonging to sequence type 231 harbouring rapidly disseminating *blaOXA*-232 located on ColKP3 plasmid in Kuwait**
A. Al Fadhli (Kuwait, Kuwait), W. Jamal, V. Rotimi*

3673 **Prevalence and impact of meropenem-resistant among nonresistant OXA-48-producing *Klebsiella pneumoniae***
N. Bustos De Godoy, L. Lopez-Cerero (Seville, Spain), M. Sánchez, E. Recacha, M. Conejo, A. Pascual Hernandez*

3877 **Effect of biocides on the mobilisation of plasmid-encoded OXA-48 carbapenemases from *Klebsiella pneumoniae* growing in biofilms**
P. Pérez-Palacios, A. Gual-De-Torrella (Seville, Spain), M. Delgado-Valverde, J. Oteo, A. Pascual Hernandez, F. Fernández-Cuenca*

4376 **Identification of genetic factors increasing carbapenem resistance in *Klebsiella pneumoniae* with *bla*OXA-48**
M. Cremanns (Bochum, Germany), S. Gatermann, N. Pfennigwerth*

4513 **Diversity of ESBL- and carbapenemase-producing *Enterobacteriaceae* with emergence of *mcr-1* and carbapenem transferable resistance in a cancer clinical setting in Egypt**
M. Mersal (Porto, Portugal), J. Palmeira, H. Ferreira*

4620 **The application of CRISPR/Cas9-based genome editing in knocking out the *bla*NDM-1 gene to study the mechanisms of pandrug resistance in clinical isolates**
X. Yu (Hangzhou, China), Y. Xiao*

4896 **IS*26*-mediated transfer of *bla*NDM-1 as the main route of resistance transmission during a polyclonal, multispecies outbreak in a German hospital**
R. Weber (Wernigerode, Germany), M. Pietsch, A. Frühauf, Y. Pfeifer, M. Martin, D. Luft, S. Gatermann, N. Pfennigwerth, M. Kaase, G. Werner, S. Fuchs*

4929 **Rapid detection of OXA-23-, OXA-40- and OXA-58-mediated carbapenem resistance in *Acinetobacter baumannii***
S. Mertins (Cologne, Germany), P. Higgins, C. Thunissen, O. Gilleman, P. Mertens, H. Seifert, M. Kroenke, A. Klimka*

4994 **A retrospective study to evaluate the epidemiology, standard of care, outcomes and resource utilisation in patients with confirmed or suspected infection by a carbapenem-resistant Gram-negative organism in the UK: the CARBAR study part 2**
S. Goldenberg (London, United Kingdom), A. Dodgson, G. Barlow, B. Parcell, L. Jones, M. Albur, P. Wilson, D. Enoch, A. Marek, D. Manissero, C. Longshaw, K. Tone, S. Lopes*

5021 **The resistance ratchet tightens: widespread penicillin-binding protein-3 insensitivity in carbapenemase-producing *Escherichia coli***
S. Mushtaq (London, United Kingdom), M. Ellington, N. Woodford, D. Livermore*

5075 **Characterisation of resistance-increasing determinants of OXA-48-bearing clinical isolates of *Klebsiella pneumoniae***
L. Höfken (Bochum, Germany), M. Cremanns, S. Gatermann, N. Pfennigwerth*

5659 **Characterisation of carbapenemase-producing *Enterobacterales* isolates with phenotypic and genotypic methods in southern Hungary**
M. Gajdács (Szeged, Hungary), M. Ábrók, L. Andrea, L. Jánvári, A. Toth, K. Burian, G. Terhes*

5729 **Investigation of antibiotic susceptibilities, clonal relationships and carbapenems resistance mechanisms of *Serratia marcescens* obtained between 2011 and 2019 in a university hospital**
G. Hazırolan (Ankara, Turkey), S. Nigiz, A. Gundogdu, G. Altınkanat-Gelmez, M. Hasdemir, F. Bayrakdar, D. Gür*

6385 **A mobilisable plasmid spreads the *bla*GES-6 carbapenemase gene among multidrug-resistant *Enterobacter cloacae* complex isolates**
J. Rodríguez Lozano (Santander, Spain), M. Garcillan, M. Lucas, L. Martinez-Martinez, J. Aguero, J. Calvo-Montes*

6648 **Mitigating the fitness costs of carbapenemase-encoding clinical plasmids in *Escherichia coli*: Piggy-backing on environmental adaptation**
J. Kloos, J. Alves Gama (Tromsø, Norway), J. Hegstad, O. Samuelsen, P. Johnsen*

7080 **Detection of the novel variant of NDM-type metallo-β-lactamase: significance of D130N amino acid substitution**
P. Starkova (Saint Petersburg, Russian Federation), O. Sulian, D. Likholetova, V. Ageevets, I. Lazareva, J. Sopova, S. Sidorenko*

7167 **Co-production of two types of carbapenemases in *Enterobacterales* from Poland**
E. Literacka (Warsaw, Poland), R. Izdebski, A. Baraniak, P. Urbanowicz, M. Herda, K. Malinowska, D. Żabicka, W. Hryniewicz, M. Gniadkowski*

7182 **The impact of H-NS-like protein on IncX3 plasmid dissemination and stability**
L. Baomo (Guangzhou, China), C. Zhuo, L. Shui, Y. Guo*

7382 **Carbapenem hetero-resistance in blood isolates of OXA-48-producing *Klebsiella pneumoniae* and *Escherichia coli***
A. Bıçakçıgil, B. Sancak (Ankara, Turkey)*

7438 **Hospital outbreak of *Klebsiella pneumoniae* producing GES-1 or GES-5 β-lactamases in Poland**
E. Literacka (Warsaw, Poland), R. Izdebski, D. Żabicka, A. Baraniak, P. Urbanowicz, I. Żak, I. Sowa-Sierant, M. Herda, K. Malinowska, W. Hryniewicz, M. Gniadkowski*

7551 **Emergence of "high risk clone" *Klebsiella pneumoniae* ST307 producing KPC-3 and NDM-1 in Argentina**
D. Cejas, M. Ferrara, F. Magariños, C. Alfonso, A. Elena, G. Gutkind (Buenos Aires, Argentina), M. Radice*

7878 **Evaluation of carbapenem resistance in *Enterobacteriaceae* isolated from intensive care unit using phenotypic and genotypic methods**
N. Shaikh (Mumbai, India), L. Drego, A. Shetty, C. Rodrigues*

8158 **Impact of porin deficiency and expression levels of environmental CRH-1 and CRP-1 class A β-lactamases on carbapenem and ceftazidime resistance**
F. Brunetti, B. Ghiglione, D. Gudeta, R. Figueroa, G. Gutkind (Buenos Aires, Argentina), L. Guardabassi, P. Power*

8401 **Local prevalence of molecular resistance mechanisms in carbapenem-resistant *Enterobacteriaceae* at a tertiary healthcare centre in Lebanon**
O. Zmerli (Beirut, Lebanon), S. Saliba, A. Chamieh, C. Afif, E. Azar*

8687 **X-ray induced changes in substrate specificity of OXA-48**
M. Dabos (Le Kremlin-Bicêtre, France), M. Mondini, E. Deutsch, T. Naas*

9346 **Evolutionary insights of multidrug-resistant hypervirulent ST23 *Klebsiella pneumoniae* predominantly driven by ICEKp**
C. Shankar (Vellore, India), J. Jacob, K. Vasudevan, M. Venkatesan, S. Anandan, V. Balaji*

Session accepted as Mini-oral ePoster Session

Carbapenemases learn geography: they are everywhere!

1524 **Epidemiology of carbapenemase-producing *Enterobacterales* in the Netherlands in 2018**
C. Wielders (Bilthoven, Netherlands), L. Schouls, D. Notermans, A. Hendrickx, E. Kuijper, A. Schoffelen, S. De Greeff*

1786 **Temporal and regional prevalence of carbapenemase-producing *Enterobacterales* in Switzerland from 2013 to 2018**
M. Gasser (Bern, Switzerland), A. Ramette, R. Zbinden, J. Schrenzel, P. Nordmann, D. Perisa, A. Kronenberg*

2785 **National pathogen surveillance for carbapenem-resistant *Enterobacteriaceae* in Japan, 2017-2018**
M. Matsui (Tokyo, Japan), S. Suzuki, M. Sugai*

2918 **Prevalence of different resistance mechanisms in carbapenemase-producing organisms in Kenya: a phenotypic study**
A. Amulele (Kilifi, Kenya), J. Waichungo, A. Mwanzu, E. Machanja, D. Wareham, J. Berkley, N. Gordon*

3121 **National survey of carbapenemase-producing *Klebsiella pneumoniae* and *Escherichia coli* in Belgium in 2019**
T. Huang (Yvoir, Belgium), P. Bogaerts, C. Berhin, M. Hoebeke, Y. Glupczynski, O. Denis*

3748 **High levels of carbapenem resistance in paediatric bloodstream infection across WHO regions influenced by variation in relative pathogen prevalence**
A. Cook (London, United Kingdom), Y. Yau, J. Bielicki, M. Sharland*

9107 **Occurrence of carbapenemase-producing *Klebsiella pneumoniae* and *Escherichia coli* in Spain: CARBA-ES-2019 prospective multi-centre study**
Z. Moure (Madrid, Spain), A. Avila, V. Bautista, M. Cano, D. Gijón, M. González, I. Gracia-Ahufinger, X. Mulet, M. Delgado-Valverde, C. Pitart, A. Rivera, G. Ruíz-Crrascoso, M. Viñado, J. Oteo*

9400 **KpnBR: Brazilian genomic database for monitoring resistance and virulence of *Klebsiella pneumoniae***
L. Cerdeira (Sao Paulo, Brazil), B. Fuga, A. Quaresma, R. Nakamura, D. Fuentes, L. Rodrigues, F. Esposito, B. Cardoso, C. Levy, E. Vespero, R. Ribas, A. Pitondo, N. Lincopan*

9543 **2002-2009 versus 2010-2017: comparison of carbapenem non-susceptibility trends over time among bloodstream *Klebsiella pneumoniae*, *Acinetobacter baumannii* and *Pseudomonas aeruginosa* isolates from Greek hospitals: data from the Electronic System for the surveillance of antimicrobial resistance, WHOnet Greece**
M. Polemis (Athens, Greece), K. Tryfinopoulou, A. Vatopoulos*

Session accepted as Paper Poster Session

Carriage of resistant enterobacteria: a gut feeling!

1315 **Resistance to extended-spectrum β-lactams, aminoglycosides and quinolones in multidrug-resistance *Enterobacterales* isolated in patients receiving an allogeneic haematopoietic stem cell transplantation: the ENTHERE-SCT Study. PI16/01415**
M. Fernández-Martínez (Santander, Spain), C. González Rico, M. Bermudez-Rodriguez, I. Gracia-Ahufinger, I. García-García, L. Vázquez, J. Aguado Garcia, C. Martín Calvo, L. Martinez-Martinez, J. Calvo-Montes, M. Fariñas*

2469 **Prevalence of carriage and characterisation of extended-spectrum beta-lactamase-producing *Escherichia coli* in healthy pregnant women living in Madagascar**
M. Milenkov (Lyon, France), E. Westeel, S. Rasoanandrasana, L. Rahajamanana, R. Rakotomalala, O. Clermont, L. Raskine, L. Samison, H. Endtz, A. Andremont, F. Komurian-Pradel, L. Armand-Lefevre*

4062 **Household transmission of carbapenemase-producing *Enterobacteriales*: a prospective case-ascertained cohort study**
K. Marimuthu (Singapore, Singapore), Y. Mo, M. Ling, A. Koutoucheva, S. Fenlon, D. Bertrand, D. Lye, B. Ang, E. Perencevich, O. Ng, B. Cooper, N. Nagarajan, S. Chen, T. Barkham*

4276 **Increased carriage of ESBL-producing *Enterobacteriaceae* among men who have sex with men**
E. Van Dulm (Amsterdam, Netherlands), W. Van Bilsen, A. Matser, I. Linde, Y. Van Duijnhoven, J. Prins, M. Prins, A. Boyd, A. Van Dam*

4510 **Epidemiology of ESBL-producing *Enterobacteriaceae* among healthcare students, Portuguese Red Cross Health School of Lisbon, Portugal**
C. Fournier (Fribourg, Switzerland), M. Aires De Sousa, B. Fuster, P. Nordmann, L. Poirel*

5363 **Prevalence of and risk factors for extended-spectrum beta-lactamase genes carriership in a middle-aged and elderly population-based cohort**
M. Mulder, P. Arp, D. Radjabzadeh, J. Kiefte-De Jong, A. Uitterlinden, C. Klaassen, R. Kraaij, W. Goessens, B. Stricker, A. Verbon (Rotterdam, Netherlands)*

6457 **Faecal carriage of extended-spectrum beta-lactamase-producing members of order *Enterobacterales* among patients in Bulgarian hospitals**
P. Stankova (Sofia, Bulgaria), R. Markovska-Davidkova, T. Stoeva, L. Boyanova, M. Murdjeva, A. Petrova, D. Ivanova, D. Dimitrova, M. Sredkova, Y. Marteva-Proevska, T. Velinov, I. Mitov*

6720 **Longitudinal large-scale survey on *bla*CTX-M faecal carriage in children from Bolivian Guaraní indigenous communities**
S. Boncompagni (Siena, Italy), T. Di Maggio, A. Mantella, M. Micieli, A. Villagrán, M. Spinicci, M. Strohmeyer, M. Cecchetti, H. Gamboa Barahona, V. Poma, A. Bartoloni, G. Rossolini, L. Pallecchi*

6919 **Healthy carriage of colistin-, ESC- and carbapenem-resistant *Enterobacterales* in workers in Lebanese pastries**
A. Hiba (Lyon, France), M. Osman, J. Madec, M. Hamze, M. Haenni*

7875 **Community faecal carriage of extended-spectrum beta-lactamase-producing *Escherichia coli* in Niger**
H. Jacquier (Paris, France), A. Page, M. Coldiron, B. Assao, A. Bridier-Nahmias, F. Chau, B. Condamine, E. Denamur, O. Guindo, M. Mélanie, C. Langendorf, V. De Lastours*

Session accepted as 2-Hour Oral Session

Clinical and molecular epidemiology of key antimicrobial-resistant enterobacteria: the devil lies in the details

721 **Genomic analysis of carbapenemase-encoding plasmids from *Klebsiella pneumoniae* across Europe highlights three major patterns of dissemination**
S. David (Cambridge, United Kingdom), V. Cohen, S. Reuter, T. Giani, G. Rossolini, E. Feil, H. Grundmann, D. Aanensen*

1159 **Transmission dynamics of multidrug-resistant *Escherichia coli* sequence type 131 in the community**
Y. Mo (Singapore, Singapore), M. Moore, K. Vignesvaran, W. Yeung, S. Peng, E. Tan, M. Chua, L. Zhou, I. Seah, P. Tambyah*

1908 **Burden and impact of carbapenem resistance caused by *Enterobacterales* in a Bangladeshi hospital: an epidemiological, clinical and molecular study**
R. Farzana (Cardiff, United Kingdom), L. Jones, A. Rahman, K. Sands, E. Portal, I. Boostrom, M. Pervin, B. Hassan, A. Barratt ?, T. Walsh*

2488 **Community outbreak of OXA-48-producing *Escherichia coli* linked to a food premises: New Zealand, 2018-19**
C. Thornley (Lower Hutt, New Zealand), M. Kelly, M. Bloomfield, A. Nesdale, X. Ren*

2942 **Carbapenemase-producing and colistin-resistant *Enterobacteriaceae* in intensive care unit patients from Mediterranean countries, 2019**
S. Borges Dos Santos, S. Diene, B. Amina, K. Zerouali, D. Ghaith, R. El-Mahdy, S. El Tayeb, A. Hammami, I. Boutiba, R. Husni, Z. Daoud, L. Mereghetti, P. François, N. Van Der Mee-Marquet (Tours, France)*

6240 **Evidence of high prevalence, transmission rate and persistence of *Escherichia coli* ST131-Rx among residents of nursing homes in south Spain (JPI-ST131TS project)**
E. Salamanca (Seville, Spain), L. Lopez-Cerero, M. Delgado-Valverde, J. Rodríguez-Baño, A. Pascual Hernandez*

6376 **A multi-year decline of multidrug-resistant *Escherichia coli* in French nursing homes and primary care: are we on the good track?**
S. Thibaut (Nantes, France), T. Coeffic, D. Boutoille, G. Birgand, J. Caillon, P. Network*

6629 **The population structure of extended-spectrum beta-lactamase-producing *Enterobacteriaceae* in households following hospital discharge and long-term care facilities is species dependent: MODERN-studies from 5 European countries (2017- 2019)**
T. Verschuuren (Utrecht, Netherlands), J. Dick, M. Riccio, E. Salamanca, S. Bunk, N. Conzelmann, D. Martak, D. Hocquet, E. Tacconelli, J. Rodríguez-Baño, S. Harbarth, I. Autenrieth, A. Fluit, S. Peter, J. Kluytmans*

6673 **Identifying the drivers of multidrug-resistant *Klebsiella pneumoniae* at a European level**
V. Kachalov (Zurich, Switzerland), H. Nguyen, S. Balakrishna, L. Salazar Vizcaya, R. Sommerstein, S. Kuster, A. Hauser, P. Abel Zur Wiesch, E. Klein, R. Kouyos*

7521 **Prospective nested case-control study on colistin-resistant *Enterobacterales* in the Netherlands**
K. Vendrik (Leiden, Netherlands), A. De Haan, D. Notermans, P. Bijkerk, A. Schoffelen, S. De Greeff, C. Wielders, M. Mennen, A. Hendrickx, E. Kuijper, L. Schouls*

Session accepted as Mini-oral Flash Session

Colistin resistance and other resistance mechanisms in the horizon

1894 **Identification of novel mobile colistin resistance gene *mcr*-10**
C. Wang, Y. Feng, Z. Zong (Chengdu, China)*

3486 **Widespread distribution of the acquired colistin resistance gene, *mcr*-9, amongst *Enterobacterales* in England and Wales**
M. Ellington (London, United Kingdom), T. Dallman, D. Meunier, K. Hopkins, N. Woodford*

5117 **Colistin resistance in human *Salmonella* spp. isolates collected from Italian Enter-Net surveillance during the period 2016-2018**
D. Fortini, S. Owczarek, A. Dionisi, I. Benedetti, L. Busani, C. Lucarelli, L. Villa (Rome, Italy), A. Garcia-Fernandez*

5188 **Plasmid-mediated colistin resistance among human clinical *Enterobacterales* isolates: surveillance in the Czech Republic, 2018-2019**
M. Zelendova, V. Jakubu, I. Jamborova, K. Pomorska, M. Medvecky, H. Zemlickova, M. Dolejska (Brno, Czech Republic)*

5240 **Sequential time-kill experiments to characterize lypopolysaccharide-modifying genes involved in polymyxin resistance in *Escherichia coli* and *Klebsiella pneumoniae* carrying *mcr*-1**
H. Ih (Poitiers, France), N. Gregoire, W. Couet, S. Marchand, J. Buyck*

5664 **An OXA-48 variant hydrolysing carbapenems, expanded-spectrum cephalosporins and aztreonam: welcome OXA-793**
M. Dabos (Le Kremlin-Bicêtre, France), R. Bonnin, L. Dortet, T. Naas*

5873 **A novel plasmid-mediated RND family efflux pump confers tigecycline resistance in *Klebsiella pneumoniae***
S. Sun (Beijing, China), H. Gao, Y. Liu, L. Jin, R. Wang, X. Wang, Q. Wang, H. Wang*

6675 **Within-patient evolution of a clinical isolate of *Escherichia coli* uncovers an IS26-linked amplification of *bla*TEM-1 leading to piperacillin-tazobactam resistance**
T. Edwards (Liverpool, United Kingdom), J. Mason, P. Roberts, C. Parry, J. Van Aartsen, A. Howard, A. Roberts, E. Adams, A. Hubbard*

8886 **Inter- and intraspecies spread of *mcr*-1 between twenty-nine distinct *Enterobacteriaceae* isolates from one patient**
H. Xu (Hangzhou, China), B. Zheng, Y. Xiao*

9444 **Investigation of colistin resistance mechanisms in *Klebsiella pneumoniae* strains**
B. Borsa (Linköping, Sweden), G. Karabiyik, I. Karalti, B. Guvenc-Tuna, I. Acuner*

Session accepted as Paper Poster Session

Commercial AST methods: what's new?

1079 **ETEST Eravacycline for antimicrobial susceptibility testing of *Enterobacteriaceae* and *Enterococcus* spp.: performance results from a multi-centre study**
L. Blanchard (Marcy-l'Étoile, France), T. Armstrong, D. Gerald, Y. Ying, M. Kresken, J. Carpenter, V. Sauvonnet, G. Zambardi*

1138 **Evaluation of the accuracy of the panel for antimicrobial susceptibility testing of *Enterobacteriaceae* and carbapenemase detection**
H. Cho (Seoul, South Korea), Y. Park, J. Kim, J. Choi, S. Ha, Y. Cha*

1813 **Does automated susceptibility testing overcall temocillin resistance?**
M. Campbell (Oxford, United Kingdom)*

2300 **Multi-centre evaluation of cephalexin MIC results for *Enterobacterales* using EUCAST breakpoints on MicroScan dried Gram-negative MIC panels**
O. Garner, C. Emery, A. Harrington, S. Desjarlais, C. Hastey, R. Brookman, Z. Lockett, J. Chau (West Sacramento, United States)*

2304 **Luminogenic phosphatase substrate for rapid susceptibility testing of Gram-positive strains**
V. Chalansonnet (La Balme-les-Grottes, France), F. Macé, S. Orenga*

2366 **Using T2Dx and rapid AST with blood culture pre-sampling for combined ID and AST before blood culture positivity**
C. Malmberg (Uppsala, Sweden), L. Flinkfeldt, P. Yuen, J. Fernberg, H. Öhrn, C. Johansson, T. Tängdén, J. Kreuger*

2724 **Phenotypic testing of ceftriaxone susceptibility on the Pheno system in characterised *Enterobacterales***
A. Bhalodi (Tucson, United States), N. Magnano, R. Humphries*

3715 **Comparative study of two susceptibility testing methods for carbapenem-resistant *Klebsiella pneumoniae* clinical isolates**
A. Tychala, A. Stamou, P. Mantzana, G. Meletis, F. Netsika, I. Gkeka, D. Papadopoulou, H. Katsanou, G. Kagkalou, O. Vasilaki, M. Kachrimanidou, L. Skoura, E. Protonotariou (Thessaloniki, Greece)*

3779 **An evaluation of an automated broth microdilution platform versus the EUCAST disk diffusion methodology**
P. D'Arcy-Grover (Southampton, United Kingdom), I. Taylor*

3822 **A low-cost nanoliter droplet handling system for pathogen identification and antimicrobial susceptibility testing on microtitre plates**
Q. Yi (Beijing, China), W. Du, Y. Xu*

4069 **Rapid generation of a standard inoculum direct from positive blood cultures using electrical biosensor technology**
E. Deak (Menlo Park, United States), S. Putney, Y. Ngo, W. Yip, K. Vo, T. Abbey, M. Herget*

4538 **Evaluation of a new commercial fosfomycin agar dilution-kit against reference agar dilution**
L. Davies, L. Jones, F. Demetrio, S. Pomponio, F. Brocco, M. Wootton (Cardiff, United Kingdom)*

4673 **Antimicrobial screening of 2208 UK isolates (2003-2018) using novel *Legionella* Medium (LASARUS)**
E. Portal (Cardiff, United Kingdom), K. Sands, B. Afshar, V. Chalker, B. Spiller*

4887 **A multi-site study comparing a commercially-prepared dried MIC susceptibility system to the CLSI/ISO broth microdilution method for cefepime-taniborbactam (formerly cefepime/VNRX-5133) using Gram-negative non-fastidious organisms**
T. Lewis (Oakwood Village, United States), D. Staats, N. Holliday, C. Knapp, S. Killian, B. Olson, C. Pike, E. Higdon, R. Schoone, T. Fritsche, A. Gattis, N. Waugh, K. Doing, P. Von Stein, A. Goer, K. Knight, A. Butler, D. Paisey, S. Cusick, G. Moeck*

5636 **Evaluation of *Bacillus anthracis* agar-based susceptibility testing by Etest for ciprofloxacin, levofloxacin, doxycycline and tetracycline**
B. Cherney (Atlanta, United States), P. Michel, J. Bugrysheva, A. Gargis, T. Kongphet-Tran, C. Lascols, H. Mclaughlin, D. Sue*

5834 **Evaluation of antimicrobial susceptibility testing assays for ceftazidime-avibactam and ceftolozane-tazobactam with Gram-negative bacteria directly from positive blood culture on the Pheno system**
N. Oppermann, A. Ndobegang, A. Sikorski, A. Taku, D. Gamage, C. Chantell, R. Humphries (Los Angeles, United States)*

6316 **Clinical evaluation of FASTinov kits for ultra-rapid antimicrobial susceptibility testing directly from positive blood cultures**
A. Silva-Dias, B. Pérez-Viso, R. Gomes, I. Martins-Oliveira, A. Rodrigues, R. Canton Moreno, C. Pina-Vaz (Porto, Portugal)*

6486 **Detection of colistin resistance in *Pseudomonas* and *Acinetobacter* by the ATB PSE EU strips**
S. Petre, E. Pillon (La Balme Les Grottes, France), M. Roland*

6516 **Evaluation of different commercial methods for fosfomycin susceptibility testing of *Staphylococcus aureus***
F. Campanile, A. Aprile (Catania, Italy), C. Bonomo, C. Imbrosciano, A. Mirabile, D. Bongiorno, S. Stefani, M. Mezzatesta*

6925 **ETEST Imipenem-relebactam for antimicrobial susceptibility testing of *Enterobacteriaceae* and *Pseudomonas aeruginosa*: performance results from a multi-centre study**
C. Anglade (Marcy L'étoile, France), S. Garrett, J. Richards, D. Leanne, C. Burnham, O. Garner, M. Wootton, G. Zambardi, D. Halimi*

6998 **Performance of the Accelerate Pheno system in a tertiary care hospital in Germany**
B. Berinson (Hamburg, Germany), F. Olearo, A. Both, M. Aepfelbacher, H. Rohde*

7138 **Comparative evaluation of the Phoenix and Vitek2 systems for ceftaroline-susceptibility testing in clinical isolates of methicillin-resistant *Staphylococcus aureus* (MRSA)**
L. Rivas, C. Varela, L. Porte, P. Rojas, C. Espinoza Farias, C. Fuenzalida, V. Sanfurgo, C. Zumaran, R. Martinez, M. Quezada, F. Moya, F. Silva, B. Barraza, S. Braun, F. Valdivieso, M. Mulhauser, M. Lafourcade, P. García, J. Munita (Santiago, Chile)*

7195 **Validation of three MicroScan antibiotic susceptibility testing microplates designed for low-resource settings**
J. Ronat (Paris, France), S. Oueslati, A. Natale, O. Vandenberg, J. Jacobs, T. Naas*

8081 **Evaluation of the PROMPT inoculation system with the MicroScan antibiotic susceptibility testing microplate designed for low-resource settings**
J. Ronat (Paris, France), S. Oueslati, A. Natale, O. Vandenberg, J. Jacobs, T. Naas*

8813 **Antimicrobial susceptibility testing directly from positive blood culture with the Reveal Rapid AST System: clinical results for Gram-negative pathogens**
R. Tibbetts, S. George, P. Rhodes, P. Singh, L. Samuel (Detroit, United States)*

8814 **Evaluation of a urinalysis predictive model and the performance of direct-from-urine susceptibility testing**
C. Doern (Richmond, United States), S. Hedrick, L. Matthews, A. Bryson, K. Bradbrook, C. Jay, N. Taylor, A. Sima, M. Jamerson*

8971 **Multi-centre study performance results of ETEST delafloxacin for antimicrobial susceptibility testing against Gram-positive organisms and *Pseudomonas aeruginosa***
C. Anglade (Marcy L'étoile, France), T. Armstrong, C. Burnham, H. Dwight, M. Wootton, G. Zambardi, V. Sauvonnet*

Session accepted as Paper Poster Session

Culture-based approaches for carbapenemase screening and confirmation

1755 **Evaluation of a new commercial disc susceptibility kit for detection and differentiation of carbapenemases produced by *Enterobacterales***
E. Marrs, A. Anyakwo, J. Hobson, J. Perry (Newcastle upon Tyne, United Kingdom)*

1984 **Additional testing and prevalence of *Enterobacterales* with elevated carbapenem MIC in the Netherlands, 2014-2018**
S. Woudt (Bilthoven, Netherlands), A. Schoffelen, A. Reuland*

2016 **Evaluation of the performance of three chromogenic culture media for the detection of carbapenemase producing *Enterobacterales* to manage healthcare-associated infections**
C. Fulchiron (La Balme les Grottes, France), J. Oliger, J. Pujol, G. Durand*

3091 **How to screen OXA-244, a difficult to detect emerging OXA-48 variant**
E. Cécile (Le Kremelin Bicêtre, France), L. Biez, D. Girlich, A. Jousset, R. Bonnin, T. Naas, L. Dortet*

3719 **Systematic comparison of three commercially available combination disc tests for carbapenemase detection in *Enterobacterales* isolates**
J. Sattler (Cologne, Germany), A. Brunke, A. Hamprecht*

6123 **Evaluation of the carbapenem inactivation method (CIM) as a predictor for carbapenemase-producing Gram-negative bacteria**
F. Hurren, K. Chua (Heidelberg, Australia), M. Leroi*

6280 **Comparative evaluation of CHROMagar COL-APSE, MicroScan Walkaway, ComASP Colistin, and Colistin MAC test diagnostic efficiencies in detecting colistin-resistant Gram-negative bacteria**
A. Sephpfane, N. Mbelle, J. Osei Sekyere (Pretoria, South Africa)*

7406 **External quality assessment panel on detection of carbapenem-resistant Gram-negative pathogens within the NeoOBS study**
T. Vilken (Dilbeek, Belgium)*

8200 **Rapid detection and characterisation of the Ambler class of carbapenem-resistant *Enterobacteriaceae* with the mCIMplus assay**
M. Petit, F. Caméléna (Paris, France), M. Rouveau, M. Lafaurie, S. Bonacorsi, A. Birgy, B. Bercot*

8304 **Retrospective and prospective evaluation of the rapid carbapenem inactivation method test for AmpC-producers**
A. Muntean (Bucharest, Romania), M. Muntean, S. Oueslati, A. Jousset, D. Girlich, S. Bernabeu, F. Guérin, V. Cattoir, C. Dragomirescu, M. Popa, T. Naas*

Session accepted as Paper Poster Session

Dissecting resistance trends in polymyxins

456 **Insights of colistin resistance and flexible transmission of *mcr-1***
Y. Yu, X. Li, X. Liao (Guangzhou, China), J. Sun, Y. Liu*

459 **Clinical and molecular perspectives of colistin-resistant *Klebsiella* from an oncology centre in a lower-middle income country**
K. Abdul Ghafur (Chennai, India), C. Shankar, S. Rajendran, T. Ma, V. Balaji*

490 **Rough-type and loss of the LPS due to *lpx* genes deletions are associated with colistin resistance among multidrug-resistant *Escherichia coli* clinical isolates not harbouring *mcr* genes**
M. Savari (Ahvaz, Iran), N. Emam, M. Moosavian*

1675 **Low horizontal transfer rate of *mcr-8* may constrain the spread of *mcr-8* genes**
Q. Yang (Cardiff, United Kingdom), T. Walsh*

2478 **Serotype is associated with high rate of colistin resistance among clinical isolates of *Salmonella* from China**
Q. Luo (Hangzhou, China), H. Fu, X. Yu, Y. Wang, Y. Xiao*

2791 **First epidemiological report on colistin- and carbapenem-resistant *Enterobacteriaceae* isolates obtained from selected tertiary hospitals in south-eastern Nigeria**
U. Ugah (Abakaliki, Nigeria), T. Udeani*

2939 **Emergence of mobile *mcr-8* colistin resistance in *Klebsiella pneumoniae* from clinical infections of hospitalised patients in Bangladesh**
R. Farzana (Cardiff, United Kingdom), L. Jones, A. Barratt ?, A. Rahman, K. Sands, E. Portal, Q. Yang, T. Walsh*

3439 **Role of AcrAB-TolC multidrug efflux pump in *mcr-1*-mediated colistin resistance**
W. Liang (Guangzhou, China), Z. Zhao, D. Lin, S. Feng, L. Liang, J. Li, X. Wen, C. Shen, G. Tian*

4183 **The intestinal carriage of colistin-resistant *Enterobacteriaceae* in a tertiary care hospital setting and whole genome sequence data analysis of *mcr*-1 positive *Escherichia coli* isolates**
J. Tkadlec (Prague, Czech Republic), E. Smelikova, A. Baráková, M. Cabrnochova, G. Tereza, R. Karpiskova, O. Nyc, P. Drevinek, M. Krutova*

4769 **Molecular detection of the *mcr*-1 mobile colistin resistance gene in healthy humans and a dog with skin infection from Portugal**
J. Menezes (Lisbon, Portugal), A. Belas, I. Cunha E Silva, M. Pomba*

5943 **Coproduction of *mcr*-9 and KPC-2 by archived clinical *Enterobacter* spp. strains from Colombia**
L. Rojas Coy (Cleveland, United States), W. Shropshire, S. Marshall, S. Rudin, E. De La Cadena, A. Dinh, M. Villegas, B. Hanson, C. Arias, R. Bonomo*

6110 **Persister response of *Klebsiella pneumoniae* to colistin exposure**
C. Vatansever (Istanbul, Turkey), N. Atac, B. Ozer, B. Kiliçoğlu, M. Berkkan, U. Guler, D. Baskurt, E. Sever, O. Dogan, F. Can*

6237 **Stable mutants and persisters variants are involved in heteroresistance to colistin in wild-type *Klebsiella pneumoniae* of clinical origin**
I. Sánchez León (Córdoba, Spain), C. Elias-Lopez, L. Martinez-Martinez*

6409 **Comparison of colistin-resistant *Klebsiella pneumoniae* strains in five Greek hospitals**
M. Maisi (Heraklion, Greece), G. Tsioulos, E. Maisi, I. Choudalaki, P. Giakkoupi*

6455 ***mcr-8*-mediated colistin resistance in a carbapenem-resistant *Klebsiella pneumoniae* isolate**
R. Bonnin, S. Bernabeu, F. Jaureguy, T. Naas, L. Dortet (Paris, France)*

6666 **Genetic characterisation of multidrug-resistant *Klebsiella pneumoniae* harbouring colistin resistance gene *mcr-1* from North India**
A. Pathak (Lucknow, India), S. Singh, K. Prasad*

6896 **Rapid detection of colistin-resistant *Klebsiella pneumoniae* using colistin drop test**
V. Rocha (Salvador, Brazil), D. Nascimento, M. Sales, A. Martins, J. Azevedo, A. Malheiros, L. Ataide, M. Reis, J. Reis*

7048 **Colistin hetero-resistant *Klebsiella pneumoniae* and *Escherichia coli* blood isolates**
Ü. Liste, E. Kırbaş (Ankara, Turkey), A. Bıçakçıgil, B. Sancak*

7172 **Hetero-resistance to colistin in *Stenotrophomonas maltophilia* isolates: challenges in colistin susceptibility testing**
Ü. Liste, A. Bıçakçıgil, C. Özkuyumcu, B. Sancak (Ankara, Turkey)*

8334 **Acquired resistance to colistin in *Enterobacteriaceae* isolated at university hospital of Algiers**
B. Mohamed Azzedine (Algiers, Algeria), D. Fazia, L. Farah, M. Tazir, W. Amhis*

8532 **First national survey on colistin resistance among *Escherichia coli* in Belgium**
O. Denis (Brussels, Belgium), P. Bogaerts, C. Berhin, M. Hoebeke, W. Bouchahrouf, Y. Glupczynski, T. Huang*

8895 **Diversity of colistin resistance mechanisms in carbapenemase-producing *Klebsiella pneumoniae* isolated in Bulgaria from 2013 to 2018**
K. Ivanova (Sofia, Bulgaria), I. Ivanov, S. Sabtcheva, V. Dobrinov, M. Nedyalkov, E. Dobreva, R. Hristova, T. Kantardjiev*

9409 **Molecular surveillance of *mcr* gene in gut microbiome of healthy individuals, acute diarrhoea and inflammatory bowel diseases patients from India**
S. Banerjee (New Delhi, India), T. Senapati, J. Verma, A. Mani, A. Kapil, B. Das*

9513 **Clonality and genetic determinants of resistance in paired isolates of *Klebsiella pneumoniae* with divergent polymyxin B phenotypes**
S. Sampaio, R. Carvalho, M. Mimica, C. Da Silva, A. Lima, K. Lima, D. Rocha, J. Mello-Sampaio (São Paulo, Brazil)*

Session accepted as Mini-oral Flash Session

Emerging resistance to new and last resort drugs

1271 **Characterisation of KPC-50, a novel transferable KPC-3 variant conferring resistance to ceftazidime-avibactam in a colistin-resistant *Klebsiella pneumoniae* from Switzerland**
L. Poirel (Fribourg, Switzerland), X. Vuillemin, A. Masseron, M. Juhas, S. Mancini, R. Zbinden, S. Tiziani, U. Bechtel-Grosch, P. Nordmann*

3424 **Genomic characterisation of meropenem/vaborbactam resistant KPC-producing *Klebsiella pneumoniae* strains isolated from bacteraemic patients**
P. Gaibani (Bologna, Italy), M. Re, S. Ambretti*

3810 **A silent *mcr-9* and a novel class A beta-lactamase in *Citrobacter telavivum* sp. nov. colonising hospital patients**
T. Goncalves Ribeiro (Porto, Portugal), R. Izdebski, P. Urbanowicz, Y. Carmeli, M. Gniadkowski, L. Peixe*

4051 **Chemical genomics to reverse the colistin resistance of MDR *Klebsiella pneumoniae***
B. Jana (Brighton, United States), K. Baker, A. Cain, W. Doerrler, L. Guardabassi*

5028 **Acquired resistance to fosfomycin through acquisition of an IS*Ecp1-bla*CTX-M-14 tandem in a *Klebsiella pneumoniae* clinical isolate**
N. Kieffer, L. Poirel (Fribourg, Switzerland), L. Mueller, P. Nordmann*

5510 **Mechanisms of resistance in *Pseudomonas aeruginosa* against ceftazidime-avibactam and ceftolozane-tazobactam from Qatar**
M. Sid Ahmed (Doha, Qatar), F. Ahmad Khan, H. Abdel Hadi, A. Sultan, M. Al-Maslamani, A. Al-Khal, B. Söderquist, E. Ibrahim, A. Omrani, J. Jass*

7656 **Multiple mutational possibilities allow ceftazidime-avibactam resistance in KPC-type carbapenemase**
H. Claire Amaris, S. Bonacorsi, H. Jacquier, M. Mélanie, A. Choudhury, B. Bercot, O. Tenaillon, A. Birgy (Paris, France)*

9106 **Characterisation of *mcr-5* action suggests a unified mechanism for polymyxin resistance**
Y. Feng (Hangzhou, China)*

Session accepted as Mini-oral ePoster Session

EUCAST rapid disk diffusion: the story so far

3616 **Evaluation of EUCAST rapid antimicrobial susceptibility testing (RAST) on blood cultures in a clinical laboratory**
P. Rydström (Växjö, Sweden), E. Jonasson*

4028 **Evaluation of rapid AST in blood cultures using CHROMagar Mueller-Hinton orientation agar**
B. Mnif (Sfax, Tunisia), F. Zouari, S. Gouiaa, N. Sallem, A. Hammami*

4543 **Usefulness of RAST-EUCAST directly from blood culture bottles combined with rapidly interpreted antibiogram reading to detect ESBL/carbapenemase-producing *Enterobacterales***
V. Cerrudo Lopez (Madrid, Spain), J. Cortes Cuevas, S. García-Fernández, R. Canton Moreno, M. Morosini, A. Sanchez Diaz*

4978 **The EUCAST Rapid AST directly from positive blood culture bottles: breakpoints for additional antimicrobial agents for *Escherichia coli*, *Klebsiella pneumoniae* and *Pseudomonas aeruginosa***
E. Jonasson, E. Matuschek, G. Kahlmeter (Växjö, Sweden)*

5113 **Direct-from-blood-culture disk diffusion to determine antimicrobial susceptibility of *Escherichia coli* and *Klebsiella pneumoniae***
V. Cortazzo (Roma, Italy), T. D'Inzeo, B. Fiori, G. Menchinelli, F. Liotti, L. Giordano, B. Posteraro, M. Sanguinetti, T. Spanu*

5127 **Automated rapid antimicrobial susceptibility testing from positive blood cultures using Copan WASPLab**
C. Verduin, S. Derksen, J. Stalpers (Veldhoven, Netherlands), T. Liebregts, M. Nijs, A. Jansz*

6278 **Evaluation of the rapid antimicrobial susceptibility testing (RAST) from positively-flagged blood cultures**
T. Ko (Taipei, Taiwan), P. Chuang, C. Hsu, T. Lee, P. Hsueh*

6845 **EUCAST rapid AST directly from positive blood culture bottles: breakpoints for *Acinetobacter baumannii***
E. Jonasson, E. Matuschek (Växjö, Sweden), G. Kahlmeter*

6934 **Evaluation of the EUCAST rapid antimicrobial susceptibility testing directly from positive blood cultures for *Escherichia coli* and *Staphylococcus aureus* in a routine laboratory**
E. Jonasson (Växjö, Sweden), P. Rydström*

Session accepted as Paper Poster Session

Gram-negatives behaving badly: antimicrobial resistance in non-enteric GNR

227 **Genome-wide analysis of resistance-related transposable elements in multidrug-resistant *Haemophilus parainfluenzae* clinical isolates**
Y. Sierra Urueña (Barcelona, Spain), A. González Díaz, D. Berbel Palau, A. Carrera-Salinas, D. Vázquez-Sánchez, M. Cubero, F. Tubau, J. Càmara, C. Ardanuy Tisaire, S. Marti*

1357 **Roles of the FadRACB system in formaldehyde detoxification and antibiotic susceptibility in *Stenotrophomonas maltophilia***
L. Li, C. Wu, Y. Lin, S. Pan, T. Yang (Taipei, Taiwan)*

1982 **Spatial and temporal genomic homogeneity among *Haemophilus influenzae* serotype f**
A. González Díaz (Barcelona, Spain), M. Pinto, M. Cubero, J. Langereis, A. Van Der Ende, P. Bajanca-Lavado, C. Ardanuy Tisaire, S. Marti*

2157 **Rising clarithromycin resistance in *Helicobacter pylori* in a Hong Kong regional hospital and molecular characterisation by next-generation sequencing**
C. Lau (Hong Kong, Hong Kong), W. Chan, C. Au, T. Chan, T. Chan, S. Ma, B. Tang*

2348 **Co-trimoxazole resistance in *Stenotrophomonas maltophilia***
A. Magnus (Copenhagen, Denmark), J. Knudsen*

3145 **Antimicrobial resistance surveillance data of *Helicobacter pylori* in Belgium (2016-2019)**
T. Huang (Yvoir, Belgium), O. Denis, C. Berhin, M. Hoebeke, W. Bouchahrouf, Y. Glupczynski, P. Bogaerts*

5045 **Mutations in PBP3 conferring beta-lactams resistance in *Haemophilus parainfluenzae***
D. Pablo Marcos (Santander, Spain), L. Armendariz, M. Siller Ruiz, J. Aguero, J. Calvo-Montes*

5055 **Dual RNase and β-lactamase activity of a single enzyme encoded in most Archaea**
S. Diene (Marseille, France), L. Pinault, N. Armstrong, S. Azza, V. Keshri, K. Saber, E. Chabrière, G. Caetano-Anolles, J. Rolain, P. Pontarotti, D. Raoult*

6151 **Whole genome sequencing and phenotypic characterisation of non-typeable *Haemophilus influenzae* in Hong Kong: 2000-2016**
C. Li, D. Cleary, Y. Yeoh, J. Ho, N. Rahman (Shatin, Hong Kong), D. Nanayakkara, J. Yang, N. Lo, S. Clarke, M. Ip*

7143 **Molecular detection of mutations involved in *Helicobacter pylori* antimicrobial resistance in Ecuador**
J. Zurita (Quito, Ecuador), G. Sevillano, V. Penaherrera, M. Echeverria, C. Zurita, A. Paz Y Mino, H. Navarrete, H. Working Group*

7441 **Evaluation of *Stenotrophomonas maltophilia* non-susceptibility and associated risk factors: a multi-centre analysis**
C. Bland, N. White, J. Lin, J. Wagner, K. Stover, B. Bookstaver, D. Chastain (Albany, United States), H. Matson, M. Motes, B. Jones*

7620 **Limited multidrug-resistant efflux pump overexpression among multidrug-resistant *Escehrichia coli* of ST131**
J. Camp (Freiburg, Germany), S. Schuster, M. Vavra, T. Schweigger, J. Rossen, W. Kern*

9061 **The rational of antibiotic failure in *Helicobacter pylori***
S. Ghafourian, E. Aboualigalehdari (Ilam, Iran), B. Badakhsh*

Session accepted as 1-Hour Oral Session

Important resistance issues in enterococci

1177 **Mechanisms of linezolid resistance in Belgian *Enterococcus* isolates (2013-2019)**
K. Loens (Antwerp, Belgium), S. Van Koeveringe, H. Goossens, V. Matheeussen*

1573 **Prevalence and outcome of ampicillin-susceptible but penicillin-resistant *Enterococcus faecalis* bacteraemia: a multi-centre retrospective study**
E. Rosselli Del Turco (Bologna, Italy), M. Bartoletti, S. Carvalho Brugger, S. Ambretti, M. Garcia, M. Giannella, R. Pascale, L. Raumer, P. Viale, J. Pericàs Pulido*

4548 **Risk factors and outcomes associated with the carriage of tigecycline-non-susceptible vancomycin-resistant *Enterococcus faecium***
J. Kessel (Frankfurt, Germany), J. Bender, G. Werner, M. Griskaitis, E. Herrmann, A. Lehn, H. Serve, K. Zacharowski, S. Zeuzem, M. Vehreschild, T. Wichelhaus, V. Kempf, M. Hogardt*

4905 **Molecular epidemiology of vancomycin-resistant enterococci: changing paradigms at the crossroads of Europe**
C. Correa-Martinez (Münster, Germany), A. Jurke, J. Schmitz, S. Kampmeier, A. Mellmann*

5195 **First vancomycin-variable enterococci from France: molecular mechanisms of phenotypic susceptibility**
Z. Mamou (saint gregoire, France), A. Zouari, S. Potrel, A. Collet, G. Auger, V. Cattoir*

Session accepted as Paper Poster Session

In vitro activity of ceftolozane/tazobactam

777 **Susceptibility of β-lactam-resistant *Pseudomonas aeruginosa* to last-line antibiotics stratified by carbapenemase production**
N. Ho, Y. Ng, B. Cheng, J. Teo, K. Chew (Singapore, Singapore)*

1215 **Emergence of non-susceptibility among Gram-negative respiratory pathogens from a phase III clinical trial for treatment of nosocomial pneumonia (ASPECT-NP)**
M. Motyl (Kenilworth, United States), M. Castanheira, M. Johnson, B. Yu, J. Huntington, P. Carmelitano, C. Bruno, C. De Anda, E. Rhee*

1350 ***In vitro* activity of ceftolozane/tazobactam against clinical isolates of carbapenem-resistant *Pseudomonas aeruginosa* from Japan hospitals**
T. Nakamura (Kyoto, Japan), M. Fujiwara*

2575 **Ceftolozane/tazobactam-resistant *Pseudomonas aeruginosa* isolates in a teaching hospital in central Italy**
M. Gianluca (Ancona, Italy), L. Brescini, A. Brenciani, A. Antonelli, V. Di Pilato, S. Castelletti, S. Fioriti, T. Giani, G. Rossolini, A. Giacometti, O. Cirioni*

2689 ***In vitro* activity of ceftolozane/tazobactam and comparators against *Pseudomonas aeruginosa* isolates collected in the United States: SMART 2018**
K. Kazmierczak (Schaumburg, IL, United States), J. Raddatz, K. Young, M. Motyl, D. Sahm*

2711 ***In vitro* activity of ceftolozane-tazobactam against *Enterobacterales* and *Pseudomonas aeruginosa* from patients with bloodstream infections in the Asia/Pacific region: SMART 2018**
S. Lob, K. Kazmierczak (Schaumburg, United States), W. Chen, T. Khan, K. Young, M. Motyl, D. Sahm*

3036 **Characterisation of ceftolozane/tazobactam resistance among *Enterobacterales* and *Pseudomonas aeruginosa* isolates recovered during the SUPERIOR study using whole genome sequencing**
M. Hernández García (Madrid, Spain), S. García-Fernández, M. García-Castillo, G. Bou Arevalo, E. Cercenado, M. Delgado-Valverde, A. Oliver, C. Pitart, J. Rodríguez-Lozano, N. Tormo, D. Lopez, J. Diaz-Regañon, R. Canton Moreno*

3052 **Confronting ceftolozane/tazobactam susceptibility in multidrug-resistant *Enterobacterales* isolates and whole genome sequencing results (STEP study)**
M. Hernández García (Madrid, Spain), S. García-Fernández, M. García-Castillo, J. Cristino, M. Feijo Pinto, E. Goncalves, V. Alves, A. Vieira, E. Ramalheira, L. Sancho, J. Diogo, R. Ferreira, D. Fonseca E Silva, C. Antunes Chaves, L. Pássaro, L. Paixao, R. Canton Moreno*

4176 **Activity of ceftolozane/tazobactam against prevalent Gram-negative pathogens across Asia: PACTS 2016-2018**
M. Tulloch (Sydney, Australia), D. Shortridge, M. Motyl, P. Moise, W. Chen*

4302 ***In vitro*** **activity of ceftolozane-tazobactam and comparators against beta-lactam-resistant pathogens isolates collected from patients with urinary tract, intra-abdominal and lower respiratory infections in Lebanon and Jordan (SMART Study Data 2016-2017)**
A. Hajj, T. Itani (Beirut, Lebanon), W. Hayajneh, A. Adaime, N. Hakime, M. Mallah Hamdan, J. Maalouf, R. Alsamarneh, M. Motyl, D. Sahm, I. Alekseeva, D. Karam Sarkis*

8680 **Activity of ceftolazone-tazobactam and combinatorial regimens against a contemporary collection of carbapenem-resistant *Pseudomonas aeruginosa***
C. Black (San Antonio, United States), J. Shurko, C. Chen, D. Burgess, G. Gawrys, G. Lee*

Session accepted as Paper Poster Session

It's a gas: anaerobes and AMR

2315 **Descriptive epidemiological analysis of antimicrobial resistance in strict anaerobes in Scotland, 2013-2018**
J. Wilson, A. Zalewska, M. Lockhart (Glasgow, United Kingdom), E. Mcardle, W. Malcolm*

2410 **Evaluation of the antimicrobial activity of ridinilazole and six comparators against Chinese, Japanese and South Korean isolates of *Clostridioides difficile***
D. Collins (West Leederville, Australia), Y. Wu, K. Tateda, H. Kim, R. Vickers, T. Riley*

3345 **Antimicrobial-resistant *Bacteroides fragilis* detected from blood culture in 2 tertiary hospitals**
K. Ohgane (Iruma-gun, Japan), M. Kodana, A. Onodera, K. Imai, J. Sakai, T. Kawamura, S. Takeuti, N. Tarumoto, K. Mitsutake, K. Ikebuchi, S. Maesaki, T. Maeda*

3386 **The antimicrobial susceptibility profile and prevalence of known anaerobic resistance genes in less common anaerobic Gram-negative bacteria, isolated in the Netherlands**
K. Boiten (Groningen, Netherlands), W. Baas, P. Buijs, J. Rossen, A. Veloo*

3414 **Pandrug-resistant *Bacteroides fragilis* clinical isolates in the Netherlands: true or fiction**
K. Boiten (Groningen, Netherlands), E. Kuijper, F. Smit, L. Bode, L. Schüle, A. Schoffelen, D. Notermans, S. Woudt, H. Winter, J. Van Prehn, A. Veloo*

3928 **Aetiology and antimicrobial susceptibility of anaerobic bacteria causing serious infections in a tertiary hospital of Madrid**
J. López-Pintor (Madrid, Spain), A. Sánchez-Díaz, P. Ruiz-Garbajosa, R. Canton Moreno, M. Morosini Reilly, S. García-Fernández*

4489 **Antimicrobial susceptibility in *Clostridioides difficile* varies according to European region and isolate source**
J. Freeman (Leeds, United Kingdom), V. Viprey, V. Tkalec, D. Ewin, W. Spittal, E. Clark, J. Vernon, W. Fawley, A. Benson, G. Davis, M. Rupnik, M. Wilcox, K. Davies*

5626 **The effect of intestinal alkaline phosphatase and physical activity on the course of experimental colitis in obese mice**
D. Wójcik (Kraków, Poland), M. Surmiak, M. Hubalewska-Mazgaj, Z. Śliwowski, S. Kwiecień, T. Brzozowski*

6955 **Molecular analysis of metronidazole-resistant *Bacteroides* strains from Kuwait**
Z. Baaity (Szeged, Hungary), W. Jamal, K. Burian, V. Rotimi, J. Soki*

Session accepted as Paper Poster Session

KPC-producing enterobacteria

2979 **Genetic characterisation of co-produced KPC-3, CTX-M-15 and SHV-1 β-lactamases in carbapenem-resistant *Klebsiella pneumonia* ST512 causing bloodstream infections in an endemic tertiary hospital**
A. Piccirilli, M. Perilli, L. Maccacaro, A. Bazaj, L. Naso, V. Piccirilli, B. Segatore, G. Amicosante, G. Cornaglia, G. Lo Cascio (Verona, Italy)*

3282 **Plasmid diversity among genetically related *Klebsiella pneumoniae bla*KPC-2 and *bla*KPC-3 isolates collected in the Dutch national surveillance**
A. Hendrickx (Bilthoven, Netherlands), F. Landman, A. De Haan, D. Borst, S. Witteveen, M. Van Santen, H. Van Der Heide, L. Schouls*

3511 **Vertical and horizontal dissemination of an IncA/C plasmid harbouring *rmtB* 16S-rRNA methylase conferring resistance to amikacin and plazomicin among KPC-producing *Klebsiella pneumoniae* in a Brazilian tertiary centre**
M. Roch, P. Dantas, R. Sierra, W. Martins, K. Sands, T. Walsh, E. Medeiros, A. Gales, D. Andrey (Geneva, Switzerland)*

4671 **Absence of the Type I-E CRISPR-Cas system in *Klebsiella pneumoniae* clonal complex 258 is associated with dissemination of *bla*KPC plasmid in this clonal complex**
Z. Ying (Shanghai, China), T. Yu, X. Jiang*

5123 **Characterisation of carbapenemase-producing *Enterobacter* spp. isolates recovered in a tertiary hospital in Madrid, Spain between 2005 and 2018**
M. Mateos, M. Hernández García (Madrid, Spain), R. Del Campo, L. Martínez García, D. Gijón, P. Ruiz-Garbajosa, M. Morosini Reilly, R. Canton Moreno*

6800 **Analysis and characterisation of *rmtB*-bearing plasmids disseminated in various species of *Enterobacterales* isolated from clinical specimens of hospitalised patients in Greece**
K. Nafplioti, H. Moraitou, P. Giannopoulou (Holargos, Greece), P. Chra, M. Damala, E. Vogiatzakis, E. Trikka-Graphakos, V. Baka, E. Prifti, M. Souli, I. Galani*

6819 **Epidemic of carbapenem-resistant *Klebsiella pneumoniae* in a tertiary referral hospital for an annual surveillance in China**
Y. Jiang (Hangzhou, China), Q. Shi, D. Zhao, P. Zhang, Y. Wang, J. Quan, X. Han, R. Yan, H. Liu, X. Wu, X. Hua, Y. Yu*

8303 **Genomic features of Argentinean KPC-2 producing *Klebsiella pneumoniae* ST25 and comparative genomics with carbapenem susceptible ST25 isolates**
D. Cejas, V. Di Pilato, L. Henrici De Angelis, S. Di Gregorio, L. Pallecchi, F. Arena, G. Rossolini, G. Gutkind (Buenos Aires, Argentina), M. Radice*

8602 **Vertical transmission of the gene *bla*KPC-3 in clinical isolates of carbapenemase resistant *Klebsiella pneumoniae***
C. Ferreira (Porto, Portugal), J. Rocha, S. Bikkarolla, K. Frykholm, S. Pohjanen, M. Brito, C. Lameiras, O. Nunes, F. Westerlund, C. Manaia*

9415 **Prevalence of genes encoding 16S rRNA methyltransferase in carbapenemase-producing *Serratia* spp. in south Brazil**
L. Bail (Ponta Grossa, Brazil), C. Sanches Ito, L. Arend, K. Nogueira, F. Tuon*

Session accepted as Paper Poster Session

Metallo-beta-lactamases and OXAs on the spot

425 **Persistence of high-risk clones of carbapenem-resistant *Klebsiella pneumoniae* in a tertiary hospital in Valencia, Spain**
B. Fuster Escriva (Oliva, Spain), N. Tormo, C. Salvador Garcia, M. Belda, C. Gimeno Cardona*

597 **Occurrence of NDM-1-producing *Morganella morganii* and *Proteus mirabilis* in a single patient, Portugal: probable *in vivo* transfer by conjugation**
M. Aires De Sousa, J. Ortiz De La Rosa, M. Goncalves, A. Costa, P. Nordmann, L. Poirel (Fribourg, Switzerland)*

1269 **Characterisation of NDM-producing *Klebsiella pneumoniae* isolates from different Roman hospitals**
C. Venditti (Rome, Italy), O. Butera, S. Darezzo, A. Vulcano, V. Puro, S. Lanini, G. Adamo, G. Ippolito, C. Nisii, A. Di Caro*

3818 **Complex polyclonal outbreak of *bla*VIM-1-harbouring and *mcr-9*-coharbouring *Enterobacter cloacae* complex linked to drains in a German hospital**
M. Malecki, P. Higgins, K. Xanthopoulou, H. Seifert, F. Mattner, A. Wendel (Cologne, Germany)*

4054 **Carbapenemase-producing *Klebsiella pneumoniae* in a Tunisian university hospital: emergence of hypervirulent strains**
B. Mnif (Sfax, Tunisia), N. Sallem, F. Zouari, A. Hammami*

4188 **Oxacillinase-48-like (OXA-48) carbapenemases along with New Delhi metallo-β-lactamase in a neonatal unit**
S. Naha, S. Mukherjee, K. Sands, P. Chattopadhyay, S. Mukherjee, S. Basu (Kolkata , India)*

4434 **Dissemination of carbapenem-non-susceptible *Klebsiella pneumoniae* from Oman**
M. Coorens, H. Al Farsi (Stockholm, Sweden), I. Sylvin, Z. Al-Muharrmi, S. Al-Azri, A. Al Jardani, C. Giske*

4508 **Detection and successful containment of a NDM-1-producing *Proteus mirabilis* clone spread in an Italian sub-acute care unit**
A. Mercato (Grotte, Italy), I. Bitar, V. Mattioni Marchetti, F. Marchesini, M. Mancinelli, S. Bracco, V. Rognoni, A. Anesi, E. Nucleo, R. Migliavacca*

4602 **Whole genome sequencing investigation into a single-site outbreak of NDM-mediated carbapenem resistance disseminated across multiple species predominantly via IncL/M plasmids**
N. Ellaby (London, United Kingdom), J. Turton, J. Clark, A. Roche, R. Manuel, J. Paul, B. Patel, J. Dave, N. Woodford, M. Ellington*

5311 **Molecular epidemiology and genetic characteristics of New Delhi metallo-β-lactamase among Gram-negative bacteria in a tertiary care hospital of north India**
S. Singh (Lucknow, India), A. Singh, A. Pathak, C. Sahu, K. Prasad*

6148 **Extensively drug-resistant *Klebsiella pneumoniae* ST383 co-harbouring OXA-48 and NDM-5 outbreak at a tertiary care centre in Lebanon**
O. Zmerli (Beirut, Lebanon), A. Chamieh, S. Saliba, Z. Daoud, C. Afif, E. Azar*

6160 **Phenotypic and molecular investigation of ST11 NDM-1-producing *Klebsiella pneumoniae* isolates persisting between 2015 and 2018 in a Bulgarian hospital**
T. Kostyanev (Wilrijk, Belgium), R. Vatcheva-Dobrevska, B. Xavier, V. Dicheva, P. Stefanowa, C. Lammens, H. Goossens, S. Malhotra-Kumar*

6350 **Integrated molecular surveillance of carbapenem-resistant *Enterobacterales* in Germany**
R. Kramer (Berlin, Germany), K. Kremer, J. Hans, S. Haller, A. Reuss, N. Pfennigwerth, Y. Pfeifer, B. Neumann, G. Werner, T. Eckmanns, S. Gatermann*

6561 **Investigation of increased prevalence of IMP carbapenemases by next-generation sequencing in Wales**
M. Wootton (Cardiff, United Kingdom), M. Mentasti, K. Prime, S. Khan, K. Sands, J. Watkins, S. Corden, T. Connor, L. Jones*

6877 **Investigation of a hospital outbreak of multi-drug resistant *Klebsiella pneumoniae* ST307, including isolates producing OXA-244 carbapenemase**
L. Jones (Cardiff, United Kingdom), M. Mentasti, K. Sands, J. Watkins, M. Morgan, S. Lingard, K. Prime, S. Khan, M. Bull, E. Davies, S. Corden, B. Healy, T. Connor, M. Wootton*

7221 **Regional outbreaks of *Enterobacter cloacae* complex NDM-1 in Poland, 2015-19**
R. Izdebski (Warsaw, Poland), P. Urbanowicz, M. Biedrzycka, D. Żabicka, E. Literacka, W. Hryniewicz, M. Gniadkowski*

7290 **Dissemination of OXA-244-producing *Escherichia coli* in Germany**
J. Hans (Bochum, Germany), B. Neumann, R. Kramer, K. Kremer, S. Haller, N. Pfennigwerth, A. Reuss, Y. Pfeifer, G. Werner, T. Eckmanns, S. Gatermann*

7294 **Emergence of *Klebsiella quasipneumoniae* carrying New Delhi metallo-β-lactamase (*bla*NDM-1) gene in a Brazilian hospital**
B. Boettger (Sao Paulo, Brazil), A. Pignatari*

7341 **Regional dissemination of *Klebsiella pneumoniae* ST147 NDM-1 in Poland**
M. Biedrzycka, R. Izdebski (Warsaw, Poland), A. Baraniak, M. Machulska, P. Urbanowicz, D. Żabicka, E. Literacka, W. Hryniewicz, M. Gniadkowski*

7351 **OXA-48 producing *Klebsiella pneumoniae* in non-hospitalised elderly patients in Zagreb, Croatia**
J. Vranes (Zagreb, Croatia), S. Šuto, B. Bedenic, A. Mlinaric-Dzepina, S. Likić, S. Kibel, J. Knezevic, M. Anusic, V. Ticic, A. Grisold*

7454 **Epidemic clonal lineages of *Enterobacteriales* producing VIM-type carbapenemases in Poland, 2013-18**
R. Izdebski (Warsaw, Poland), D. Żabicka, E. Literacka, P. Urbanowicz, A. Baraniak, W. Hryniewicz, M. Gniadkowski*

8992 **Unexpected detection of clinical isolates of *Proteus mirabilis* producing OXA-48 but susceptible to carbapenems and piperacillin-tazobactam**
M. Artacho (Málaga, Spain), R. Pedraza Merino, M. Causse, M. Muñoz De La Rosa, E. Perez-Nadales, C. Pitart, M. Hernández García, J. Vila Estape, R. Canton Moreno, M. Egea, L. Martinez-Martinez*

9072 **Emergence of *bla*VIM-2 and detection of *bla*VIM-24 in *Pseudomonas* sp. from clinical samples in Brazil**
I. Santos (Rio de Janeiro, Brazil), N. Pereira, O. Conceição-Neto, B. Costa, L. Da Silva Pontes, M. Chaves Silveira, C. Rocha-De-Souza, A. D'Alincourt Carvalho Assef*

9209 **The emergence of new STs of *bla*NDM-positive hypervirulent *Klebsiella pneumoniae* isolates in an oncology hospital, Russia**
P. Starkova (Saint Petersburg, Russian Federation), I. Lazareva, V. Ageevets, J. Sopova, V. Gostev, I. Tsvetkova, M. Lebedeva, S. Sidorenko*

9373 **Multidrug-resistant *Klebsiella pneumoniae* ST231: the new endemic super bug of India?**
C. Shankar (Vellore, India), J. Jacob, K. Vasudevan, B. Abirami, S. Anandan, V. Balaji*

9593 **Genomic epidemiology of NDM-producing *Enterobacteriaceae* in Portuguese hospitals**
V. Manageiro (Lisbon, Portugal), E. Ferreira, M. Caniça*

Session accepted as Paper Poster Session

MIC: are all methods equal?

150 **Assessment of trimethoprim-sulfamethoxazole susceptibility testing methods for fastidious *Haemophilus* spp.**
Y. Sierra Urueña (Barcelona, Spain), A. González Díaz, F. Tubau, A. Carrera-Salinas, J. Moleres, P. Bajanca-Lavado, J. Garmendia, M. Domínguez Luzon, C. Ardanuy Tisaire, S. Marti*

1108 **Reduced *in vitro* killing of methicillin-resistant *Staphylococcus aureus* blood culture isolates by vancomycin as the bacterial inocula increases**
A. Alsaeed, J. Rubin, S. Sanche, H. Deneer, J. Blondeau (Saskatoon, Canada)*

3564 **Benzylpenicillin gradient tests underestimate MICs for penicillin non-susceptible *Streptococcus pneumoniae***
F. Nilsson, E. Matuschek (Växjö, Sweden), G. Kahlmeter*

3658 **Area of technical uncertainty for ciprofloxacin in *Enterobacterales*: evaluation of MIC values using the E-test method**
V. Viaggi, E. Meroni, O. Spezia, S. Tonolo, B. Pini, F. Luzzaro (Lecco, Italy)*

4613 **Evaluation of commercial media for susceptibility testing of *Neisseria gonorrhoeae***
L. Davies, M. Cole, C. Horner, F. Ismail, Z. Ivanov, H. Fifer, L. Jones, R. Howe, M. Wootton (Cardiff, United Kingdom)*

4746 **Stability studies with tigecycline in bacterial growth medium and impact of stabilising agents: a pre-requisite for *in vitro* susceptibility testing**
L. Amann (Hamburg, Germany), E. Ruda Vicente, M. Rathke, A. Broeker, S. Wicha*

5137 **Comparison of methods to evaluate the activity of ceftolozane/tazobactam against clinical isolates of carbapenem-resistant *Pseudomonas aeruginosa* from Chile**
R. Martinez, L. Rivas, J. Fuentes, M. Spencer, M. Lam, P. Rojas, V. Moreno, L. Fuenzalida, L. Porte, F. Silva, M. Cifuentes, B. Barraza, B. Hervé, M. Acuña, D. Ramírez, P. García, J. Munita (Santiago, Chile)*

5433 **Performance of VITEK 2 AST-GN meropenem/vaborbactam for antimicrobial susceptibility testing of *Enterobacteriaceae* and *Pseudomonas aeruginosa*: a multi-centre study**
S. Franklin (St. Louis, United States), H. Dwivedi, G. Procop, M. Traczewski, O. Garner, P. Deol*

6184 **The Insertion Sequence (IS) disruption of *mgrB* gene is critical for colistin susceptibility testing efficiency of Sensititre in carbapenem-resistant *Klebsiella pneumoniae***
B. Ozer (Istanbul, Turkey), C. Vatansever, B. Gundogdu, O. Dogan, F. Can*

8897 **Fosfomycin susceptibility testing by different methods in multidrug-resistant urinary *Klebsiella pneumoniae* isolates**
Z. Semerci, A. Ilki (Istanbul, Turkey)*

Session accepted as Paper Poster Session

Molecular and phenotypic investigation of resistance in staphylococci

369 **Molecular characterisation of *Staphylococcus aureus* clinical strains from endotracheal tubes of patients with intensive care unit-acquired pneumonia**
R. Cabrera (Barcelona, Spain), L. Fernandez Barat, A. Motos, R. López, N. Vázquez Burgos, M. Panigada, F. Alvarez-Lerma, Y. Lopez, L. Muñoz, P. Castro, J. Vila Estape, A. Torres*

497 **Investigation of hetero-VISA among MRSA isolates in Gaziantep, Turkey**
D. Gazel, M. Erinmez (Gaziantep, Turkey), A. Büyüktaş Manay, Y. Zer*

Abstract Categories 2020

1194 **Mutant prevention concentration values of linezolid, moxifloxacin and vancomycin against *Staphylococcus pseudintermedius* strains recovered from humans**
L. Blondeau (Saskatoon, Canada), J. Rubin, R. Kanthan, S. Sanche, H. Deneer, J. Blondeau*

1298 **Effect of short-term antimicrobial therapy on the tolerance and antibiotic resistance of multidrug-resistant *Staphylococcus capitis***
X. Yu (Hangzhou, China)*

1479 **Risk factors associated with daptomycin non-susceptible *Staphylococcus aureus* bloodstream infections**
S. Gudipati, A. Vahia (Detroit, United States), M. Perri, R. Tibbetts, M. Zervos, G. Suleyman*

1933 **Nasal methicillin-resistant *Staphylococcus aureus* colonisation among adults and children in Russia: predominance ST22-subclone "Gaza Strip"**
V. Gostev (Saint Petersburg, Russian Federation), K. Ivanova, E. Kalisnikova, A. Kruglov, I. Ryabchenko, S. Zyryanov, O. Kalinogorskaya, M. Wolkowa, L. Zhelezova, E. Martens, S. Sidorenko*

1942 **Involvement of *walK* gene mutations in antibiotic resistance increase in daptomycin-unsusceptible methicillin-resistant *Staphylococcus aureus***
A. Hugo Campano, N. Gómez Casanova, J. Munoz-Bellido (Salamanca, Spain)*

2274 **Molecular characterisation of methicillin-resistant *Staphylococcus aureus* isolates from the United Arab Emirates: emergence of novel strains and variants**
A. Senok (Dubai, United Arab Emirates), R. Nassar, H. Celiloglu, A. Nabi, M. Alfarsi, S. Weber, E. Müller, A. Reissig, D. Gawlik, S. Monecke, R. Ehricht*

3388 **Minimum Inhibitory Concentration distributions and putative new resistance mechanisms for mecillinam and trimethoprim in *Staphylococcus saprophyticus***
F. Jansåker (Copenhagen, Denmark), J. Monk, O. Lawal, S. Mollerup, J. Iversen, M. Goncalves, P. Paixão, E. Goncalves, C. Toscano, J. Empel, M. Brzozowska, M. Domínguez Luzon, M. Fraqueza, H. De Lencastre, M. Miragaia, H. Westh, J. Knudsen*

3626 **Genomic analysis of Panton-Valentine leukocidin-positive methicillin-resistant *Staphylococcus aureus* in hospitalised patients in Germany by whole genome sequencing: 2015-2018**
S. Klein (Heidelberg, Germany), J. Hannesen, P. Zanger, K. Heeg, S. Boutin, D. Nurjadi*

3980 **Direct detection of PBP2a using the high-resolution Orbitrap mass spectrometer and rapid discrimination of antibiotic resistance in *Staphylococcus aureus* using the Acrion system**
J. Neil (Cambridge, United States), A. Verma, M. Viirtola, W. Mcgee, S. Kronewitter, J. Stephenson*

4245 **Investigation of linezolid resistance mechanisms of *Staphylococcus epidermidis* isolates collected in Gauteng, South Africa**
K. Addison, K. Strydom, E. Hoosien, Y. Bolukaoto, M. Kock, M. Ehlers (Pretoria, South Africa)*

4271 **Bloodstream infections caused by *Staphylococcus aureus* non-susceptible to daptomycin: clonal and clinical aspects**
D. Fernandes, R. Wladyka, A. Ferreira, S. Nouer (Rio de Janeiro, Brazil), K. Dos Santos*

4533 **Rapid *nuc* and *mecA* gene testing by polymerase chain reaction is useful to choose appropriate antibiotics in *Staphylococcus aureus* bacteraemia**
M. Ikemachi (Kobe, Japan), Y. Go, H. Takekawa, K. Miyagawa*

4550 **The temporal dynamics of *Staphylococcus aureus* carriage among healthcare workers in a tertiary referral hospital with a history of endemic methicillin-resistant *Staphylococcus aureus*, investigated by whole genome sequencing**
A. Kearney (Dublin, Ireland), P. Kinnevey, M. Earls, T. Poovelikunnel, G. Brennan, A. Shore, H. Humphreys, D. Coleman*

4596 **Linezolid resistance mechanisms in *Staphylococcus capitis* and *Staphylococcus haemolyticus* isolates collected in Gauteng, South Africa**
K. Addison, K. Strydom, E. Hoosien, Y. Bolukaoto, M. Kock, M. Ehlers (Pretoria, South Africa)*

4868 **Methicillin-resistant *Staphylococcus aureus* bacteraemia: clinical-epidemiological characteristics and evolution of oxacillin resistance in 17 years**
L. Vinuela, G. Santillana, R. Martinez, P. Bardon, C. García, E. Clavijo, M. García López (Málaga, Spain)*

5220 **Worldwide dissemination of linezolid-resistant *Staphylococcus epidermidis* clones**
N. Faria, N. Bogas, C. Torres, A. Robinson, E. Petinaki, J. Empel, N. Ishiwada, B. Kahl, F. Campanile, H. De Lencastre, F. Laurent, M. Miragaia (Oeiras, Portugal)*

5241 **Penicillin-binding protein 2a temperature-sensitive folding defect: a new path to tackle methicillin resistance in *Staphylococcus aureus***
M. Roch (Geneva, Switzerland), E. Lelong, R. Sierra, O. Panasenko, A. Renzoni, W. Kelley*

5844 **Evaluation of a culture surveillance application for the detection of methicillin-resistant *Staphylococcus aureus* in the clinical setting**
M. Bois, E. Mcelvania, M. Gosnell, C. Orny, V. Jean-Marc, J. Lemstra, M. Van Der Lei (Drachten, Netherlands), R. Marcelpoil*

6393 **A study of virulence factors and antimicrobial resistance in *Staphylococcus epidermidis* isolates from ocular infections**
N. Hussain Ahmed (Delhi, India), A. Basu, G. Satpathy, B. Tezpur, N. Sharma, R. Chawla*

6434 **Stepwise *in vitro* daptomycin resistance selection of *Staphylococcus aureus*: accumulation mutations and heteromutations**
V. Gostev (Saint Petersburg, Russian Federation), O. Kalinogorskaya, J. Sopova, I. Tsvetkova, M. Velizhanina, S. Sidorenko*

7457 **Prevalence and molecular characteristics of *Staphylococcus aureus* carrying Panton-Valentine leukocidin genes isolated from patients accessing at emergency department in 2016-2018 period**
A. Lai (Milan, Italy), A. Bergna, S. Rimoldi, A. Ridolfo, M. Gismondo, C. Balotta, M. Galli, G. Zehender*

7590 **qPCR to detect *mecA* in faecal samples: a tool for assessing resistance burden amongst pets and their owners in the microbiological 'fast age'?**
S. Frosini (Hatfield, United Kingdom), G. Gallow, J. Menezes, A. Belas, C. Saraiva Marques, C. Aboim, M. Pomba, A. Loeffler*

7951 **Penicillin-binding protein 2 (PBP2), PBP2a and PBP4 clone-specific polymorphisms are not associated to ceftaroline- (CPT) susceptibility in Chilean clinical isolates of methicillin-resistant *Staphylococcus aureus* (MRSA)**
M. Spencer, R. Martinez, L. Rivas, M. Rojas, R. Rios, A. Dinh, L. Diaz, J. Reyes, B. Hanson, P. García, C. Arias, J. Munita (Santiago, Chile)*

8280 **Decline of the Brazilian endemic clone and dominance of internationally disseminated lineages among MRSA from bacteraemic patients in Porto Alegre, Brazil**
C. Würdig Riche (Porto Alegre, Brazil), R. Mamede, R. Pereira, J. Carriço, C. Dias, M. Ramirez*

8302 **Study of penicillin-susceptible *Staphylococcus aureus* in patients with bacteraemia. a multi-centre study in Spanish hospitals**
O. Mama, C. Aspiroz, L. Ruiz, E. Cercenado, J. Azcona-Gutierrez, L. Lopez-Cerero, F. Castillo, A. López-Calleja, C. Alonso, P. Berdonces, J. Torroba Alvarez, J. Calvo, M. Zarazaga, C. Torres (Logroño, Spain)*

8411 **Performance of the PBP2a (Alere-Abbott) immunochromatographic test on early primary cultures from positive MRSA/MR-CoNS blood cultures**
C. Munier (Lyon, France), C. Dupieux, C. Kolenda, M. Bes, O. Dauwalder, F. Vandenesch, A. Tristan, F. Laurent*

8630 **Evaluation of an immunochromatographic assay for rapid identification of PBP2a-positive *Staphylococcus aureus***
R. Sainz Rodriguez (Málaga, Spain), M. Valverde Troya, M. Gasca Santiyan*

8786 **Linezolid resistance in coagulase-negative *Staphylococcus* spp. in six private hospitals in Sao Paulo, Brazil**
P. Santos (Sao Paulo, Brazil), A. Marchi, A. Blikstad Mauro, E. Kusano, C. Rodrigues, L. Bello, E. Siqueira Ayub, F. Porfirio, M. Yano, L. Perdigao Neto, L. Camera Pierrotti, S. Figueiredo Costa, V. Castro-Lima*

Session accepted as 2-Hour Oral Session

Molecular epidemiology and detection of resistant staphylococci

2678 **Epidemiology of the *Staphylococcus aureus* CA-MRSA USA300 in Belgium**
M. Argudín (Brussels, Belgium), D. Martiny, N. Yin, A. Deplano, C. Nonhoff, A. Meghraoui, C. Michel, M. Hallin*

3040 **An emerging methicillin resistance mechanism due to loss-of-function of the GdpP protein in *mec* gene-negative staphylococci undetected by reference methods**
G. Durand (La Balme Les Grottes, France), C. Dupieux-Chabert, M. Bes, C. Gustave, B. Fruiquière, C. Fulchiron, L. Munoz, S. Rivat, A. Ranc, F. Vandenesch, F. Laurent, A. Tristan, P. Martins Simoes*

3801 **Genomic analysis reveals persistence and microevolution of methicillin-resistant *Staphylococcus aureus* in recurrent carriers**
K. Barasevich, C. Giske, I. Fröding, U. Tollström, M. Ullberg, H. Fang (Stockholm, Sweden)*

3838 **Increase of daptomycin-resistant *Staphylococcus aureus* with a possible link to antiseptic wound treatment in three medical centres in Cologne, Germany**
A. Wendel (Cologne, Germany), R. Otchwemah, F. Mattner, H. Oberländer, C. Tellez-Castillo, R. Skov, G. Werner, F. Layer, B. Strommenger*

4648 **The dissemination and molecular characterisation of clonal complex 361 methicillin-resistant *Staphylococcus aureus* in Kuwait hospitals, 2016-2018**
E. Udo, E. Sarkhoo (Jabriya, Kuwait), S. Boswihi, E. Müller, S. Monecke, R. Ehricht*

4709 **Accessory gene regulator (*agr*) functionality differences among closely related methicillin-resistant *mec*C-*Staphylococcus aureus***
C. Huber, I. Stamm, W. Ziebuhr, G. Marincola, M. Bischoff, B. Strommenger, G. Jaschkowitz, T. Marciniak, C. Cuny, W. Witte, J. Doellinger, C. Schaudinn, A. Thürmer, L. Epping, T. Semmler, A. Lübke-Becker, L. Wieler, B. Walther (Berlin, Germany)*

5207 **Nasopharyngeal carriage of methicillin-resistant *Staphylococcus aureus* in newly HIV-diagnosed, antiretroviral therapy naïve adults, Dar es Salaam, Tanzania**
J. Manyahi (Bergen, Norway), S. Moyo, S. Aboud, N. Langeland, B. Blomberg*

5735 **Lineage CC398 among methicillin-susceptible and methicillin-resistant *Staphylococcus aureus* isolates of blood cultures. A multi-centre study in Spanish hospitals**
O. Mama, C. Aspiroz, L. Ruiz, M. Iniguez-Barrio, E. Cercenado, J. Azcona-Gutierrez, L. Lopez-Cerero, C. Seral, A. Rezusta, C. Alonso, A. Bellés Bellés, P. Berdonces, J. Torroba Alvarez, M. Siller, M. Zarazaga, C. Torres (Logroño, Spain)*

6906 **Zooming into the CoNS group on a species level exposes high heterogenicity in prevalence and antibiotic resistance: an in-depth data analysis in the MALDI-TOF era**
M. Berends (Groningen, Netherlands), C. Luz, Y. Roelofs, J. Arends, G. Andriesse, C. Glasner, A. Friedrich*

8544 **Changing profile of invasive disease-causing *Staphylococcus aureus* in Australia**
S. Baines (Melbourne, Australia), S. Giulieri, A. Gonçalves Da Silva, N. Holmes, G. Coombs, S. Pang, T. Stinear, B. Howden*

Session accepted as Paper Poster Session

Molecular methods for carbapenemase detection

343 **Expediting antibiotic therapy management of critically ill patients with pneumonia by the detection of the main carbapenemase and ESBL-encoding genes directly from bronchoalveolar lavage**
M. Boattini (Turin, Italy), G. Bianco, M. Iannaccone, C. Costa, R. Cavallo*

593 **Evaluation of a new commercial assay for detection and characterisation of carbapenemase genes**
G. Eltringham (Newcastle upon Tyne, United Kingdom), M. Suwara, M. Bakheit, S. Stack, E. Gillies, J. Perry*

1054 **Establishment and clinical application of a multiple touchdown PCR for detection of carbapenemase genes**
X. Li (Nanjing, China), N. Sun, L. Zhang, B. Yu, W. Wang, X. Yao, J. Yu*

1800 **Application of a new molecular biology method for carbapenem-resistant *Enterobacteriaceae* detection in rectal swabs**
G. Parisi (Rome, Italy), A. Denaro, S. D'Inzeo, R. D'Arrigo, D. Gallone, B. Mariani, R. Oliverio*

2126 **Evaluation of a novel high-definition PCR multiplex assay to identify nine genetic targets associated with multidrug-resistant organisms**
D. Gerstbrein, B. Mesich, N. Ledeboer, M. Faron, B. Buchan (Milwaukee, United States)*

4657 **Performance of the Xpert Carba-R assay versus the ChromID CARBA SMART for the detection of carbapenemase-producing Gram-negative bacteria from rectal swabs**
S. Vasoo (Singapore, Singapore), C. Kang, P. Hon, W. Lin, J. Leong, J. Loh, W. Lian, A. Tan, Y. Sun, J. Kum, B. Poh, S. Mendis, P. Rao, A. Chow, O. Ng, K. Marimuthu, B. Ang, P. De*

5630 **Surveillance of circulating carbapenemase genes with automated molecular system (BD Max) at a healthcare centre in Buenos Aires, Argentina**
M. Zárate (Buenos Aires, Argentina), G. Weltman, G. Serruto, P. Mainetti, B. Wisner, J. Zaracho*

6146 **Novodiag CarbaR+ assay for the detection of carbapenemase-producing bacteria**
S. Bernabeu (Le Kremlin-Bicêtre, France), D. Girlich, W. Bouchahrouf, S. Oueslati, I. Langlois, N. Arangia, C. Begasse, T. Huang, P. Bogaerts, Y. Glupczynski, T. Naas*

6472 **Development of LAMP-based multiplex real-time assay for rapid detection of genes of NDM, VIM, KPC and OXA-48 carbapenemase groups**
A. Nosova (Moscow, Russian Federation), Y. Savochkina, A. Ibragimova, G. Shipulin*

7215 **Evaluation of the Revogene Carba C assay for detection and differentiation of carbapenemase-producing bacteria**
D. Girlich, M. Laguide, L. Dortet, T. Naas (Le Kremlin Bicêtre, France)*

7386 **Utility of Xpert Carba-R in identifying carbapenem resistance in blood culture isolates in critically ill patients**
V. Krishna (Chennai, India), R. Vimal Kumar, S. Uma*

7945 **Development and preliminary evaluation of Multidrug Resistance Direct Flow Chip kit, a molecular method for a rapid detection of multiple antibiotic resistance markers**
J. Carrero (Granada, Spain), A. Galiana, D. Gomez, A. Olmo, M. Ruiz, N. Gonzalo-Jiménez*

9179 **Molecular and cultural tests in a multi-centre point prevalence surveillance study on carbapenem-resistant *Enterobacteriaceae* in long-term care facilities' residents in northern Italy area**
G. Lo Cascio (Verona, Italy), A. Azzini, A. Bazaj, G. Be, L. Lambertenghi, N. Salerno, I. Coledan, F. Mazzaferri, L. Maccacaro, E. Concia, E. Tacconelli, G. Cornaglia*

9301 **Evaluation of the EasyScreen ESBL/CPO kit for the detection of ß-lactam resistance genes**
C. Gonzalez (Le Kremlin-Bicêtre, France), S. Oueslati, D. Girlich, L. Dortet, T. Naas*

Session accepted as Mini-oral ePoster Session

Novel methods for RAST of XDR Gram-negatives

3257 **Rapid, direct antimicrobial susceptibility testing of positive blood cultures within 4 hours using ATP bioluminescence detection and machine learning method**
S. Kawabe (Kokubunji-shi, Tokyo, Japan), Y. Uchiho, H. Noda, A. Matsui, H. Niimi, I. Kitajima*

5695 **Implementing rapid susceptibility testing directly from positive blood cultures in the routine laboratory workflow for sepsis**
P. Mantzana, E. Kandyliotou, M. Kyriakopoulou, F. Netsika, M. Arhonti, A. Tychala (Thessaloniki, Greece), G. Meletis, O. Vasilaki, G. Kagkalou, E. Protonotariou, L. Skoura*

6194 **Rapid phenotypic susceptibility testing of *Neisseria gonorrhoeae* using Graver-Wade medium, broth microdilution, and the flow cytometry-assisted susceptibility test (FAST)**
M. Kopczyk, T. Paton, K. Mulroney, T. Inglis, C. Carson (Crawley, Australia)*

6690 **Impaired membrane integrity as a marker for colistin susceptibility: a flow cytometry method for rapid AST in *Pseudomonas aeruginosa* and *Acinetobacter* spp.**
O. Ekelund, E. Sturegård, T. Schön, S. Somajo (Karlskrona, Sweden)*

7658 **The flow cytometry-assisted susceptibility test (FAST) accurately predicts colistin MICs for Gram-negative bacilli directly from positive blood culture in less than four hours**
T. Paton (Perth, Australia), K. Mulroney, M. Kopczyk, C. Carson, T. Inglis*

8222 **Colistin MIC determination by a rapid flow cytometry assay**
D. Fonseca E Silva (Porto, Portugal), R. Gomes, I. Martins-Oliveira, A. Silva-Dias, B. Pérez-Viso, R. Canton Moreno, H. Ramos, A. Rodrigues, C. Pina-Vaz*

8310 **Evaluation of FAST-Prep Liquid Colony for early antimicrobial sensitivity testing of positive blood culture by disk diffusion method**
A. Khine (Richmond Hill, Canada), N. Fernandez, L. Pandey, A. Talebpour, S. Novak, T. Alavie*

Session accepted as Paper Poster Session

Phenotypic AST: still important!

272 **Adjunction of daptomycin for the treatment of bacterial meningitis: *in vitro* study**
T. Maldiney, D. Bonnot, N. Anzala, S. Albac, D. Labrousse, E. Varon, C. Neuwirth, D. Croisier, P. Chavanet (Dijon, France)*

567 **Can Rapid Antimicrobial Susceptibly Testing (RAST) improve the time to the optimal therapy for bloodstream infections?**
F. Olearo (Hamburg, Germany), B. Berinson, M. Christner, H. Rohde*

2191 **Evaluation of EUCAST disk diffusion criteria to screening *mecA* gene in species of *Staphylococcus epidermidis*-like group**
V. Pietta Perez (João Pessoa, Brazil), M. Da Silva, A. Rossato, P. Alves D'Azevedo*

2220 **Effective antimicrobial combination testing: linking rapid microcalorimetry screening to *in vivo* efficacy**
K. Kragh (Copenhagen, Denmark), D. Gijón, A. Maruri, A. Antonelli, M. Coppi, M. Kolpen, S. Crone, C. Tellapragada, B. Hasan, C. De Vogel, W. Van Wamel, A. Verbon, C. Giske, G. Rossolini, R. Canton Moreno, N. Frimodt-Moller*

2528 ***In vitro* evaluation of ceftolozane/tazobactam-aztreonam and ceftolozane/tazobactam-fosfomycin combinations by time-kill assays against SPM-1-producing *Pseudomonas aeruginosa* clinical strains**
G. Santos, G. Cuba (São Paulo, Brazil), C. Silva Nodari, A. Streling, R. Cayô Da Silva, A. Gales, A. Pignatari, D. Nicolau, C. Kiffer*

3141 **The predictive value of disc diffusion assay results for resistance in Gram-negative bacteraemia: a UK district general hospital experience**
T. Swaine (London, United Kingdom), C. Dominic, R. Buchanan*

3358 **EUCAST improved screening algorithm for beta-lactam resistance in *Haemophilus influenzae***
E. Matuschek (Växjö, Sweden), J. Ahman, J. Thegerström, F. Resman, S. Bengtsson, G. Kahlmeter*

3918 **EUCAST temocillin breakpoints and antimicrobial susceptibility testing guidelines**
C. Giske (Stockholm, Sweden), E. Matuschek, R. Canton Moreno, J. Turnidge, G. Kahlmeter*

4152 **Variations in categorical agreement between fosfomycin agar dilution and disk diffusion using standard and high inoculum protocols for *Klebsiella pneumoniae* testing**
A. Krueger, H. Brigman, J. Anderson, E. Smith, E. Hirsch (Minneapolis, United States)*

4934 **A rapid adenosine triphosphate bioluminescence-based assay for predicting antibiotic combinations against dividing and non-dividing live carbapenem-resistant *Enterobacteriaceae***
Y. Cai (Singapore, Singapore), N. Begam, N. Fauzi, H. Wong, T. Lim, J. Teo, T. Tan, J. Sim, A. Kwa*

6128 **Evaluation of ceftolozane-tazobactam disk diffusion testing of *Pseudomonas aeruginosa* in a multi-centre UK study**
J. Diggle, I. Monahan, A. Alvarez Buylla, E. Manu, M. Allen, T. Planche, M. Wootton (Cardiff, United Kingdom)*

6618 **A study comparing the performance of an eravacycline oxoid antimicrobial susceptibility testing disc against an FDA-cleared predicate device**
K. Church (Basingstoke, United Kingdom), D. Carpenter, M. Olesky*

7039 **SynAST, a reliable *in vitro* synergy test as support for New Delhi metallo-beta-lactamase *Klebsiella pneumoniae* infection therapy**
A. Leonildi (Pisa, Italy), C. Giordano, E. Tagliaferri, M. Falcone, G. Tiseo, S. Barnini, F. Menichetti*

8345 **Ceftazidime-avibactam/aztreonam synergism assay against carbapenem-resistant *Enterobacteriales* and *Pseudomonas aeruginosa* carrying metallo-beta-lactamases**
J. Barbosa, K. Moraes (sao paulo, Brazil), E. Sanchez Espinoza, L. Perdigao Neto, S. Santos, A. Marchi, R. Ruedas Martins, T. Guimaraes, F. Rossi, S. Figueiredo Costa*

8652 ***In vivo* and *in vitro* synergistic activity of colistin combining with meropenem and sulbactam against multidrug-resistant and pandrug-resistant *Acinetobacter baumannii* clinical isolates**
C. Kulah (Zonguldak, Turkey), E. Subasi, A. Atalar*

9317 **AST for fastidious bacteria: a reliable automation to standardise the EUCAST disk diffusion test**
M. Paolucci (Brescia, Italy), C. Lacchini, N. Schepis, L. Navarria*

Session accepted as 2-Hour Oral Session

Predicting resistance from whole genome analysis

1007 **Impact of lung transplantation on the phylogenetic diversity of *Pseudomonas aeruginosa* isolates from end-stage cystic fibrosis patients**
R. Datar (La Balme Les Grottes, France), A. Coello Pelegrin, S. Orenga, A. Perry, J. Samuel, A. Van Belkum, H. Goossens, V. Chalansonnet*

1073 **Predicting *Pseudomonas aeruginosa* susceptibility phenotypes from whole genome sequence resistome analysis**
S. Cortes-Lara (Palma, Spain), C. Lopez Causape, E. Del Barrio-Tofiño, A. Oliver*

1293 **Whole genome sequencing to detect antimicrobial resistance-associated determinants in *Staphylococcus epidermidis***
K. Cole (Brighton, United Kingdom), B. Young, D. Wilson, B. Atkins, J. Paul, M. Llewelyn*

1644 **Prediction of antibiotic resistance in *Helicobacter pylori* by whole genome sequencing and open-source bioinformatics tools**
A. Miqueleiz, A. Blanco Suárez, C. Alba Rubio, P. Urruzuno, K. Thorell, T. Alarcon Cavero (Madrid, Spain)*

2540 **Quantifying the intestinal load of genes of antibiotic resistance among two paediatric patient populations: not all "positives" are equal**
E. Dahdouh (Madrid, Spain), F. Lázaro Perona, E. Cendejas, G. Ruíz-Crrascoso, J. Mingorance*

4828 **Understanding discordance between observed and WGS-predicted resistance: a study of amoxicillin-clavulanate in *Escherichia coli***
T. Davies (Oxford, United Kingdom), N. Stoesser, A. Sheppard, M. Abuoun, P. Fowler, J. Swann, T. Quan, D. Griffiths, A. Vaughan, M. Morgan, H. Phan, K. Jeffery, M. Andersson, M. Ellington, O. Ekelund, N. Woodford, A. Mathers, R. Bonomo, D. Crook, T. Peto, M. Anjum, A. Walker*

4940 **Bioinformatic fake news: the important but under-appreciated caveats of identifying resistance genes from whole genome sequencing data**
T. Davies (Oxford, United Kingdom), A. Sheppard, J. Swann, N. Stoesser, M. Ellington, N. Woodford, T. Peto, D. Crook, M. Anjum, A. Walker*

5917 **Heuristic identification of carbapenemase-encoding plasmids by short-read sequencing data: validation by ONT long-read hybrid assembly of a large Singaporean carbapenem-resistant *Enterobacteriaceae* collection**
W. Xu (Singapore, Singapore), S. Prakki, N. Thevasagayam, L. Wang, K. Marimuthu, I. Venkatachalam, J. Teo, O. Ng*

6130 **Metagenomic analyses of antibiotic resistance genes in gut microbiome of healthy people in Korea: high carriage rate of *bla*CTX-M, *bla*CMY-2 and plasmid-mediated quinolone resistance genes**
J. Kim (Guri, South Korea), M. Seo, K. Park, H. Park, H. Hwang, B. Kim, M. Rho, H. Pai*

9602 **Big data analysis of all bacterial genomes establishes a triple whammy of carbapenemases, ICEs and multiple clinically-relevant bacteria**
J. Tomaz Santos Botelho (Porto, Portugal), J. Cordeiro Melro Mourão, A. Roberts, L. Vieira Peixe*

Session accepted as Paper Poster Session

Proteomics beyond bacterial identification

256 **Evaluation of a novel method for detection of carbapenem hydrolysis with an automated software (Clover BioSoft) by MALDI-TOF MS**
E. Gato, G. Méndez, L. Mancera Pascual, G. Bou Arevalo, M. Oviaño García (A Coruña, Spain)*

1658 **Accurate differentiation of carbapenemases by MALDI-TOF MS-typing: employment of bioinformatics**
E. Gato, J. Arca Suárez, B. Rodiño, G. Méndez, M. Arroyo, L. Mancera Pascual, G. Bou Arevalo, M. Oviaño García (A Coruña, Spain)*

3385 **MBT STAR-Carba assay: going beyond the routine protocol**
M. Złoch (Toruń, Poland), M. Peer, K. Sparbier, M. Kostrzewa, B. Buszewski*

4575 **Extended antibiotic panel to analyse the susceptibility of *Enterobacteriaceae* by the MALDI-TOF MS-based MBT FAST Assay**
K. Sparbier, O. Drews, M. Peer, I. Nix, E. Idelevich, K. Becker, M. Kostrzewa (Bremen, Germany)*

5896 **Quantitative detection of bacterial resistance by meropenem hydrolysis using MALDI-TOF MS**
C. Wilhelm (Porto Alegre, Brazil), M. Carneiro, P. Wink, A. Barth*

5960 **Evaluation of a liquid chromatography and tandem mass spectrometry-based Carba detection method using the Acrion system for clinical isolates expressing multiple carbapenemases**
W. Mcgee (Watertown, United States), S. Kronewitter, J. Haakana, J. Neil, M. Hutchins, S. Gurung, M. Viirtola, A. Verma, J. Stephenson*

6476 **Optimisation of the MALDIxin test for the rapid identification of colistin resistance in *Klebsiella pneumoniae* using MALDI-TOF MS**
L. Dortet (Paris, France), S. Bernabeu, P. Bogaerts, R. Bonnin, T. Naas, A. Filloux, G. Larrouy-Maumus*

8514 **Direct detection of intact *Klebsiella pneumoniae* carbapenemase (KPC) enzymes from bacterial isolates using liquid chromatography coupled with high-resolution Orbitrap mass spectrometry**
W. Mcgee (Watertown, United States), M. Faron, J. Neil, S. Kronewitter, B. Buchan, J. Stephenson, N. Ledeboer*

8627 **A rapid method for direct detection of intact OXA-48-like carbapenemases using liquid chromatography and high-resolution Orbitrap mass spectrometry**
W. Mcgee (Watertown, United States), S. Kronewitter, A. Verma, M. Viirtola, J. Neil, J. Stephenson*

8718 **Antimicrobial susceptibility testing by MALDI-TOF MS of lipids determines true MICs in six hours**
M. Sorensen, E. Nilsson, F. Gardner, S. Ramadan, D. Goodlett, R. Ernst (Baltimore, United States)*

8742 **Rapid MALDI-TOF MS-based method for vancomycin-resistant *Enterococcus faecium* detection**
A. Candela (Madrid, Spain), L. Quiroga, M. Arroyo, A. Ruiz, E. Cercenado, G. Méndez, M. Marín, P. Muñoz, L. Mancera Pascual, B. Rodriguez-Sanchez*

9635 **Characterisation of extended-spectrum β-lactamases by mass spectrometric analysis**
S. Lee (Seoul, South Korea), W. Yang, H. Suh, H. Jang, Y. Park, S. Hwang, J. Baek*

Session accepted as Paper Poster Session

Rapid non-molecular methods for detection of beta-lactam and polymyxin resistance

2215 **A novel spectrophotometric assay for rapid detection and differentiation of KPC-, MBL- and OXA-48-producing *Enterobacteriaceae***
D. Tsakogiannis, G. Vrioni (Athens, Greece), D. Marinou, M. Mavrouli, A. Tsakris, J. Routsias*

3593 **Detection of carbapenemases in *Pseudomonas* and *Acinetobacter* by the Mast Carba PAcE kit**
D. Fournier, K. Jeannot (Besançon, France), L. Gabriel, P. Triponney, J. Rousselot, A. Potron, P. Plésiat*

4015 **Rapid detection of piperacillin/tazobactam resistance and extended spectrum resistance to β-lactams/β-lactamase inhibitors in clinical isolates of *Escherichia coli***
Á. Rodríguez Villodres (Seville, Spain), A. Gutiérrez-Linares, J. Pachon-Diaz, J. Lepe, Y. Smani*

4389 **Direct detection of extended-spectrum beta-lactamases in bacteria isolated in blood culture bottles using a lateral flow assay**
G. Cuesta Chasco (Barcelona, Spain), J. Bosch, Y. Zboromyrska, C. Pitart, A. Vergara, F. Morales, E. Rubio Garcia, B. Fidalgo, M. Fernández, C. Casals-Pascual, J. Vila Estape*

4985 **Direct-from-Blood-Culture NG-Test CTX-M Multi and Carba 5 assay to predict extended-spectrum β-lactam resistance of *Escherichia coli* and *Klebsiella pneumoniae***
L. Giordano (Rome, Italy), T. D'Inzeo, B. Fiori, V. Cortazzo, G. Menchinelli, F. Liotti, M. Ventriglia, G. De Angelis, B. Posteraro, M. Sanguinetti, T. Spanu*

5053 **Evaluation of the rapid ResaPolymyxin *Acinetobacter/Pseudomonas* NP test for rapid screening of colistin resistance in non-lactose fermenters**
H. Jung (Pretoria, South Africa), J. Pitout, B. Mitton, K. Strydom, C. Kingsburgh, N. Mbelle, M. Ehlers, M. Kock*

5398 **Polymyxin B broth disk elution as a screening test to determine polymyxin B susceptibility in *Enterobacterales***
N. Cielo, T. Belmonte, M. Preussler Mott, G. Rosa Da Cunha, N. Tolfo, C. Würdig Riche (Porto Alegre, Brazil), R. Maya Cardoso Da Silva, O. Hallal Ferreira Raro, C. Dias, J. Caierao*

6570 **Investigation of carbapenemases by RESIST-4 O.K.N.V immunochromatographic lateral flow assay in *Enterobacteriaceae* isolates**
M. Yasar (Izmir, Turkey), F. Cilli, Y. Tekintas, F. Polat, M. Hosgor-Limoncu*

7362 **Evaluation of the RESIST-4 O.K.N.V. K-SeT test for the detection of carbapenemase production in *Enterobacterales***
A. Both, L. Jánvári, A. Hanczvikkel, A. Toth (Budapest, Hungary)*

7380 **Improved NG-test Carba5 assay for the detection of previously undetected IMP-variants**
H. Volland (Gif sur Yvette, France), D. Girlich, M. Laguide, V. Paris, M. Laroche, S. Oueslati, L. Dortet, P. Plésiat, S. Simon, T. Naas*

8336 **Comparison of four ESBL detection tests directly from blood cultures and urine samples**
F. Caméléna (Paris, France), H. Kafando, A. Ly, P. Thiebot, M. Rouveau, T. Sophie, M. Lafaurie, B. Bercot*

8551 **Evaluation of the new BL-RED electrochemical test for the detection of 3GC-resistant *Enterobacteriaceae* directly from positive blood cultures**
C. Durand, A. Boudet (Nîmes, France), J. Lavigne, A. Pantel*

8610 **High-throughput bacterial phenotyping to characterise antimicrobial resistance mechanisms**
B. Warne (Cambridge, United Kingdom), J. Bartholdson Scott, S. Forrest, M. Maes, S. Sridhar, M. Török, G. Dougan*

Session accepted as 1-Hour Oral Session

RAST and antimicrobial stewardship

1442 **Clinical impact of rapid susceptibility testing in Gram-negative bloodstream infections**
V. Antón Vázquez (London, United Kingdom), C. Suarez, S. Adjepong, T. Planche*

2390 **Improving Outcomes and Antibiotic Stewardship for patients with bloodstream Infections (IOAS): a quasi-experimental multi-centre analysis of time to optimal therapy**
A. Bhalodi (Tucson, United States), S. Macvane, M. Morgan, M. Ben-Aderet, M. Madhusudhan, J. Kolev, R. Dare, E. Rosenbaum, K. Wolfe, B. Ford, D. Ince, P. Kinn, K. Percival, R. Humphries*

3322 **Implementation of EUCAST rapid antimicrobial susceptibility testing combined with routine infectious disease bedside consultation**
T. Valentin (Graz, Austria), T. Loizenbaur, E. König, J. Prattes, S. Wunsch, C. Zurl, R. Krause, I. Zollner-Schwetz*

5846 **Impact of rapid antimicrobial susceptibility testing on antimicrobial stewardship and clinical outcomes of patients with Gram-negative rod bloodstream infection**
C. Hogan (Palo Alto, Canada), B. Ebunji, N. Watz, K. Kapphahn, J. Rigdon, E. Mui, L. Meng, W. Alegria, M. Holubar, S. Deresinski, N. Banaei*

7466 **Very good results for the use of the RAST methodology and for identification of agents of sepsis directly from the blood cultures by MALDI-TOF to optimise antibiotic therapy**
J. Mamani Pariona, F. Oliveira, P. Scotoni, T. Zaccariotto, N. Lincopan, C. Levy (Campinas, Brazil)*

Session accepted as Paper Poster Session

Resistance issues in special circumstances

371 **Impact of biocide residues on *Escherichia coli* antimicrobial susceptibility**
R. Wesgate (Cardiff, United Kingdom), J. Maillard, S. Fanning, Y. Hu*

442 **Antimicrobial resistance and pathogenicity of *Corynebacterium striatum* clinical isolates collected from three tertiary hospitals in China**
J. Wang, Y. Han (Hohhot, China)*

2396 **Elucidation of environment-dependent antibiotic resistance mechanisms**
H. Machado (La Jolla, United States), Y. Seif, N. Dillon, H. Tsunemoto, J. Pogliano, V. Nizet, B. Palsson, A. Feist*

2670 **Potentiation of quinolones activity against *Escherichia coli* by supression of SOS response and oxidative detoxification systems**
S. Díaz Díaz (Seville, Spain), E. Recacha, J. Machuca Bárcena, A. García-Duque, J. Blazquez, A. Pascual Hernandez, F. Docobo Perez, J. Rodriguez Martinez*

3101 **Identified beta-lactamase genes in *Aeromonas* species: an experience from Qatar**
A. Husain (Doha, Qatar), S. Skariah, M. Sid Ahmed, M. Badawi, H. Ahmedullah, M. Al-Maslamani, A. Al-Khal, H. Al Soub, A. Sultan, E. Ibrahim, H. Ziglam*

3418 **Enhancing fosfomycin activity via glycerol-3-phosphate transporter activation**
M. Ortiz Padilla (Seville, Spain), I. Portillo Calderón, B. De Gregorio Laria, J. Rodríguez-Baño, A. Pascual Hernandez, J. Rodriguez Martinez, F. Docobo Perez*

3790 **Unveiling the role of nisin on resistance development by diabetic foot staphylococci: mutant selection window and horizontal gene transfer**
M. Costa, E. Cunha, L. Tavares, M. Oliveira (Lisbon, Portugal)*

4124 **Characterising a novel mechanism of inducible carbapenem reistance in toxigenic *Corynebacterium diphtheriae***
B. Forde (Brisbane, Australia), A. Henderson, G. Playford, D. Paterson, S. Beatson*

4264 **Prevalence of macrolide resistance mutations in *Mycoplasma pneumoniae* from patients with respiratory tract infections in European Russia**
I. Edelstein (Smolensk, Russian Federation), A. Romanov, A. Kuzmenkov, N. Alyabyeva, T. Pleskachevskaia, M. Erschova, I. Ivanova, A. Ignatkova, O. Romashov, E. Groshenkova, R. Kozlov*

4342 **Significant increase in the prevalence of macrolide resistance-mediating mutations in *Mycoplasma genitalium* from 2014 to 2019**
G. Khayrullina (Moscow, Russian Federation), T. Makhova, E. Goloveshkina, G. Alexander*

4380 **Spontaneous and clinically relevant *tet*(A)-dependent tigecycline resistance development**
J. Jagdmann (Uppsala, Sweden), D. Andersson, H. Nicoloff*

4699 **Carbapenem-resistant *Pseudomonas aeruginosa* in cystic fibrosis children**
E. Samoylova, O. Shamina (Moscow, Russian Federation), I. Novikova, T. Savinova, A. Lazareva*

5546 **A novel variant of CTX-M β-lactamase in a clinical strain of *Serratia marcescens***
P. Celejewski-Marciniak, R. Wolinowska, M. Wroblewska (Warsaw, Poland)*

5835 **Two antibiotics are better than one: using functional genomics to elucidate mechanisms of action in combination therapy**
G. Sullivan (North Ryde, Australia), R. Maharjan, N. Delgado, A. Cain*

5948 **Induction of erythromycin resistance in *Bordetella* sp. confirmed by whole genome sequencing**
W. Fong (Westmead, Australia), V. Timms, E. Sim, T. Nguyen, V. Sintchenko*

6164 **The rates of antimicrobial resistance in leprosy are higher among cases diagnosed in France than in those diagnosed in African countries (WHO sentinel surveillance network)**
A. Chauffour (Paris, France), E. Lecorche, F. Mougari, A. Aubry, A. Randrianantoandro, K. Mamoudou, M. Gado, B. Cauchoix, R. Johnson, V. Jarlier, E. Cambau*

6229 **Antimicrobial susceptibility of medically important *Nocardia* species in Korea**
K. Hur (Seoul, South Korea), K. Park, M. Kim, H. Sung*

6312 **Do bacterial growth conditions affect antibiotic resistance evolution?**
J. Littler (Coventry, United Kingdom), F. Harrison*

6831 **Pandrug-resistant *Ralstonia mannitolilytica* isolates from a cystic fibrosis patient after lung transplantation**
M. Hernandez (Valladolid, Spain), B. Suberviola, L. Alvarez-Montes, C. Díaz Ríos, M. Siller, J. Rodríguez-Lozano, A. De Malet, I. Perez Del Molino, L. Armendariz, M. Fariñas, J. Calvo-Montes, A. Ocampo-Sosa*

6855 **Molecular epidemiology of *Achromobacter xylosoxidans* in the airways of cystic fibrosis patients: a longitudinal study**
S. Kampmeier (Münster, Germany), A. Mellmann, B. Kahl*

7866 **Piperacillin-tazobactam resistance developed during febrile neutropenia**
C. Gomes (São Paulo, Brazil), E. Sanchez Espinoza, M. Farrel Côrtes, A. Marchi, T. Guimaraes, F. Rossi, L. Perdigao Neto, V. Rocha, S. Figueiredo Costa*

9132 **Aminoglycoside resistance mechanisms in invasive *Klebsiella pneumoniae* and *Escherichia coli*: a threat of *rmtC* mediated resistance**
I. Uzun (Istanbul, Turkey), T. Celik, B. Aksu, N. Ulger Toprak, M. Hasdemir*

Session accepted as Paper Poster Session

Resistance issues in streptococci

1280 **Multiple mutations in dihydrofolate reductase gene in cotrimoxazole-resistant *Streptococcus pneumoniae* isolated from HIV adults in a community setting, Tanzania**
J. Manyahi (Bergen, Norway), S. Moyo, S. Aboud, N. Langeland, B. Blomberg*

2003 **Whole genome analysis of non-PCV13 emergent serotypes 8, 12F, 9N and 22F causing invasive pneumococcal disease in Spain**
A. González Díaz (Barcelona, Spain), J. Càmara, M. Ercibengoa Arana, E. Cercenado, N. Larrosa, M. Quesada, D. Fontals, M. Cubero, J. Marimon Ortiz De Zarate, J. Yuste, C. Ardanuy Tisaire*

2277 **Colonisation dynamics of *Streptococcus pneumoniae* in a remote African population: a prospective cohort study**
F. Schaumburg (Münster, Germany), A. Flamen, A. Alabi, J. Ehrhardt, M. Van Der Linden*

2376 **Emergence of the uncommon multiple drug-resistant non-PCV13 serotype 13/ST2754-clone among paediatric nasopharyngeal pneumococci isolated in Russia: 2010-2018**
E. Brzhozovskaya (Moscow, Russian Federation), N. Alyabyeva, T. Savinova, O. Ponomarenko, A. Mirzaeva, T. Kulichenko, Y. Mikhaylova, D. Shagin, N. Mayanskiy*

2996 **In the absence of pressure, physical interaction within nasopharyngeal pneumococcal biofilms leads to acquisition of cephalosporin resistance but not to capsule switch events**
X. Wu (Hangzhou, China), L. Santiago, Y. Tzeng, D. Stephens, J. Vidal*

3451 **Resistance patterns and serotype distribution of *Streptococcus pneumoniae* isolates responsible for respiratory tract infections in Poland, 2006-2018**
A. Gołębiewska (Warsaw, Poland), I. Waśko, P. Ronkiewicz, M. Kiedrowska, I. Wróbel, A. Bojarska, B. Zieniuk, A. Kuch, E. Sadowy, W. Hryniewicz, A. Skoczyńska*

3556 **Identification of a multidrug-resistance cluster in clinical isolates of *Streptococcus pyogenes* that confers resistance to macrolides, lincosamides, tetracyclines, chloramphenicol and co-trimoxazole**
D. Berbel Palau, G. López De Egea, J. Càmara (Barcelona, Spain), A. González Díaz, M. Cubero, F. Tubau, M. Domínguez Luzon, C. Ardanuy Tisaire*

4352 **Clonal spread of multidrug-resistant penicillin-nonsusceptible *Streptococcus agalactiae***
J. Chang (Goyang-si, South Korea), H. Sung, M. Kim*

4634 **Comparative genomics and virulence of human and animal *Streptocccus agalactiae* (Group B *Streptococcus)***
Y. Yang (Hong Kong, Hong Kong), Y. Yeoh, C. Li, D. Nanayakkara, J. Rothen, M. Morach, R. Stephan, S. Schmitt, C. Ewers, J. Reyes-Velez, U. Gilli, M. Crespo-Ortiz, M. Crumlish, G. Revathi, M. Luo, L. Zheng, H. Zhou, K. Fung, C. Daubenberger, S. Johler, M. Ip*

5523 **A multi-centre evaluation of the US prevalence and regional variation in macrolide-resistant *Streptococcus pneumoniae* from blood or respiratory cultures among adult patients**
V. Gupta (Naperville, United States), K. Yu, J. Schranz, H. Jokinen-Gordon, S. Gelone*

6432 **Collateral responses to fluoroquinolone resistance in *Streptococcus pneumoniae***
A. Liakopoulos (Leiden, Netherlands), M. Buffoni, D. Rozen*

7777 **Emergence of penicillin non-susceptible Group B streptococci within the hypervirulent CC17 clone colonising pregnant women in Portugal: a genomic analysis**
R. Mamede, J. Melo-Cristino, M. Ramirez (Lisbon, Portugal), E. Ferreira Martins*

8796 **Genetic diversity of invasive, non-invasive and colonising Group B *Streptococcus* isolates in Southern Brazil**
O. May-Fuerscchutte, E. Alves, A. Vilela, F. Barazetti, J. Palmeiro, M. Scheffer (Florianopolis, Brazil), M. Bazzo*

8985 **Antimicrobial susceptibility of *Streptococcus dysgalactiae* subspecies *equisimilis* isolates recovered from invasive infections in Portugal**
A. Castro, J. Melo-Cristino, M. Ramirez, M. Pinho (Lisbon, Portugal)*

Session accepted as Paper Poster Session

Resistance mechanisms to new beta-lactamase inhibitor combinations

1179 **Non-lethal concentrations of ceftazidime and ceftazidime-avibactam select for multiple-resistant genotypes**
C. Fröhlich (Tromsø, Norway), J. Alves Gama, P. Johnsen, H. Leiros, O. Samuelsen*

2259 **Dual therapy with aztreonam & ceftazidime/avibactam against multi-drug resistant *Stenotrophomonas maltophilia* on tricuspid valve endocarditis**
J. Alexander (Orlando, United States), A. Carr, S. Minor, D. Navas*

2569 **Baseline resistance to ceftazidime-avibactam and aztreonam-avibactam in carbapenemase-producing *Enterobacterales* from Argentina mediated by the co-expression of PER ESBL: role of imipenem-relebactam and aztreonam-relebactam as therapeutic alternatives**
F. Pasteran (Buenos Aires, Argentina), J. De Mendieta, M. Rapoport, S. Ramirez, D. Faccone, C. Lucero, P. Ceriana, A. Corso*

3771 **Genomic and transcriptomic approach to unravel the resistance mechanisms to ceftazidime-avibactam in *Pseudomonas aeruginosa* and *Enterobacter cloacae***
A. Bösch (St. Gallen, Switzerland), S. Schmitt, M. Held, J. Findlay, A. Egli, H. Seth-Smith, V. Hinic, V. Gisler, H. Fankhauser, M. Oberle, P. Kohler, S. Seiffert, N. Oliver, B. Babouee Flury*

4607 **A novel KPC-3 variant associated with CAZ/AVI resistance in an *Klebsiella pneumoniae* ST512 causing bacteraemia**
A. Knezevich (Trieste, Italy), M. Coppi, A. Antonelli, V. Di Pilato, T. Giani, S. Di Bella, C. Maurel, M. Zatta, S. Fossati, M. Bortolin, E. Piccoli, R. Luzzati, G. Rossolini, M. Busetti*

4981 **Ceftazidime-avibactam resistance and restoration of carbapenem susceptibility in KPC-producing *Klebsiella pneumoniae* infections**
S. Van Asten (Leiden, Netherlands), M. Boattini, G. Bianco, M. Kraakman, C. Costa, R. Cavallo, A. Bernards*

5145 **Mechanism of ceftazidime-avibactam resistance in carbapenem-resistant *Escherichia coli* isolated in the Arabian Peninsula**
A. Sonnevend (Pécs, Hungary), A. Ghazawi, V. Di Pilato, A. Antonelli, G. Rossolini, T. Pal*

6113 **Mutations variability of KPC-3 carbapenemase related to ceftazidime/avibactam resistance found in *Klebsiella pneumoniae* strains isolated in Verona, Italy**
S. Cavallini, I. Unali, I. Di Nolfo, A. Bertoncelli, A. Mazzariol (Verona, Italy)*

7310 **Impact of porin deletions on the *in vitro* antimicrobial activity of cefepime-taniborbactam (formerly cefepime/VNRX-5133) in *Klebsiella pneumoniae***
T. Uehara (Malvern, United States), S. Vernacchio, B. Miller, C. Chatwin, G. Moeck, C. Burns, D. Pevear, D. Daigle*

7410 **Evaluation of *in vitro* susceptibility and molecular resistance mechanisms to ceftazidime-avibactam in clinical isolates of *Pseudomonas aeruginosa* from five Latin American countries**
E. De La Cadena (Bogota, Colombia), T. Appel, M. Mojica, J. García-Betancur, C. Pallares, M. Villegas*

9045 **Unusual mechanisms of resistance to ceftazidime-avibactam in *Klebsiella pneumoniae***
E. Sanchez Espinoza, L. Perdigao Neto, M. Farrel Côrtes (Sao Paulo, Brazil), T. Orsi, R. Ruedas Martins, E. Lira, I. Boszczowski, C. Dantas De Maio Carrilho, T. Guimaraes, A. Sara Levin, S. Figueiredo Costa*

Session accepted as Paper Poster Session

Resistance to key drugs in enterococci

768 **Linezolid-resistant strains of *Enterococcus faecium* in the Czech Republic from 2009 to 2018**
L. Malisova (Prague, Czech Republic), V. Jakubu, M. Musilek, H. Zemlickova*

998 **Carrier prevalence of vancomycin-resistant *Enterococcus faecium* (VREfm) among patients admitted to emergency departments in Copenhagen (Denmark) compared with VREfm prevalence of the background population**
I. Rubin (Frederiksberg, Denmark), M. Pinholt, H. Calum, C. Pahl Kavalris, M. From-Hansen, M. Stangerup, H. Westh, J. Knudsen*

1020 **Gene expression analysis of transport channels in *Enterococcus faecium***
Z. Alhareth (Leicester, United Kingdom), K. Laird, L. Smith, J. Dixon, L. Owen*

1735 **Genome-based surveillance of clinical vancomycin-resistant *Enterococcus faecium* reveals increased prevalence of *vanB*-type isolates of ST117/CT71 in German hospitals, 2010-2016**
B. Neumann (Wernigerode, Germany), M. Kresken, G. Werner*

1828 **Improved detection of van-B bearing *E. faecium* isolates in a German hospital laboratory by a modified routine workflow for antimicrobial susceptibility testing**
C. Scherer (Bielefeld, Germany)*

2257 **Clonal attack: number of vancomycin-susceptible, -variable and -resistant *E. faecium* clones in individual rectal swabs**
K. Nielsen (Copenhagen, Denmark), S. Radmer, K. Knudsen List, N. Frimodt-Moller*

2466 **Duration of colonisation with vancomycin-resistant *Enterococcus faecium* in a large ST796 *vanB* hospital outbreak: a cohort study**
V. Piezzi, Y. Schmiedel, T. Kaspar, M. Baechli, P. Bittel, J. Marschall, R. Sommerstein (Bern, Switzerland)*

2826 **Molecular epidemiology of vancomycin-resistant enterococcus in parts of China**
H. Sun (Beijing, China), L. Chang, Y. Xu*

3164 **Daptomycin plus fosfomycin or ceftaroline is active *in vitro* against high-level aminoglycoside-resistant and vancomycin-resistant or vancomycin-susceptible *Enterococcus* spp. strains**
C. Garcia-De-La-Maria (Barcelona, Spain), J. García-González, D. Panesso, M. Cañas Pacheco, A. Dahl, D. Fuster, B. Vidal, A. Perissinotti, E. Sandoval, J. Tolosana, E. Quintana, M. Almela, J. Ambrosioni, M. Moreno Camacho, C. Arias, J. Miró Meda*

3530 **Non-vancomycin antibiotic resistance genes in vancomycin-resistant *E. faecium*: variation linked to MLST and mis-match between aminoglycoside resistance geno- and phenotypes**
Z. Adamecz (Copenhagen, Denmark), K. Nielsen, N. Kirkby, N. Frimodt-Moller*

4238 **Detection of low-level *vanB*-type vancomycin-resistant *Enterococcus faecium* with agar screen methods**
S. Van Koeveringe, K. Loens, I. Mermans, H. Jansens, H. Goossens, V. Matheeussen (Edegem, Belgium)*

4450 **Vancomycin-resistant *Enterococcus faecium:* admission prevalence, sequence types and risk factors: a cross-sectional study in 7 German university hospitals over 5 years**
A. Rohde (Berlin, Germany), A. Walker, M. Behnke, T. Chakraborty, S. Eisenbeis, J. Falgenhauer, H. Gölz, G. Häcker, F. Hölzl, N. Kaeding, W. Kern, A. Kola, E. Kramme, A. Mischnik, S. Peter, S. Rieg, J. Rupp, F. Schwab, H. Seifert, D. Tobys, E. Tacconelli, A. Weber, K. Xanthopoulou, J. Zweigner, P. Higgins, P. Gastmeier*

4852 **Antimicrobial susceptibility of vancomycin-resistant *Enterococcus faecium* and linezolid-resistant *Enterococcus faecium* isolated from blood culture in haematological patients: results of multi-centre study in Russia**
A. Fedorova Mironova (Moscow, Russian Federation), G. Klyasova, I. Frolova, S. Khrulnova, A. Vetokhina, T. Kaporskaya, I. Molchanova*

4904 **Prevalence of resistant and virulence genes in *Enterococcus faecium* and *Enterococcus faecalis* isolated from blood culture in haematological patients in Russia**
A. Fedorova Mironova (Moscow, Russian Federation), S. Khrulnova, G. Klyasova*

5036 **Molecular epidemiology of invasive vancomycin-resistant *Enterococcus faecium* isolates**
L. Nürnberger (Essen, Germany), D. Schmidt, J. Steinmann, P. Rath*

5136 **Molecular epidemiology of colonising and infecting vancomycin-resistant *Enterococcus faecium* in Germany**
K. Xanthopoulou (Cologne, Germany), J. Wille, A. Walker, Y. Stelzer, V. Persy, S. Peter, H. Seifert, P. Higgins*

5192 **Vanco-Test: a rapid test for detection of vancomycin-resistant enterococci**
A. Bertoncelli, I. Rizzotti, A. Mazzariol (Verona, Italy)*

5505 **High-throughput culture-based vancomycin-resistant enterococci screening using artificial intelligence**
A. Nowag, H. Wisplinghoff (Cologne, Germany), X. Quante, S. Giglio, S. Wirth, B. Pohl, N. Jazmati*

5612 **Increasing importance of *Enterococcus faecium* as an aetiological agent of healthcare-associated bloodstream infections**
H. Marchel, M. Wroblewska (Warsaw, Poland)*

6070 **Comparative genomics of global linezolid-resistant *Enterococcus faecalis* strains unveils a chromosomal hotspot for *optrA* acquisition**
A. Freitas (Porto, Portugal), A. Tedim, C. Novais, V. Fernandez Lanza, L. Vieira Peixe*

6235 **Phenotypic susceptibility testing for vancomycin-resistant enterococci in less than 4 hours using the flow cytometry-assisted susceptibility test**
K. Mulroney, T. Paton (Perth, Australia), M. Kopczyk, A. Chakera, C. Carson, T. Inglis*

6473 **Major changes detected in penicillin-binding proteins of vancomycin-resistant *Enterococcus faecalis* by sequencing and homology modeling**
N. Caglayan, B. Sancak, E. Aybakan, Z. Kanlidere, O. Oflaz, T. Kocagoz (Istanbul, Turkey)*

6579 **Possible horizontal transfer of enterococcal IS*1216V*-mediated composite transposon between enterococci and methicillin-resistant *Staphylococcus aureus***
W. Hung (Kaohsiung City, Taiwan), C. Chang*

7269 **Large diffusion of OptrA- and PoxtA-producing linezolid-resistant *Enterococcus* spp. among healthy children from rural communities of the Bolivian Chaco**
I. Baccani (Florence, Italy), A. Antonelli, M. Tortorella, T. Di Maggio, M. Spinicci, M. Strohmeyer, F. Mariotti, H. Gamboa Barahona, D. Rojo Mayaregua, V. Poma, L. Pallecchi, A. Bartoloni, G. Rossolini*

7872 **Genetic context of the *poxtA* gene that confers resistance to linezolid in enterococci**
L. Dejoies (Rennes, France), S. Schutz, A. Zouari, S. Potrel, A. Collet, G. Auger, M. Sassi, V. Cattoir*

9246 **Detection of linezolid-resistant enterococci carrying *optr*A and/or *poxt*A in raw-frozen dog foods commercialised in the EU: trend or threat?**
L. Finisterra, C. Novais, B. Duarte, L. Vieira Peixe, A. Freitas (Porto, Portugal)*

9311 **Genomic characterisation of clinical *Enterococcus faecium* from Tunisia: remarkable identity with ampicillin-resistant strains obtained from animals/meat in the same area**
A. Freitas (Porto, Portugal), H. Elghaieb, C. Novais, B. Duarte, M. Abbassi, L. Vieira Peixe*

Session accepted as Paper Poster Session

Resistome characterisation of Gram-negatives

152 **Whole genome sequencing of *Pseudomonas aeruginosa* isolates from across the United Kingdom: population structure and molecular predictors of resistance**
T. Planche (London, United Kingdom), A. Witney, A. Alvarez Buylla, M. Allen, E. Manu, I. Monahan, M. Wootton*

2184 **Whole genome sequence of a pan-resistant *Klebsiella pneumoniae* sequence type 11 harbouring an IncR-F33:A-:B- plasmid carrying multiple resistance determinants identified in Japan in 2016**
S. Nishida (Tokyo, Japan), Y. Ono*

2519 **Whole genome sequence-based PCR for the rapid identification of *Pseudomonas aeruginosa* ST175 high-risk clone isolates directly from clinical samples**
G. Cabot (Palma, Spain), P. Lara-Esbri, X. Mulet, A. Oliver*

4382 **Whole genome sequence analysis of antimicrobial resistance genes in Global Priority Superbugs**
N. Perera (Teddington, United Kingdom), C. Fedorchuk, J. Sutcliffe, J. Sohn, R. Mclaughlin, J. Lopera*

4384 **Pathogenic potential and antimicrobial resistance genomic analysis of human gut commensal *Escherichia coli***
B. Pakbin, P. Lisotto, E. Raangs, A. Friedrich, J. Rossen, S. García Cobos (Madrid, Spain)*

5374 **Insights in the resistome of multidrug-resistant *Pseudomonas aeruginosa* strains isolated in Romania from nosocomial infections and wastewater**
I. Gheorghe (Bucharest, Romania), I. Czobor, L. Popa, I. Avram, A. Haitham, S. Mohsin, S. Paraschiv, M. Surleac, V. Cristea, M. Popa, L. Marutescu, D. Otelea, V. Lazar, M. Chifiriuc*

6026 **Resistome analysis of new bacterial species isolated at at the Institut Hospitalo-Universitaire Méditerranée**
S. Khabthani, M. Hamel, S. Diene, V. Merhej, J. Rolain (Marseille, France)*

8535 **An outbreak of hypervirulent and multidrug-resistant clone (ST2096) *Klebsiella pneumoniae* silently transmitting in a Saudi Arabia western region hospital: a clinical and molecular surveillance study**
S. Hala, A. Chakkiat, M. Alshehri, A. Alsaedi, A. Althaqafi, G. Alahmadi (Jeddah, Saudi Arabia), M. Kaaki, M. Alazmi, B. Alhaj Hussein, M. Yaseen, R. Ghazali, H. Zowawi, A. Alamri, A. Pain*

9224 **Genomic surveillance at the regional scale: antimicrobial-resistant *Klebsiella pneumoniae* ST11 isolates in the Valencian community, Spain**
N. Garcia-Gonzalez (Paterna, Spain), F. Gonzalez-Candelas*

9369 **Hybrid genome based approach for investigation of molecular basis of international high risk clone ST357 *Pseudomonas aeruginosa* circulating in India**
A. Pragasam (Vellore, India), J. Jacob, K. Vasudevan, V. Narasiman, S. Anandan, V. Balaji*

9476 ***De novo* hybrid genome assembly and genome analysis of polymyxin- and carbapenem-resistant clinical isolate *Klebsiella pneumoniae***
M. Zubasheva (Moscow, Russian Federation), D. Shcherbinin, G. Speshilov, V. Zhukhovitsky*

Session accepted as Mini-oral ePoster Session

State-of-the-art detection of carbapenemases and colistin resistance

2137 **Rapid detection of ceftazidime/avibactam-resistant *Enterobacteriaceae* by VITEK MALDI-TOF mass spectrometry using direct-on-target microdroplet growth assay**
S. Huang (ShangHai, China), B. Hu, W. Guo, J. Pan, B. Wang, Z. Chunmei, Y. Ma, Y. Shan, Y. Zhang*

3402 **Evaluation of CARBA PAcE, a novel rapid test for detection of carbapenemase-producing *Enterobacterales***
J. Sattler (Cologne, Germany), A. Brunke, A. Hamprecht*

3854 **Rapid detection of colistin resistance using a newly developed protocol for MALDI-TOF MS**
N. Perrot (La Balme les Grottes, France), D. Dechaume, F. Javerliat, K. Pinkston, V. Girard, G. Zambardi, J. Charrier*

4577 **Comparative evaluation of MAST Carba PAcE, RESIST-4 O.K.N.V. and NG-Test Carba 5 kits in the detection of carbapenemase production in clinical isolates**
J. Lee (London, United Kingdom), Z. Sadouki, I. Balakrishnan, E. Wey*

5090 **Rapid detection of bacteria resistant to the last resort antibiotics using MALDI Biotyper Sirius: the MALDIxin test**
C. Furniss, L. Dortet, R. Bonnin, S. Le Hello, K. Sparbier, O. Drews, A. Filloux, M. Kostrzewa, D. Mavridou, G. Larrouy-Maumus (London, United Kingdom)*

7144 **Blue-Carba complete**
A. Lima, D. Rocha, K. Lima, S. Sampaio, J. Mello-Sampaio (São Paulo, Brazil)*

7814 **Evaluation of different methods for the detection and differentiation of mechanisms of resistance in carbapenemase-producing *Enterobacterales* at a large district hospital, UK**
S. Parikh, H. Kandil (Watford, United Kingdom)*

8371 **Detection and identification of intact carbapenemases using liquid chromatography and tandem mass spectrometry from microbial lysates in a rapid carba method using the Acrion system**
W. Mcgee (Watertown, United States), A. Verma, M. Viirtola, S. Kronewitter, J. Neil, J. Haakana, J. Stephenson*

8578 **Directly detecting imipenemase (IMP) carbapenemase with high-resolution Orbitrap mass spectrometry**
W. Mcgee, S. Kronewitter, M. Viirtola, A. Verma, J. Neil, D. Sarracino, M. Hutchins, S. Gurung, J. Stephenson (Raleigh, United States)*

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Surveillance of carbapenemase-producing *Enterobacterales*

835 **Epidemiology of carbapenemase-producing *Klebsiella pneumoniae* in Northern Portugal: predominance of KPC-2 and OXA-48**
E. Lopes, M. Saavedra, E. Costa, H. De Lencastre, L. Poirel, M. Aires De Sousa (Lisbon, Portugal)*

2000 **Report of the national reference centre for multidrug-resistant Gram-negative bacteria on carbapenemases in Germany in 2019**
N. Pfennigwerth (Bochum, Germany), J. Schauer, M. Cremanns, J. Hans, A. Anders, S. Gatermann*

2566 **Rapid increase in occurrence of carbapenem-resistant *Enterobacteriaceae* in healthy rural residents in Shandong province, China, from 2015 to 2017**
B. Chen, B. Berglund, S. Wang, S. Börjesson, H. Yin, Z. Bi, M. Nilsson, Z. Bi, L. Nilsson (Linköping, Sweden)*

2819 **Types of carbapenemases produced by Gram-negative bacteria detected isolated in cancer hospital in 2017-2019**
V. Aginova, N. Dmitrieva, P. Irina (Moscow, Russian Federation), Z. Grigoryevskaya, N. Bagirova, S. Dyakova, I. Tereshchenko, I. Klyuchnikova*

3417 **Whole genome sequencing: epidemiologic surveillance of carbapenemases present in *Enterobacteriaceae* isolated at Sant Pau Hospital (Barcelona) in 2018**
E. Miró (Barcelona, Spain), D. Miniac, R. Altaba, M. Rubio, A. Rivera, F. Navarro*

3668 **Detection of ST131, ST410 and ST69 *Escherichia coli* KPC-2/3, OXA-181, and VIM-1 -producers from a long-term care facility in Milan, Italy**
F. Marchesini, A. Abu-Alsha'Ar, A. Mercato, M. Mancinelli (Pavia, Italy), V. Mattioni Marchetti, E. Fogato, F. Lattanzi, E. Nucleo, R. Migliavacca*

4211 **Investigation of carbapenem- and tigecycline-resistant *Klebsiella pneumoniae* in a Greek hospital**
A. Mavroidi (Athens, Greece), E. Palla, O. Kordanouli, S. Likousi, K. Zourla, E. Merkouri, E. Platsouka*

4802 **Carbapenemase-producing organisms in high-risk units of a district general hospital in London**
S. De Saram (London, United Kingdom), N. Mukombe, J. Lucas, R. Forbes, M. Mirfenderesky, N. Draz*

4810 **Surveillance and molecular typing of carbapenem-resistant *Enterobacteriaceae* in neonatal intensive care units in Italy**
M. Agosta (Rome, Italy), D. Bencardino, F. Andreoni, M. Argentieri, B. Lucignano, L. Mancinelli, M. Onori, L. Pansani, A. Sisto, M. Magnani, P. Bernaschi*

5338 **Carbapenemase-producing *Enterobacterales* among urinary isolates from community in Belgrade, Serbia**
S. Brkić (Belgrade, Serbia), D. Topalov, D. Božić, N. Stojanović, I. Cirkovic*

6454 **Molecular characterisation of carbapenemase-producing *Enterobacterales* (CPE) in London, UK**
B. Patel (London, United Kingdom), K. Hopkins, D. Meunier, N. Mustafa, N. Ellaby, M. Doumith, S. Hopkins, N. Woodford*

6540 **One-year surveillance report of carbapenem- and colistin-resistant Gram-negative bacteria within the MERCyCAT project**
M. Marí Almirall, L. Muñoz, N. Ferrando, C. Cosgaya Castro, V. Moya, M. Piquet, R. Rodríguez, F. Ballester, P. Ciruela Navas, Y. Zboromyrska, C. Pitart, J. Vila Estape, I. Roca (Barcelona, Spain)*

6718 **Epidemiology of carbapenem resistance genes in clinical isolates in South India**
A. Rohit (Chennai, India), J. P, B. Raghuraman, D. I, S. Dorairajan, K. Iddya*

6883 **Molecular epidemiology of carbapenemase-producing *Escherichia coli* in northern Spain studied by molecular typing techniques and next-generation sequencing**
X. Vázquez, V. García Menéndez, M. De Toro, P. Lumbreras Iglesias, J. Rodriguez-Lozano, A. Canut, P. De La Iglesia, B. Iglesias, A. Mora Gutiérrez, J. Blanco, M. Rodicio, J. Fernández (Oviedo, Spain)*

7024 **Evolutionary trajectories of carbapenemase-producing *Escherichia coli***
R. Patino-Navarrete, I. Rosinski-Chupin, N. Cabanel, L. Gauthier, J. Takissian, J. Madec, M. Hamze, R. Bonnin, T. Naas, P. Glaser (Paris, France)*

7768 **Epidemiology of carbapenemases isolated from *Enterobacteriaceae* other than *Klebsiella pneumoniae* and *Escherichia coli* in Belgium (2015-2018)**
O. Denis (Brussels, Belgium), P. Bogaerts, C. Berhin, W. Bouchahrouf, M. Hoebeke, Y. Glupczynski, T. Huang*

8324 **Antimicrobial susceptibility of *Enterobacterales* and *Pseudomonas aeruginosa* to carbapenems and occurrence of carbapenemase producers: results from SMART study in South Serbia, 2012-2018**
B. Kocic (Nis, Serbia), S. Mladenovic-Antic, M. Dinic, D. Stankovic-Djordjevic, R. Velickovic Radovanovic, R. Mitic, J. Petrovic, M. Randjelovic, S. Hawser*

8434 **One-year prospective analysis of carbapenem-resistant strains isolated from a tertiary urinary centre in Romania**
M. Muntean (Bucharest, Romania), A. Muntean, M. Preda, I. Sandu, V. Jinga, T. Naas, M. Popa*

9281 **Increase of carbapenemase-producing *Enterobacteriaceae* in a Portuguese hospital from 2016 to 2019**
R. Ramos Figueiredo, P. Gama, C. Cortes (Torres Novas, Portugal)*

Session accepted as Paper Poster Session

Surveillance of resistance: novel agents and novel concepts

1045 ***In vitro* surveillance of eravacycline against Gram-negative pathogens, including multidrug-resistant isolates, collected from European hospitals in 2018**
S. Hwang, S. Hawser, I. Morrissey (Monthey, Switzerland), N. Kothari, E. Efimova, M. Olesky*

1331 **Comparative *in vitro* activity of cefepime-enmetazobactam and other agents against 3rd-generation cephalosporin-resistant and extended-spectrum β-lactamase-producing clinical isolates of *Enterobacterales* collected between 2016-2018**
A. Belley (Beaconsfield, Canada), S. Hawser, I. Morrissey, F. Monti, N. Khotari, P. Knechtle*

2372 **Using the Antibiotic Spectrum Index (ASI) score to assess antibiotic exposure for patients with Bloodstream Infections (BSI): an analysis of the Accelerate PhenoTest BC Kit (AXDX) IOAS study**
S. Macvane (Tucson, United States), A. Bhalodi, M. Morgan, M. Ben-Aderet, M. Madhusudhan, J. Kolev, R. Dare, E. Rosenbaum, K. Wolfe, B. Ford, D. Ince, P. Kinn, K. Percival, R. Humphries*

2739 **Antimicrobial susceptibility and carbapenem co-resistance among piperacillin/tazobactam-resistant *Pseudomonas aeruginosa*: SMART Asia/Pacific 2016-2018**
S. Lob, K. Kazmierczak (Schaumburg, United States), W. Chen, K. Balwani, T. Khan, K. Young, M. Motyl, D. Sahm*

3290 ***In vitro* activity of cefiderocol against Gram-negative pathogens from different infection types**
A. Santerre Henriksen (Jyllinge, Denmark), C. Longshaw, Y. Yamano*

4888 **Surrogate analysis of ertapenem to predict activity of tebipenem against *Escherichia coli* and *Klebsiella pneumoniae* collected from UTIs in Europe and the United States in 2019**
I. Critchley (Cambridge, United States), N. Cotroneo, M. Pucci, A. Jain, R. Mendes*

5323 **Antimicrobial activity of plazomicin and old aminoglycosides against clinical isolates of *Enterobacterales* collected worldwide in 2018**
H. Sader (North Liberty, United States), J. Streit, L. Duncan, J. Gogtay, C. Carvalhaes, M. Castanheira*

5478 ***In vitro* activity of imipenem-relebactam plus aztreonam against metallo-β-lactamase producing *Pseudomonas aeruginosa***
N. O'Donnell (Albany, United States), V. Putra, G. Belfiore, B. Maring, K. Young, T. Lodise*

5565 **Antimicrobial activity of cefepime in combination with taniborbactam (formerly VNRX-5133) against clinical isolates of *Enterobacterales* from Europe collected from 2018-2019 surveillance**
M. Hackel (Schaumburg, United States), D. Sahm, M. Wise*

5577 **Antimicrobial activity of cefepime in combination with taniborbactam (formerly VNRX-5133) against a European 2018-2019 surveillance collection of *Pseudomonas aeruginosa***
M. Hackel (Schaumburg, United States), D. Sahm, M. Wise*

5601 **Change of antimicrobial susceptibility testing guidelines from CLSI to BRCAST: impact of breakpoint change on the susceptibility of clinical isolates in a tertiary care hospital in Brazil**
Â. Celestino De Souza, P. Barth (Porto Alegre, Brazil), L. Lutz, M. Brasil Da Silva, V. Aquino, E. Wurdig Roesch, D. Castro Pereira*

6381 **Antimicrobial resistance surveillance in low- and middle-income countries: can we estimate resistance in bloodstream infections from other types of specimen?**
K. Vihta (Oxford, United Kingdom), N. Gordon, N. Stoesser, T. Quan, C. Tyrrell, D. Eyre, N. White, D. Crook, T. Peto, A. Walker*

6753 **Activity of cefiderocol and comparator antibiotics on an Italian multi-centre collection of carbapenem-resistant Gram-negative clinical isolates**
M. Coppi (Florence, Italy), A. Antonelli, C. Cervini, L. Mosconi, E. Riccobono, G. Baldi, F. Luzzaro, T. Lopizzo, T. Spanu, T. Giani, G. Rossolini*

6781 **Rapid, reproducible resistance analysis for all: the AMR package for R**
M. Berends (Groningen, Netherlands), C. Luz, B. Sinha, A. Friedrich, C. Glasner*

7274 ***In vitro* activity of cefiderocol, a siderophore cephalosporin, against multidrug-resistant isolates of Gram-negative bacilli from France**
S. Oueslati, L. Dortet, T. Naas (Le Kremlin Bicêtre, France)*

8011 ***In vitro* antibacterial activities of cefiderocol (S-649266) against multidrug-resistant *Acinetobacter baumannii***
J. Abdul-Mutakabbir (Detroit, United States), L. Nguyen, P. Maassen, K. Stamper, K. Lev, R. Kebriaei, K. Kaye, M. Rybak*

9115 **Levonadifloxacin (WCK 771), a recently approved benzoquinolizine fluoroquinolone exhibits potent *in vitro* activity against methicillin- and quinolone-resistant *Staphylococcus aureus*: a report from Indian tertiary care hospital**
Y. Devi Bakthavatchalam, A. Shankar, H. R, V. Balaji (Vellore, India)*

9459 ***In vitro* activity of novel β-lactam and β-lactam enhancer combination, cefepime-zidebactam (WCK5222) against Gram-negative clinical isolates with high-level carbapenem resistance rate: report from a large tertiary care centre in India**
S. Vijayakumar, B. Abirami, V. Balaji (Vellore, India)*

Session accepted as Paper Poster Session

Susceptibility to avibactam, relebactam, and vaborbactam combinations

473 **Antimicrobial activity of ceftazidime-avibactam, ceftolozane-tazobactam and comparators tested against *Pseudomonas aeruginosa* and *Klebsiella pneumoniae* isolates collected from US medical centres in 2016-2018**
H. Sader (North Liberty, United States), C. Carvalhaes, J. Streit, T. Doyle, M. Castanheira*

802 ***In vitro* activity of ceftazidime-avibactam (CAZ-AVI) and comparators against Gram-negative pathogens isolated from patients in Canadian hospitals in 2009-2018: CANWARD surveillance study**
P. Lagacé-Wiens (Winnipeg, Canada), H. Adam, M. Baxter, J. Karlowsky, A. Walkty, G. Zhanel*

1089 ***In vitro* activity of ceftazidime/avibactam against ceftazidime-resistant *Enterobacterales* and *Pseudomonas aeruginosa* from hospitalised patients in Germany: 2016-17**
M. Kresken (Rheinbach, Germany), M. Korte-Berwanger, N. Pfennigwerth, S. Gatermann*

1313 **Aztreonam-avibactam activity against carbapenemase-producing *Enterobacterales* collected in Europe, Asia and Latin America (2017-2019)**
H. Sader (North Liberty, United States), T. Doyle, R. Mendes, V. Kantro, M. Castanheira*

1316 **Antimicrobial activity of aztreonam-avibactam and comparator agents when tested against a large collection of contemporary *Stenotrophomonas maltophilia* isolates collected from medical centres worldwide**
H. Sader (North Liberty, United States), C. Carvalhaes, S. Arends, L. Duncan, R. Flamm, M. Castanheira*

1603 ***In vitro* activities of ceftazidime-avibactam and comparator agents against *Enterobacterales* and *Pseudomonas aeruginosa* from Turkey collected through the ATLAS global surveillance programme 2013-2018**
S. Pacha, M. Hackel (Schaumburg, United States), G. Stone, D. Sahm*

1620 ***In vitro* activities of ceftazidime-avibactam and comparator agents against *Enterobacterales* and *Pseudomonas aeruginosa* from Israel collected through the ATLAS global surveillance programme 2013-2018**
M. Person, M. Hackel (Schaumburg, United States), G. Stone, D. Sahm*

1627 ***In vitro* activity of aztreonam-avibactam and comparator agents against *Enterobacterales* from Europe collected during the ATLAS global surveillance programme 2015-2018**
K. Kazmierczak (Schaumburg, United States), F. Arhin, D. Sahm*

2037 ***In vitro* activities of ceftazidime-avibactam and comparator agents against *Enterobacterales* from Europe stratified by region, ATLAS global surveillance programme 2018**
M. Estabrook, K. Kazmierczak (Schaumburg, United States), G. Stone, D. Sahm*

2042 ***In vitro* activities of ceftazidime-avibactam and comparator agents against *Pseudomonas aeruginosa* from Europe stratified by region: ATLAS global surveillance programme 2018**
M. Wise, K. Kazmierczak (Schaumburg, United States), G. Stone, D. Sahm*

2062 ***In vitro* activity of ceftazidime-avibactam and comparators against isolates of *Enterobacterales* and *Pseudomonas aeruginosa* collected from paediatric patients as part of the ATLAS global surveillance program: 2013-2018**
K. Kazmierczak (Schaumburg, United States), M. Hackel, G. Stone, D. Sahm*

2063 ***In vitro* activities of ceftazidime-avibactam and comparator agents against *Enterobacterales* from Europe stratified by infection type from the ATLAS global surveillance programme 2016-2018**
M. Estabrook, K. Kazmierczak (Schaumburg, United States), G. Stone, D. Sahm*

2071 ***In vitro* activities of ceftazidime-avibactam and comparators against *Pseudomonas aeruginosa* from Europe stratified by infection type: ATLAS global surveillance programme 2016-2018**
M. Wise, K. Kazmierczak (Schaumburg, United States), G. Stone, D. Sahm*

2074 ***In vitro* activities of ceftazidime-avibactam and comparator agents against Gram-negative isolates from China as part of the ATLAS global surveillance programme 2018**
M. Hackel (Schaumburg, United States), G. Stone, D. Sahm*

2123 **Activity of meropenem-vaborbactam and single-agent comparators against *Enterobacterales* isolates, including KPC-producing isolates, from European patients hospitalised with pneumonia (2014-2018)**
D. Shortridge (North Liberty, United States), L. Deshpande, L. Duncan, J. Streit, M. Castanheira*

2308 ***In vitro* activity of ceftazidime-avibactam against *Enterobacterales* and *Pseudomonas aeruginosa* from central Europe and Israel: ATLAS global surveillance programme 2018**
K. Kristóf (Budapest, Hungary), V. Adamkova, A. Adler, E. Gospodarek-Komkowska, A. Rafila, S. Billova, B. Mozejko-Pastewka, F. Kiss*

2334 **Multi-centre evaluation of meropenem/vaborbactam MIC results for *Enterobacterales* and *Pseudomonas aeruginosa* using EUCAST breakpoints on MicroScan dried Gram-negative MIC panels**
A. Harrington, S. Desjarlais, O. Garner, M. Traczewski, D. Beasley, C. Hastey, R. Brookman, Z. Lockett, J. Chau (West Sacramento, United States), B. L. Zimmer*

2360 ***In vitro* activities of aztreonam-avibactam and comparator agents against carbapenemase-producing *Enterobacterales* collected during the ATLAS global surveillance programme 2015-2018**
K. Kazmierczak (Schaumburg, United States), F. Arhin, D. Sahm*

2375 ***In vitro* activity of imipenem/relebactam against Gram-negative organisms collected globally from patients with different infection types: SMART 2018**
S. Lob, K. Kazmierczak (Schaumburg, United States), K. Young, M. Motyl, F. Siddiqui, D. Sahm*

2385 **Unravelling the potential utility of novel β-lactam/β-lactamase inhibitors against *Enterobacter cloacae* complex**
E. Mccreary (Pittsburgh, United States), A. Rubio, A. Iovleva, E. Kline, C. Jones, Y. Doi, R. Shields*

2694 ***In vitro* activity of imipenem/relebactam against *Pseudomonas aeruginosa* isolates collected from patients in Europe: SMART 2018**
N. Kothari, S. Hawser (Monthey, Switzerland), S. Lob, K. Kazmierczak, K. Young, P. Moise, M. Motyl, F. Siddiqui, D. Sahm*

2706 **Activity of imipenem/relebactam against non-*Morganellaceae Enterobacterales* and *Pseudomonas aeruginosa* isolates from 6 countries in western Europe: SMART 2016-2018**
N. Kothari, S. Hawser (Monthey, Switzerland), S. Lob, K. Kazmierczak, M. González-Del Vecchio, K. Young, M. Motyl, F. Siddiqui, D. Sahm*

2728 ***In vitro* activity of imipenem/relebactam against *Klebsiella pneumoniae* and *Pseudomonas aeruginosa* isolates from patients with respiratory tract infections in the Asia/Pacific region: SMART 2015-2018**
S. Lob, K. Kazmierczak (Schaumburg, United States), W. Chen, Y. Khoo, K. Balwani, K. Young, M. Motyl, D. Sahm*

2733 ***In vitro* activity of imipenem/relebactam against Gram-negative organisms collected from patients in Colombia: SMART 2015-2018**
S. Lob, K. Kazmierczak (Schaumburg, United States), J. Pavia, K. Young, M. Motyl, D. Sahm*

2741 ***In vitro* activity of imipenem/relebactam against *Klebsiella pneumoniae* and *Pseudomonas aeruginosa* isolates from Patients in intensive care unit and non-intensive care unit wards in the Philippines: SMART 2016-2018**
S. Lob, K. Kazmierczak (Schaumburg, United States), W. Chen, G. Abello, M. Villanueva, K. Young, M. Motyl, D. Sahm*

2752 **Antimicrobial activity of aztreonam-avibactam and comparator agents tested against contemporary (2019) clinical *Enterobacterales* isolates**
H. Sader (North Liberty, United States), C. Carvalhaes, S. Arends, R. Mendes, M. Castanheira*

3695 ***In vitro* activity of imipenem/relebactam against non-*Morganellaceae Enterobacterales*, *Pseudomonas aeruginosa* and *Acinetobacter baumannii* isolates from patients with respiratory tract infections in the United States: SMART 2016-2018**
K. Kazmierczak (Schaumburg, United States), D. Depestel, K. Young, M. Motyl, D. Sahm*

4145 **Retrospective analysis of the *in vitro* activity of imipenem/relebactam against KPC-encoding *Enterobacterales***
K. Young (Kenilworth, United States), D. Hilbert, M. Motyl, M. Wise, K. Kazmierczak*

5262 **Adapting technology to provide nationwide testing for highly-resistant infections in the United States: aztreonam-avibactam susceptibility testing of metallo-β-lactamase-producing *Enterobacteriaceae***
S. Malik (Atlanta, United States), A. Bhatnagar, M. Karlsson, D. Lonsway, J. Lutgring, J. Huang, S. Gumbis, A. Brown*

5559 **Increasing frequency of OXA-48-producing *Enterobacterales* worldwide and activity of ceftazidime-avibactam, meropenem-vaborbactam and comparators against these isolates**
M. Castanheira (North Liberty, United States), T. Doyle, P. Rhomberg, H. Sader, R. Mendes*

5579 ***In vitro* susceptibility of carbapenem-resistant *Enterobacteriaceae* from the Arabian Peninsula to ceftazidime-avibactam, aztreonam-avibactam and other rescue antibiotics**
T. Pal (Al Ain, United Arab Emirates), A. Sonnevend, A. Ghazawi, D. Darwish, G. Bharathan, R. Hashmey, T. Ashraf*

6807 **Activity of imipenem-relebactam and meropenem-vaborbactam against ceftazidime-avibactam-resistant *Klebsiella pneumoniae* isolates producing KPC carbapenemases**
I. Galani, E. Angelidis, V. Papoutsaki, I. Karaiskos (Athens, Greece), L. Galani, H. Giamarellou, M. Souli, A. Antoniadou*

6945 **German multi-centre study on standardised *in vitro* testing of ceftazidime-avibactam against extensively drug-resistant clinical *Pseudomonas aeruginosa* isolates from 2017-2019**
R. Stauf (Nuremberg, Germany), J. Abel, E. Molitor, G. Hischebeth, A. Halfmann, S. Becker, J. Steinmann*

7898 **Activity of imipenem-relebactam against *Enterobacterales* and *Pseudomonas aeruginosa* isolates collected in Latin America and Brazil from 2017-2018: results from the Study for Monitoring Antimicrobial Resistance Trends (SMART)**
E. Beirao (Sao Paolo, Brazil), F. Tuon, S. Rodrigues, T. Klain De Andrade, F. Serra, M. Della Negra De Paula, T. Bueno Polis, A. Gales*

8142 **Comparative *in vitro* activity of ceftolozane/tazobactam, ceftazidime/avibactam, meropenem/vaborbactam, and imipenem/relebactam against susceptible and resistant *Pseudomonas aeruginosa***
J. Pogue (Ann Arbor, United States), K. Kaye, V. Marshall, A. Smith, C. Young, P. Lephart, J. Mills, O. Albin, T. Patel*

8873 **Activity of imipenem-relebactam against a genetically diverse collection of carbapenemase-producing and non-producing carbapenem-resistant *Enterobacteriaceae***
C. Chen (San Antonio, United States), W. So, S. Dallas, N. Wiederhold, R. Benavides, G. Gawrys, K. Reveles, J. Shurko, G. Lee*

Session accepted as Paper Poster Session

The spread of successful clones and resistance genes

466 **Prevalence of ESBL *Klebsiella pneumoniae* infections in Nigeria: a systematic review**
U. Abubakar (Kuantan, Malaysia)*

836 **Faecal carriage of extended-spectrum beta-lactamase producing *Enterobacteriaceae* at hospital admission in Portugal: a prospective survey**
M. Aires De Sousa (Lisbon, Portugal), E. Lopes, M. Godinho Gonçalves, A. Pereira, A. Costa, H. De Lencastre, L. Poirel*

1562 **Acquired resistome of *Escherichia coli***
M. Petitjean (Bagnolet, France), O. Clermont, B. Condamine, E. Denamur, E. Ruppé*

1674 **Georeferencing patients infected by Gram-negative bacteria producing extended-spectrum beta-lactamase, Pereira city, Colombia, 2012-2017**
J. Hoyos Pulgarin (Medellin, Colombia), D. Arias, A. Alzate, G. Moreno, J. Olaya, I. Cortés, C. Vargas*

2762 **CTX-M type extended-spectrum beta-lactamase in *Serratia marcescens* in Japan**
H. Baba (Sendai, Japan), H. Kanamori, Y. Suzuki, S. Endo, H. Yano, M. Kaku*

3061 **Comparison of *Escherichia coli* multilocus sequence typing from the UK, Saudi Arabia and Kazakhstan indicates that UK sepsis rates are directly related to carriage of pathogenic *E. coli* strains in the community**
A. Almusallam, J. Mathias, M. Toleman (Cardiff, United Kingdom), D. Babenko*

4027 **Significant increase of CTX-M-15-ST131 and emergence of CTX-M-27-ST31 *Escherichia coli* high-risk clones causing healthcare-associated bacteraemia of urinary origin in Spain (ITUBRAS-2 project)**
F. Becerra (Madrid, Spain), D. Gijón, I. Merino Velasco, S. Gómez-Zorrilla, A. Siverio, D. Berbel Palau, C. Sanchez Carrillo, E. Cercenado, A. Rivera, A. De Malet, M. Xercavins, E. Ruiz, L. Canoura-Fernández, J. Martínez Martínez, S. Salvo, J. Del Pozo, M. Cuesta, D. Lopez, J. Diaz-Regañon, R. Canton Moreno, A. Oliver, J. Horcajada, P. Ruiz-Garbajosa*

4137 **CTX-M-15 and CTX-M-14 genes in UK *Escherichia coli* are found as often on the chromosome as they are on plasmids**
A. Almusallam, D. Babenko, J. Mathias, D. Wareham, M. Toleman (Cardiff, United Kingdom)*

4454 **Diversity of beta-lactamase genes carried by multidrug-resistant *Enterobacteriaceae* clinical isolates in Georgia**
N. Latif, T. Aptsiauri, M. Nozadze, N. Butskhrikidze, T. Didbaridze, P. Imnadze, M. Washington, S. Walls, N. Trapaidze (Tbilisi, Georgia)*

4748 **Detection of virulence genes and capsule types in *Klebsiella pneumoniae* isolated from blood cultures in patients with haematological malignancies**
S. Khrulnova (Moscow, Russian Federation), A. Korobova, A. Fedorova Mironova, I. Frolova, G. Klyasova*

4995 **Genomic analysis of the subclades C2/H30Rx and C1-M27 of *Escherichia coli* ST131 high-risk clone across Hungary**
T. Kinga (Budapest, Hungary), A. Toth, L. Jánvári, E. Ungvári, I. Damjanova, D. Szabo*

5084 **Prevalence and molecular epidemiology of high-risk clones among third-generation cephalosporin-resistant and carbapenem-resistant *Klebsiella pneumoniae* in Germany**
K. Xanthopoulou (Cologne, Germany), J. Wille, A. Walker, Y. Stelzer, V. Persy, C. Imirzalioglu, K. Lucassen, H. Seifert, P. Higgins*

5798 **Clonal expansion of extended-spectrum β-lactamase-producing *Escherichia coli* ST131in bloodstream infections of Ecuadorian patients from 2009 to 2018**
J. Zurita (Quito, Ecuador), G. Sevillano, A. Paz Y Mino, N. Haro*

5800 **Clonal diversity of uropathogenic *Escherichia coli* strains from Zimbabwe**
F. Takawira, J. Pitout, T. Mashe, A. Tarupiwa, M. Ehlers, S. Zinyowera, M. Kock (Pretoria, South Africa)*

6371 **Molecular characterisation of *Escherichia coli* isolated from children admitted with bloodstream infection in Dar es Salaam, Tanzania**
S. Moyo, J. Manyahi (Bergen, Norway), A. Hubbard, B. Blomberg, A. Roberts, N. Langeland*

7819 **ESBL- and/or carbapenemase-producing *Klebsiella pneumoniae* with multidrug-resistant phenotypes as a main cause of non-*Escherichia coli Enterobacterales* healthcare-associated bacteraemia of urinary origin episodes in Spain**
F. Becerra (Madrid, Spain), D. Gijón, I. Merino Velasco, S. Gómez-Zorrilla, A. Siverio, D. Berbel Palau, C. Sanchez Carrillo, E. Cercenado, A. Rivera, A. De Malet, M. Xercavins, E. Ruiz, L. Canoura-Fernández, J. Martínez Martínez, S. Salvo, J. Del Pozo, M. Cuesta, D. Lopez, J. Diaz-Regañon, R. Canton Moreno, A. Oliver, J. Horcajada, P. Ruiz-Garbajosa*

8531 **Emergence of plasmid-mediated AmpC genes in *Enterobacter cloacae* complex strains from a sepsis outbreak in a neonatal intensive care unit**
E. Hernandez Alonso (Paris, France), V. Faraut-Derouin, M. Evevrin, M. Villet, M. Bilan, P. Jatteau, D. De Luca, F. Doucet-Populaire, N. Bourgeois-Nicolaos*

Session accepted as Paper Poster Session

Water and surfaces as reservoir for resistance

532 **Are residual waters vehicles of transmission of resistance mechanisms? DARWIN JPI AMR-2016 study**
E. Torres Sangiao (Santiago de Compostela, Spain), A. Dieguez, E. Rabuñal-Rey, S. Balboa, M. Quintela-Bujan, R. De La Cruz Moreno, M. Paul, S. Sørensen, J. Kreft, D. Graham, A. Dechesne, B. Smets, J. Romalde, C. García-Riestra*

3469 **Pathogenic, antimicrobial-resistant *Escherichia coli* in low-income settings household soils: origins and genomic diversity**
M. Montealegre (Dübendorf, Switzerland), A. Talavera Rodríguez, S. Roy, M. Hossain, V. Fernandez Lanza, M. Islam, T. Julian*

3496 **Public health implications of prevalent antibiotic resistance genes and integrons in commensal *Escherichia coli* inhabiting a major Indian river**
S. Nambram (New Delhi, India), J. Virdi, M. Kumar*

3608 **Detection of OXA-244 producing *Escherichia coli* of ST131 from surface water of Pavia urban area, northern Italy**
F. Marchesini (Borgarello, Italy), M. Spalla, A. Mercato, M. Mancinelli, V. Mattioni Marchetti, G. Pilla, R. Sconfietti, R. Migliavacca, E. Nucleo*

4846 **Colistin-resistant Gram-negative bacteria isolated from humid compartments of high risk hospital units**
G. Fleres (Groningen, Netherlands), A. Mirabile, M. Lokate, N. Couto, J. Rossen, A. Friedrich, S. García Cobos*

6465 **Reconstruction of plasmids by shotgun sequencing of various environmental DNA: from hospital biofilms to wastewater treatment plants**
G. Bricheux (Aubiere, France), C. Hilpert, F. Bernard, C. Hennequin, C. Forestier, O. Traore, D. Debroas*

7504 **Common and distinctive genomic features of clinical and environmental third-generation cephalosporin-resistant *Klebsiella pneumoniae***
J. Rocha (Porto, Portugal), C. Ferreira, D. Mil-Homens, M. Brito, C. Lameiras, A. Fialho, I. Henriques, M. Gomila, C. Manaia*

8317 **Detection of *bla*KPC-2 in a conjugative IncP-6 plasmid in *Escherichia coli* isolated from wastewater in Romania**
L. Popa, A. Negu?, I. Czobor (Bucharest, Romania), I. Gheorghe, S. Mohsin, M. Mitache, M. Popa, L. Marutescu, M. Chifiriuc*

8574 **Investigating the effect of wastewater treatment systems on antimicrobial resistance and virulence factors**
C. Bertelli (Lausanne, Switzerland), S. Courtois, M. Rosikiewicz, T. Pillonel, S. Berlendis, S. Aeby, B. Galofre, G. Medema, J. Loret, G. Greub*

8993 **Carbapenem resistance mechanisms uncovered by nanopore sequencing in wastewater canalisations from Ghana**
J. Delgado Blas (Madrid, Spain), E. Marin Rodriguez, C. Valenzuela, C. Serna Bernaldo, N. Montero, C. Saba, B. Gonzalez-Zorn*

9034 **Association of carbapenemase-producers in hospital effluents with carbapenemase-producer's infection incidence and sewages heavy metals concentrations: results from the Canalis project**
L. Romero-Oraá (Seville, Spain), J. Borrego-Jiménez, F. Galan-Sanchez, R. Tejero-García, M. Rojo Martin, M. Rodríguez-Mateos, A. Pérez-Pérez, V. Merino Bohórquez, L. Lopez-Cerero*

9330 **Clinical class 1 integron patterns and relative antibiotic resistance gene carriage in urban compartments**
M. Quintela-Bujan (Newcastle Upon Tyne, United Kingdom), M. Abouelnaga, J. Romalde, M. Gomez Lopez, B. Allen, D. Frigon, D. Graham*

9452 **KPC-producing and colistin-resistant *Klebsiella pneumoniae* ST258 persistence during wastewater treatment plant processes**
I. Czobor (Bucharest, Romania), I. Gheorghe, L. Popa, M. Surleac, S. Paraschiv, D. Otelea, L. Marutescu, M. Popa, S. Mohsin, M. Chifiriuc*

Session accepted as Mini-oral ePoster Session

We are not alone: One Health in AMR

690 **Dissemination of a *bla*NDM-1-carrying IncA/C2 plasmid in a broiler flock: a possible real-life scenario**
S. Hadziabdic (Berlin, Germany), J. Fischer, B. Malorny, I. Szabo*

1541 **One Health surveillance of extended-spectrum beta-lactamase-producing *Enterobacteriales* in urban and rural Malawi**
D. Cocker (London, United Kingdom), A. Singer, T. Morse, C. Jewell, A. Roberts, N. Feasey*

3202 **Bacteriophage-controlling dominant sequence types of carbapenem-resistant *Escherichia coli* in Bangladesh**
J. Mathias (Cardiff, Wales, United Kingdom), D. Babenko, A. Almusallam, R. Farzana, M. Toleman*

3623 **Seawater: a risk for transmission of antimicrobial resistance?**
K. Fitzhenry, B. Hooban, A. Joyce, N. Cahill, B. Wong Ngie Xiong, B. Mahon, L. O'Connor, M. Cormican, P. Hickey, S. Keane, D. Morris (Galway, Ireland)*

4227 **Colistin-resistant *Enterobacteriaceae* in Belgian broiler and pig farms**
S. De Koster (Antwerp, Belgium), M. Ringenier, C. Lammens, M. Kluytmans - Van Den Bergh, J. Kluytmans, J. Dewulf, H. Goossens*

4318 **Quantification and characterisation of antibiotic resistance in greywater discharged to the environment**
S. Porob, H. Craddock (Beer Sheva, Israel), Y. Motro, O. Sagi, M. Gdalevich, N. Davidovitch, Z. Ronen, J. Moran-Gilad*

4319 **Tracing of ESBL-producing and ciprofloxacin-resistant *Escherichia coli* in Belgian broiler and pig farms: a longitudinal study**
S. De Koster (Antwerp, Belgium), M. Ringenier, C. Lammens, D. De Coninck, M. Kluytmans - Van Den Bergh, J. Kluytmans, J. Dewulf, H. Goossens*

5271 **A One Health approach identifies the environment surrounding food animals as a potential reservoir of *bla*CTX-M genes in the community in Vietnam**
M. Nguyen Ngoc (Antwerp, Belgium), H. Thi Thu Hoang, B. Xavier, C. Lammens, T. Hoang, H. Le Thanh, N. Thi Pham, A. Dang Duc, H. Goossens, S. Malhotra-Kumar*

8162 **Persistence of antimicrobial resistance genes in treated sewage water intended for reuse**
M. Dropa (São Paulo, Brazil), J. Da Silva, T. Knöbl, M. Vieira Cunha, R. Araujo, C. Brandão, M. Razzolini, M. Sato*

Session accepted as Mini-oral Flash Session

XDR Gram-negatives on the run

1291 ***Acinetobacter baumannii* complex, the beast of the weakest**
O. Perovic (Johannesburg, South Africa), W. Strasheim, M. Lowe, R. Mokokotleng, M. Smith, A. Singh-Moodley*

2020 ***In vitro* dynamics and mechanisms of resistance development to imipenem and imipenem/relebactam in *Pseudomonas aeruginosa***
M. Gomis Font (Palma de Mallorca, Spain), G. Cabot, I. Sánchez-Diener, L. Zamorano, A. Oliver*

4551 **Ongoing dissemination of OXA-244 carbapenemase-producing *Escherichia coli* in Switzerland**
P. Nordmann (Fribourg, Switzerland), A. Masseron, J. Kessler, A. Demord, L. Poirel*

5299 **Molecular diversity of carbapenem-resistant *Enterobacteriaceae* (CRE) in Singapore**
J. Teo (Singapore, Singapore), C. Tang, S. Ong, S. Lee, J. Ho, S. Tan, Y. Cai, T. Lim, T. Tan, J. Sim, R. Ong, A. Kwa*

6126 **Collateral treatment effects in *Pseudomonas aeruginosa* on antibiotic susceptibility and virulence mechanisms**
T. Van Der Schalk (Antwerp, Belgium), B. Xavier, C. Lammens, S. Kumar-Singh, H. Goossens, S. Malhotra-Kumar*

6391 **Unexpected genetic diversity among KPC-producing *Klebsiella pneumoniae* in France**
R. Bonnin (Le Kremlin-Bicêtre, France), A. Jousset, A. Chiarelli, E. Cécile, P. Glaser, T. Naas, L. Dortet*

6966 **Genomic surveillance of carbapenemase-producing *Enterobacterales* over 5 years reveals transmission clusters of clones and plasmids and extensive diversity of bacterial species encoding carbapenemases**
C. Ludden (London, United Kingdom), E. Mcgrath, N. Delappe, W. Brennan, B. Blane, J. Parkhill, M. Cormican, S. Peacock*

7832 **Complex sharing of *Klebsiella pneumoniae* carbapenemase (KPC) plasmids in patients harbouring multiple KPC-positive organisms**
A. Mathers (Charlottesville, United States), H. Parikh, D. Eyre, K. Barry, N. Stoesser, A. Sheppard, D. Crook, A. Walker*

8065 **Evolutionary dynamics of carbapenem resistance genes among different international clones of *Acinetobacter baumannii*: resistance and dissemination implications**
S. Vijayakumar (Tamil Nadu, India), J. Jacob, K. Vasudevan, V. Balaji*

8137 **Colistin heteroresistance in carbapenemase-producing *Acinetobacter baumannii***
D. Machado (Lisbon, Portugal), S. Gothe, M. Martins, T. Pacheco, J. Batista, C. Toscano, M. Viveiros*

Abstract Programme

4. Diagnostic bacteriology & general microbiology

- Diagnostic bacteriology – culture based and general microbiology
- Lab management, automation and QC
- MALTI-TOF and other proteomic methods
- Molecular diagnostics (incl POCT and syndromic testing)
- Molecular and genomic typing and surveillance
- Whole genome sequencing (diagnostic)
- Microbiome studies (incl One Health aspects)
- Clinical metagenomics
- Bioinformatics tools & pipelines
- Other

Session accepted as Paper Poster Session

Bioinformatics for WGS: what's in the pipeline

1495 **Swiss Pathogen Surveillance Platform: development of a surveillance database for molecular epidemiology of multidrug-resistant pathogens**
A. Lebrand, C. Bertelli, D. Blanc, J. Dauvillier, A. Gleizes, G. Greub, V. Hinard, E. Hodcroft, V. Lazarevic, S. Moretti, R. Neher, V. Perreten, T. Roloff, J. Schrenzel, H. Seth-Smith, D. Terumalai, A. Egli (Basel, Switzerland)*

1981 **BacterialTyper: a bioinformatics pipeline for the integrative analysis of bacterial whole genome sequencing**
J. Sanchez-Herrero, A. Lacoma (Badalona, Spain), B. Molina-Moya, M. Gimenez, S. Molinos, C. Prat, L. Sumoy*

6882 **Assigning the plasmidome: a novel approach to compare plasmids independent of host and incompatibility type**
N. Strepis (Rotterdam, Netherlands), J. Severin, C. Klaassen*

7740 **Arakki: a workflow-based system for virus identification in the clinic**
M. Abouelhoda (Riyadh, Saudi Arabia), M. Selvaraju, M. Shokrof, Z. Shah, Y. Alnakhli, T. Alamoudi, H. Aljafar*

7811 **LUISA: Low Cost Unit for Sequencing Applications**
L. Cerdeira (Sao Paulo, Brazil), R. Wick, L. Judd, M. Lam, K. Wyres, K. Holt*

8422 **Enabling phyletic-based comparison and visualization of genomic islands for tens to hundreds of microbial genomes**
C. Bertelli (Lausanne, Switzerland), K. Gray, A. Lim, N. Woods, G. Winsor, A. Spencer, J. Peltier, F. Brinkman*

8664 **IntFinder: a freely-available user-friendly web tool for detection of class 1 integrons in next-generation sequencing data using k-mer alignment**
K. Loaiza Conza (Hellerup, Denmark), D. Ortega-Paredes, M. Kristofer Johansson, A. Ferrer Florensa, O. Lund, V. Bortolaia*

8989 **Virulence factor prediction: comparison of databases and their use for *Staphylococcus aureus* genomes analysis**
T. Pillonel (Lausanne, Switzerland), C. Bertelli, F. Tagini, J. Schrenzel, G. Greub*

9081 **Implementing a scalable bioinformatics infrastructure to enable national clinical pathogen genomics services**
M. Bull, A. Gaskin (Cardiff, United Kingdom), J. Southgate, A. Price, T. Connor*

9208 **Improved taxon identification from similarity searches using Taxonomic Vote**
N. Garcia-Gonzalez (Paterna, Spain), F. Gonzalez-Candelas*

Session accepted as Paper Poster Session

Bloodstream infections: fast diagnosis using molecular tools

105 **Comparison of molecular rapid diagnostic testing panels for Gram-negative bacteraemia using Desirability Of Outcome Ranking Management of Antimicrobial Therapy (DOOR-MAT)**
K. Claeys (Baltimore, United States), R. Smith, S. Leekha, J. Johnson*

467 **Investigation of positive blood culture bottles with the hemoFISH test: a beacon-based fluorescence *in situ* hybridisation technique**
D. Dündar, D. Er (Kocaeli, Turkey), B. Mutlu*

961 **Multi-centre evaluation of the BIOFIRE FILMARRAY BCID 2 Panel for the detection of microorganisms and resistance markers in positive blood cultures**
K. Holmberg (Salt Lake City, United States), Y. Lu, S. Vourli, S. Pournaras, K. Everhart, A. Leber, R. Barr, J. Daly, T. Henry, A. Johnson, J. Balada-Llasat, D. Rhoads, M. Jacobs, K. Mckinley, A. Harrington, F. Zhang, G. Berry, M. Jeong, R. She, M. Fantini, G. Dirani, S. Zannoli, V. Sambri, U. Spaulding, K. Bourzac*

1018 **Analytical performance evaluation of the BIOFIRE Blood Culture Identification 2 (BCID2) panel**
B. Flaherty (Salt Lake city, United States), M. Buccambuso, N. Francis, J. Manwaring, J. Southwick, J. Larsen, J. Arce, K. Mylroie, E. Ong, K. Ekins, J. Gann, T. Dawson, H. Burton, C. Russell, J. Brooksby, S. Hansen, C. Dubost, C. Cantrell, E. Amiott*

2386 **T2Bacteria panel in diagnostics of sepsis: the first experience at the University Hospital Centre Zagreb**
I. Marekovic (Zagreb, Croatia), Z. Bosnjak, S. Pleško, V. Tripkovic*

2708 **Detection of *Enterobacterales* and associated antimicrobial resistance genes with the BIOFIRE FILMARAY Blood Culture Identification 2 (BCID2) panel**
J. Antosch (Salt Lake City, United States), D. Judd, J. Stone, K. Koch, T. Robinson, I. Kavetska, B. Flaherty, M. Buccambuso, K. Holmberg, Y. Lu, M. Rogatcheva, U. Spaulding*

2720 **Resolution of discrepant results observed during the clinical evaluation of investigational use only prototype of the BIOFIRE FILMARRAY Blood Culture Identification 2 (BCID2) panel**
K. Koch, I. Kavetska, T. Robinson, J. Antosch, J. Stone, K. Holmberg, Y. Lu, J. Peterson, Z. Lu, M. Rogatcheva, U. Spaulding (Salt Lake City, United States)*

2960 **The comparison of the rapid blood identification results within/after 8 hours from positive signal of blood culture bottle**
H. Kim (Daejeon, South Korea), K. Choi, M. Koo, J. Kim, S. Koo*

3642 **Optimisation of duplex next-generation digital PCR assays for molecular diagnosis of infection**
I. Merino Velasco (Salamanca, Spain), A. Ortega, M. Dominguez-Gil, J. Eiros, J. Bermejo-Martin, A. Tedim*

5044 **Evaluation of the Sepsis Flow Chip kit for the molecular diagnosis of bloodstream infections**
S. Zannoli (Pievesestina di Cesena, Italy), G. Masciarelli, M. Pedna, V. Sambri*

5640 **Comparison of three rapid diagnostic blood culture identification panels for Gram-negative bloodstream infections**
R. Smith, S. Hitchcock, J. Johnson (Baltimore, United States), K. Claeys*

5852 **Evaluation of an investigation-use-only prototype of the BIOFIRE FILMARRAY Blood Culture Identification 2 (BCID2) panel for detection of bacteria, yeast, and antimicrobial resistance markers from positive blood cultures**
A. Vasilakopoulou, A. Tarpatzi, S. Vourli, P. Tsilikis, Y. Lu, K. Holmberg, U. Spaulding, K. Koch, A. Alvanidi, N. Koumasi, S. Pournaras (Athens, Greece)*

6019 **The effectiveness of two rapid identification technologies in Gram-negative bacteraemia without antimicrobial stewardship interventions**
L. Nguyen (Loma Linda, United States), D. Chong, J. Vo, J. Lee, T. Ho*

6694 **Prospective, non-interventional, multi-centre clinical study of the T2Resistance system for detection resistance genes in bacterial bloodstream infections: an interim analysis**
T. Walsh (New York, United States), A. Mencacci, R. Paggi, E. Douka, C. Vrettou, O. Guzman, R. Smith, T. Lowery*

7011 **Evaluation of T2MR in a Greek university intensive care unit**
E. Douka (Athens, Greece), I. Papachatzakis, C. Vrettou, E. Mizi, E. Perivoliotis, S. Zakynthinos*

7031 **Impact of the FilmArray Blood Culture Identification Panel (BCID) compared to VITEK-MS and the VITEK-2 ID/AST instrument in the diagnosis and management of bloodstream infections in a 24-hour laboratory setting**
R. Davidson (Halifax, Canada), D. Haldane, J. Leblanc, I. Davis, Z. Hussain, G. Patriquin, H. Alsidairi, T. Hatchette*

7403 **The use and impact of a rapid molecular assay in the diagnosis and management of bloodstream infections in Botswana: a prospective clinical trial**
J. Pernica (Hamilton, Canada), T. Arscott-Mills, K. Lechiile, M. Bapabi, M. Mokomane, M. Vandendorpe, B. Moorad, T. Rantleru, A. Gezmu, T. Machiya, C. Sayikanmi, B. Barker, C. Yansouni, A. Mace, S. Dittrich, D. Goldfarb*

9525 **Early diagnosis in sepsis: T2 bacteria magnetic resonance assay versus blood culture**
P. Elizabet, J. Esteban Moreno, R. Fernández Roblas, I. Gadea Gironés, M. Alicia, N. Carrasco Antón (Madrid, Spain)*

Session accepted as Paper Poster Session

Clinical challenges and culture-based diagnostics

1518 **Clinical and microbiological characteristics in men with non-obstructive acute pyelonephritis**
J. Lee (Goyang, South Korea), M. Park, S. Kwon, H. Choi, K. Kim, S. Bae, S. Cho*

1544 **Clinical factors associated with empirical antibiotics resistance in febrile patients with urinary tract calculus**
J. Lee, M. Park, S. Kwon, H. Choi, K. Kim (Incheon, South Korea), S. Bae, G. Song*

1653 **High diagnostic yield of splenic core biopsy in patients with pyrexia or inflammation of unknown origin: a descriptive analysis of imaging (including FDG-PET) and pathological findings at a major tertiary centre**
Y. Yim (London, United Kingdom), G. Wallis, J. Saeed, S. Voo, I. Proctor, C. Mcnamara, M. Brown*

1842 **A selective culture medium for screening ceftazidime/avibactam resistant Gram-negative isolates**
P. Nordmann (Fribourg, Switzerland), M. Sadek, C. Tinguely, L. Poirel*

2044 **Are *Pseudomonas aeruginosa* biofilms a major issue in non-cystic fibrosis bronchiectasis?**
L. Fernandez Barat (Madrid, Spain), R. López, N. Vázquez Burgos, V. Alcaraz, G. Scioscia, P. Oscanoa, L. Bueno, A. Motos, R. Amaro, L. Lingren, D. Martinez, R. Cabrera, L. Muñoz, J. Vila Estape, N. Hoiby, A. Torres*

3136 **Contaminating microflora at a tuberculosis test: dependence on medium for primary inoculation**
A. Lyamin (Samara, Russian Federation), D. Ismatullin, A. Zhestkov, A. Kovalyov, T. Persiyantseva, A. Kozlov, O. Kondratenko*

3551 **Validation of Colorex (CHROMagar) Serratia agar on WASP/WASPLab in screening for Serratia marcescens in neonatal intensive care units using the ESwab**
M. Gaskin (Hamilton, Canada), J. Korver, D. Yamamura*

4099 **The type of agar may affect the string test result and virulence gene detection of hyper-mucoviscous *Klebsiella pneumoniae***
K. Furusawa (Tokyo, Japan), K. Fujita, M. Gorai-Nishimura, W. Aoki, Y. Mano, T. Suzuki, Y. Akatsu, Y. Saito, M. Seike, A. Gemma, N. Furuya*

5277 **Performance of the NTM Elite agar for the detection of non-tuberculous mycobacteria in sputum samples of patients with cystic fibrosis**
E. Andre (Leuven, Belgium), L. Raymaekers, S. Deiwick, J. Gafsi, P. Van Bleyenbergh, L. Dupont, B. Kahl, N. Lorent*

5940 **Bacteriological study of kidney stones**
H. Bento Da Cruz (Porto, Portugal), C. Santos, H. Ramos*

6764 **A proof-of-concept evaluation of biphasic blood culture bottles for low-resource settings**
S. Ombelet (Antwerp, Belgium), A. Natale, J. Ronat, T. Naas, J. Jacobs*

7586 **Efficient inactivation of clinically relevant antimicrobial drug concentrations by two resin-containing media in simulated paediatric blood cultures**
F. Liotti (Rome, Italy), G. Menchinelli, L. Giordano, G. De Angelis, T. Spanu, M. Sanguinetti, B. Posteraro*

7686 **Fever of unknown origin: a prospective observational study from a tetriary university hospital**
S. Vlachos, D. Bassoulis (Athens, Greece), M. Samarkos, G. Patavoukas, C. Siafarikas, F. Ntziora, E. Apostolidi, N. Sypsas, G. Daikos, M. Psichogiou*

8577 **Chorioamnionitis: time for changes in management?**
B. Crespo Estrada (Santa Cruz De Tenerife, Spain), I. Gutíerrez González, C. Alegría, N. Hernando, B. Reyes*

9221 **An audit of cadaveric liver and kidney organ transport fluid microbiology cultures in a tertiary referral centre**
R. Patel (Birmingham, United Kingdom), M. David*

9445 **Culture-dependent analysis of the bacterial profile of breast milk samples from women with diagnosis of subacute lactational mastitis**
M. Lung, A. García Señán (Barcelona, Spain), Y. Roca, M. López, E. López Gimeno, M. Viñado*

Session accepted as Paper Poster Session

Current challenges in laboratory automation

1995 **Evaluation of a fully automated prototype version of the BD Kiestra ID/AST system**
J. Snyder, G. Thomson, K. Jamros, S. Heckman, S. Abdelghani, K. Thomson (Louisville, United States)*

2463 **Performance evaluation of the BD Kiestra ID/AST prototype for automatic colony picking, Bruker MALDI Biotyper target plate spotting and Phoenix AST panel preparation and loading**
G. Sarton-Lohéac, A. Coste, G. Prod'Hom, C. Bertelli, A. Croxatto (Lausanne, Switzerland)*

2581 **Evaluation of Colibrí for antimicrobial susceptibility testing**
J. Bayette (Montpellier, France), A. Roché, T. Bayol, R. Fournier, G. Teissier*

2594 **Evaluation of Colibrí for the identification of Gram-negative bacilli**
A. Roché, G. Teissier, R. Fournier, P. Mion, J. Bayette (Montpellier, France)*

2600 **PhenoMATRIX TAG and Colibrí for a faster workflow of the management of urine specimens**
A. Roché, G. Teissier, R. Fournier, T. Bayol, P. Mion, J. Bayette (Montpellier, France)*

3097 **Laboratory productivity index and efficiency gains at 3 benchmark BD Kiestra TLA sites**
K. Renić, K. Lehmann (Ontario, Canada)*

3106 **Artificial intelligence and automation of microbiology: the urinalysis 3.0**
A. Michel, C. Eymard, K. Santos, L. Chanel, A. Luzzati, P. Roy-Azcorra, J. Sauzon, M. Guillaumont, G. Pipaud, P. Girardo, F. Christine, G. Lina, F. Laurent, F. Vandenesch, C. Roure-Sobas, O. Dauwalder (Lyon, France)*

3672 **Impact of BD urine culture application on clinical microbiology laboratory activity**
F. D'alò, A. Cesarini, R. Paggi (Perugia, Italy), D. Pietrella, A. Repetto, E. Cenci, A. Mencacci*

3991 **Flexible implementation of microbiology laboratory automation using BD's solution of standalone instruments**
S. Raghunandan, S. Reinholt, B. Pfrommer, A. Cardenas (Sparks, United States)*

4039 **Evaluation of the implementation of diagnostic automation into the bacteriology laboratory as part of pathology modernisation**
G. Mohammad (London, United Kingdom), J. Turner*

4063 **Evaluating emerging technologies in microbiology: what if your gold-standard isn't gold?**
L. Brenton (Fitzroy, Australia), M. Waters, T. Stanford*

5442 **Improvement of blood cultures processing with full automation in microbiology**
B. Osnaghi, L. Vismara, P. Mirri, M. De Paschale, A. Gatti, S. Cavallari, P. Melloni, E. Vasconi, L. Rodolfi, M. Cassani, A. Bortignon, M. Barzani, M. Cozzi, V. Accardo, C. Zago (Legnano, Italy), P. Clerici*

7311 **Measuring the impact on turnaround time by implementation of a new fully-automated random, continuous-access molecular platform in a large microbiology department**
L. Martínez García (Madrid, Spain), M. Rodriguez, C. Rodríguez, B. Romero, R. Canton Moreno, J. Galán*

7853 **Impact of total laboratory automation systems on efficiency, cost and clinical outcomes: a systematic review**
M. Wimmer, D. Makhija, K. Guo (Sparks, United States), D. Gary*

Session accepted as Paper Poster Session

Diagnosing bloodstream infection

481 **Reducing paediatric blood culture contamination rates: a benefit to arterial catheter-drawn cultures**
M. Meir (Haifa, Israel), O. Naserldeen, H. Dabaja-Younis, Y. Geffen, I. Kassis*

2092 **Blood culture contamination is commonly associated with divergent blood culture sets**
E. Ben-Chetrit (Jerusalem, Israel), P. Levin*

2280 **Laboratory stewardship initiative on repeat blood culture collection practices led to reduction of collection rates but electronic best practice alerts are needed to sustain reduction rates**
J. Gastaldo, P. Ozbolt, K. Krupinski-Shaw, K. Kerr, S. Hohman, S. Antonara (Columbus, United States)*

2590 **Impact of a training activity on collecting blood samples regarding a correct bloodstream infections diagnosis: The risks of overseeing the foundations**
S. Velasco De La Fuente (Canalejas De Peñafiel, Spain), A. Rodriguez Fernandez, V. Arranz García, S. Alonso Madrazo, A. De Malet, J. Calvo-Montes*

5989 **Rapid identification of positive blood culture, short-incubation subcultures by MALDI-TOF MS comparing pre-conditioned and non-conditioned culture media adapted to laboratory automation**
C. Reimers, E. Grabsch, K. Lui, A. Batey, K. Chua (Heidelberg, Australia), M. Leroi*

6053 **Simplification of direct MALDI-TOF MS identification from positive blood culture broth**
J. Brotto, E. Grabsch, K. Chua (Heidelberg, Australia), M. Leroi*

6191 **Direct MALDI-TOF MS identification from positive blood cultures: rapid sepsityper**
M. Cordovana (Bologna, Italy), S. Ambretti*

6468 **Bacterial contamination of umbilical cord blood collected at Ankara University cord blood bank**
P. Yurdakul-Mesutoglu (Ankara, Turkey), E. Gencer-Oncul, H. Yalim Akin, M. Beksac*

6499 **Polymicrobial species identification from positive blood cultures with high-resolution Orbitrap mass spectrometry**
H. Peltoniemi, M. Damsbo, I. Ritamo, M. Viirtola (Vantaa, Finland), A. Rantakari*

6536 **Evaluation of a sub-culturing solution directly from manual blood cultures in low-resource settings**
A. Natale (Paris, France), S. Oueslati, S. Ombelet, J. Ronat, O. Vandenberg, T. Naas, J. Jacobs*

6580 **Identification of microorganisms in polymicrobial blood culture bottles using short-term culture MALDI-TOF MS**
A. Wong (Stockholm, Sweden), M. Ullberg, V. Özenci*

6614 **Reference evaluation of two manual blood culture bottles for low-resource settings**
S. Ombelet (Antwerp, Belgium), A. Natale, J. Ronat, T. Naas, O. Vandenberg, J. Jacobs*

6645 **The impact of delayed analysis of positive blood cultures on the performance of short-term culture followed by MALDI-TOF MS**
A. Johnsson, A. Wong (Stockholm, Sweden), V. Özenci*

6701 **The clinical impact of extended blood culture incubation time**
R. Willemze, A. Kwakernaak, T. Koster, V. Hira (Gouda, Netherlands)*

6702 **Reference-setting evaluation of MicroScan panels for identification of bloodstream pathogens in low-resource settings**
S. Ombelet (Antwerp, Belgium), A. Natale, J. Ronat, T. Naas, J. Jacobs*

7649 **Evaluation of the BACT/ALERT VIRTUO in terms of time to detection, performance, workflow efficiency and impact on patient management, compared to the BACTEC FX automated blood culture system**
A. Halperin (Madrid, Spain), J. Cortes Cuevas, M. Cuesta, S. Talens, R. Birch, A. Sanchez Diaz, R. Canton Moreno*

8539 **How does blood volume cultured in Europe comply with guidelines? Results of a 125-centre ESGBIES/CTCB survey**
B. Lamy (Nice, France), A. Morisot, E. Sanchez, L. Bailly, R. Ruimy, C. Pradier, S. Albarède, J. Galinier*

8769 **The impact of rapid identification of blood culture pathogens by MALDI-TOF MS and their direct antibiotic susceptibilities on antimicrobial stewardship at a large district general hospital, United Kingdom**
N. Malik (Watford, United Kingdom), H. Kandil*

9329 **Accuracy of sepsityper methodology for identifying microorganisms directly from positive blood culture bottles using MALDI-TOF MS**
R. Gorton (London, United Kingdom), R. White, C. Baker, R. Smith*

9342 **Sepsis diagnosis: have we solved the riddle yet?**
A. Rohit (Chennai, India), A. Dangari, M. Prasad, A. Jenifer, S. Dorairajan, C. Boahen, V. Kumar*

Session accepted as Mini-oral ePoster Session

Diagnostic stewardship in real life

572 **Time to positivity of blood cultures and its role in the diagnosis of bacteraemia**
A. Aguirre Quinonero (Vitoria, Spain), M. Marroyo-Salazar, E. Saez De Adana Arroniz, A. Canut*

5464 **Impact of artificial intelligence on time to result in culture-based MRSA screening**
A. Nowag, N. Jazmati, S. Giglio, S. Wirth, B. Pohl, X. Quante, H. Wisplinghoff (Cologne, Germany)*

6090 **Benchmarking blood culture turnaround times in an automated laboratory, at a tertiary teaching hospital**
M. Sullivan, E. Grabsch, K. Chua (Heidelberg, Australia), M. Leroi*

6313 **A prolonged incubation time is not needed for cultures obtained from acute periprosthetic joint infections**
D. Talsma (Groningen, Netherlands), J. Ploegmakers, P. Jutte, G. Kampinga, M. Wouthuyzen-Bakker*

7756 **What clinicians and researchers should know about machine learning for infection management: review of methods, targeted outcomes and reporting of future technologies**
C. Luz (Groningen, Netherlands), M. Vollmer, J. Decruyenaer, M. Nijsten, C. Glasner, B. Sinha*

7801 **Impact of unique blood culture sampling in the emergency departments of Strasbourg University Hospital, France**
P. Boyer (Strasbourg, France), A. Chabaud, P. Bilbault, D. Menahem, E. Fonti, V. De Peyrecave, T. Lavigne, B. Jaulhac*

8976 **Dipstick urinalysis: an alternative screening test for urine cultures to rule out negatives?**
F. Doganci, M. Karaoglan, B. Erdir, S. Aslan, O. Ozel, A. Ilki (Istanbul, Turkey)*

9276 **Turn around time and performances of blood cultures with regard to hospital organisation**
G. Pean De Ponfilly (Paris, France), H. Benmansour, E. Lecorche, F. Mougari, A. Munier, S. Temim, H. Jacquier, E. Cambau*

Session accepted as Paper Poster Session

Gastrointestinal infections and molecular diagnosis

866 **Application of a multiplex polymerase chain reaction test for diagnosing bacterial enteritis in children in a real-life clinical setting**
E. Lee (Seoul, South Korea), H. Lee, S. Han*

947 **Should a molecular bacterial syndromic approach totally replace culture for the diagnosis of gastrointestinal tract infections ?**
A. Boudet (Nîmes, France), R. Stephan, A. Pantel, M. Carles, C. Enault, S. Charachon, J. Lavigne, H. Marchandin*

1519 **Evaluation of the Qiastat-Dx Gastro-intestinal Panel at the University Hospital of Liege (Belgium)**
J. Schmitt, C. Diop (Liege, Belgium), L. Schoneveld, C. Meex, P. Melin, M. Hayette*

1583 **Evaluation of the filmarray GI panel in the microbiological diagnosis and management of the patient with infectious gastroenteritis**
J. Parra Martinez, R. Carranza González (Albacete, Spain), M. Castano Aroca, V. Solves Ferriz, F. Ferrer Amate, C. Sáinz De Baranda Camino*

1801 **Impact of ribotype on *Clostridioides difficile* diagnostics**
K. Rizzardi (Solna, Sweden), T. Åkerlund, T. Norén, A. Matussek*

2685 **Evaluation of the Novodiag Bacterial GE+ kit for the diagnosis of intestinal bacterial infections**
C. Roy, D. Robert, D. Boraud, A. Buissonniere, L. Benejat, A. Ducournau, F. Megraud, E. Bessède, P. Lehours (Bordeaux, France)*

2736 **Diagnostic utility of stool polymerase chain reaction in enteric fever: experience from a high-incidence London hospital**
D. Hsu (London, United Kingdom), S. Tiberi, R. Buchanan, C. Rosmarin*

3084 **Development of a biosensor for the detection of *Campylobacter jejuni***
S. Shams (Qom, Iran), B. Bakhshi, T. Tohidi Moghadam*

4406 **Improved diagnostic of acute gastrointestinal disease by a multiplex real-time PCR semi-automated method for the detection of enteropathogens**
B. Fidalgo (Barcelona, Spain), E. Rubio Garcia, V. Pastor, M. Parera, C. Aylagas, P. Salvador, A. Fernández, M. Fernández, G. Cuesta Chasco, A. Vergara, M. Valls, M. Alvarez Martinez, M. Marcos, C. Ballesté, J. Vila Estape, M. Martinez, C. Casals-Pascual*

6094 **Evaluation of a Point-of-Care molecular system for rapid detection of toxigenic *Clostridioides difficile* in paediatric patients: impact on diagnostic yield and time to result**
J. Saucedo, S. Garcia, M. Fernandez De Sevilla, S. Simó, E. Altero, M. Monsonis, C. Muñoz-Almagro, P. Brotons De Los Reyes (Esplugues de Llobregat, Spain)*

7755 **Prospective evaluation of three rapid multiplex PCR assays for the detection of gastrointestinal pathogens from stool samples**
K. Villageois-Tran (Clichy, France), N. Argy, L. Noel, C. Pauc, T. Montagne, P. Lehours, L. Benejat, A. Ducournau, A. Le Guern, S. Lefevre, S. Miladinovic, S. Houze, B. Visseaux, L. Armand-Lefevre*

7793 **Evaluation of Novodiag C. difficile and GenePOC CDiff test for quick and accurate detection of *Clostridioides difficile* infection**
A. Petersson (Lund, Sweden), L. Rebihic, S. Karlsson Sobirk*

7991 **Performances of BD MAX Cdiff assay for detection of toxigenic *Clostridioides difficile* in 1321 clinical stool specimens using FecalSwab**
A. Ranc (Lyon, France), O. Dauwalder, S. Celia, A. Tristan, B. Coralie, K. Santos, F. Sonia, P. Duraffourg, F. Vandenesch, F. Laurent*

8443 **Laboratory evaluation of a cartridge-based multiplex PCR assay for the detection of gastrointestinal pathogens**
C. Holmes, P. Bird (Leicester, United Kingdom)*

Session accepted as 2-Hour Oral Session

Genomic epidemiology: from local to global

48 **The phylogenetic landscape and nosocomial spread of the multidrug-resistant opportunist *Stenotrophomonas maltophilia***
M. Groschel (Boston, United States), C. Meehan, I. Barilar, M. Diricks, A. Gonzaga, M. Steglich, O. Conchillo-Sole, I. Scherer, U. Mamat, C. Luz, K. De Bruyne, C. Utpatel, D. Yero, I. Gibert, X. Daura, S. Kampmeier, N. Abdul Rahman, M. Kresken, T. Van Der Werf, I. Alio, W. Streit, K. Zhou, T. Schwartz, J. Rossen, U. Schaible, M. Farhat, U. Nübel, J. Rupp, J. Steinmann, S. Niemann, T. Kohl*

997 **Genomic epidemiology and resistome analysis of *Helicobacter pylori***
T. Domanovich-Asor, Y. Motro, B. Khalfin, H. Craddock (Beer Sheva, Israel), A. Peretz, J. Moran-Gilad*

6585 **The distribution, transmission and adaptation of *Klebsiella* species in multiple clinical and non-clinical settings**
H. Thorpe, J. Corander, T. Kallonen, S. Brisse, V. Passet, J. Lopez Fernandez, C. Parada Rodrigues, L. Matthews, S. Mitchell, R. Reeve, S. David, C. Merla, M. Corbella, C. Ferrari, D. Sassera, E. Feil (Bath, United Kingdom)*

6677 ***Bordetella pertussis* in the Netherlands, 2015-2019: a sharp increase in *prn*-deficient isolates**
R. Mariman (Leiderdorp, Netherlands), C. Schot, J. Groot, F. Reubsaet, R. Noomen, T. Bosch*

7168 **Genomic analysis of Group B streptococci colonising pregnant women in Portugal reveals the emergence of novel genetic lineages resulting from capsular switching**
E. Ferreira Martins, R. Pedrosa, J. Melo-Cristino, M. Ramirez (Lisbon, Portugal)*

7623 **The role of mobile genetic elements and virulence factors in the typing of vancomycin-resistant *Enterococcus faecium* outbreak isolates of a successful MLST ST117 cluster type 24**
P. Lisotto (Groningen, Netherlands), N. Couto, S. Rosema, M. Lokate, X. Zhou, E. Bathoorn, H. Harmsen, A. Friedrich, J. Rossen, M. Chlebowicz*

7865 **Understanding the *Corynebacterium diphtheriae* population through whole genome sequencing**
N. Groves (London, United Kingdom), M. Chand, D. Litt, S. Rose, C. Gower, A. Enefer, G. Amirthalingam, N. Fry*

8122 **Phylogenetic and taxogenomic approaches to elucidate the *Citrobacter* genus**
T. Goncalves Ribeiro (Porto, Portugal), C. Rodrigues, L. Peixe*

8981 **A genomic snapshot of antimicrobial resistance in *Campylobacter fetus***
B. Duim (Utrecht, Netherlands), A. Zomer, T. Looft, A. Timmerman, J. Wagenaar, L. Van Der Graaf-Van Bloois*

Session accepted as 1-Hour Oral Session

Implementing metagenomics in clinical practice

1080 **Metagenomic sequencing of urine to differentiate infected from contaminated samples**
G. Hayward (Oxford, United Kingdom), A. Walker, T. Peto, D. Foster, D. Eyre, T. Street, N. Sanderson, L. Barker, G. Rodger, D. Crook, M. Llewelyn*

3903 **Long-read compared to short-read next-generation sequencing of the 16S-23S rRNA region for the identification of bacterial species in clinical samples: a pilot study**
E. Van Zanten, G. Wisselink, R. Benus, M. Kooistra-Smid (Groningen, Netherlands)*

5057 **Utilising long-read shotgun sequencing to study the lower respiratory tract microbiome from endotracheal aspirate samples**
J. Rodriguez Ruiz (Antwerp, Belgium), M. Nguyen Ngoc, B. Xavier, J. Coppens, C. Lammens, V. Matheeussen, H. Goossens, S. Malhotra-Kumar*

6426 **Same-day diagnosis of severe pneumonia on intensive care using long-read whole gene 16S rRNA gene sequencing on single-sample flowcells**
R. Baldan, P. Cliff, S. Burns, R. Batra, G. Smith, N. Groves, A. Cerda, S. Lewis, J. Edgeworth (London, United Kingdom), M. Chand*

7764 **Metanet: synchronisation and quality assessment of methods for rapid metagenomics-based pathogen detection**
R. Schlaberg, L. Schüle, P. Oberhettinger, S. Bletz, D. Harmsen, J. Rossen (Groningen, Netherlands), A. Mellmann, K. Prior, M. Pedersen, H. Westh, N. Couto, S. Peter, A. Friedrich*

Session accepted as Paper Poster Session

Improvements in diagnosis

1184 **Does C Diff Quik Chek display the same sensitivity than C Diff Quik Chek Complete for GDH detection?**
C. Gateau (Paris, France), R. Syed-Zaidi, A. Youssouf, V. Lalande, J. Couturier, F. Barbut*

1459 **Two novel fastidious anaerobes from the genus *Bacteroides* isolated from chicken gastrointestinal tracts**
S. Králová (Brno, Czech Republic), L. Davidova Gerzova, M. Medvecky, I. Rychlik, M. Cigánek, A. Cizek*

1798 **Serodiagnosis of Lyme borreliosis: is IgM in serum more harmful than helpful?**
H. Hillerdal, A. Henningsson (Jönköping, Sweden)*

1952 **A comparative prospective study for the qualitative detection of *Helicobacter pylori* specific antigens in stool samples at Sheffield Teaching Hospitals Foundation Trust, England**
S. Coleman (Sheffied, United Kingdom), S. Davies, H. Carr*

3099 **Discordant *Clostridioides difficile* diagnostic assay and treatment practice: a retrospective observational study**
L. Lenggenhager (Geneva, Switzerland), M. Zanella, A. Poncet, L. Kaiser, J. Schrenzel*

3939 ***Staphylococcus lugdunensis*: coloniser or pathogen: outlining the clinical importance: a study of 295 clinical samples from hospital patients received for culture at the department of Medical Microbiology, SI Lillehammer, Norway, from November 2016 to November 2019**
S. Hartzen (Lillehammer, Norway), C. Dahlseide, A. Hartzen*

4817 ***Campylobacter* concisus prevalence in microscopic colitis: a cultivation study**
M. Aagaard (Aalborg, Denmark), K. Kirk, H. Nielsen, I. Tarpgaard, J. Hansen, H. Nielsen*

5434 **The importance of CXCL13 cytokine as a biomarker in the molecular diagnosis of Lyme neuroborreliosis versus multiple sclerosis**
T. Carreira (Lisboa, Portugal), F. Geraldo Dias, A. Armada, M. Vieira*

6678 **Early syphilis infection: a clinical case**
M. Bozhilova, D. Velcheva (Sofia, Bulgaria)*

6738 **Diagnosing disseminated histoplasmosis in an AIDS patient: the role of bone marrow evaluation**
N. Mussá (Lisbon, Portugal), D. Carvalho, S. Ismail, J. Melo-Cristino*

6768 **Stool multiplex PCR for Shiga toxin-producing *Escherichia coli* sufficiently equals with culture for clinical diagnosis and follow-up**
A. Jääskeläinen (Helsinki, Finland), S. Salmenlinna, J. Antikainen, A. Pätäri-Sampo*

7368 **Faster and more sensitive diagnostics of *Shigella* by *Shigella* specific PCR and improved culture**
C. Lindsten (Halmstad, Sweden), H. Wirdelius, D. Palmér, F. Mårtensson, A. Ljung, P. Nilsson*

7605 **Group B *Streptococcus* vaginal colonisation from antenatal screening to 2 months after delivery: results from a prospective cohort study in France**
C. Plainvert (Paris, France), O. Anselem, C. Joubrel, V. Marcou, E. Falloukh, A. Frigo, F. El Alaoui, P. Ancel, P. Jarreau, L. Mandelbrot, F. Goffinet, C. Poyart, A. Tazi*

8660 **Antibiotic resistance in anaerobic infections in a hospital in Tenerife**
B. Crespo Estrada (Santa Cruz De Tenerife, Spain), I. Gutíerrez González*

9614 **Prevalence and susceptibility profile of *Corynebacterium glucuronolyticum* in semen cultures**
A. Rodríguez Achaerandio (Vitoria, Spain), E. Insagurbe Saez Camara, A. Palomares Casado, S. Guerra Merino, A. Fernández De Romarategui Gómez, R. Salazar Calleja, A. Canut*

Session accepted as Mini-oral ePoster Session

Innovative approaches for faster ID/AST from positive blood cultures

1678 **Decreasing reporting time of blood cultures by workflow optimisation with the WASPLab system**
S. D'Haese (Leuven, Belgium), K. Claes, M. Van Ranst, K. Lagrou, M. Depypere, K. Jeuris, K. Standaert, A. Verdonck, S. Desmet*

5002 **How to accelerate bacteria identification from positive blood culture in a routine microbiology laboratory with the aid of MALDI-TOF MS: a simple and rapid in-house protocol**
P. Barth (Porto Alegre, Brazil), Â. Celestino De Souza, L. Lutz, E. Wurdig Roesch, V. Aquino, D. Castro Pereira*

5204 **Time-to-result quantification for different blood culturing workflows in an external microbiology laboratory setting**
J. Fonville (Veldhoven, Netherlands), M. Van Den Broek, A. Jansz, T. Liebregts*

6854 **Identification of microorganisms direct from signal positive blood culture using Acrion system**
J. Salo (Vantaa, Finland), S. Gurung, O. Niiranen, N. Chant, M. Wilks*

7161 **Light scatter AST for positive blood cultures, how impactful on antimicrobial therapy management of septic patient?**
A. Curtoni (Torino, Italy), D. Ghibaudo, L. Imperatore, C. Veglio, G. Bianco, S. Corcione, S. Scabini, C. Costa, L. Scaglione, F. De Rosa, R. Cavallo*

7261 **Prospective evaluation of BinaxNOW for rapid identification of *Streptococcus pneumoniae* from positive blood culture bottles**
K. Žnidar (Ljubljana, Slovenia), D. Tratnik, M. Pirs, M. Mueller-Premru*

7357 **Speeding up identification and antimicrobial susceptibility testing of bacteria from positive blood cultures by the use of Alifax HB&L system**
Y. Wang (Beijing, China), Y. Dai, D. Li, H. Sun, Y. Zhao, Y. Xu*

9244 **Easy technique for ultra-fast identification of positive blood cultures with MALDI-TOF MS**
F. Bressant, M. Messy, H. Rodriguez-Villalobos, A. Verroken (Brussels, Belgium)*

9520 **Rapid identification of bacteria directly from positive blood cultures by a modified method using a Serum Separator Tube (SST) and MALDI-TOF MS**
O. Carretero, G. Rivas, C. Loras, M. Orellana Miguel (Madrid, Spain)*

Session accepted as Paper Poster Session

Mass spectrometry for microbial detection, identification and typing

179 **A rapid direct from specimen MALDI-TOF MS diagnostic for bacterial and fungal pathogens**
D. Goodlett (Baltimore, United States), M. Sorensen, F. Gardner, L. Leung, C. Chandler, E. Nilsson, R. Ernst*

929 **Pilot evaluation of machine learning for the classification of *Streptococcus pneumoniae* PCV-13 serotypes from non-PCV13 serotypes based on MALDI-TOF MS analysis**
J. Zintgraff (Caba, Argentina), M. Rocca, D. Napoli, M. Moscoloni, G. Ayala, C. Lara*

1891 **Typing of *emm1* Group A streptococci using MALDI-TOF MS**
M. Sakuma, K. Shima (Kyoto, Japan), S. Funatsu, K. Ogata, M. Morozumi, S. Iwata*

1980 **Rapid identification of uropathogens by combining Alfred 60 system with matrix-assisted laser desorption ionisation-time of flight mass spectrometry technology**
K. Athamna (Hadera, Israel), A. Zbriger, M. Shapira, Y. Tal, S. Freimann*

2459 **Comparison of two commercial platforms for identification of bacteria and *Candida* isolates at species-level by MALDI-TOF MS in Shenzhen, China**
W. Lau (Shenzen, China), J. Chan, S. Lo, L. Yan, Y. Ting, L. Caiyuan, L. Huijuan, K. Yuen*

2746 **A *Peptoniphilus* species nova closest to *P. harei* from human clinical materials but which was misidentified by Bruker Biotyper as *P. indolicus***
K. Bernard, D. Wiebe, A. Veloo (Groningen, Netherlands), A. Ebbinge*

3117 **Identification of clinical isolates of *Tannerella forsythia* by MALDI-TOF mass spectrometry**
T. Teržan (Ljubljana, Slovenia), M. Pirs, M. Furlan, P. Hrvat, V. Cvitković-Špik, T. Cerar Kišek, K. Seme*

3477 **Differentiation of the members of the *Staphylococcus aureus* complex by MALDI-TOF using the VITEK MS platform**
B. Celliere (La Balme les Grottes, France), V. Monnin, M. Bes, F. Laurent, A. Ranc, S. Arend, P. Courault, F. Vandenesch, G. Durand, A. Tristan, V. Girard*

4880 ***Achromobacter* identification using *nrdA* gene phylogeny and MALDI-TOF MS**
M. Rumigny (La Balme les Grottes, France), F. Allard, V. Collin, C. Meunier, D. Giraud, V. Monnin, V. Girard, F. Javerliat*

5534 **Accurate discrimination of *Shewanella* algae from *Shewanella putrefaciens* with Acrion system: an under-reported marine pathogen**
J. D'Addiego (Basingstoke, United Kingdom), J. Räbinä, S. Gurung, J. Knuuttila, J. Chew, M. Hutchins, A. Socas, P. Wacklin, N. Chant*

6537 **Accurate identification species of *Enterobacter cloacae* complex with Acrion system**
J. D'Addiego (Basingstoke, United Kingdom), J. Räbinä, S. Gurung, O. Niiranen, J. Knuuttila, N. Chant, P. Wacklin*

6581 **Evaluation of a new automated Acrion system for rapid identification of microorganisms and detection of antimicrobial resistance markers directly from blood cultures in an Italian hospital**
F. Liotti (Rome, Italy), M. Viirtola, J. Salo, O. Niiranen, M. Sanguinetti, B. Posteraro*

6672 **Rapid MALDI-TOF MS-based pneumococci confirmation by a standardised semi-automated workflow**
M. Peer, I. Nix, E. Idelevich, I. Burckhardt, S. Zimmermann, K. Sparbier, K. Becker, M. Kostrzewa (Bremen, Germany)*

6835 **High accuracy identification of ten common blood culture isolates by Acrion system**
H. Friedrich (Vantaa, Finland), M. Viirtola, H. Amdahl, I. Ritamo, J. Knuuttila, A. Rantakari, P. Wacklin*

6908 **Direct detection and identification of microorganisms from clinical urine specimens by high-resolution mass spectrometry**
M. Viirtola (Vantaa, Finland), A. Rantakari, I. Ritamo, H. Amdahl, J. Knuuttila, H. Peltoniemi, H. Friedrich, K. Haapasalo, S. Jokiranta*

7593 **Typing of *Clostridioides difficile* isolates by MALDI-TOF MS**
A. Calderaro, M. Buttrini (Parma, Italy), S. Montecchini, S. Covan, A. Ruggeri, M. Martinelli, S. Larini, M. Arcangeletti, C. Chezzi, F. De Conto*

8818 **Improved specie identification of *Staphylococcus argenteus* with MALDI-TOF MS using an extended MSP library**
U. Tjörnstrand, H. Seid, A. Petersson, B. Nilson (Lund, Sweden)*

9225 **Comparison of a new MALDI-TOF MS platform, Autof MS1000, with Bruker Biotyper for mucoid bacterial strains identification**
Q. Zhang (Zhengzhou, China), Y. Youhua, Q. Ma, Y. Li*

9638 **Misidentification of *Staphylococcus argenteus* by MALDI-TOF MS**
H. Tsang (Hong Kong, Hong Kong), S. Leung, S. Wong*

Session accepted as Paper Poster Session

Metagenomics goes clinical

1003 **Rapid, sensitive diagnosis of bloodstream infection using clinical metagenomics**
L. Moragues Solanas (Norwich, United Kingdom), A. Rogers, G. Kay, S. La Fauci, W. Mullen, J. O'Grady*

1171 **Rapid identification of pathogens, antibiotic resistance genes and plasmids in blood cultures by nanopore sequencing**
A. Taxt, E. Avershina, S. Frye, U. Naseer, R. Ahmad (Hamar, Norway)*

2477 **Comparative analysis of diagnostic utility of microbial metagenomic next-generation sequencing among different sample types**
Q. Miao (Shanghai, China), B. Hu, J. Pan, W. Jin*

3226 **Clinical impact of metagenomic next-generation sequencing of plasma cell-free DNA for the diagnosis of infectious diseases: a multi-centre retrospective cohort study**
C. Hogan (Palo Alto, Canada), S. Yang, O. Garner, D. Green, C. Gomez, J. Dien Bard, B. Pinsky, N. Banaei*

3698 **Diagnosis of bone and joint infections using nanopore metagenomic sequencing of synovial fluids and tissue samples**
C. Kolenda (Lyon, Finland), T. Street, N. Sanderson, C. Taunt, M. Llewelyn, B. Atkins, D. Crook, D. Eyre*

3948 **Utilisation of next-generation sequencing testing for diagnostic dilemmas: experience at a tertiary care centre**
M. Santarossa (Maywood, United States), R. Ukani, K. Walding, A. Harrington, N. Clark, G. Reid*

4022 **Clinical metagenomic sequencing of positive blood cultures as a tool for rapid microbiological diagnosis**
K. Govender (Oxford, United Kingdom), T. Street, D. Crook, D. Eyre*

4317 **Whole metagenome shotgun-sequencing in a case of hyperammonaemia syndrome following lung transplantation**
C. Michel (Brussels, Belgium), V. Lazarevic, N. Leduc, M. Raimo, C. Knoop, J. Schrenzel, M. Hallin, M. Hites, D. Grimaldi*

5047 **The incremental clinical value of metagenomic next-generation sequencing when applied to microbiological diagnosis of skin and soft tissue infections**
Q. Wang (Shanghai, China), Q. Miao, J. Pan, W. Jin, Y. Ma, Y. Zhang, Y. Su, L. Na, B. Hu*

5494 **Blood virome in febrile Tanzanian children**
S. Cordey (Geneva, Switzerland), F. Laubscher, M. Hartley, T. Junier, K. Keitel, M. Docquier, N. Guex, C. Iseli, G. Vieille, P. Le Mercier, A. Gleizes, J. Samaka, T. Mlaganile, F. Kagoro, J. Masimba, Z. Said, H. Temba, C. Tapparel, M. Zanella, I. Xenarios, J. Fellay, V. D'Acremont, L. Kaiser*

5858 **Clinical impact of metagenomics next-generation sequencing in patients with suspected central nervous system infection: a real-world study**
Q. Zhang (Shanghai, China), J. Ai, W. Zhang*

6332 **Integrated diagnosis by metagenomic and host transcriptomic of pulmonary infection in solid organ transplant patients**
L. Castain (Nantes, France), G. Gricourt, D. Vanessa, A. Rodallec, C. Bressollette-Bodin, B. Imbert-Marcille, C. Rodriguez*

6682 **Pan-pathogen microbiological diagnosis by accredited routine clinical metagenomics: one-year experience**
P. Woerther (Créteil, France), R. Lepeule, D. Vanessa, G. Gricourt, C. Lamoureux, V. Fihman, S. Fourati, F. Botterel, C. Angebault, J. Pawlotsky, C. Rodriguez*

6850 **Rescue diagnosis of a cerebral nocardiosis by accredited clinical metagenomics: a case report**
V. Courbin, Q. Riller, G. Gricourt, D. Vanessa, R. Lepeule, J. Pawlotsky, C. Rodriguez, P. Woerther (Créteil, France)*

7238 **Comparative analysis of kitome identification methods in viral metagenomic data**
A. Bal, J. Becker, G. Oriol, M. Sabatier, G. Destras, P. Sesques, G. Salles, B. Lina, F. Mallet, A. Pachot, F. Reynier, F. Morfin, T. Sophie, V. Cheynet, K. Brengel-Pesce, L. Josset (Lyon, France)*

7886 **Clinical metagenomics next-generation sequencing for diagnosis of suspected clinical infections, a prospective multi-centre cohort study**
J. Ai (Shanghai, China), H. Zhang, Y. Zhang, J. Ma, W. Zhang*

8055 **Next-generation sequencing for kinetics of the respiratory microbiota of intensive care unit intubated patients**
S. Meyer (Limoges, France), T. Daix, B. Francois, D. Chainier, A. Gay, M. Ploy, P. Vignon, O. Barraud*

8070 **The rapid clinical diagnosis of lower respiratory infection by an unbiased real-time metagenomics methods in validated intensive care unit patients**
H. Zhang (Shanghai, China), J. Ai, Q. Zhang, W. Zhang*

8863 **Rapid, non-invasive detection of *Legionella* and resolution of species diversity in clinical infections using the Karius test, a microbial cell-free DNA sequencing test for pathogen detection**
A. Ahmed (Redwood City, United States), S. Dalai, D. Hong, L. Blair, M. Lindner, D. Hollemon, S. Bercovici, T. Blauwkamp, M. Kertesz, A. Macintyre*

9069 **Direct sequencing from clinical samples in the diagnostic microbiology laboratory without capital expenditure or specialised bioinformatic training is possible using nanopore technology**
A. Alcolea Medina (London, United Kingdom), C. Nicfhogartaigh, J. Lambourne, R. Serafino-Wani, M. Wilks*

9251 **Long-read sequencing for the diagnosis and characterisation of pathogens in severe pneumonia: the role of simulation and standards in clinical metagenomics pipeline development**
M. Chand (London, United Kingdom), N. Groves, G. Amos, V. Chalker*

9458 **Application of a user-friendly, end-to-end metagenomics platform for rapid pathogen identification in children with osteoarticular infections**
R. Stinnett, N. Ramchandar, H. Xie, S. Flygare, T. Schwarz, K. Broadbent, A. Davis, L. Farnaes, R. Schlaberg (Salt Lake City, United States)*

9503 **Application of a comprehensive, user-friendly metagenomic sequencing platform for rapid pathogen identification in a paediatric population with meningitis and encephalitis**
R. Stinnett, N. Ramchandar, K. Broadbent, T. Schwarz, S. Flygare, H. Xie, J. Foley, A. Davis, L. Farnaes, R. Schlaberg (Salt Lake City, United States)*

Session accepted as 2-Hour Oral Session

Microbiome and human disease: from top to bottom

595 **Longitudinal analysis of lung microbiota in intensive care unit patients undergoing mechanical ventilation**
L. Alagna (Milano, Italy), A. Peri, L. Mancabelli, C. Milani, F. Magni, S. Del Bianco, A. Vargiolu, E. Picetti, S. Rossi, T. Tonetti, R. Fumagalli, L. Galimberti, M. Guarnieri, G. Migliorino, L. Chatenoud, I. Sala, A. Bandera, G. Citerio, A. Gori*

1744 **Characterisation of the microbial community in patients with pharyngeal gonorrhoea infection**
C. Foschi (Bologna, Italy), C. Ceccarani, T. Camboni, C. Consolandi, M. Salvo, V. Gaspari, A. D'Antuono, M. Belletti, M. Re, M. Severgnini, A. Marangoni*

3552 **The role of the eye microbiome in health and disease states of the lacrimal system**
Y. Yagel (Beer Sheva, Israel), Y. Motro, T. Kornhauser, S. Kordeluk, S. Green, J. Moran-Gilad, E. Tsumi*

3553 **Intestinal microbiome in critical care patients: association with patient status and outcome**
E. Rubio Garcia (Barcelona, Spain), A. Vergara, M. Fernández, B. Fidalgo, G. Cuesta Chasco, F. Aziz, M. Hernandez-Tejero, J. Fernandez, A. Soriano, J. Vila Estape, C. Casals-Pascual*

4102 **Diversity of the gut microbiome before haematopoietic cell transplantation is an independent predictor of respiratory failure and sepsis requiring intensive care in the post-transplant period**
F. Adhi (Cleveland Heights, United States), E. Littmann, E. Pamer, J. Peled*

6133 **Diagnosis of invasive pneumococcal disease in children by using a classification method based on nasopharyngeal microbiota signatures**
D. Henares-Bonilla (Esplugues de Llobregat, Barcelona, Spain), R. Cabrera-Rubio, N. Timoneda, M. Fernandez De Sevilla, A. Fernandez, P. Brotons De Los Reyes, A. Mira, C. Muñoz-Almagro*

6309 **Role of the gut microbiota in the anastomotic leakage after colorectal surgery**
P. Hernández (Madrid, Spain), M. Ponce-Alonso, J. Barquín, A. Caminoa-Lizarralde, E. Conde, B. Romero, J. García-Pérez, R. Del Campo*

6590 **Evolution of cutaneous bacterial microbiota of pressure ulcers in patients with spinal cord injury**
C. Dunyach-Remy (Nîmes, France), A. Gélis, S. Bastide, A. Yahiaoui-Martinez, J. Lavigne, A. Sotto*

6971 **Individuals at risk of developing rheumatoid arthritis possess a unique microbiome**
C. Rooney (Leeds, United Kingdom), S. Mitra, K. Mankia, I. Moura, P. Emery, M. Wilcox*

Session accepted as Paper Poster Session

Microbiome impact in health and disease

32 **Metatranscriptomic analysis reveals active bacterial communities in diabetic foot infections**
F. Sadeghpour Heravi (Sydney, Australia), M. Zakrzewski, K. Vickery, H. Hu*

228 **Gut microbiome interferes with host tryptophan metabolism pathway and regulates basal anxiety-like behaviour**
J. Shafiq (Karachi, Pakistan), B. Khan, G. Abbas, A. Ahmed*

810 **A new perspective: microbiota, the role of *Streptococcus gallolyticus* in childhood colorectal cancer**
A. Büyükcam (Ankara, Turkey), C. Akyüz, N. Gursoy, D. Orhan, B. Otlu, B. Sancak, A. Kara*

1471 **Relationship between intestinal microbiota and infantile colic**
C. Haddad, T. Itani (Beirut, Lebanon), A. Moukarzel, D. Karam Sarkis*

1802 **Changes in the gut microbiota due to smoking in patients with inflammatory bowel disease**
T. Ohkusa (Tokyo, Japan), K. Uchiyama, E. Miyauchi, H. Arakawa, S. Koido, N. Sato, H. Ono*

1832 **Bacterial profile associated with oral cancer: metagenomic analysis in oral micro-niches**
D. Garcia Robayo (Chia, Colombia), F. Gamboa, H. Tupaz Erira*

2221 **Microbiome analysis of samples from patients with idiopathic pulmonary fibrosis in the A Coruña University Hospital, Spain: a pilot study**
K. Conde (A Coruña, Spain), J. Vallejo, L. Alvarez-Fraga, S. Rumbo-Feal, B. Rodiño-Janeiro, G. Bou Arevalo, C. Montero Martínez, I. Vidal García, M. Poza Dominguez*

2731 **Assessment of quantitative composition of *Bacteroides fragilis* in children with coeliac disease at the time of diagnosis and after a six-month period of diet**
A. Krawczyk (Krakow, Poland), D. Salamon, K. Kowalska-Duplaga, Z. Grzenda-Adamek, A. Kozioł-Kozakowska, K. Fyderek, T. Gosiewski*

3498 **The female reproductive tract microbiome and its relationship with infertility and hydrosalpinx**
Y. Yagel (Beer Sheva, Israel), A. Weintraub, E. Pardo, S. Green, Y. Motro, J. Moran-Gilad*

4187 **Vaginal microbiota in Japanese women undergoing infertility treatment**
A. Matsumoto (Saitama, Japan), Y. Yamagishi, S. Takahashi, Y. Kuroki, A. Minemura, K. Oka, M. Takahashi, H. Mikamo*

4451 **Microbiota as a marker of mucoid *Pseudomonas aeruginosa* and *Haemophyillus influenzae* in non-cystic fibrosis bronchiectasis**
R. López, L. Fernandez Barat (Madrid, Spain), N. Vazquez, V. Alcaraz, L. Bueno, R. Cabrera, G. Scioscia, P. Oscanoa, R. Amaro, A. Torres*

4471 **Characterisation of healthy gut microbiome subjects following a mediterranean diet**
S. Vazquez Cuesta (Madrid, Spain), N. Lozano, L. Villar Gomara, L. Alcalá, M. Marín, P. Muñoz, E. Bouza, E. Reigadas Ramirez*

4479 **Determining the lung microbiome of chronic obstructive pulmonary disease patients from hospitals in Pretoria, South Africa using IS-Pro method and 16S rDNA sequencing**
T. Goolam Mahomed (Pretoria, South Africa), R. Peters, G. Pretorius, A. Goolam Mahomed, V. Ueckermann, A. Stoltz, M. Kock, M. Ehlers*

4629 **Surface ocular microbiome in dry eye syndrome: a preliminary study**
C. Foschi, P. Versura, C. Consolandi, M. Severgnini, M. Re, A. Marangoni (Bologna, Italy)*

5440 **Differences in the lower respiratory tract microbiota in patients with severe pneumonia of viral or bacterial origin**
J. Marimon Ortiz De Zarate (Donostia-San Sebastian, Spain), A. Perez-Gavilán, M. Ercibengoa, N. Azcue, M. Alonso, L. Vidaur*

5575 **A multi-omics approach to understanding the aetiology of Q fever fatigue syndrome**
R. Raijmakers (Nijmegen, Netherlands), M. Roerink, A. Jansen, S. Keijmel, R. Gacesa, Y. Li, L. Joosten, J. Van Der Meer, M. Netea, C. Bleeker-Rovers, C. Xu*

6236 **Characterisation of vaginal microbiota in pregnant women with preterm prelabor rupture of the foetal membranes**
A. Vergara (Barcelona, Spain), T. Cobo, E. Rubio Garcia, J. Bosch, J. Vila Estape, C. Casals-Pascual*

6544 **Differences in nasopharyngeal microbiota composition according to the severity of human rhinovirus infection in the first 1000 days of life**
N. Timoneda, D. Henares-Bonilla, R. Cabrera-Rubio, A. Fernandez, D. Penela, P. Brotons De Los Reyes, Y. Jordan García, A. Mira, C. Muñoz-Almagro, C. Launes (Barcelona, Spain)*

6790 **Long-term effect of dietary preferences and nutritional regimes on intestinal microbiota diversity and composition**
M. Hora, A. Gundogdu (Kayseri, Turkey)*

6794 **Chemotherapies for acute lymphoblastic leukaemia may have a long-term impact on bacterial gut microbiota**
M. Payen (Paris, France), A. Cointe, A. Pascault, G. Mohamed, M. Fadh, S. Delannoy, P. Fach, A. Baruchel, A. Monjault, S. Bonacorsi, A. Birgy*

6839 ***Akkermansia muciniphila* in multiple sclerosis**
E. Tarasova (St. Petersburg, Russian Federation), I. Abdurasulova, A. Ivanov, A. Matsulevich, I. Kudrjavtsev, M. Serebryakova, I. Nikiforova, A. Ilves, E. Ivashkova, I. Stoliarov, V. Ulyantsev, M. Suvorova, V. Klimenko*

7021 **Interplay between genetic disorders and gut microbial community: Rubinstein-Taybi syndrome as a model**
G. Bassanini, E. Di Fede, E. Colombo, C. Ceccarani, E. Ottaviano, V. Massa, C. Gervasini, E. Borghi (Milan, Italy)*

7370 **Gut microbiota of full-term and late preterm newborns in Moscow**
P. Tatiana, E. Isaeva, V. Muravieva, A. Gordeev (Moscow, Russian Federation), A. Melkumyan, L. Lyubasovskaya, M. Mesyan, L. Timofeeva, V. Zubkov, G. Sukhikh*

7582 **Faecal microbiota in Romanian ankylosing spondylitis patients**
M. Oprea (Bucharest, Romania), D. Cristea, D. Predateanu, V. Bojinca, M. Trandafir, S. Dinu, S. Ciontea, C. Usein*

7893 **Studying the association of the human vaginal microbiome with HPV infection using enriched metagenomic sequencing**
A. Latsuzbaia (Dudelange, Luxembourg), A. Wienecke-Baldacchino, M. Herold, I. Karabegovic, J. Tapp, M. Fischer, F. Mühlschlegel, J. Mossong*

7960 **The microbial aetiology of the acute appendicitis: the possible role of microbiota in the disease**
E. Munukka (Turku, Finland), S. Vanhatalo, S. Sippola, M. Gunell, J. Grönroos, P. Huovinen, A. Hakanen, P. Salminen*

8400 **Dynamic study of microbial interactions in the skin microbiota of patients with epidermal necrolysis (DynaMiCut)**
J. Lavaud, C. Rodriguez, S. Oro, N. De Prost, G. Gricourt, F. Kouby, V. Desmontant, C. Hua, F. Botterel, B. Costes, E. Melloul, L. Roisin, P. Wolkenstein, J. Decousser, O. Chosidow, C. Bernigaud, P. Woerther (Créteil, France)*

8629 ***Lactobacilus iners* in vaginal microbial community**
K. Trajkova, K. Popovska Jankovic, B. Curcic, O. Petrovski, A. Dimovski, M. Petrovska (Skopje, Macedonia)*

8758 **Dysbiosis in a triplet with an autism spectrum disorder: a case study**
S. Hazan (Ventura, United States), J. Daniels, A. Papoutsis*

8760 **Correlation between vaginal microbiota diversity and human papilloma virus induced cervical carcinogenesis in population of Santander, Colombia**
L. Torrado García (Bucaramanga, Colombia), B. Rincon-Orozco, R. Martinez Vega, N. Jones-Cifuentes*

Session accepted as Paper Poster Session

Modulation of the microbiota

999 **Modulation of the microbiota by oral intake of a synbiotic mixture in healthy volunteers: a single-centre one-armed pilot study**
I. Rubin (Frederiksberg, Denmark), S. Mollerup, M. Pinholt, M. Pedersen, T. Kallemose, H. Westh, A. Petersen*

1730 **Effects of penicillin V on the intestinal microbiota in patients with pharyngo-tonsillitis**
P. Edquist (Stockholm, Sweden), K. Rystedt, C. Giske, K. Hedin, S. Mölstad, M. Ringman, G. Skoog Ståhlgren, P. Sundvall, C. Edlund*

3435 **Preliminary analysis of a pilot study using a new oral encapsulated formulation of faecal microbiota**
V. Rico Caballero (Barcelona, Spain), A. Aira, E. Rubio Garcia, C. Casals-Pascual, A. Vergara, J. Martínez Martínez, A. Soriano*

3809 **Using metagenomics to study the impact of hospital stay on the human gut resistome**
M. Yokoyama (Brighton, United Kingdom), L. Peto, A. Walker, M. Llewelyn*

4119 **Long-term exposure to ceftriaxone sodium induces alteration of gut microbiota accompanied by anxiety-like and depression-like behaviours in mice**
Z. Zhao (Chengdu, China), L. Zhou, C. Tao*

4298 **Effects of spectrum of antibiotics on microbiome compositions and resistome levels**
K. Nielsen (Copenhagen, Denmark), M. Olsen, A. Palleja, S. Ebdrup, N. Sørensen, O. Lukjancenko, R. Marvig, K. Møller, N. Frimodt-Moller, F. B. Hertz*

4942 **Bacterial consortium: the evolution of the Faecal Microbiota Transplantation (FMT)**
G. Quaranta (Rome, Italy), G. Fancello, R. Graffeo, G. Ianiro, G. Cammarota, M. Sanguinetti, L. Masucci*

4998 **Donor selection in the Belgian Ghent Stool Bank: a relief to help**
H. Hamerlinck (Ghent, Belgium), J. Vandevijver, E. Naessens, S. Vandendriessche, L. Coorevits, J. Boelens, B. Verhasselt*

5420 **Early microbiome changes associated with the novel, targeted-spectrum antibiotic ACX-362E compared to oral vancomycin**
K. Garey (Houston, United States), K. Begum, C. Lancaster, A. Gonzales-Luna, D. Bui, M. Hu, M. Silverman, M. Alam*

5805 **Disease prevention not decolonisation: a cohort study for faecal microbiota transplantation for patients colonised with multidrug-resistant organisms**
R. Ghani (London, United Kingdom), B. Mullish, J. Mcdonald, A. Ghazy, H. Williams, G. Satta, E. Brannigan, M. Gilchrist, N. Duncan, R. Corbett, J. Pavlu, A. Innes, M. Thursz, J. Marchesi, F. Davies*

5833 **Impact of different antimicrobial exposures on the gut microbiome and resistome characterised by metagenomic sequencing**
L. Peto (Oxford, United Kingdom), N. Fawcett, T. Peto, D. Crook, M. Llewelyn, A. Walker*

6174 **Change of gut microbiome and resistome of the patients with *Clostridioides difficile* infection and those with chronic obstructive pulmonary diseases compared with healthy population**
J. Kim (Guri, South Korea), M. Seo, M. Bae, B. Kim, M. Rho, H. Pai*

6210 **Gut microbiota of healthy volunteers with or without stool carriage of *Klebsiella pneumoniae* in an area with invasive *Klebsiella pneumoniae* syndrome**
Y. Huang (New Taipei, Taiwan), C. Liao*

6230 **Characterisation of the human gut microbiome in a high antibiotic use and resistance setting in Vietnam**
B. Vu Thi Ngoc (Hanoi, Vietnam), H. Ho Bich, M. Oomen, T. Huy, H. Rogier Van Doorn, H. Wertheim, J. Penders*

6942 **Gut microbiome characterisation in irritable bowel syndrome patients following faecal microbiota transplant: a case report study**
M. Surleac, S. Paraschiv (Bucharest, Romania), C. Apostolescu, D. Otelea*

7323 **Recruiting donors for faecal microbiota transfer: a one year experience**
A. Aira (Barcelona, Spain), V. Rico Caballero, E. Rubio Garcia, C. Casals-Pascual, A. Soriano*

7691 **Ceftriaxone and cefotaxime have similar impact in emergence of resistance in gut microbiota from hospitalised patients**
P. Benoit (Paris, France), O. Jiang, A. Mizrahi, J. Zahar, A. Le Monnier*

7778 ***Bacteroides* as a next-generation of probiotics in neonatology**
L. Lyubasovskaya, P. Tatiana, V. Muravieva, E. Isaeva, D. Serdyukova, A. Gordeev, N. Shabanova (Moscow, Russian Federation), G. Sukhikh*

8565 **Is periodic screening of donor faeces with temporary quarantine storage effective in preventing transmission of multidrug-resistant organism during faecal microbiota transplantation?**
K. Vendrik (Leiden, Netherlands), E. Terveer, S. Nooij, E. Boeije-Koppenol, I. Sanders, J. Keller, E. Van Lingen, E. Berssenbrugge, H. Verspaget, E. Kuijper, J. Van Prehn*

8593 **What constitutes a healthy faecal microbiome?**
S. Mitra, A. Buckley, I. Moura, D. Ewin, W. Spittal, E. Clark, K. Bentley, J. Freeman (Leeds, United Kingdom), M. Wilcox*

8930 **Impact of selective digestive and oropharyngeal decontamination on the gut microbiome and resistome in intensive care patients**
B. Xavier (Antwerp, Belgium), S. Patz, N. Plantinga, B. Wittekamp, C. Lammens, D. Huson, M. Bonten, H. Goossens, P. Jorens, S. Malhotra-Kumar*

9008 **Continuous infusion versus intermittent antipseudomonal β-lactam antibiotics for acute pulmonary exacerbations of cystic fibrosis: effect on the respiratory microbiome**
K. Langan (Kensington, Australia), J. Choo, G. Rogers, D. Keating, R. Stirling, J. Wilson, A. Cheng, C. Chang, T. Kotsimbos, A. Peleg*

9401 **Longitudinal microbiome analysis defines expected and aberrant antibiotic effects on the human respiratory microbiome**
E. Clarke, E. Lautenbach, E. Reesey, M. Wernovsky, P. Tolomeo, B. Kelly (Philadelphia, United States)*

Session accepted as Paper Poster Session

Molecular and genomic typing and characterisation of pathogens

587 **Next-generation infection prevention: integrated whole genome sequencing and clinical epidemiology analysis to detect actionable carbapenem-resistant *Acinetobacter baumanii* transmission hotspots**
S. Ong (Singapore, Singapore), P. Rao, Z. Wei, B. Poh, S. Prakki, L. Wang, V. Ong, B. Ang, P. De, O. Ng, K. Marimuthu*

2352 **Molecular epidemiology of carbapenem-resistant *Acinetobacter baumannii* in the United States, 2013–2017**
S. Mckay (Atlanta, United States), J. Daniels, V. Albrecht, N. Vlachos, V. Stevens, J. Rasheed, M. Karlsson, A. Laufer-Halpin*

2596 **Whole genome sequencing for *Neisseria meningitidis* for health protection action**
S. Shaaban (Glasgow, United Kingdom), L. Macdonald, H. Murdoch, F. Johnston, R. Ure, K. Scott, D. Brown, A. Smith, M. Holden, C. Cameron*

2980 **Molecular epidemiology and spatiotemporal analysis of carbapenem-resistant *Acinetobacter baumannii* in networks hospital in southern Thailand**
S. Chusri (Songkhla, Thailand), T. Hortivakul, K. Singkhamanan, A. Chukamnerd, K. Silpapojakul*

3133 **Clonal characterisation of *Acinetobacter baumannii* strains in a public hospital in Brazil**
A. Andrade, L. Arend (Curitiba, Brazil), J. Cieslinski, V. Stadler Tasca Ribeiro, L. Kraft, J. Telles, F. Tuon*

3339 **A common protocol for the simultaneous processing of multiple bacterial species for whole genome sequencing**
K. Raven (Cambridge, United Kingdom), S. Girgis, B. Blane, A. Akram, D. Leek, N. Brown, S. Peacock*

3359 **Invasive *Haemophilus influenzae* type b (Hib) disease in children in Italy, after 20 years of routine use of conjugate Hib vaccines**
M. Giufre' (Rome, Italy), E. Lindh, R. Cardines, M. Cerquetti*

4611 **Genetic diversity of *Pseudomonas aeruginosa* isolates colonising the lungs of cystic fibrosis patients at two academic hospitals in the Gauteng Province, South Africa**
T. Hamiwe (Pretoria, South Africa), R. Green, D. White, S. Klugman, L. Van Bruwaene, A. Goga, M. Kock, M. Ehlers*

4742 **Genomic analysis of *Bordetella pertussis* strains causing disease in Italy and in Argentina, 2013 - 2016**
L. Ambrosio (Rome, Italy), G. Buttinelli, C. Concato, G. Linardos, P. Leone, I. Schiavoni, D. Bottero, G. Fedele, D. Hozbor, P. Stefanelli*

4768 **Retrospective analysis of *Bordetella pertussis* isolates collected by the National Reference Centre for Whooping Cough in France since 1995: focus on vaccine antigen-deficient isolates**
V. Bouchez, S. Guillot, A. Landier, N. Armatys, J. Toubiana, S. Brisse (Paris, France)*

5025 **Epidemiological typing of *Neisseria gonorrhoeae* with whole genome sequencing: a vital supplement in transmission surveillance**
K. Haij Bhattarai (Stockholm, Sweden), E. Ericsson, F. Dyrkell, D. Arnellos, G. Bratt, M. Ullberg, N. Björkström, H. Fang*

5082 **Evaluation of meningococcal B vaccine antigen variants in *Neisseria meningitidis*: Italy 2012-2018**
P. Vacca (Rome, Italy), L. Ambrosio, C. Fazio, A. Neri, A. Palmieri, A. Carannante, P. Stefanelli*

5303 **European Centre for Disease Prevention and Control system for cluster detection and interactive exploration of WGS data**
E. Alm (Stockholm, Sweden)*

6000 **Metagenomic sequencing to identify environmental reservoirs of carbapenem-resistant *Acinetobacter baumannii* associated with clinical outbreaks**
B. Forde (Brisbane, Australia), L. Roberts, P. Harris, A. Jennison, K. Hajkowicz, T. Hurst, M. Doidge, S. Beatson, D. Paterson*

6250 **Molecular epidemiology of leptospirosis in Tahiti, French Polynesia, during the 13-year-time spanning from 2007 to 2019**
H. Angermeier (Paris, France), L. Grillová, S. Lastere, M. Levy, M. Picardeau*

6834 **Phylogenetic and resistome analysis of human and animal *Acinetobacter baumannii* ST25 isolates**
A. Lupo (Lyon, France), B. Valot, E. Saras, M. Bour, E. Hirchaud, M. Haenni, P. Plésiat, J. Madec, A. Potron*

7177 **Genomic surveillance of *Bordetella pertussis* in Austria**
A. Cabal Rosel (Vienna, Austria), D. Schmid, M. Hell, E. Mustafa, J. Möst, E. Leitner, F. Allerberger, W. Ruppitsch*

7799 **Prevalence, antimicrobial susceptibility and molecular typing of *Legionella pneumophila* in hot water systems in Morocco**
A. Assaidi (Beni Mellal, Morocco), M. Ellouali, H. Latrache, H. Zahir, C. Ginevra, S. Jarraud, M. Mliji*

7838 **Multi locus sequence typing of *Treponema pallidum* subspecies *pallidum* in Barcelona**
C. Fernández Naval (Barcelona, Spain), M. Arando, M. Espasa, A. Anton, M. Fernández-Huerta, J. González-López, J. Serra Pladevall, T. Pumarola-Suñé, M. Vall, J. Esperalba*

8858 **Macrolide-resistant *Mycoplasma pneumoniae* detection**
S. Leung (Hong Kong, Hong Kong)*

9062 **National survey of *Neisseria gonorrhoeae* isolates by whole genome sequencing in France in 2018**
A. Braille, M. Mainardis, M. Merimèche, T. Poncin, D. Viriot, N. Schnepf, H. Jacquier, C. Bébéar, J. Molina, F. Lot, N. Ndeikoundam, B. Bercot (Paris, France)*

Session accepted as Paper Poster Session

Molecular and genomic typing of Gram-negatives

1598 **Routine use of whole genome sequencing for *Salmonella* Enteritidis surveillance in the Netherlands in 2019**
M. Van Den Beld (Bilthoven, Netherlands), R. Pijnacker, A. Verbruggen, K. Van Der Zwaluw, S. Kuiling, E. Franz*

3377 **Distribution of capsular types among multi-resistant *Klebsiella pneumoniae* in the south of Spain by using a whole genome sequence-based solution**
L. Lopez-Cerero (Seville, Spain), M. Urrutikoetxea-Gutierrez, J. Machuca Bárcena, M. Delgado-Valverde, I. López-Hernández, F. Fernández-Cuenca, A. Pascual Hernandez*

3781 ***Escherichia coli* ST457: an emerging pathogen with wildlife and food-producing animals' reservoirs**
K. Nesporova (Brno, Czech Republic), E. Wyrsch, I. Jamborova, A. Valček, I. Literak, S. Djordjevic, M. Dolejska*

3952 **Developing a pragmatic framework for genomics-informed surveillance of endemic *Salmonella* Typhimurium in Australia**
P. Andersson, W. Pitchers, D. Hennessy, M. Valcanis, J. Gregory, Z. Cutcher, M. Easton, B. Howden (Parkville, Australia), D. Williamson*

4182 **Improved surveillance of Shiga toxin-producing *Escherichia coli* after implementation of whole genome sequencing at the Belgian National Reference Centre**
F. Crombe, O. Soetens, S. Leenen, N. Hammami, B. Verhaegen, S. Denayer, D. Pierard (Brussels, Belgium)*

4826 **Molecular characteristics and clonal diversity of carbapenemase-producing *Klebsiella pneumoniae* isolated from blood culture in patients with haematological malignancies**
S. Khrulnova (Moscow, Russian Federation), G. Klyasova, K. Tandilova, A. Korobova, A. Fedorova Mironova, I. Frolova, B. Biderman*

5250 **Genomic analyses of carbapenem-resistant *Klebsiella pneumoniae* in Singapore: resistance and virulence determinants**
J. Teo, C. Tang (Singapore, Singapore), S. Lee, T. Lim, Y. Cai, J. Sim, T. Tan, R. Ong, A. Kwa*

5787 **Phenotypical and molecular characterisation of non-lactose fermenting *Escherichia coli* isolated from outpatients with urinary tract infection in a private health centre in Santiago, Chile**
K. Ocares, C. Sanhueza, F. Morales, C. Tapia, G. Hermosilla, M. Ulloa (Santiago, Chile)*

5867 **Comparing *Klebsiella pneumoniae* isolates from invasive infections versus carriage in Vietnam: genotypes and capsule types**
B. Vu Thi Ngoc (Hanoi, Vietnam), S. Brisse, K. Holt, H. Tran Thi Kieu, D. Nguyen Thi Ngoc, T. Dao Tuyet, T. Nguyen Vu, H. Rogier Van Doorn, H. Wertheim*

6414 **Continuous genomic surveillance of the third generation cephalosporin-resistant *Enterobacteriaceae* circulating in intensive care units of a 1600 bed university hospital, France**
F. Gravey (Caen, France), M. Fines-Guyon, C. Isnard, F. Ethuin, D. Samba, D. Du Cheyron, C. Daubin, A. Mouet, C. Lesteven, O. Join-Lambert, M. Auzou, F. Guérin, S. Le Hello*

7314 **Molecular characterisation of 15 strains of OXA-181-producing *Klebsiella pneumoniae* in Spain**
N. Romaní Rodés (Badalona, Spain), A. Moreno-Mingorance, M. Quesada, N. Larrosa, M. Gimenez, J. González-López*

7423 **Unexpected genomic variability among *Enterobacterales* causing bloodstream infections in European neonates and infants less than 90 days**
L. Folgori (Milan, Italy), A. Piazza, F. Comandatore, A. Witney, Y. Hsia, N. Russell, K. Laing, I. Monahan, M. Perini, G. Zuccotti, T. Planche, P. Heath, M. Sharland*

7643 **Clones diversity of ESBL-producing *Escherichia coli* from vultures in Canary Islands**
I. Carvalho (Vila Real, Portugal), C. Safia, M. Tejedor-Junco, M. González-Martín, J. Alberto Corbera, A. Suárez-Pérez, G. Igrejas, C. Torres, P. Poeta*

8635 **Characterisation of a newborn species: *Klebsiella spallanzanii***
M. Corbella (Pavia, Italy), C. Merla, C. Parada Rodrigues, G. Batisti Biffignandi, V. Passet, T. Kallonen, P. Marone, C. Bandi, D. Sassera, Z. Zong, C. Jukka, E. Feil, S. Brisse*

8701 **Molecular epidemiology of carbapenem-resistant *Klebsiella pneumoniae* isolates in France 2018**
M. Budia (Le Kremlin-Bicêtre, France), R. Bonnin, L. Dortet, T. Naas*

Session accepted as Paper Poster Session

Molecular and genomic typing of Gram-positives

517 **Prevalence and serotype distribution of *Streptococcus agalactiae* colonisation among pregnant women in Taiwan**
C. Yu-Fen (Changhua, Taiwan), F. Yu-Ping, C. Lee*

723 **Typing of MRSA isolates from bloodstream infections in the Dutch-German border region and Berlin**
N. Couto (Groningen, Netherlands), E. Raangs, J. Rossen, J. Hellkamp, J. Elias, R. Köck, A. Friedrich*

989 **The evolving landscape of group A *Streptococcus* in marginalised populations in England and Wales**
J. Coelho, N. Groves, R. Daniel, K. Broughton, C. Brown, L. Utsi, D. Leeman, K. Sinka, I. Oliver, D. Ready (London, United Kingdom)*

1336 **Emergence of a mupirocin-resistant, methicillin-susceptible *Staphylococcus aureus* clone associated with skin and soft tissue infections in Greece**
N. Giormezis (Patras, Greece), A. Doudoulakakis, K. Tsilipounidaki, M. Militsopoulou, G. Kalogeras, V. Stamouli, F. Kolonitsiou, E. Petinaki, E. Lebessi, I. Spiliopoulou*

1363 **Genetic structure characteristics and treatment for *Listeria monocytogenes* infections**
W. Yu (Hangzhou, China), Y. Huang, L. Guo, J. Zhang, Y. Zhan, L. Zhang, Y. Qiu*

1954 **Molecular and clinical characterisation of methicillin-resistant *Staphylococcus aureus* isolates carrying Panton-Valentine leucocidin in Northern Bavaria, Germany, 2009-2016**
T. Szumlanski (Nürnberg, Germany), A. Simbeck, R. Ziegler, S. Monecke, R. Ehricht, T. Holzmann, R. Bertram, W. Schneider-Brachert, J. Steinmann*

2447 **Molecular epidemiological survey of *Staphylococcus lugdunensis* isolates with different copies of the repeat region in the gene encoding the von Willebrand factor-binding protein**
J. Lu (Taoyuan, Taiwan), L. Lin*

2586 **Genomic and phenotypic characterisation of invasive neonatal and colonising Group B *Streptococcus* isolates from Slovenia, 2001-2018**
T. Perme, D. Golparian, M. Mueller-Premru, M. Bombek Ihan, M. Lučovnik, L. Kornhauser Cerar, P. Fister, J. Lozar Krivec, A. Ihan, Š. Grosek, M. Unemo, S. Jeverica (Ljubljana, Slovenia)*

2717 **Diversity of methicillin-resistant staphylococci among wild Iberian hares: detection of *mec*A-methicillin-resistant staphylococci strains**
V. Silva (Vila Real, Portugal), J. Pereira, L. Maltez, E. Ferreira, V. Manageiro, M. Caniça, J. Capelo, G. Igrejas, P. Poeta*

4781 **Prospective surveillance of invasive group A streptococcal disease in the Netherlands**
L. Rumke (Utrecht, Netherlands), S. Vestjens, A. Van Der Ende, B. De Gier, N. Van Sorge, B. Vlaminckx*

5037 **The unexpected stability of Group B *Streptococcus* clones/serotypes colonising the genitourinary tract of healthy young women**
M. Ksiezarek, A. Guimarães, V. Martins, J. Rocha, S. Ugarcina Perovic, F. Grosso (Porto, Portugal), L. Vieira Peixe*

5651 **Prevalence and molecular characterisation of methicillin-susceptible *Staphylococcus aureus* carrying Panton-Valentine leucocidin gene isolated from patients with invasive infections and nasal carriers**
D. Tapia, C. Sanhueza, C. Campusano, I. Gallardo, L. Porte (Santiago, Chile), C. Varela, M. Ulloa*

6303 **Paediatric invasive pneumococcal disease in Portugal: dominance of serotype 3 and increase in serotype 8 four years after PCV13 inclusion in the national immunization plan**
C. Silva-Costa, J. Gomes-Silva, L. Prados, M. Ramirez (Lisbon, Portugal), J. Melo-Cristino*

6305 **Clinical and bacterial characteristics of paediatric invasive infections caused by *Streptococcus pyogenes***
C. Gouveia, L. Varandas, M. Ramirez (Lisbon, Portugal), J. Melo-Cristino, A. Friães*

6485 **The PCV13 serotypes still account for a large fraction of invasive pneumococcal disease in adults three-years after PCV13 introduction in the paediatric vaccination schedule (Portugal: 2015-2018)**
C. Silva-Costa, J. Gomes-Silva, I. Teodoro, M. Ramirez (Lisbon, Portugal), J. Melo-Cristino*

6986 **Genomic analysis of invasive *Streptococcus pyogenes* isolated in 2013 and 2018 from Hungary**
K. Kristóf, P. Farkas, M. Iván, E. Ungvári, T. Erdősi, A. Toth (Budapest, Hungary)*

7196 **Characterisation of Group B streptococci (GBS) colonising pregnant women in Belgium, 2018: antimicrobial susceptibility profile and distributions of capsular-types, pili-types and sequence-types**
C. Meex (Liège, Belgium), S. Douillez, A. Kinet, R. Sacheli, P. Melin*

8772 **Genomic epidemiology of paediatric invasive Group A *Streptococcus* infections in British Columbia, Canada**
I. Sekirov (Vancouver, Canada), W. Demczuk, I. Martin, S. David, M. Naus, J. Srigley, L. Hoang*

9094 ***Streptococcus agalactiae* in adults in England and Wales 2014-2015, large scale recombination and capsular shifting**
U. Khan (Cardiff, United Kingdom), E. Jauneikaite, R. Andrews, V. Chalker, B. Spiller*

9231 **Sharing of MLVA clusters of *Listeria monocytogenes* among bovine and human invasive clinical isolates**
I. Drigo (Fontane di Villorba, Italy), E. Mazzolini, C. Bacchin, A. Barberio, L. Barco, M. Cocchi, L. D'este, M. Favretti, T. Gallo, A. Gattuso, A. Lettini, E. Schiavon, A. Tavella, F. Agnoletti*

Session accepted as Paper Poster Session

Molecular diagnosis of genital infections

287 **Screening of *Chlamydia trachomatis* and *Neisseria gonorrhoeae* in female sex workers: pooled versus single site testing**
N. Verougstraete, V. Verbeke, A. De Cannière, E. Padalko, L. Coorevits (Ghent, Belgium)*

293 **Sexually-transmitted infections detection using real-time PCR Allplex in the east coast of Spain**
B. Fuster Escriva (Oliva, Spain), M. Belda, M. Ocete, C. Gimeno Cardona*

1075 **Evaluation of simultaneous detection of pathogens associated with sexual transmitted infection and vaginal disorders on a real-time qPCR microfluidics platform in an asymptomatic female college student's cohort**
M. Montesinos Hernández (Brussels, Belgium), M. Hallin, L. Triki, B. Tuglu, S. Lorea, A. De Vleeschouwer, S. Henrard, Z. Kipouros, M. Delforge, J. Goffard*

1319 **MYCOPLASMA IST3, a new *in vitro* medical device to aid the diagnosis of urogenital mycoplasma infection: performance results from an international multi-centre trial**
Y. Bala (Marcy L'étoile, France), I. Boostrom, J. Minic Vasic, A. Barratt ?, E. Chanard, J. Gluvakov, B. Spiller, L. Devigne*

1677 **ESwab collection device allows both detection of human papilloma virus with molecular assays and culture with WASP automation**
R. Gatej, M. Giuca, S. Constanda (Bucharest, Romania), R. Musat, M. Dinescu*

1728 **Evaluation of the Aptima BV assay for detection of bacterial vaginosis by comparison with the BD MAX vaginal panel assay**
S. Voogd, B. Ridwan, D. Willemse-Erix ('s-Hertogenbosch, Netherlands), S. Lutgens-Dumont, M. Hermans*

4351 **Evaluation of a multiplex PCR in genital ulceration diagnosis**
L. Verdurme (Saint-Ouen-l'Aumône, France), A. Lheude, E. Hedbaut, S. Trombert Paolantoni, N. Day, S. Haim-Boukobza*

4805 **Molecular detection of *Mycoplasma amphoriforme* and *Ureaplasma* species from patient samples previously investigated for *Mycoplasma pneumoniae* infection in England and Wales between 2016 – 2017**
S. Rehman, S. Maddocks, B. Afshar, J. Day, V. Chalker, M. Beeton (Cardiff, United Kingdom)*

4827 **Rapid molecular *Chlamydia trachomatis/Neisseria gonorrhoeae* testing is now a reality**
B. Van Der Pol (Birmingham, United States), L. Crane, S. Taylor, J. Lebed, A. Ermel, L. Mena, C. Mcneil, A. Sukhija-Cohen*

4839 **Comparison of analytical performances of the new Qiagen NeuMoDx CT/NG assay with the Abbott RealTime CT/NG assay for detecting *Chlamydia trachomatis* and *Neisseria gonorrhoeae***
S. Svraka-Latifovic (Hilversum, Netherlands), T. Dzebisasjvili, R. Doorn, C. Timmerman, L. Bakker, R. Nijhuis, J. Dorigo-Zetsma*

4911 **Clinical validation of the BD CT/GC/TV2 for BD MAX system in vaginal, endocervical and female urine specimens**
B. Van Der Pol (Birmingham, United States), E. Torres-Chavolla, S. Kodsi, C. Cooper, T. Davis, K. Fife, S. Taylor, M. Augenbraun, L. Bachmann, C. Gaydos*

4946 **Clinical validation of the BD CTGCTV2 for BD MAX system assay in male urine specimens**
B. Van Der Pol (Birmingham, United States), E. Torres-Chavolla, S. Kodsi, C. Cooper, T. Davis, K. Fife, S. Taylor, M. Augenbraun, L. Bachmann, C. Gaydos*

5059 **Method comparison: Abbott Alinity m STI (CT, NG, MG, TV) vs Hologic Aptima CT/NG & Aptima MG**
M. Obermeier (Berlin, Germany), S. Breuer, J. Dhein, R. Ehret*

5528 **Epidemiology of sexually-transmitted infections in women with suspected pelvic inflammatory disease admitted to gynaecology emergency unit of an Italian hospital**
S. Fiorentini (Brescia, Italy), A. Pirozzi, A. Matteelli, V. Marchese, R. Stellini, M. Traversi, F. Caccuri, S. Rubessa, M. Gulletta*

5703 **Comparison of two molecular methods for the diagnosis of sexually-transmitted pathogens**
M. Adelantado Lacasa, A. Gil-Setas, E. Erviti, X. Beristain Rementeria, I. Arregui, C. Ezpeleta Baquedano (Pamplona, Spain)*

6640 **Assessment of the performance of the Vaginosis kit Aptima BV on Panther system from vaginal samples during a 3-month period at Nantes university hospital**
L. Ruffier D'Epenoux, A. Guillouzouic, P. Bemer, S. Corvec (Nantes, France)*

6822 **Molecular *cpn60*-targeted PCR sequencing to assess the diagnostic characteristics of the Nugent Score diagnosis of bacterial vaginosis in reproductive age Kenyan women**
T. Fear (Toronto, Canada), E. Shvartsman, J. Russell, M. Richmond, C. Perciani, S. Vancuren, J. Hill, P. Sandstrom, K. Macdonald*

6823 **Performance of two commercial multiplex PCR assays on the detection the aetiologies of sexually-transmitted infections in men who have sex with men**
T. Lee (Taipei, Taiwan), K. Lin, S. Chang, C. Hung, P. Hsueh*

7110 **Extending the NeuMoDx CTNG test to liquid-based cytology specimens: a performance evaluation**
L. Gong (Ann Arbor, United States), C. Lounds, M. Olson, E. Craig, C. Couture, M. Mastronardi, B. Wu, S. Brahmasandra*

7394 **Performance evaluation of a novel *Trichomonas vaginalis* and *Mycoplasma genitalium* assay in urine and swab specimens**
C. Lounds, L. Gong (Ann Arbor, United States), A. Ripley, E. Strand, C. Butcher, W. Marshall, M. Mastronardi, B. Wu, S. Brahmasandra*

7502 **Use ESwab in sexually-transmitted disease diagnosis by STD Direct Flow Chip Kit**
T. Soler Maniega (Madrid, Spain), N. Zurita Cruz, A. Fraile Torres, S. Gómez De Frutos, A. García, L. Cardeñoso*

7700 **Evaluation of a multiplex real-time PCR assay for detection of the aetiologic agents of vaginitis**
P. Salmerón (Barcelona, Spain), P. García, M. Fernández-Huerta, C. Fernández Naval, T. Pumarola-Suñé, Y. Hoyos-Mallecot, J. Serra Pladevall*

8491 **A study to investigate the utility of confirmatory testing of oropharyngeal samples positive for *Neisseria gonorrhoeae* by Cobas 4800 CT/NG test**
S. Jones (Cardiff, United Kingdom), R. Drayton, C. Knapper, M. Perry*

8592 **Performance and comparison of the rapid VivalyticSTI multiplex assay for the detection of sexually-transmitted infections (STI) in specimens from male patients attending an STI dermatologist practice**
G. Lang (Vienna, Austria)*

Session accepted as Paper Poster Session

Molecular diagnosis: additional aspects

2022 **The impact of transport media, shipping time and DNA extraction kits on the absolute abundance of key vaginal bacterial species**
T. Haahr, J. Jensen (Copenhagen, Denmark)*

3297 **A highly sensitive, non-amplification detection method of nucleic acids in bacilli and viruses**
E. Ito (Tokyo, Japan), N. Kawada, Y. Kyosei, M. Okamatsu, Y. Sakoda, T. Yoshimura, R. Takeuchi, T. Ohta, K. Nakaishi, S. Watabe*

3965 **Evaluation of multiplex PCR for rapid detection of bacteria and antibiotic resistance in spontaneous bacterial peritonitis: a pilot study**
J. Tan (London, United Kingdom), N. Burke, N. Roth, D. Owen, J. Ryan, M. Morgan, R. Westbrook, E. Wey*

4106 **Highly sensitive and specific detection and serotyping of five prevalent *Salmonella* serovars by multiple cross displacement amplification**
X. Zhang (Sutherland, Australia), M. Payne, Q. Wang, V. Sintchenko, R. Lan*

4255 **Evaluation of the Allplex *H. pylori* and ClariR Assay PCR kit on gastric biopsies**
Q. Jehanne, L. Benejat, F. Megraud, E. Bessède, P. Lehours (Bordeaux, France)*

4458 **qPCR inhibitors/enhancers: the interference in the reaction by drugs used for patient treatment or ingested by the patients**
E. Machetti-Mareca, R. Morales Hernández, C. Escolar (Zaragoza, Spain), M. Gil-Rodríguez*

6205 **Hypervirulent *Klebsiella pneumoniae* bloodstream infections in adults: results from a retrospective study in a French intensive care unit**
C. Gonnin, P. Jaubert, C. Poyart, J. Charpentier, H. Poupet, A. Doloy, J. Mira, A. Tazi, N. Gastli (Paris, France)*

6601 **Viral versus bacterial infection diagnosis: Affimer proteins as alternative molecular recognition reagents**
M. Ajayi (Leeds, United Kingdom), D. Tomlinson, M. Mcpherson*

7920 **Automation of laboratory developed tests using CSF, transport medium, and whole-blood specimens on the NeuMoDx molecular system**
C. Lounds, B. Zgheib, P. Mateas, C. Couture (Ann Arbor, United States), M. Mastronardi, B. Wu, S. Brahmasandra*

8181 **Molecular testing of the bone marrow in post-mortem samples for the detection of fatal disseminated infections**
M. Navarro (Barcelona, Spain), J. Hurtado, P. Castillo, N. Rakislova, A. Martinez-Palhares, I. Casas, M. Freire, L. Ferreira, M. Lacerda, W. Monteiro, L. Marimon, J. Vila Estape, Q. Bassat, C. Menéndez, J. Ordi, M. Martinez*

8354 **Development of an in-house cell-SELEX methodology for *Acinetobacter baumannii* aptamers selection**
M. Farrel Côrtes (Sao Paulo, Brazil), T. Marli Bes, B. Déo, E. Cerdeira Sabino, S. Figueiredo Costa, C. Santos*

Session accepted as 1-Hour Oral Session

Molecular testing and multiplex panel approaches for diagnosis

3983 **Assessing impact of Multiplex PCR Point-of-Care testing in patients with respiratory tract infection: a French national study**
O. Dauwalder (Lyon, France), C. Jean-Sebastien, P. L'Aour Dufour, J. Berthiller, E. Bravant, A. Vabret, N. Lévêque, C. Payan, J. Plantier, M. Lafon, P. Bruno, S. Bonacorsi, L. Caudrelier, J. Izopet, F. Laurent, G. Lina, F. Vandenesch, B. Lina*

4090 **Discriminating bacterial and viral infection using a rapid host gene expression test**
E. Tsalik (Durham, United States), R. Henao, J. Montgomery, M. Aydin, E. Lydon, E. Ko, E. Petzold, C. Cairns, S. Glickman, E. Quackenbush, S. Kingsmore, A. Jaehne, E. Rivers, R. Langley, V. Fowler, M. Mcclain, R. Crisp, G. Ginsburg, T. Burke, A. Hemmert, C. Woods*

6914 **TRanscripts to Identify Meningitis (TRIM) test: a novel and accurate host transcript based multiplex PCR assay to rule-out bacterial meningitis**
J. Flatley, M. Wnek, T. Prince, P. Leidinger-Kaufmann, A. Gustin, J. Saikia, F. Mcgill, T. Solomon, M. Griffiths (Liverpool, United Kingdom)*

7249 **The effects of introduction of a syndromic PCR sputum testing in intensive care unit pneumonia patients in a tertiary trauma centre**
D. Kluczna (Hull, United Kingdom), P. Burns, D. Wearmouth, P. Lillie*

Session accepted as Mini-oral Flash Session

Molecular tools for bacterial diagnosis: how, when and why to use them?

3069 **Syndromic tests for meningitis: patient screening before testing allows a high efficient medical value**
O. Dauwalder (Lyon, France), C. Jean-Sebastien, L. Chelghoum, B. Visseaux, C. Gustave, D. Dupont, P. Girardo, H. Salord, M. Bouscambert-Duchamp, G. Billaud, M. Milon, G. Lina, F. Morfin, F. Laurent, M. Wallon, D. Descamps, B. Lina, F. Vandenesch*

5944 **Do DNA based NAAT tests lead to over diagnosis of *Chlamydia trachomatis* infections?**
A. Todd (Sydney, Australia), W. Huston, N. Lima*

6917 **Molecular pathogen identification and resistance gene detection from positive blood cultures**
A. Brachner, L. Marki, H. Enroth (Skövde, Sweden), B. Ronacher*

6926 **Towards an enhanced diagnosis of relapsing fevers by the use of dried blood spots**
E. Talagrand-Reboul (Strasbourg, France), P. Boyer, A. Grillon, C. Bartel, L. Baldinger, M. Engel, L. Zilliox, B. Jaulhac, N. Boulanger*

6941 **Diagnostic evaluation of the new FluoroType MRSAfast assay for the detection of MRSA from clinical swab specimens**
S. Dargel, B. Herberth, M. Eckart (Nehren, Germany), V. Allerheiligen, T. Brodegger*

7018 **Clinical evaluation of ChromaCode's HDPCR tick-borne pathogen panel**
L. Petersen (Lebanon, United States), J. Lefferts, G. Tsongalis*

7587 **Five different *Borrelia* species identified in synovial fluids from patients in Sweden**
K. Ornstein (Kristianstad, Sweden), A. Petersson*

7879 **Diagnostic challenges in Whipple's disease: an update**
J. Kikhney, A. Wießner, V. Moos, M. Wolters, H. Rohde, A. Moter (Berlin, Germany)*

7940 **Evaluation of the performances of BD MAX enteric bacterial panel and extended enteric bacterial panel for detection of gastrointestinal pathogens in clinical stool specimens using FecalSwab**
S. Celia, O. Dauwalder, A. Tristan, B. Coralie, K. Santos, F. Sonia, P. Duraffourg, F. Vandenesch, F. Laurent, A. Ranc (Lyon, France)*

Session accepted as 2-Hour Oral Session

New diagnostic approaches in the lab

1958 **Detection of viable microorganisms and molecular Gram categorisation from whole blood in less than 4 hours**
A. Kadoom (Oxford, United Kingdom), D. Lockhart, H. Bennett, A. Rogers, J. Turner, Y. Kadoom, S. La Fauci, P. Jay, W. Mullen, S. Thaker*

3806 **Development of electronic nano-sensors for the specific *in situ* detection of *Escherichia coli***
Y. Benserhir (Rennes, Algeria), A. Salaun, S. Dutertre, O. Loreal, L. Pichon, A. Jolivet-Gougeon*

5469 **Faecal calprotectin could help distinguish *Clostridioides difficile* infection from *C.difficile* colonisation**
C. Suárez Carantoña (Madrid, Spain), L. Viteri Noel, J. Fernández Sedeño, A. Rodriguez Torres, D. Mora Pimentel, F. Martin Jusdado, S. García-Fernández, R. Escudero Sánchez, J. Cobo Reinoso*

6135 **Lensless imaging for non-destructive and label-free identification directly on agar**
I. Zamoun, A. Maire, P. Schiavone, P. Marcoux (Grenoble, France), T. Yescas González, E. Picard, M. Zelsmann, E. Hadji, D. Peyrade*

7094 **Rapid distinction of capsulated *Acinetobacter baumannii* using a density gradient method**
H. Kon, N. Rakovitsky, D. Schwartz, Y. Carmeli, J. Lellouche (Tel-Aviv, Israel)*

7267 **Rapid diagnostics of bloodstream infections using sybodies and nanobodies as capturing agents**
L. Huber, M. Sorgenfrei (Zurich, Switzerland), R. Melissa, H. Keserue, P. Keller, M. Seeger*

7385 **Loop-primer endonuclease cleavage loop-mediated isothermal amplification technology for singleplex or multiplex target detection and single-nucleotide polymorphism identification**
O. Higgins (Galway, Ireland), T. Smith*

7860 **Fighting antimicrobial resistance with breath analysis**
E. Adams (Liverpool, United Kingdom), E. Brodrick, J. Covington, N. Feasey, J. Skinner, M. Radice, D. Sanders*

9460 **Direct detection of *Escherichia coli* in clinical samples by an ultrasensitive fluorescent copper nanoparticles-aptasensor**
Y. Xiao (Chengdu, China), P. Zhang, L. Wang, Z. Wang, J. Geng*

Session accepted as Paper Poster Session

New *in vitro* and *in silico* diagnostics

35 **Evaluation of EUCAST rapid antimicrobial susceptibility testing (RAST) directly from blood culture bottles**
S. Waled, Y. Soo, S. Ng, Y. Peh, K. Chew (Singapore, Singapore)*

223 **Evaluation of diagnostic method with sonication and culturing of orthopaedic implant-associated infection at Karolinska University Hospital, Sweden**
B. Saeedi, D. Kartout Boukdir (Stockholm, Sweden)*

383 **Neural networks for prediction of minimum inhibitory concentration**
E. Carlsson, F. Dyrkell (Gothenburg, Sweden), T. Lundh*

909 **Performance of the urine flow cytometer Sysmex UF-5000 in rapid diagnosis of urinary tract infections**
K. Haugum (Trondheim, Norway), M. Haugan, J. Skage, M. Tetik, A. Jakovljev, H. Schjelderup Nilsen*

1098 **Laser light scattering technology in the diagnosis of infections in children on dialysis**
L. Boronina (Ekaterinburg, Russian Federation), E. Samatova*

1166 **Comparison of the Accelerate Pheno rapid diagnostic system with standard of care for diagnosing Gram-negative bloodstream infections: bacterial identification, antimicrobial sensitivity and turnaround time**
L. Snell (London, United Kingdom), J. Vink, L. Rowley, T. Awokiyesi, A. Taylor, R. Rusek, D. Jeyaratnam, S. Goldenberg*

1405 **A clinical predictive model of multidrug resistance in neutropenic cancer patients with bloodstream infection due to *Pseudomonas aeruginosa* (IRONIC study)**
C. Gudiol, A. Albasanz (Barcelona, Spain), J. Laporte, N. Pallarès, A. Mussetti, I. Ruiz, P. Puerta, E. Abdala, C. Oltolini, M. Akova, M. Montejo Baranda, M. Mikulska, P. Martín-Dávila, F. Herrera, O. Gasch Blasi, L. Drgona, H. Paz Morales, A. Brunel, E. Garcia, B. Isler, W. Kern, I. Morales, G. Maestro, M. Montero, S. Kanj, O. Sipahi, S. Calik, I. Marquez, J. Marin, M. Gomes, P. Hemmati, R. Araos, M. Peghin, J. Del Pozo, L. Yáñez, R. Tilley, A. Manzur, A. Novo, J. Carratalà*

2136 **Predicting phenotypic polymyxin resistance in *Klebsiella pneumoniae* through machine learning analysis of genomic data**
N. Macesic (Melbourne, Australia), O. Bear Don'T Walk Iv, I. Pe'Er, N. Tatonetti, A. Peleg, A. Uhlemann*

2303 **Visual antibiogram of *Staphylococcus aureus* using machine learning demonstrates multidrug resistance as associations between individual antimicrobials**
C. Cazer (Ithaca, United States), L. Westblade, M. Simon, R. Magleby, M. Castanheira, S. Jenkins, Y. Grohn*

2316 **Optimisation of blood components sterility testing: impact of small volumes in analytical sensitivity**
D. Vay, F. Gotta, L. Carrabba, R. Mazzeo, A. Rocchetti (Alessandria, Italy)*

2369 **Turnaround time for pathogen identification and antimicrobial susceptibility testing of bronchoalveolar lavage specimens in U.S. acute care hospitals**
S. Macvane (Tucson, United States), N. Oppermann, R. Humphries*

2676 **Evaluation of the RIDA QUICK *Helicobacter* and RIDASCREEN *Helicobacter* kits on stool samples for *Helicobacter pylori* diagnosis**
A. Buissonniere, L. Benejat, E. Bessède, F. Megraud, P. Lehours (Bordeaux, France)*

3793 **CXCL13, a new marker in the diagnosis of Lyme neuroborreliosis?**
A. Barbry (Lyon, France), C. André, A. Carricajo, A. Doleans Jordheim, F. Christine, P. Girardo, A. Boibieux, F. Laurent, G. Lina, F. Vandenesch, C. Roure-Sobas*

4963 **Value of pneumococcal urinary antigen testing in a recent series of *Streptococcus pneumoniae* bacteraemia**
A. García Caballero (Madrid, Spain), M. Serrano Tomás, D. Marcos Mencía, J. Fortun Abete, M. Moya, R. Canton Moreno, A. Sanchez Diaz*

5051 **Sensitivity of the pneumococcal urinary antigen ImmuView in proven or probable pneumococcal pneumonia**
G. López De Egea (L'Hospitalet de Llobregat, Spain), A. González Díaz, M. Domínguez Luzon, C. Ardanuy Tisaire*

5578 **Comparison of bacterial recovery of stored sonication fluid cultures using liquid broth and solid media obtained from orthopaedic implant-associated infections**
M. Kurihara, I. Nayara Marcelino Santos, B. Castro, A. Pignatari, M. Salles (Sao Paulo, Brazil)*

6220 **Typing of *Salmonella enterica* by Fourier-transform infrared spectroscopy**
M. Cordovana (Bologna, Italy), N. Mauder, S. Pongolini, L. Soliani, S. Ambretti, M. Kostrzewa*

6290 **Predicting co-amoxiclav resistance in *Escherichia coli* bloodstream infections using machine learning methods and bacterial genome-wide association studies**
K. Vihta (Oxford, United Kingdom), T. Davies, N. Stoesser, S. Earle, D. Wilson, D. Eyre, S. Lipworth, D. Clifton, S. Kouchaki, D. Crook, T. Peto, A. Walker*

6483 **Validation of FASTmar kit, a flow cytometric assay for detection of main mechanisms of beta-lactams resistance directly from positive blood cultures**
I. Martins-Oliveira, R. Gomes, B. Pérez-Viso, A. Silva-Dias, L. Vieira Peixe, Â. Novais, R. Canton Moreno, A. Rodrigues, C. Pina-Vaz (Porto, Portugal)*

7413 **Education for diagnostic stewardship needs fresh approaches in the digital era: lessons from an attempt to reduce inappropriate urine cultures**
A. Ang (Singapore, Singapore)*

7915 **Usefulness of flow cytometry as a screening technique in the detection of bacterial vaginosis and vaginitis**
J. Peñate (Cádiz, Spain), I. Guerrero Lozano, S. Rodríguez-Pallarés, F. Galan-Sanchez, M. Rodriguez-Iglesias*

7995 **Evaluation of the CAMPYLOBACTER QUIK CHECK to detect *Campylobacter* in stool samples**
J. Franco (Bordeaux, France), L. Benejat, A. Ducournau, F. Megraud, P. Lehours, E. Bessède*

Session accepted as Mini-oral Flash Session

No time to lose: rapid diagnostics

1556 **Rapid carbapenemase detection using the CARBA5 lateral flow device**
H. Ciesielczuk (London, United Kingdom)*

2496 **Proof of concept of a low-cost tropicalised device to detect bacterial growth in equipment-free blood cultures: results from the Turbidimeter pilot study**
L. Hardy (Antwerp, Belgium), E. Corsmit, J. Jans, K. Kaur, R. Baets, J. Jacobs*

4321 **Optimal detection of multidrug-resistant Gram-negatives from stools**
C. Fournier, M. Sadek, L. Poirel, P. Nordmann (Fribourg, Switzerland)*

6088 **Improving culture of *Neisseria gonorrhoeae*, by immediate plating and incubation at a venereology clinic**
L. Brendefur Corwin (Oslo, Norway), P. Campbell, K. Jakobsen, M. Ledaal, B. Moayeri, G. Syversen, F. Müller, T. Leegaard, J. Vildershøj Bjørnholt, A. Olsen*

6374 **New approach for determination of antimicrobial susceptibility to amoxicillin by an acoustic sensor-based on a slot mode**
O. Guliy (Saratov, Russian Federation), B. Zaitsev, O. Karavaeva, I. Borodina*

6439 **Can UF-5000 body fluid mode be an alternative for cerebrospinal fluid cell count?**
E. Baran (Istanbul, Turkey), A. Ilki*

8027 **Rapid identification of methicillin-resistant *Staphylococcus aureus* (MRSA) in clinical microbiology labs by infrared spectral fingerprinting following growth on agar supplemented with cefoxitin**
T. Tsutsumi (Montreal, Canada), C. Frenette, N. Doherty, J. Sedman, A. Ismail*

9383 **Faster turn-around-time for blood cultures after relocation of blood culture units at Karolinska University laboratory**
K. Ininbergs (Stockholm, Sweden), S. Sheikholeslami, M. Kedfors Holm, K. Hedman, S. Dhillon, M. Ullberg, A. Kelly, V. Özenci*

Session accepted as Paper Poster Session

Respiratory infections: what to expect from molecular tools?

418 **The INHALE trial: designing a prescribing algorithm to aid antibiotic choices for the FilmArray Pneumonia Panel Plus**
Z. Dhesi, V. Enne (London, United Kingdom), V. Gant, D. Livermore*

828 **Performance of a PCR-based syndromic panel compared to routine culture and microscopy in patients suspected of pneumonia**
V. Andrews (Lund, Sweden), M. Pinholt, U. Schneider, L. Søes, K. Schønning, G. Lisby*

1346 **Multinational performance evaluation of the BIOFIRE FILMARRAY Pneumonia *plus* (PN*plus*) panel**
C. Ginocchio (Durham, United States), C. Garcia, B. Mauerhofer, C. Rindlisbacher*

1502 **Microbiological validation of the BIOFIRE FILMARRAY Pneumonia Panel plus: a single-centre experience**
V. Hinic, B. Nickel, V. Bättig, N. Khanna, D. Stolz, M. Tamm, A. Blaich, D. Goldenberger, A. Egli (Basel, Switzerland)*

2307 **Impact of respiratory panel PCR assay on antibiotic use in patients with community-acquired pneumonia admitted to intensive care unit**
A. Hamon (Paris, France), X. Repessé, M. Welti, G. Geri, C. Duran, A. Vieillard Baron, E. Salomon, E. Gault, A. Dinh*

2803 **Evaluation of the RIDA GENE CAP Bac real-time PCR assay for diagnosis of community-acquired pneumonia from human bronchoalveolar lavage (BAL)**
A. Hiergeist (Regensburg, Germany), S. Foerster, A. Simons, U. Reischl*

3908 **BIOFIRE FILMARRAY pneumonia panel in the evaluation of severe lower respiratory tract infections**
E. Kyriazopoulou (Athens, Greece), A. Karageorgos, L. Liaskou-Antoniou, P. Koufargyris, A. Safarika, G. Adamis, A. Antoniadou, E. Giamarellos-Bourboulis*

4143 **Laboratory evaluation of the BIOFIRE FILMARRAY pneumonia panel *plus* compared to standard-of-care testing at a private laboratory in Cape Town, South Africa**
P. Naicker, L. Suleman (Cape Town, South Africa), F. Khan, A. Haripersad, J. Hellig, E. Naicker, Q. Labuschagne, H. Naicker, F. Van Der Merwe, M. Hlazo, T. Poole, S. Cass, J. Wojno, A. Brink*

4252 **Evaluation of the FILMARRAY pneumonia plus panel for rapid diagnosis of hospital-acquired pneumonia**
L. Cremet (Nantes, France), M. Bouras, B. Gaborit, E. Persyn, V. Riche, B. Rozec, K. Lakhal, A. Roquilly, S. Gibaud*

4553 **Multi-centre study for the evaluation of BioFire FilmArray Pneumonia Plus for the rapid microbiological diagnosis of low respiratory tract infections**
E. Riccobono (Florence, Italy), T. Spanu, F. Allegrucci, C. Tiberio, S. Ambretti, P. Bottino, V. Ghisetti, G. Lo Cascio, G. Rossolini*

4625 **Evaluation of a highly specific sample-to-result real-time PCR assay for detection and typing of *Bordetella pertussis*, *Bordetella parapertussis* and *Bordetella holmesii* in nasopharyngeal aspirates, nasopharyngeal swabs and sputum samples**
G. Linardos, G. Ricciotti, L. Piccioni, C. Concato (Rome, Italy)*

4669 **Evaluation of the potential clinical impact of BioFire FilmArray Pneumo Plus for the treatment of VAP in intensive care unit patients, Careggi University Hospital, Florence**
B. Viaggi, E. Riccobono (Florence, Italy), M. Bendinelli, V. Zucchelli, T. Giani, G. Rossolini*

4932 **Patient management and indication for influenza A/B and respiratory syncytial virus Point-of-Care testing in the emergency room and possible gains by syndromic respiratory testing**
U. Schneider (Copenhagen, Denmark), M. Holm, D. Bang, R. Petersen, S. Mortensen, R. Trebbien, G. Lisby*

4966 **Unyvero multiplex PCR on broncho-alveolar lavage for rapid microbiologic and antibiotic susceptibility documentations in immunocompromised patients under antibiotic therapy admitted to the intensive care unit**
J. Tankovic (Paris, France), J. Baudel, R. Dahoumane, S. Gallah, L. Benzerara, N. Veziris, E. Maury, B. Guidet*

5583 **Evaluation of a quantitative multiplex PCR panel for the diagnosis of pneumonia: how do we optimise utilisation?**
S. Whittier (Edison, United States), M. Lopez, Y. Chen*

6311 **Microbiological Point-of-Care analysis of endotracheal aspirate from intubated patients admitted to the intensive care unit**
D. Ørsnes Christensen (Copenhagen, Denmark), D. Kur, J. Brandt, M. Hindborg, C. Sørensen, M. Kolpen, C. Jensen, F. B. Hertz, J. Bangsborg, M. Bestle*

7035 **Evaluation of Biofire Filmarray Pneumonia for the detection of pathogen bacteria in respiratory infections**
M. Bermúdez Ruiz, M. Valverde Troya, F. Ana María, C. Mediavilla, B. Palop (Málaga, Spain), I. De Toro Peinado*

8185 **Procalcitonin diagnostic performance for differentiating bacterial from viral infection in adults and children with lower respiratory tract infection**
M. Paz (Tirat Carmel, Israel), C. Papan, A. Argentiero, N. Mastboim, L. Shani, T. Gottlieb, M. Stein, E. Simon, G. Kronenfeld, N. Avni, O. Boico, T. Ilan-Ber, E. Eden, E. Farinelli, I. Testa, M. Pasticci, D. Mezzetti, K. Perruccio, U. Hakim, A. Simon, J. Liese, M. Knuf, S. Schneider, S. Esposito, T. Tenenbaum*

8492 **Microbiological performances and clinical impact of the FilmArray Pneumonia Panel Plus on critically ill with severe pneumonia**
A. Verroken (Brussels, Belgium), J. Favresse, H. Rodriguez-Villalobos, P. Laterre*

9059 **Impact assessment of the results of BIOFIRE FILMARRAY pneumonia panel plus for the detection of pathogenic bacteria and individualised therapeutic targeting**
C. Gómez-Camarasa, V. García-Casas, M. Yuste Ossorio, N. Chueca Porcuna (Granada, Spain)*

9633 **The potential impact of molecular rapid identification of pneumonia by The BIOFIRE FILMARRAY pneumonia panel on antimicrobial stewardship and patient management at a large district general hospital, United Kingdom**
H. Kandil (Watford, United Kingdom), R. Hilson, V. Page*

Session accepted as Mini-oral ePoster Session

Strategies for studying the human microbiome

1631 **Insights into vaginal metabolic profiles throughout pregnancy**
C. Foschi, L. Laghi, C. Zhu, G. Patuelli, S. Zagonari, M. Pedna, V. Sambri, A. Marangoni (Bologna, Italy)*

2684 **(In)stability of female urinary microbiota: who's resident and who's passing by**
M. Ksiezarek (Porto, Portugal), S. Ugarcina Perovic, J. Rocha, F. Grosso, L. Vieira Peixe*

3425 **Stool versus rectal swab for microbiome composition analysis in critical care patients**
E. Rubio Garcia (Barcelona, Spain), A. Vergara, M. Fernández, B. Fidalgo, G. Cuesta Chasco, F. Aziz, M. Hernandez-Tejero, J. Fernandez, A. Soriano, J. Vila Estape, C. Casals-Pascual*

5081 **MiSeq protocol for 16S rDNA community profiling revisited with exact ribosomal sequence variants**
J. Matern (Münster, Germany), D. Hagenfeld, K. Prior, B. Ehmke, D. Harmsen*

6217 **The microbiome of nasal samples from an all-age, healthy, UK cohort reveals the epidemiology of potentially protective bacterial genera**
D. Cleary (Southampton, United Kingdom), M. Asai, K. Moore, S. Clarke*

7894 **Nasal microbiota: is it the war between staphylococci and corynebacteria?**
J. Rigaill, A. Barray (Lyon, France), M. Gavid, Y. Lelonge, F. Laurent, P. Berthelot, J. Rasigade, P. Verhoeven*

8113 **Application of direct MALDI-TOF MS analysis in routine study of gut microbiota of newborns**
P. Tatiana (Moscow, Russian Federation), A. Gordeev, V. Muravieva, E. Isaeva, L. Lyubasovskaya, A. Melkumyan, A. Skorobogatiy, S. Trubinov, G. Sukhikh*

8519 **Detection of respiratory *Mycoplasmataceae* during prolonged mechanical ventilation**
E. Clarke, E. Lautenbach, E. Reesey, M. Wernovsky, P. Tolomeo, B. Kelly (Philadelphia, United States)*

Session accepted as Paper Poster Session

Update on metagenomics applications for clinical microbiology

1 **The impact of microbiome DNA enrichment methods on host DNA depletion efficiency and bacterial community structure of infected tissue samples**
F. Sadeghpour Heravi (Sydney, Australia), M. Zakrzewski, K. Vickery, H. Hu*

2956 ***Clostridium butyricum* 588 modifies lipid metabolism in gut microbiome and colon tissue to protect antibiotic-induced colon epithelial damages**
T. Ariyoshi (Saitama, Japan), M. Hagihara, Y. Kuroki, S. Higashi, K. Oka, M. Takahashi, Y. Yamagishi, H. Mikamo*

3802 **Development of fungal mock community standards for mycobiome studies**
N. Perera (Teddington, United Kingdom), S. Suh, M. Hunter, J. Lopera, S. King, A. Mccluskey, B. Benton*

4523 **Polybrominated diphenyl ethers disruption of human gut microbiota**
R. Cruz, J. Palmeira (Aveiro, Portugal), Z. Martins, M. Faria, H. Ferreira, A. Marques, S. Casal, S. Cunha*

4535 **Microbial profile shift and miRNAs circulating in the saliva: what is their clinical correlation?**
M. Santagati, M. Ragusa, F. Mirabella, M. Scillato, A. Spitale (Catania, Italy), G. Mongelli, R. Rizzo, M. Purrello, S. Stefani*

4838 **Automated isolation of microbial DNA from human samples**
H. Block (Hilden, Germany), S. Magyar, D. O'Neil, M. Sprenger-Haussels*

5108 **Evaluation of 16S rRNA metagenomics workflow performance by spike-in and *in silico* experiments**
V. Scherz (Lausanne, Switzerland), S. Aeby, G. Greub, C. Bertelli*

5516 **Comparison of different platforms and analysis tools in microbiome analysis**
C. Scholz, A. Kretzschmar, A. Nowag, F. Sack, M. Polke, S. Stepanow, N. Jazmati, H. Wisplinghoff (Cologne, Germany)*

6667 **Evaluation of various stool collection devices for gut microbiome analysis**
M. Castro Camargo (Bristol, United Kingdom), A. Theodoridou, L. Hillary, H. Bacchus, J. Patil*

6842 **Human-like miRNA detection of bacterial origin in human gut microbiome**
A. Soyturk, A. Gundogdu (Kayseri, Turkey), U. Nalbantoglu*

6892 **Evaluation of QIAseq 16S/ITS screening panel kit sequencing 6 regions to analyse 16S microbiota**
M. Payen (Paris, France), B. Philippe, S. Delannoy, P. Fach, A. Monjault, S. Bonacorsi, A. Birgy*

7093 **Evaluation the presence of leukocytes and bacterial communities of sputum from cystic fibrosis patients**
F. Volpato (Porto Alegre, Brazil), D. Lima Morales, P. Rampelotto, P. Maróstica, A. Barth*

8084 **Impact of saponin-based host DNA depletion on respiratory resistome measures**
E. Reesey, E. Clarke, E. Lautenbach, M. Wernovsky, P. Tolomeo, B. Kelly (Philadelphia, United States)*

8684 **Salivary microbiota profiling for discrimination between individuals in forensic science**
V. Scherz (Lausanne, Switzerland), S. Aeby, L. Falquet, F. Taroni, C. Bertelli, G. Greub*

8805 **Linking the resistome to the microbiome: a culture-free method links plasmid, virus, and antimicrobial resistance genes to their hosts in complex microbial populations**
I. Liachko (Seattle, United States)*

9441 **Phased-primer library preparation improves 16S rRNA metagenomics sequencing quality with limited impact on output**
V. Scherz (Lausanne, Switzerland), S. Aeby, G. Greub, C. Bertelli*

Session accepted as Paper Poster Session

Update on surveillance of Gram-negative bacteria

1041 **Healthcare-associated infections reporting in developing countries: challenges and corrective measures**
N. Dehghan-Nayeri, L. Rostamnia, A. Seifi (Tehran, Iran), S. Varaei, A. Akbari Sari, H. Haghani, V. Ghanbari*

1378 **Infection incidence among patients colonised with carbapenem-resistant *Enterobacteriaceae* (CRE) and microbial aetiology**
E. Sala, R. Mauri (Como, Italy), M. Valli, B. Pini, S. Cimetti, E. Pozzoli, P. Corti, C. Finco, L. Pusterla, G. Catanoso*

1566 **A mock-outbreak of carbapenem-resistant *Klebsiella pneumoniae*: using whole genome sequencing to correlate clinical and environmental samples and provide clues to improve infection control in real-time**
A. Simões (Oeiras, Portugal), T. Touret, N. Faria, S. P. Ladeiro, J. Costa, A. Bispo, M. Serrano, C. Palos, M. Miragaia, R. Leite, R. Sá-Leão*

2164 **Systematic assessment of available data on the incidence of bloodstream infections and hospital-acquired pneumonia caused by carbapenem-resistant *Acinetobacter baumannii* in Europe: the ABOUT-MDRO-CRAB study**
B. Anaya-Baz (Seville, Spain), N. Maldonado, Z. Palacios Baena, V. Palomo, M. Pezzani, S. Chiesi, E. Razzaboni, M. Compri, E. Tacconelli, J. Rodríguez-Baño*

2168 **Systematic assessment of available data on the incidence of hospital-acquired pneumonia and bloodstream infections due to carbapenem-resistant *Pseudomonas aeruginosa* in Europe: the ABOUT-MDRO-CRPA project**
B. Anaya-Baz (Seville, Spain), N. Maldonado, Z. Palacios Baena, V. Palomo, M. Pezzani, S. Chiesi, E. Razzaboni, M. Compri, E. Tacconelli, J. Rodríguez-Baño*

2888 **Interest of rapid detection of emerging extensively drug-resistant bacteria by PCR associated with temporary dedicated team for high-risk patients**
M. Otto, C. Darles, J. Plantamura, P. Rossi, M. Walker, E. Sennavoine, B. Ducret, Y. Auroy, F. Janvier (Toulon, France)*

2965 **Endemicity of carbapenemase-producing *Enterobacteriaceae* in Hong Kong**
S. Wong (Hong Kong, Hong Kong), V. Cheng*

3048 **Characterisation of carbapenemase-producing *Serratia marcescens* clinical isolates recovered in a hospital in Madrid (Spain) using whole genome sequencing**
M. Hernández García, B. Pérez-Viso (Madrid, Spain), M. Morosini Reilly, P. Ruiz-Garbajosa, R. Del Campo, R. Canton Moreno*

3508 **Which anatomic sites should be screened for carbapenem-resistant *Acinetobacter baumannii*?**
A. Nutman (Tel-Aviv, Israel), J. Lellouche, D. Schwartz, A. Lerner, P. Elmalih, R. Rov, A. Vaturi, D. Ben-David, Y. Carmeli*

3509 **Management and cost-analysis of a *Klebsiella pneumoniae* carbapenemase-producing cluster in the cardiac intensive care unit in Vicenza hospital, Italy**
S. Mondino (Vicenza, Italy), V. Manfrin, M. Rassu, R. Cazzaro, D. Brodesco, A. Diquigiovanni, L. Zaghis, I. Zecchinato, M. Zanon, E. Bovolenta, S. Zanovello, S. Barra*

3814 **Determining the value of sequential screening to detect carbapenemase-producing *Enterobacteriales***
J. Henderson (London, United Kingdom), H. Ciesielczuk, M. Wilks, S. Nelson*

3912 **Rectal colonisation by drug-resistant bacteria in nursing home residents in Crete, Greece**
K. Moschou, P. Ioannou (Heraklion, Greece), E. Moraitaki, D. Stafylaki, G. Vougiouklakis, S. Maraki, G. Samonis, D. Kofteridis*

4383 **Diverse populations of carbapenem-resistant *Klebsiella pneumoniae* isolated in rectal colonisation cultures from intensive care units of a single tertiary centre in Greece**
E. Protonotariou (Thessaloniki, Greece), C. Kotzamanidis, T. Papadopoulos, D. Pilalas, A. Tychala, D. Papadopoulou, F. Netsika, G. Meletis, A. Zdragas, M. Symeon, L. Skoura*

4545 **Longitudinal genomic analysis of IMP-1 metallo-β-lactamase-producing *Enterobacteriaceae* at a tertiary care hospital in north-east Japan**
H. Kanamori (Sendai, Japan), Y. Makino, H. Baba, K. Oshima, T. Aoyagi, K. Tokuda, S. Endo, H. Yano, M. Kaku*

5018 **The use of carbapenemase real-time PCR directly from rectal swab for control carbapenem-resistant *Enterobacteriaceae* cross-transmission in a kidney transplant ward**
M. Freire (Sao Paulo, Brazil), A. Cury, D. Garcia, F. Spadao, W. C. G. Valentin, F. Jota De Paula, F. Rossi, E. David Neto, W. Nahas, L. Pierrotti*

5746 **Emergence and spread of plasmid carrying *bla*IMP and *mcr*-9 in *Enterobacteriaceae* isolated from hospitalised patients in West London from 2016 to 2019**
A. Boonyasiri (Bangkok, Thailand), F. Davies, F. Bolt, E. Jauneikaite, A. Ledda, S. Mookerjee, H. Abbas, A. Abdolrasouli, J. Otter, M. Gilchrist, T. Galletly, E. Brannigan, J. Turton, M. Ellington, G. Larrouy-Maumus, J. Rodriguez-Manzano, X. Didelot, A. Holmes*

6093 **Carbapenem-resistant *Enterobacteriaceae*: a 7-year surveillance at Keimyung University Dongsan Hospital and changes after moving to a new location**
N. Ryoo (Daegu, South Korea), H. Kang, D. Kim, W. Lee, J. Ha, D. Jeon, S. Suh*

6592 **Epidemiological and genomics insights into the first outbreak of an extensive drug-resistant NDM-1-producing *Klebsiella pneumoniae* in Portugal**
Â. Novais (Porto, Portugal), R. Ferraz, M. Viana, P. Martins Da Costa, L. Vieira Peixe*

6634 **Diagnostic yield of pharyngeal, axillary, inguinal and rectal swab samples for multidrug-resistant Gram-negative detection in intensive care patients**
S. Román Soto (Madrid, Spain), M. Alguacil Guillén, A. Quintás-Viqueira, A. Robustillo, G. Ruíz-Crrascoso*

6688 **Endemic situation regarding OXA-48-producing *Klebsiella pneumoniae* in north-west Spain**
E. Gato (A Coruña, Spain), M. Gude Gonzalez, F. Fernández-Cuenca, A. Pascual Hernandez, A. Pérez, A. Fernández González, G. Bou Arevalo*

6726 **Colonisation and infection with carbapenemase-producing *Enterobacteriaceae* (CPE) in high-risk patients in a private hospital setting in Istanbul, Turkey**
M. Ozdamar (Kocaeli, Turkey), E. Hakko, I. Karaman, M. Topaloglu, S. Turkoglu*

6749 **Whole genome sequencing in an outbreak of *Serratia marcescens* in a neonatal intensive care unit of a tertiary care centre in Italy**
B. Saccani (Brescia, Italy), L. Signorini, F. Castelli, E. Van Hauwermeiren, R. Marzollo, M. Motta, M. Ricca, S. Fiorentini, A. Caruso, R. Pezzotta, C. Bandi, P. Marone*

6758 **Prediction Model for carbapenemase-producing *Enterobacterales* colonisation upon admission to hospital in an endemic geographic area**
C. Papafotiou (Athens, Greece), S. Bampali, S. Roussos, V. Sypsa, T. Moussouli, M. Samarkos, M. Psichogiou, K. Spyridopoulou, A. Karapanou, G. Daikos*

6828 **An outbreak of carbapenem-resistant *Serratia marcescens* carrying *bla*KPC in an intensive care unit between 2010 and 2013: which is the role of environment?**
M. Farrel Côrtes (Sao Paulo, Brazil), G. Melo, A. Soares, R. Ruedas Martins, T. Guimaraes, S. Figueiredo Costa*

7118 **Detection of unexpected emerging extensively drug-resistant bacteria: experience of a French university hospital, 2012-2018**
N. Khanafer (Lyon, France), X. Jarrige, D. Hilliquin, C. De Bastiani, O. Dauwalder, E. Munier-Marion, P. Vanhems*

7164 **Genomic features involved in intra-hospital transmission of *Pseudomonas aeruginosa***
J. Liese, M. Desch, S. Peter, R. Eggeling, N. Pfeifer, M. Willmann (Tübingen, Germany)*

7426 **Molecular epidemiology and spatiotemporal analysis of carbapenem-resistant *Enterobacteriaceae* among network hospitals in southern Thailand**
S. Chusri (Songkhla, Thailand), T. Hortivakul, K. Kaewnirat, A. Chukamnerd, K. Silpapojakul*

7532 **Rectal isolates display high-negative predictive value for bloodstream infections with (ESBL+) Gram-negative bacteria in neonates with suspected sepsis in a low-resource setting neonatal care unit**
A. Lenglet (Amsterdam, Netherlands), J. Schuurmans, K. Charles, E. Borgundvaag, C. Badjo, K. Clezy, M. Lekkerkerker, C. Ariti, M. Mcrae, H. Wertheim, J. Hopman*

7600 **Screening for carbapenemase-producing *Enterobacteriaceae***
A. Sarian (Preston, United Kingdom), N. Mughal, L. Moore*

7625 **Incidence of hospital-acquired bloodstream infections caused by *Klebsiella pneumoniae* and impact of different preventive strategies: need to going back to basics?**
F. Tassinari, M. Astengo, A. Battaglini, F. Butera, G. Noberasco, I. Schenone (Genoa, Italy), D. De Florentiis, A. Battistini, L. Sticchi, G. Icardi, A. Orsi*

7779 **Notification of hospital-acquired infections events: the French experience**
I. Poujol (Saint-Maurice Cedex, France), S. Sophan, L. Audrey, S. Yann, M. Colomb-Cotinat, A. Berger-Carbonne*

8094 **Intra- and inter-facilities spread of multidrug-resistant *Enterobacteriaceae* across a large nursing homes network**
C. Legeay, B. Fuchs, T. Haudebourg, C. Poulain, F. Raymond, S. Corvec, G. Birgand (London, United Kingdom)*

8204 **Screening of colonisation for carbapenemase-producing *Enterobacterales*: impact in the empiric antibiotic choice of carbapenemase-producing *Klebsiella pneumoniae* infection in a Portuguese hospital**
A. Cipriano (Loulé, Portugal), M. Pereira, A. Read, F. Carneiro, M. Monteiro, M. Soares, V. Alves*

8344 **The role of a monthly active surveillance programme for multidrug-resistant Gram-negative bacteria in a neonatal intensive care unit: impact evaluation of preventive measures**
L. Saporito, G. Graziano (Palermo, Italy), F. Mescolo, V. Insinga, G. Rinaudo, A. Aleo, C. Bonura, M. Vitaliti, C. Maida, M. Giuffè*

8526 **Screening of risk groups detects only a minority of patients with carbapenemase-producing Gram-negative bacilli**
A. Wagemakers (Amsterdam, Netherlands), L. Cadenau, R. Van Mansfeld*

9086 **Random forest and multilevel multivariable analyses to assess risks for colonisation with multidrug-resistant Gram-negatives in 27 long-term care facilities in high endemic settings**
A. Azzini, G. Lo Cascio (Verona, Italy), G. Be, I. Coledan, L. Lambertenghi, N. Salerno, L. Naso, A. Bazaj, M. Mirandola, A. Gorska, F. Russo, G. Napoletano, F. Mazzaferri, G. Cornaglia, E. Concia, E. Tacconelli*

9508 **Parenteral colistin therapy induces rapid selection of colistin-resistant bacteria in human gut: first report from India**
S. Banerjee (New Delhi, India), J. Verma, T. Senapati, A. Mani, M. Soneja, A. Biswas, N. Wig, B. Das, A. Kapil*

9594 **First description of GES-20-producing *Pseudomonas aeruginosa* in Brazil**
A. Lima, D. Rocha, K. Lima, S. Sampaio, J. Mello-Sampaio (São Paulo, Brazil)*

Session accepted as Mini-oral ePoster Session

WGS: real life experience

565 **Prophages, plasmid integration and lack of CRISPR-*Cas* elements underlie genome adaptation in European human-associated *Staphylococcus aureus* ST398**
J. Vlaeminck (Wilrijk, Belgium), B. Xavier, M. Berkell, L. Timbermont, C. Lammens, D. Tabor, J. Kluijtmans, W. Van Wamel, F. Coenjaerts, J. Hasan, B. François, A. Ruzin, H. Goossens, S. Malhotra-Kumar*

1806 **Novel organism verification and analysis (NOVA) study: identification of potentially novel bacterial species from a diverse spectrum of clinical isolates**
D. Goldenberger (Basel, Switzerland), A. Egli, V. Hinic, A. Blaich, T. Roloff, H. Seth-Smith*

2224 **Increased carriage of *Streptococcus pneumoniae* serotype 19A three years after a PCV13 to PCV10 vaccine switch in Belgian children**
L. Van Heirstraeten, I. Wouters, S. Desmet, C. Lammens, J. Verhaegen, H. Goossens, P. Van Damme, P. Beutels, H. Theeten (Antwerp, Belgium), S. Malhotra-Kumar*

3634 **Molecular biomarker to monitor NDM-producing *Klebsiella pneumoniae* outbreak in two Belgian hospitals: a whole genome sequencing-based infection control application**
A. Heinrichs (Brussels, Belgium), M. Argudín, L. Nienhaus, C. Nonhoff, L. Filippin, P. Bogaerts, T. Huang, Y. Glupczynski, O. Denis*

6357 **Investigating the feasibility and clinical impact of a prospective genomics workflow for hospital infection control**
N. Sherry (Heidelberg, Australia), C. Gorrie, J. Kwong, C. Higgs, R. Stuart, C. Marshall, T. Korman, R. Lee, M. Graham, M. Leroi, M. Slavin, L. Worth, H. Chan, M. Grayson, B. Howden*

6858 **Development of a high-throughput single nucleotide polymorphism (SNP) typing assay for *Klebsiella pneumoniae***
E. Shaidullina (Smolensk, Russian Federation), E. Sheck, A. Mikotina, A. Mardanova, M. Edelstein*

8432 **Typing of carbapenemase-producing *Klebsiella pneumoniae*: IR Biotyper meets NGS**
M. Cordovana (Bologna, Italy), H. Seth-Smith, A. Deni, V. Hinic, A. Egli, S. Ambretti*

9340 **It takes two to tango: antimicrobial resistance and virulence contribute to the success of particular *Acinetobacter baumannii* clones**
F. Grosso (Porto, Portugal), L. Silva, C. Rodrigues, M. Ksiezarek, H. Ramos, L. Vieira Peixe*

Session accepted as Paper Poster Session

What's new in bacterial typing?

40 **Mass-Up: free software for the analysis of mass spectra biomarkers**
M. Ercibengoa, A. Perez Gavilan, M. Alonso Asencor, M. Alkorta Gurrutxaga, G. Cilla, J. Marimon (Donostia-San Sebastián, Spain)*

387 **A k-mer-based approach for MLST and cgMLST analysis of nanopore sequenced *Staphylococcus aureus***
O. Aspelin (Gothenburg, Sweden), F. Dyrkell, D. Arnellos*

908 **Using machine learning for improving MLST analysis of nanopore sequenced bacteria**
O. Aspelin (Gothenburg, Sweden), E. Carlsson*

1523 **High-resolution subtyping of *Escherichia coli* using optical DNA mapping**
M. Nyblom, A. Johnning, M. Wrande, M. Hitz, V. Müller, G. Goyal, K. Frykholm, A. Dvirnas, C. Giske, T. Ambjörnsson, L. Sandegren, E. Kristiansson, F. Westerlund (Gothenburg, Sweden)*

3999 **Subtyping *Escherichia coli* in spontaneous bacterial peritonitis with use of IR biotyper and whole genome sequencing**
J. Tan (London, United Kingdom), C. Leboreiro, P. Solanki, R. Westbrook, E. Wey*

4949 **K-mer based prediction of *Clostridioides difficile* ribotypes and relatedness**
M. Moore (Oxford, United Kingdom), D. Eyre*

5152 **Systematic review: transmission inference using single nucleotide polymorphism (SNP) differences between isolates of ESBL and CR-*Enterobacteriaceae*. Can a SNP cutoff be defined?**
A. Jamal (Toronto, Canada), A. Corbeil, L. Farooqi, Z. Zhong, E. Uleryk, A. Mcgeer*

5345 **Standardisation and validation of the PCR technique for detection of ST16-KL51 serotype among *Klebsiella pneumoniae* isolates**
J. Paulino, D. Andrey, W. Martins, N. Lincopan, A. Gales (São Paulo, Brazil)*

6218 **Multi-centre whole genome sequencing bioinformatic outbreak analysis proficiency test conducted in The Netherlands**
J. Coolen (Nijmegen, Netherlands), C. Jamin, P. Savelkoul, H. Wertheim, J. Rossen, S. Matamoros, L. Van Alphen*

6386 **Whole genome sequences analyses by a new easy-to-use software solution confirm a neonatal ward outbreak of MRSA CC22 being related to strains in the neighbouring region**
M. Slott Jensen, M. Chen, M. Skov, M. Kemp (Odense, Denmark)*

6535 **Biochemical description of seven putative novel species of the genus *Yersinia* identified by core-genome multilocus sequence typing (cgMLST)**
H. Angermeier (Paris, France), A. Le Guern, S. Bremont, C. Savin, J. Pizarro-Cerda*

6863 **A publicly accessible database for *Clostridioides difficile* genome sequences supports tracing of transmission chains and epidemics**
M. Frentrup, Z. Zhou, M. Steglich, J. Meier-Kolthoff, M. Göker, T. Riedel, B. Bunk, C. Spröer, J. Overmann, M. Blaschitz, A. Indra, L. von Müller, T. Kohl, S. Niemann, C. Seyboldt, F. Klawonn, N. Kumar, T. Lawley, S. García-Fernández, R. Canton Moreno, R. Del Campo, O. Zimmermann, U. Groß, M. Achtman, U. Nübel (Brunswick, Germany)*

6884 **A high-resolution whole genome multilocus sequence typing (wgMLST) scheme for easy and scalable detection of *Streptococcus pyogenes* outbreaks**
D. De Coninck, K. Vranckx (St. Martens-Latem, Belgium), J. Dombrecht*

7285 **Multimodal analysis of *Escherichia coli* isolates from patients and carriers with EPISEQ CS, a next-generation sequencing service for epidemiological surveillance**
K. Vranckx (St. Martens-Latem, Belgium), K. De Rauw, K. De Bruyne*

7412 **Fourier-transform infrared spectroscopy for bacterial typing and real-time outbreak analysis**
J. Lellouche (Tel-Aviv, Israel), N. Rakovitsky, S. Frenk, D. Schwartz, H. Kon, S. Abramov, P. Elmalih, Y. Carmeli*

8420 **Performance of core genome multi-locus sequence typing compared to capillary electrophoresis PCR ribotyping of *Clostridioides difficile***
A. Baktash (Leiden, Netherlands), B. Hornung, J. Cover, C. Harmanus, W. Smits, W. Fawley, M. Wilcox, N. Kumar, D. Eyre, A. Indra, A. Mellmann, E. Kuijper*

9387 **CRISPR typing of *Salmonella enterica* serovar Typhimurium from clinical and non-clinical sources reveals the possible transmission from environment to humans**
J. Jacob (Vellore, India), K. Vasudevan, M. Venkatesan, S. Anandan, V. Balaji*

9421 **First use of Fourier-transform infrared spectroscopy in Romania for investigating *Klebsiella pneumoniae* strains isolated from a possible cluster**
D. Talapan (Bucharest, Romania), A. Sandu, B. Lixandru, D. Iovanescu, A. Streinu-Cercel, D. Piţigoi, A. Rafila*

Session accepted as Paper Poster Session

Whole genome sequencing in outbreak analysis

301 **Whole genome analysis of vancomycin-resistant *Enterococcus faecium* causing nosocomial outbreaks suggests the occurrence of few endemic clonal lineages in Bavaria, Germany**
D. Eisenberger (Erlangen, Germany), C. Tuschak, S. Nickel, V. Lehner-Reindl, C. Höller, B. Liebl, G. Valenza*

2082 **Drain water as a potential source of in-hospital room-to-room transmission of carbapenemase-producing *Klebsiella pneumoniae***
L. Heireman (Ghent, Belgium), H. Hamerlinck, J. Boelens, S. Vandendriessche, L. Coorevits, I. Leroux-Roels, M. Chlebowicz, J. Rossen, B. Verhasselt*

2116 **Whole genome sequencing investigation of iGAS outbreak in elderly care**
J. Coelho, N. Groves, D. Ready (London, United Kingdom), C. Brown, O. Olufon, R. Manuel, K. Paranthaman, I. Braithwaite, M. Cummins, C. Ebberson, D. Lawrence, T. Lamagni, E. Wynne-Evans*

3981 **Legionnaires' disease and sleep apnea devices: retrospective analysis of a 9-year-investigation and contribution of whole genome sequencing**
C. Allam (Lyon, France), C. Ginevra, C. Campese, A. Prugne, D. Morel, L. Beraud, G. Descours, S. Jarraud*

4973 **Retrospective WGS of *Acinetobacter baumannii* over 6.5-year-period reveals former unknown structure of clusters and uncovers resistance profile**
A. Groß (Freiburg, Germany), J. Rauch, W. Ebner, H. Grundmann, S. Reuter*

6615 **Whole genome sequencing clarifies potential outbreak with extended-spectrum beta-lactamase-producing *Escherichia coli***
S. Mernelius (Jönköping, Sweden), L. Berglind*

7848 **An unusal cluster of community-acquired skin infections by a multidrug-resistant MRSA harbouring genes that encode for exfoliative toxins**
D. Notermans (Bilthoven, Netherlands), E. Denie, W. Silvis, B. Postma, S. Bantjes, A. Schoffelen, M. Dimmendaal, H. Ruijs, F. Koene-Bennett, M. Petrignani, K. Vendrik, L. Schouls, E. Kuijper*

8157 **Use of whole genome sequencing for rapid detection of a national nosocomial outbreak of *Listeria monocytogenes* associated with contaminated prepacked sandwiches in England, 2019**
G. Godbole (London, United Kingdom), S. Gharbia, T. Dallman, L. Byrne, A. Simbo, J. Mclauchlin, S. Lai, N. Phin*

9126 **A home humidifier responsible for Legionnaires' disease: input of WGS for genomic investigation in a ST1 case**
J. Couturier, C. Ginevra, G. Dhenin, S. Jolivet, D. Nesa, L. Boukari, M. Maison, S. Lapoussin, B. Salauze, S. Jarraud, F. Barbut, G. Descours (Lyon, France)*

Session accepted as Paper Poster Session

Whole genome sequencing: from molecular characterization to typing

677 **Pan-genome analysis supports the differentiation of *Bacteroides fragilis* in division I and the potentially carbapenem-resistant *cfiA*+ division II into two species**
T. Vognbjerg Sydenham (Vejle, Denmark), U. Justesen*

1976 ***In silico* identification of host-associated genomic determinants in *Escherichia coli* using bacterial genome-wide association study**
S. Tiwari (Berlin, Germany), B. Van Der Putten, V. Nguyen, M. Bootsma, R. La Ragione, S. Matamoros, T. Ngo, C. Berens, J. Leng, J. Alvarez, M. Ferrandis-Vila, J. Ritchie, A. Fruth, S. Schwarz, L. Domínguez, M. Ugarte-Ruiz, A. Bethe, C. Huber, V. Johanns, I. Stamm, R. Oldenkamp, L. Wieler, C. Ewers, M. Fivian-Hughes, C. Menge, C. Schultsz, T. Semmler*

1996 **New polysaccharide capsule identification in urogenital *Haemophilus parainfluenzae* related to capsular locus present in *Haemophilus* spp.**
A. González Díaz (Barcelona, Spain), Y. Sierra Urueña, F. Tubau, J. Ayats, M. Cubero, C. Ardanuy Tisaire, S. Marti*

2203 **Stx2k-producing *Escherichia coli* in China**
Y. Xiong (Beijing, China), X. Bai, X. Yang*

2284 **Temporal acquisition of IS*1548* in *Streptococcus agalactiae* clonal complexes**
S. Khazaal (Tours, France), R. Al Safadi, D. Osman, A. Hiron, P. Gilot*

2568 **Genomic characterisation of multidrug-resistant *Klebsiella michiganensis* strains**
P. Shibu, F. Mccuaig, M. Kujawska, L. Hall, A. Mccartney, L. Hoyles (Nottingham, United Kingdom)*

2609 **Implementing pathogen genomics effectively: a seamless service**
S. Shaaban, A. Holmes, L. Allison, D. Brown, L. Seagar, P. Saunders, R. Evans, S. Currie, C. Cameron, A. Smith-Palmer, M. Hanson, I. Laurenson, A. Smith, A. Leanord, A. Roexe, P. Croan, P. Kennedy, S. Gillespie, M. Holden, M. Lockhart (Glasgow, United Kingdom)*

2626 **NDM-1 emerging on distinct plasmid backbones from the IncL/M family**
M. Lopez (A Coruna, Spain), N. Ellaby, N. Woodford, M. Tomas, M. Ellington*

3568 **Genetic diversity of *bla*KPC gene containing IncF plasmids from epidemiologically related and unrelated *Enterobacteriaceae***
J. Stohr (Breda, Netherlands), M. Kluytmans - Van Den Bergh, V. Weterings, J. Rossen, J. Kluytmans*

4179 **Recurrence of multidrug-resistant *Klebsiella pneumoniae* ST48 at Charité, Universitätsmedizin Berlin**
F. Maechler, A. Weber (Berlin, Germany), P. Gastmeier, A. Kola*

4522 **High-throughput genome sequencing highlights *Pseudomonas aeruginosa* adaptative evolution in the urinary tract**
A. Cottalorda, S. Dahyot (Rouen, France), M. Leoz, F. Gravey, F. Aujoulat, K. Alexandre, S. Le Hello, E. Jumas-Bilak, M. Pestel-Caron*

5264 **Whole genome sequencing of heterochronous isolates of *Burkholderia cenocepacia* and *B. contaminans* from two patients with cystic fibrosis using Nanopore and Illumina platforms**
A. Bernier (Winnipeg, Canada), S. Tyson, T. Burdz, D. Wiebe, K. Bernard*

5479 **Genetic characterisation of virulence factors of non-01 non-0139 *Vibrio cholerae* strains from clinical and environmental origin isolated in Chile between 1992 and 2018**
C. Tong, C. Sanhueza, L. Porte, J. Dabanch, I. Briceño, M. Lafourcade, F. Silva, L. Castillo, G. Osorio, M. Ulloa (Santiago, Chile)*

6522 **Whole genome sequencing reveals differences between previously indistinguishable isolates of tobramycin resistant *Staphylococcus aureus***
S. Mernelius (Jönköping, Sweden), A. Jogenfors, L. Berglind, A. Matussek*

6623 **Relatedness of European *Clostridioides difficile* strains from humans, food and animals by whole genome sequencing, ribotyping and toxinotyping; results from COMBACTE-CDI**
K. Davies (Leeds, United Kingdom), V. Viprey, V. Tkalec, N. Devos, E. Santiago-Allexant, D. Ewin, W. Spittal, J. Vernon, W. Fawley, J. Dombrecht, A. Benson, G. Davis, B. Sente, M. Rupnik, P. Cleuziat, M. Wilcox*

7669 **First insight into the genome sequence of *Clostridioides difficile* strains isolated from Romanian patients**
I. Czobor (Bucharest, Romania), V. Cristea, I. Gheorghe, C. Chifiriuc, Y. Feng, X. Wang, L. Popa, M. Popa, L. Marutescu, V. Lazar, M. Popa, Z. Zong*

7698 **Optimisation of bacterial whole genome sequncing workflow for implementation in routine clinical and epidemiological applications**
C. Helsmoortel (Leuven, Belgium), L. Laenen, E. Souche, L. Dehaspe, N. Dedoncker, W. Bossuyt, S. Desmet, E. Andre*

7970 **Virulence profile and comparative genomics analysis of the emerging *Klebsiella pneumoniae* genotypes ST45, ST101 and ST629**
E. Esposito (Naples, Italy), M. Cervoni, C. Roe, L. Peixe, S. Pournaras, S. Brisse, J. Sahl, F. Imperi, R. Zarrilli*

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- Pharmacoepidemiology (incl economics and cost-effectiveness), improved prescribing and antibiotic stewardship (incl decision-support / prediction tools, behavioural aspects)
- Other

Session accepted as Paper Poster Session

Adverse effects of antibiotics: data from clinical trials

2197 **Impact of combining vancomycin with piperacillin/tazobactam or with meropenem on vancomycin-induced nephrotoxicity**
R. Tokhi, N. Kabli, M. Hantool, A. Thabit (Jeddah, Saudi Arabia)*

2538 **A retrospective matched cohort study evaluating the rate of acute kidney injury in patients with severe Gram-negative infections treated with colistin or new β-lactam + β-lactamase inhibitor antibiotics**
C. Doremus (New Jersey, United States), S. Marcella, B. Cai, R. Echols*

2889 **Antimicrobial therapy with aminoglycoside or meropenem in the intensive care unit for hospital-associated infections and risk factors for acute kidney injury**
R. Pitta, J. Gasparetto, T. De Moraes, J. Telles (Sao Paulo, Brazil), F. Tuon*

4180 **Nephrotoxicity during teicoplanin therapy in combination with piperacillin/tazobactam or other anti-pseudomonal β lactams**
C. Tai (Taipei City, Taiwan), C. Shao, C. Wang, F. Lin, C. Wu*

4310 **Effect of a serum lactate monitoring recommendation policy on patients treated with linezolid**
J. Baek (Incheon, South Korea), J. Im, J. Lee, H. Kwon*

5518 **Daptomycin and pulmonary eosinophilia: An unrecognised opportunity**
K. West (Portland, United States), A. Sheeti, G. Forrest*

5678 **Occurrence and predictors of nephrotoxicity in adult patients treated with intravenous colistin: a cohort study**
L. Graça, J. Torres, A. Silva-Pinto, F. Almeida, N. Rocha Pereira (Porto, Portugal), P. Andrade, R. Duro, C. Alves*

5874 **Impact of safety alerts and warnings on fluoroquinolone and alternative antibiotic use in Colombian outpatient care**
M. Silva-Medina Weil (Cali, Colombia), P. Ricardo, M. Palacios*

6435 **Phase II clinical data showed that lower recurrence of *Clostridiodes difficile* infection with ridinilazole is associated with minimal impact on the gut microbiota and bile acid composition**
E. Duperchy (Abingdon, United Kingdom), X. Qian, K. Yanagi, A. Kane, N. Alden, M. Lei, D. Snydman, R. Vickers, D. Roblin, K. Lee, C. Thorpe*

8138 **Real-world experience with prolonged courses of tedizolid at a large academic medical centre**
W. Alegria (Stanford, CA, United States), D. Ha, M. Holubar, L. Meng, E. Mui, S. Deresinski*

8337 **Vancomycin plus piperacillin-tazobactam and the risk for acute kidney injury: what is the effect size?**
S. Avedissian (Nebraska, United States), J. Liu, G. Pais, M. Scheetz, N. Rhodes*

8865 **Patient risk factors associated with development of acute kidney injury after combination antibiotic therapy for methicillin-resistant *Staphylococcus aureus* (MRSA) bacteraemia**
S. Tong (Melbourne, Australia), S. Johnson, D. Lye, D. Yahav, A. Cass, M. Roberts, O. Robinson, M. O'Sullivan, H. Foo, J. Nelson, N. Meagher, D. Price, J. Davis*

Session accepted as Paper Poster Session

Antibiotic hospital consumption measurements around the world

1381 **Antibiotic use in French hospitals 2012-2018: improvements to be confirmed!**
C. Dumartin (Bordeaux, France), M. Péfau, A. Jouzeau, L. Dugravot, E. Reyreaud, A. Chabaud, E. Couve-Deacon, C. Martin, M. Ploy, O. Ali-Brandmeyer, C. Rabaud, J. Claver, A. Rogues, L. Simon*

2907 **The Global Point Prevalence Survey of Antimicrobial Consumption and Resistance (Global-PPS): roll-out of a successful antimicrobial stewardship programme in Nigeria using the global-PPS tool**
O. Oduyebo, A. Roberts, O. Ola-Bello, A. Versporten (Antwerp, Belgium), I. Pauwels, C. Osuagwu, I. Fajolu, P. Oshun, H. Goossens, P. Akintan, E. Temiye*

3384 **A novel methodical approach to quantifying the value of an antibiotic: enablement-, insurance- and productivity-value**
J. Kowalik (London, United Kingdom), A. Blake, R. Russell, D. Mircea, D. Leonard, N. Meadows*

5360 **The Global Point Prevalence Survey of Antimicrobial Consumption and Resistance (Global-PPS): the results of antimicrobial prescribing in 33 hospitals in Guinea**
M. Sow (Conakry, Guinea), A. Versporten, I. Pauwels, D. Djiro, H. Goossens*

6638 **Antimicrobial stewardship in Cambodia: the importance of antimicrobial point prevalence survey and lessons learned from the field**
G. Khim (Phnom-Penh, Cambodia), F. Daily, P. Pen, R. Kong, S. Sok, S. Yim, S. Oung, J. Hessell, J. Letchford, J. Ferguson*

6805 **Trends in antimicrobial use in Brazilian hospitals: 2017 and 2018 point prevalence surveys**
A. Matos Porto (Sao Paulo, Brazil), I. Boszczowski, A. Versporten, I. Pauwels, T. Guimaraes, E. Girão, C. Carrilho, P. Esteves, T. Ferraz, C. Rodrigues, J. Capobiango, C. Donini, D. Montenegro, R. Coutinho, C. Takeda, B. Cocentino, U. Castelo Branco, M. Sampaio, M. Avelar Machado, J. Sardi Perozin, J. Carijo, J. Matos, A. Silva Machado, L. Perdigao Neto, K. Kolbe, A. Tahara, B. Bassetti, E. Alves Simoes Neto, R. Cipriano, F. Piastrelli, M. Do Monte Alves, H. Vechi, T. Varejao Strabelli, R. Focaccia Siciliano, R. Cavalcante, J. Atique, L. Passos, A. Nunes Martinelli, A. Vieira De Oliveira, H. Goossens, S. Figueiredo Costa*

7077 **Trends of antibiotic consumption in German hospitals from 2015-2018**
B. Schweickert (Berlin, Germany), M. Feig, M. Schneider, K. Groeschner, M. Behnke, L. Pena Diaz, P. Gastmeier, M. Abu Sin, D. Richter, H. Blank, H. Wehrmeyer, A. Hoffmann, T. Eckmanns*

7329 **Comparing the financial burden of hospitalised patients within the same Diagnosis Related Groups (DRGs) with and without an infection: a multi-centre evaluation in the USA**
L. Puzniak, K. Yu (New Jersey, United States), V. Gupta*

8515 **Using point prevalence methodology to evaluate antimicrobial prescribing in the UK's largest renal dialysis centre**
A. Chavda (London, United Kingdom), A. Ghazy, L. Whitney, M. Gilchrist, A. Holmes*

8521 **Nation-wide audit with feedback of antibiotic stewardship in Norwegian hospitals: a low cost initiative with many opportunities**
P. Akselsen (Bergen, Norway), M. Neteland, J. Høgli, B. Skodvin, S. Harthug*

8703 **The Global Point Prevalence Survey of Antimicrobial Consumption and Resistance (Global-PPS): results of antimicrobial prescribing at Ghana's National Referral Centre**
M. Mirfenderesky (London, United Kingdom), J. Mahungu, A. Aggor, A. Versporten, I. Pauwels, H. Goossens, D. Ankrah*

8950 **The Global Point Prevalence Survey of Antimicrobial Consumption and Resistance (Global-PPS): an opportunity to lead global stewardship actions in Belgian hospitals?**
X. Holemans (Charleroi, Belgium), C. Van Wetter, A. Versporten, O. Tassin, I. Pauwels, H. Goossens, M. Ventura*

9259 **Improving country-level antimicrobial prescribing with the implementation of a uniform and standardised surveillance method: the Global-PPS Chilean experience, year 2015 and 2017**
C. Carvajal (Santiago, Chile), A. Versporten, A. Rojas, M. Cifuentes, F. Silva, H. Goossens, J. Labarca*

9455 **Consumption of antibiotics effective against multi-resistant Gram-positive pathogens: data of German hospitals from 2015-2018**
B. Schweickert (Berlin, Germany), M. Feig, M. Schneider, K. Groeschner, W. Niklas, M. Behnke, L. Pena Diaz, P. Gastmeier, D. Richter, H. Blank, H. Wehrmeyer, T. Eckmanns, M. Abu Sin*

9634 **14-year evolution of antimicrobial consumption in a Belgian tertiary hospital based on the BeH-SAC surveillance**
F. Buyle (Ghent, Belgium), S. Callens, A. Somers, S. Commeyne, D. Vogelaers*

Session accepted as Mini-oral ePoster Session

Antibiotic prescribing in children

1178 **A global point prevalence study of antimicrobial use in the neonatal intensive care unit: the NO-More-AntibioticS and Resistance study (NO-MAS-R)**
P. Prusakov (Columbus, United States), D. Goff, P. Wozniak, A. Medoro, P. Sanchez*

3029 **A nation-wide parent survey of antibiotic use in Australian children**
R. Anderson, A. Rhodes, N. Cranswick, M. Downes, J. O'Hara, M. Measey, A. Gwee (Melbourne, Australia)*

4952 **Antibiotic consumption in very low birth weight neonates on neonatal intensive care units in Germany: a longitudinal study 3 years of national surveillance**
F. Salm, T. Kramer (Berlin, Germany), F. Schwab, M. Behnke, P. Gastmeier, C. Geffers, B. Piening*

5667 **Impact of antibiotic stewardship programme on the most utilised antibiotics' utilisation and financial expenditure in 57,357 Children Cancer Hospital Egypt inpatient setting**
E. Khaled Mohamed Abualanain, A. Elzeiny, M. Nagy, A. Kashef, A. Badie (Cairo, Egypt), A. Sameh, L. Shalaby*

5770 **Prescribing in paediatric inpatients in England, 2016: factors associated with prescribing "watch" and "reserve" antibiotics**
A. Demirjian (London, United Kingdom), R. Freeman, B. Muller-Pebody, D. Ashiru-Oredope, S. Hopkins*

6865 **Community antibiotic prescribing for children in France from 2015 to 2017: a prospective national study**
N. Trinh (Paris, France), R. Cohen, M. Lemaitre, P. Chahwakilian, G. Coulthard, T. Bruckner, D. Milic, C. Levy, M. Chalumeau, J. Cohen*

7833 **Heterogeneity of antimicrobial prescribing in large paediatric tertiary centres: implications for future interventions and benchmarking of antimicrobial stewardship activities**
M. Gilchrist (London, United Kingdom), A. Chavda, F. Chappell, C. Dalton, A. Demirjian, J. Hatcher, H. Lyall, O. Mcgarrity, J. Peters, C. Watterson, E. Whittaker, L. Whitney*

9269 **Infectious disease specialist intervention in the neonatal intensive care unit: a safe approach to reduce antibiotic exposure in neonates**
J. Armann (Dresden, Germany), B. Seipolt, M. Rüdiger, R. Berner*

Session accepted as Paper Poster Session

Antibiotic stewardship in geriatric care, nursing homes and in end-of-life contexts

821 **Introducing end-of-life considerations into a computerised decision support system for antibiotic treatment: effects on the system's recommendations and comparison to physicians' behaviour**
Y. Dishon-Benattar (Haifa, Israel), I. Pfeffer, M. Mogensen, L. Ward, L. Leibovici, E. Dagan, M. Paul*

2170 **How an inflammatory marker Point-of-Care test can reduce inappropriate antibiotic use in urinary tract infections: perceptions of physicians and nurses in Dutch nursing homes**
S. Kuil (Amsterdam, Netherlands), C. Schneeberger, M. De Jong, F. Van Leth, J. Harting*

3035 **Impact of an antimicrobial stewardship programme on antibiotic resistance profile of urinary *Enterobacteriacae* isolated from nursing home residents: a retrospective cohort study**
A. Strazzulla (Melun, France), S. Bokobza, E. Ombandza, K. Kherallah, S. Hommel, R. Draidi, C. Bonutto, D. Bonnet Zamponi, R. Gauzit, S. Diamantis*

3602 **Antibiotic use at the end-of-life in patients with advanced cancer: a systematic literature review**
A. Marra, M. Puig-Asensio (Iowa City, United States), E. Perencevich*

5774 **Antibiotic consumption in 417 nursing homes: results from a pilot survey**
C. Dumartin (Bordeaux, France), M. Péfau, A. Jouzeau, L. Dugravot, A. Chabaud, C. Martin, E. Couve-Deacon, E. Reyreaud, M. Ploy, J. Claver, O. Ali-Brandmeyer, C. Rabaud, A. Rogues, L. Simon*

6057 **Development of an antimicrobial stewardship programme for post-acute and long-term care centre by the use of telemedicine**
S. Gómez-Zorrilla (Barcelona, Spain), M. Marín, P. Garcia, D. Echeverría-Esnal, N. Prim, M. Gracia-Arnillas, E. Padilla, O. Vázquez, J. Horcajada, S. Grau*

7099 **Spectrum overly broad and duration too long: an assessment of appropriateness of antimicrobial prescriptions in older patients admitted to an Australian tertiary teaching hospital**
L. Gebremichael, R. Visvanathan, M. Warner (Adelaide, Australia)*

8884 **A new approach of antibiotic stewardship in geriatric facilities**
R. Collarino (Le Kremlin-Bicêtre, France), C. De Villelong, X. Lescure, V. Fossey-Diaz, L. Deconinck, L. Vaillant*

Session accepted as Paper Poster Session

Assessment of community and outpatient antibiotic prescribing worldwide

996 **Antibacterial prescribing in the outpatient setting: results from a longitudinal surveillance programme and a sentinel network of physicians: Switzerland, 2018**
C. Pluess-Suard (Bern, Switzerland), D. Perisa, O. Friedli, M. Mäusezahl-Feuz, A. Kronenberg*

1129 **National ambulatory care prescribing of oral antibiotics and prevalence of inappropriate prescribing in the United States, 2009 to 2016**
E. Young (San Antonio, United States), A. Yap, R. Panchal, K. Reveles*

1225 **Overuse of antibiotics in primary care: a secondary analysis of standardised patient studies across four low- and middle-income countries**
G. Sulis (Montreal, Canada), B. Daniels, A. Kwan, J. Das, M. Pai*

2258 **Community-acquired and hospital-acquired *Clostridioides difficile* infections in the context of a trans-sectoral antibiotic stewardship intervention in Berlin, Brandenburg and Thuringia**
S. Schneider, C. Schröder, F. Salm, I. Petruschke, A. Moeser, S. Hagel, M. Pletz, P. Gastmeier (Berlin, Germany)*

2698 **Impact of a national antimicrobial stewardship programme to switch from trimethoprim to nitrofurantoin for treatment of urinary tract infections on the incidence of *Escherichia coli* bloodstream infection in England, 2015–2019**
A. Au-Yeung (London, United Kingdom), A. Saei, A. Charlett, O. Nsonwu, R. Hope, B. Muller-Pebody, S. Hopkins, R. Freeman*

2716 **Antibiotic prescription practices in primary care in low- and middle-income countries: a systematic review and meta-analysis**
G. Sulis (Montreal, Canada), P. Adam, V. Nafade, G. Gore, B. Daniels, A. Daftary, J. Das, S. Gandra, M. Pai*

3186 **A computerised decision support system (CDSS) for antibiotic prescribing in primary care: Antibioclic: implementation, adoption and sustainable use in the era of extended antimicrobial resistance**
T. Delory (Paris, France), P. Jeanmougin, S. Lariven, J. Aubert, N. Peiffer-Smadja, P. Boëlle, E. Bouvet, X. Lescure, J. Le Bel*

3389 **Optimising the treatment of upper respiratory tract infections and tackling antibiotic resistance: effect of online education on physician knowledge and confidence**
J. Duffey (Matlock, United Kingdom), V. Lund, D. Hoban, B. Rubin, S. Voorn*

3464 **Ten-year trends in Estonian ambulatory antibiotics use and comparison of ESAC quality indicators with Nordic countries**
J. Lass, O. Laius, E. Linask, E. Sepp, I. Lutsar (Tartu, Estonia)*

4043 **Community antimicrobial stewardship programme in pregnant women with urinary tract infections in primary care service**
J. Asimbaya, P. Zambrano Sánchez (Quito, Ecuador)*

4398 **Variations in antibiotic prescribing among village doctors in rural Shandong province, China**
O. Dyar (Stockholm, Sweden), Y. Ding, Y. Jia, S. Qiang, C. Stålsby Lundborg*

4402 **Acceptability of selective reporting of antibiotic susceptibility testing results in primary care**
M. Simon (Chaligny, France), G. Le Dref, S. Fougnot, P. De Monchy, J. Kivits, C. Pulcini, N. Thilly*

4705 **Acceptability of a public commitment charter associated with patient information leaflets on antibiotics by general practitioners**
A. Essilini (Nancy, France), G. Le Dref, J. Kivits, A. Welter, C. Pulcini, N. Thilly*

4825 **Antibiotic use prior to seeking medical care in patients with persistent fever in four low- and middle-income countries**
B. Ingelbeen (Antwerp, Belgium), K. Koirala, K. Verdonck, B. Barbé, D. Mukendi Mulumba, T. Phe, S. El Safi, E. Bottieau, M. Van Der Sande, M. Boelaert, F. Chappuis, J. Jacobs*

5125 **Association between susceptibility to quinolones in *Escherichia coli* and tetracycline use in the community: analysis with community-specific ARIMA models**
M. Vibet, Q. Le Bastard, M. Low, B. Gottesman, J. López-Lozano, E. Montassier, E. Batard (Nantes, France)*

5799 **Evaluation of large urban-rural outpatient antibiotic stewardship programme**
L. May (Sacramento, United States), T. Chechi, H. Bettencourt, M. Wang*

5946 **Perceptions of general practitioners on antimicrobial stewardship: a nation-wide survey in Australia**
S. Saha (Melbourne, Australia), D. Kong, K. Thursky, D. Mazza*

6263 **Geodes Antibiotiques: restituting French antimicrobial consumption in the ambulatory sector using two indicators and an interactive website**
P. Cavalie (Saint Maurice, France), M. Boussac, S. Maugat, E. Lucas, A. Berger-Carbonne, L. Watier, B. Coignard*

6962 **Monitoring outpatient antibiotic utilisation using sales and reimbursement data: a population-based comparison in France, 2012-2017**
N. Trinh (Paris, France), J. Cohen, T. Bruckner, C. Levy, P. Chahwakilian, A. Bessou, D. Milic, R. Cohen, M. Chalumeau, M. Lemaitre*

7556 **Bridging the gap between human and animal antimicrobic resistance and consumption surveillance data, antibiotic policy and stewardship: the EPI-Net and ARCH projects**
M. Pezzani (Verona, Italy), F. Arieti, E. Carrara, R. Cauda, M. Compri, S. Goepel, F. Mazzaferri, E. Mazzolini, M. Mendelson, N. Mutters, N. Babu Rajendran, R. Schrijver, M. Sibani, A. Voss, E. Tacconelli*

8186 **Impact of a French regional centre infectiology hotline on antibiotic prescriptions in general medical practice**
M. Bachelet, P. Thibon, A. Lesourd, S. Dargère, F. Caron, R. Verdon, E. Fiaux (Rouen, France)*

8325 **An automated data extraction from primary-care-paediatricians' computers: a French paediatric ambulatory research in infectious diseases**
S. Béchet, A. Werner, F. Vie Le Sage, G. Thiebault, N. Gelbert, F. Cahn-Sellem, F. Kochert, C. Levy, R. Cohen (Créteil, France)*

9250 **Population-level antimicrobial consumption is associated with cultural factors in 37 high-income countries: a global ecological analysis**
C. Kenyon (Berchem, Belgium)*

9291 **Antibiotic stewardship: assessment of education and awareness tools for improving citizen involvement**
F. Grimaud (Creteil, France), X. Lescure, J. Le Bel, Y. Yazdanpanah*

9504 **Epidemiology of previous antibiotic treatment in a community setting infectious diseases consultation office**
J. Choucair (Beirut, Lebanon)*

Session accepted as Paper Poster Session

Bacteriophage therapy goes viral

865 **Bacteriophage therapy against multidrug-resistant *Acinetobacter baumannii* infections**
R. Rathore (T'bilisi, Georgia), N. Karumidze*

1268 **Quality control of therapeutic bacteriophages: the Belgian experience**
A. Leroy, L. Cuignet, C. Vanhee, E. Deconinck, P. Ceyssens (Brussels, Belgium)*

1329 **Efficacy of bacteriophage-antibiotic combinations on two different phenotypes of methicillin-resistant *Staphylococcus aureus***
R. Kebriaei, K. Lev, T. Morrisette, P. Maassen, J. Abdul-Mutakabbir, S. Morales, M. Rybak (Detroit, United States)*

1507 **Personalised production and administration of bacteriophages: lesson learned from a unique European academic collaboration to treat a patient with pandrug-resistant *Pseudomonas aeruginosa* spinal infection**
T. Ferry (Lyon, France), J. Pirnay, C. Gustave, C. Kolenda, M. Merabishvili, L. Gilles, A. Marchet, C. Barrey, T. Perpoint, F. Laurent, G. Resch*

1532 **Bacteriophages in real-life: positive and negative experience in a difficult to access old-new therapeutic**
A. Bleibtreu (Paris, France), M. Hentzien, D. Lebeaux, J. Robert, E. Haddad, A. Bellanger, É. Vallet, E. Caumes, S. Jauréguiberry*

1750 **Diversity and therapeutic potential of *Klebisella pneumoniae* bacteriophages and their depolymerases: genomics and enzymatic activity**
R. Ragupathy (Manchester, United Kingdom), J. Redfern, M. Enright*

2797 **Intravenous administration of personalised cocktail of bacteriophages as salvage therapy in combination with ceftazidime/avibactam in patients with relapsing *Pseudomonas aeruginosa* bacteraemia associated with intravascular implants: lesson to be learned from two cases**
T. Ferry (Lyon, France), A. Conrad, C. Gustave, C. Kolenda, F. Farhat, M. Catroux, F. Cazenave-Roblot, C. Triffault-Fillit, C. Fevre, C. Petitjean, C. Chidiac, J. Josse, L. Gilles, F. Laurent*

3483 **Case report: microbiological effects of phage therapy on *Pseudomonas aeroginosa* in a pneumonia patient**
A. Niessen (Utrecht, Netherlands), A. Costa, F. Nóbrega, P. Haas*

4070 ***In vitro* activity of four lytic bacteriophages specific for OXA-72-producing *Acinetobacter baumannii***
W. Martins (São Paulo, Brazil), J. Cino, E. Medeiros, M. Toleman, A. Gales*

4556 **Phage-MR003 prevents infection caused by clinical isolated methicillin-resistant *Staphylococcus aureus* in mouse wound model**
T. Suda (Mitaka, Japan), T. Hanawa, Y. Tanji, K. Miyanaga, H. Ohnishi, T. Matsuda*

5157 **Innovative antibacterial agents eradicate bacteria including persisters within mature biofilms**
J. Wubbolts (Leiden, Netherlands), H. Scheper, J. Verhagen, A. De Visser, M. Merabishvili, J. Pirnay, M. De Boer, P. Nibbering*

5553 **Effectiveness of bacteriophage-antibiotic combinations for daptomycin-resistant *Enterococcus faecium* harbouring LiaS and LiaR substitutions**
T. Morrisette (Detroit, United States), K. Lev, R. Kebriaei, J. Abdul-Mutakabbir, P. Maassen, S. Morales, C. Arias, M. Rybak*

6054 **Characterisation of phage obtained from methicillin-resistant *Staphylococcus aureus***
O. Ulusan (İzmir, Turkey), F. Sahin, M. Kıyan*

6187 **Susceptibility to bacteriophage K, biofilm formation, presence of *ica* operon and adhesins among staphylococci**
M. Plota (Patras, Greece), F. Gkartziou, N. Giormezis, F. Kolonitsiou, I. Spiliopoulou*

7992 **Bacteriophage therapy in the treatment of burn wounds**
M. Alexander, I. Grigoryan (Moscow, Russian Federation), A. Melkumyan, O. Safronova, Y. Turnikov*

8964 **Late spot evaluation reveals enhanced phage lytic activity**
D. Rezevska (Riga, Latvia), K. Racenis, J. Kroica*

9007 **Anti-biofilm activity of bacteriophage ϕWL-3 conjuncted with ciprofloxacin, fosfomycin, gentamicin, meropenem or ceftriaxone against a ciprofloxacin-ceftriaxone-resistant *Escherichia coli* clinical isolate**
L. Wang (Hefei, China), T. Tkhilaishvili, B. Bernal Andrés, A. Trampuz, M. Gonzalez Moreno*

9015 **Biofilm killing activity of bacteriophage ϕWL-3 against antibiotic-resistant *Escherichia coli* clinical isolate**
L. Wang (Hefei, China), T. Tkhilaishvili, B. Bernal Andrés, A. Trampuz, M. Gonzalez Moreno*

9063 ***In vitro* evaluation of single or combined bacteriophages targeting different *Staphylococcus aureus* clinical isolates**
J. Orcastegui Delso (Berlin, Germany), F. Kunisch, A. Trampuz, M. Gonzalez Moreno*

9153 **Bacteriophage therapy in orthopaedic and cardiovascular surgery: first clinical experience with difficult-to-treat infections**
P. Morovic (Berlin, Germany), T. Tkhilaishvili, D. Margaryan, S. Karbysheva, A. Trampuz*

Session accepted as Paper Poster Session

Clinical experience with recently approved antibiotics

1152 **Efficacy of ceftazidime-avibactam for multidrug-resistant Gram-negative bacteria infections: a retrospective evaluation in a Belgian teaching hospital**
V. Goncette, N. Layios, F. Frippiat (Liège, Belgium)*

1214 **Exposure-efficacy analyses support optimal dosing regimens of ceftolozane/tazobactam in patients with hospital-acquired pneumonia /ventilator-associated pneumonia in ASPECT-NP**
W. Gao, J. Passarell, Y. Patel, Z. Zhang, G. Lin, J. Fiedler-Kelly, C. Bruno, E. Rhee, C. De Anda, H. Feng (Kenilworth, United States)*

2946 **Optimal PK/PD target and high efficacy rates of ceftolozane-tazobactam in patients with infections caused by extensively drug-resistant *Pseudomonas aeruginosa***
E. Navarrete-Rouco, S. Luque, L. Sorlí, A. Arancon, N. Campillo, M. Montero, N. Prim, A. Benítez-Cano, E. Samso, J. Horcajada (Barcelona, Spain), S. Grau*

3088 **SUSANA project: real-world data coming from the use of new antimicrobial drugs**
P. Bonfanti (Lecco, Italy), E. Ricci, A. Pandolfo, F. Baragli, M. Merli, D. Lo Porto, S. Benedetti, N. Geremia, L. Sanna, G. Angioni, K. Falasca, I. Caramma, A. Bandera, N. Squillace, P. Maggi, A. Spolti, F. Vichi, M. Puoti, A. Cascio, G. De Socio, P. Viganò, G. Madeddu, F. Luzzaro*

3200 **Ceftolozane-tazobactam for treatment of severe ESBL-producing *Enterobacteriaceae* infections: a multi-centre nationwide clinical experience (Ceftabuse II Study)**
M. Bassetti, A. Vena, D. Giacobbe, M. Falcone, G. Tiseo, M. Giannella, R. Pascale, M. Meschiari, M. Digaetano, A. Oliva, C. Rovelli, N. Carannante, A. Losito, S. Carbonara, M. Mariani, A. Mastroianni, G. Angarano, M. Tumbarello, C. Tascini, P. Grossi, C. Mastroianni, C. Mussini, P. Viale, F. Menichetti, C. Viscoli, A. Russo (Pisa, Italy)*

4540 **Delafloxacin (DLX) in the treatment of community-acquired bacterial pneumonia (CABP): patients with PORT Risk Class III-V**
R. Alvarez-Sala, M. Popescu, L. Lawrence, S. Cammarata, D. Zinzi (Pomezia, Italy)*

4873 **Resistance to ceftolozane-tazobactam and ceftazidime-avibactam in extensively drug-resistant (XDR) and multidrug-resistant (MDR) *Pseudomonas aeruginosa*: comparing antimicrobial activity, associated risk factors and clinical outcomes**
M. Meschiari (Modena, Italy), K. Shaniko, V. Bianco, M. Sarti, G. Orlando, A. Bedini, C. Mussini*

5161 **Clinical experience with ceftazidime-avibactam (CAZ-AVI) in the treatment of infections caused by XDR *Klebsiella pneumoniae* producing OXA-48 carbapenemase**
A. Bykov, M. Suvorova, I. Sychev, E. Burmistrova, A. Ismagilov, D. Protsenko, S. Yakovlev (Moscow, Russian Federation)*

5234 **Experience after analysing a ceftazidime/avibactam national registry of infections caused by KPC-producing *Klebsiella pneumoniae***
H. Giamarellou, I. Karaiskos (Athens, Greece), A. Gkoufa, C. Routsi, G. Adamis, A. Stefos, L. Sybardi, G. Chrysos, E. Mouloudi, D. Bassoulis, L. Galani, C. Gogos, K. Pontikis, E. Papadimitriou, M. Petraki, K. Masgala, K. Arvaniti, G. Poulakou, G. Daikos*

7153 **Comparative effectiveness of ceftolozane/tazobactam versus aminoglycosides or polymyxins in multidrug-resistant *Pseudomonas aeruginosa* infections**
A. Caffrey, E. Piehl (Providence, United States), V. Lopes, L. Puzniak, K. Laplante*

7665 **Real-world multi-centre experience with eravacycline at academic hospital systems**
S. Alosaimy, K. Molina, K. Claeys, J. Andrade, J. Truong, M. King, B. Pullinger, G. Huang, T. Morrisette (Detroit, United States), A. Lagnf, M. Rybak*

8318 **Real-life experience with ceftazidime-avibactam in South Spain**
M. Nunez, A. Perez-Bailón, M. Trigo-Rodriguez, C. Castaño-Amores, N. Chueca Porcuna (Granada, Spain), A. Ruiz-Sancho, D. Vinuesa García, J. Cabeza, J. Hernández-Quero, M. Yuste*

Session accepted as Mini-oral ePoster Session
Clinical mycology: diagnosis, treatment, stewardship.

972 **Radiologic features of *Pneumocystis* pneumonia differ between patients with and without HIV Infection**
H. Wu (Kaohsiung, Taiwan), K. Wu, S. Lee, D. Chang, S. Dai, S. Kuo, C. Chou, Y. Weng, Y. Tseng, J. Chen, C. Sy, H. Tsai, Y. Chen*

3203 **Successful use of the novel antifungal olorofim in the treatment of disseminated coccioidomycosis**
E. Harvey, L. Fitton, J. Rex (Wellesley, United States), G. Thompson*

6225 **Outcomes of candidaemia caused by biofilm-forming isolates in haematological patients**
G. Klyasova (Moscow, Russian Federation), A. Malchikova, K. Tandilova, S. Kravchenko, P. Elena, V. Savchenko*

6599 **Clinical evaluation of an investigational use only *Aspergillus* galactomannan lateral flow assay at a tertiary cancer care centre**
K. Jani, T. Mcmillen, E. Babady (New York, United States)*

7859 **Performances evaluation of the first sample-to-result system for detection and quantification of *Pneumocystis jirovecii* in respiratory tract samples**
S. Patanè (Torino, Italy), G. Bovolenta, A. Camporese, R. Tedeschi, P. Stano, S. Costa, C. Bittoto, G. Stefanuto*

8095 **Effectiveness and safety of isavuconazole treatment for invasive fungal infections in solid organ transplant recipients**
A. Monforte (Barcelona, Spain), I. Los-Arcos, M. Martin, D. Campany, V. Monforte, C. Berastegui, J. Sacanell, L. Castells, I. Campos-Varela, R. Ferrer, C. Bravo, J. Gavaldà, O. Len*

8513 **Antimicrobial stewardship teams in candidaemia management: advise or take care of the patient?**
A. Alemán Alemán, N. Gómez-Manero, M. Fernández Regueras, M. Mantecón, L. Buzón Martín, M. Morán-Rodriguez, C. Navarro San Francisco (Burgos, Spain)*

9621 **Evaluation of the antifungal stewardship programme at St George's Hospital, London 2018-19**
A. Rusdiah (London, United Kingdom), T. Yau, C. Logan, T. Bicanic*

Session accepted as Paper Poster Session
Clinical PK/PD studies with beta-lactams

154 **Population pharmacokinetic/pharmacodynamic assessment of a clinical imipenem/cilastatin and relebactam dose in patients with hospital-acquired bacterial pneumonia and ventilator-associated bacterial pneumonia**
M. Patel (Kenilworth, United States), P. Patel, N. Daryani, W. Copalu, P. Kulkarni, D. Hilbert, K. Young, M. Rizk*

685 **Pharmacokinetic/Pharmacodynamic benefit of prolonged ceftazidime/avibactam infusion**
S. Baklouti, C. Massip, C. Mane, H. Guet-Revillet, M. Murris, D. Concordet, P. Gandia (Toulouse, France)*

823 **Evaluating the predictive performance of ID-ODS software in critically ill patients for piperacillin: a comparison using IV bolus and continuous infusion data**
A. Alsultan (Riyadh, Saudi Arabia), S. Wallis, J. Lipman, J. Roberts*

990 **Development of a simultaneous population pharmacokinetic model for aztreonam-avibactam**
R. Xie (Singapore, Singapore), P. Chan, M. Mcfadyen, S. Raber*

1213 **Ceftolozane/tazobactam probability of target attainment in patients with hospital-acquired pneumonia/ventilator-associated pneumonia**
Z. Zhang, Y. Patel, H. Feng (Kenilworth, United States), M. Johnson, J. Fiedler-Kelly, C. Bruno, E. Rhee, C. De Anda, W. Gao*

1633 **Utilising the full potential of model-based dosing tables: an interprofessional collaboration to develop and integrate meropenem dosing tables into clinical routine**
F. Weinelt (Berlin, Germany), M. Stegemann, A. Theloe, F. Pfäfflin, L. Dübel, A. Uhrig, S. Achterberg, R. Lorenz, H. Epple, L. Ehmann, W. Huisinga, S. Hennig, C. Kloft*

1812 **Once-daily dose ceftriaxone plus ampicillin: an alternative for *Enterococcus faecalis* infective endocarditis OPAT treatment**
L. Herrera-Hidalgo, A. Gutiérrez-Valencia, L. Rafael, L. Lopez-Cortes (Seville, Spain), A. De Alarcón, J. Gálvez-Acebal, L. Lopez-Cortes, M. Gil-Navarro*

2535 **Target attainment and pharmacokinetics of frequently used antimicrobials in surgical patients (TAPAS study)**
P. Declercq (Leuven, Belgium), E. Van Wijngaerden, G. Van De Sijpe, R. Poncelet, S. Nijs, W. Metsemakers, A. D'Hoore, A. Wolthuis, J. Wauters, I. Spriet*

2630 **Efficacy of ceftobiprole for *Pseudomonas aeruginosa* hospital-acquired pneumonia in critically ill patients: a pharmacokinetic-pharmacodynamic evaluation**
C. Mane (Toulouse, France), V. Duhalde, G. Martin-Blondel, D. Concordet, P. Gandia*

2657 **Use of therapeutic drug monitoring to optimise cephazolin dosing in the treatment of methicillin-susceptible *Staphylococcus aureus* bacteraemia**
V. Venugopalan, S. Hernandez, K. Desear, C. Peloquin, K. Cherabuddi, A. Casapao (Jacksonville, United States)*

3028 **Capillary micro-sampling versus conventional sampling to conduct a clinical pharmacokinetic study for meropenem in critically ill patients**
Y. Guerra Valero (Queensland, Australia), J. Roberts, J. Lipman, C. Fourie, T. Starr, S. Wallis, S. Parker*

3531 **New evidence-based recommendations for cefazolin prophylaxis in patients undergoing cardiac surgery with cardiopulmonary bypass**
S. Zelenitsky (Winnipeg, Canada), D. Calic, R. Ariano, R. Arora, H. Grocott*

4024 **Pharmacokinetic/pharmacodynamic simulation of cost-effective dosage regimens of ceftazidime/avibactam in patients with renal impairment**
L. Dheyriat, L. Bourguignon, M. Leroy, T. Ferry, S. Goutelle (Lyon, France)*

4150 **Impact of hypoalbuminemia and augmented renal clearance on flucloxacillin plasma concentrations: a real-life retrospective study**
D. Marriott (Sydney, Australia), A. Duckworth, G. Jones, C. Lau, D. Cattaneo*

4362 **Population pharmacokinetics of ceftriaxone administered as continuous or intermittent infusion in critically ill patients**
E. Leegwater (The Hague, Netherlands), B. Kraaijenbrink, D. Moes, I. Purmer, E. Wilms*

4908 **Plasma population pharmacokinetic modelling of cefepime and enmetazobactam in patients with complicated urinary tract infections**
M. Machacek, F. Bernhard, M. Mameli, A. Belley, P. Knechtle (St. Louis, France)*

5078 **Large variability of unbound active fraction of ceftriaxone in contrast to ciprofloxacin in plasma of critically ill patients**
T. Ewoldt, A. Abdulla (Rotterdam, Netherlands), D. Gommers, A. Muller, H. Endeman, B. Koch*

5228 **Variability in ceftazidime exposure and probability of target attainment of different dosing regimens of ceftazidime in critically ill patients with a proven or assumed *Pseudomonas aeruginosa* infection**
A. Werumeus Buning (Amsterdam, Netherlands), C. Hodiamont, N. Lechner, P. Elbers, N. Juffermans, R. Mathot, R. Van Hest*

5902 **The DECISIVE study: defining beta-lactam concentration in intensive care unit patients - pharmacokinetics of cefepime, meropenem and piperacillin in critically ill patients across Malaysian intensive care units**
M. Abdul-Aziz (Brisbane, Australia), M. Rozali, M. Othman-Jailani, A. Abd Rahman, H. Sulaiman, N. Atiya, S. Adiraju, S. Wallis, W. Wan-Mat, M. Mazlan, M. Jamaluddin, S. Hasan, B. Mat Nor, J. Roberts*

7966 **Intravenous amoxicillin in patients with various degrees of renal function: are we dosing adequately?**
F. De Velde, A. Abdulla, A. Muller, T. Van Gelder, B. Koch (Rotterdam, Netherlands)*

8074 **Dose optimization of carbapenems in critically ill patients for highly resistant *Klebsiella pneumoniae* environment: population pharmacokinetics and simulations**
A. Truong, D. Co, D. Vu (Hanoi, Vietnam), H. Nguyen, D. Hong Gam, N. Tran, D. Le, N. Vu, H. Pham, C. Bui, T. Trinh, Q. Dang, G. Nguyen, J. Lipman, J. Roberts*

8785 **A Monte Carlo simulation modelling meropenem bolus to prolonged infusion dosing and expected suppression of resistance in *Pseudomonas aeruginosa***
S. Moore (Louisville (KY), United States), M. Kays, C. Cheatham*

Session accepted as Paper Poster Session

Clinical trials: PK and dosing

832 **Can gentamicin concentrations be used to estimate glomerular filtration rate in intensive care unit patients?**
A. Smekal (Stockholm, Sweden), M. Swartling, M. Furebring, E. Nielsen, A. Larsson, M. Lipcsey*

1950 **Retrospective evaluation of appropriate dosing of cefmetazole for invasive urinary tract infection due to ESBL-producing *Escherichia coli***
K. Hayakawa, Y. Matsumura, Y. Hamada, S. Saito, M. Nagashima, K. Uemura, N. Ohmagari, Y. Doi (Pittsburgh, United States)*

3174 **Clinical and economic outcome evaluation of cefepime 4 grams/day extended infusion in pneumonia and sepsis**
E. Dionne, A. Khole, M. Campion (Worcester, United States)*

3973 **A phase I study in healthy volunteers to assess the absolute bioavailability of the bilayer tablet of sulopenem etzadroxil with probenecid**
M. Dunne (Old Saybrook, United States), M. Dai, R. Zhou, S. Aronin, J. Wald*

4426 **Human mass balance study of enmetazobactam using 14C analysed by AMS**
P. Motta (Saint-Louis, France), S. English, P. Barth*

5246 **Factors associated with inadequate intravenous colistin dosages: results from a multi-centre, cross-sectional study**
M. Mirabella (Genoa, Italy), D. Giacobbe, A. Vena, C. Saffioti, M. Rinaldi, A. Losito, F. Raffaelli, M. Mikulska, M. Giannella, P. Viale, M. Tumbarello, M. Bassetti*

5581 **The trouble with gentamicin: a realist evaluation exploring two distinct protocols for prescribing gentamicin in hospital settings**
N. Dyar (Barrack Road, United Kingdom), K. Mattick, R. Bethune*

Session accepted as Mini-oral ePoster Session

Drug combinations against multi-resistant bacteria

119 **Dynamic *in vitro* pharmacodynamics evaluation of piperacillin/tazobactam-tobramycin combination therapy against *Escherichia coli* and *Klebsiella pneumoniae* clinical isolates**
C. Sumi (Brisbane, Australia), A. Heffernan, S. Naicker, K. Cottrell, P. Harris, F. Sime, J. Roberts*

1187 **Effect of antiretroviral therapy on resistant *Escherichia coli***
R. Hammond (St Andrews, United Kingdom), A. Coates, S. Gillespie*

1224 **Exebacase resensitises methicillin-resistant *Staphylococcus aureus* to oxacillin in a rabbit model of infective endocarditis**
J. Oh, D. Lehoux, C. Cassino, W. Abdelhady, Y. Xiong, A. Bayer, R. Schuch (Yonkers, United States)*

1885 **Optimising the combination of ceftazidime/avibactam and gentamicin against KPC-producing *Klebsiella pneumoniae* (KPC-Kp) with aminoglycoside-modifying enzymes**
Y. Huang, K. Sokolowski, A. Rana, N. Kadiyala, Z. Bulman (Chicago, United States), F. Krapp, E. Ozer, A. Hauser*

4916 ***In vivo* bactericidal activity of minocycline and rifampicin combination in a lung infection model in neutropenic mice**
W. Kloezen, A. Van Der Meijden, H. Van Der Spek, M. Ten Kate, J. Mouton, A. Muller, J. Meletiadis, S. Van Den Berg (Rotterdam, Netherlands)*

7002 **Evaluation of the interactions of polymyxin B in combination with aztreonam, minocycline, meropenem and rifampicin against NDM- and OXA-48-like producing *Escherichia coli***
A. Olsson (Uppsala, Sweden), M. Hong, H. Al Farsi, C. Giske, P. Lagerbäck, T. Tängdén*

7570 **Dose-dependent *in vitro* interactions of colistin with meropenem against carbapenem-resistant Gram-negative bacteria**
J. Lellouche (Tel-Aviv, Israel), M. Amar, D. Schwartz, A. Nutman, G. Daikos, A. Skiada, E. Durante Mangoni, Y. Dishon, R. Bitterman, D. Yahav, V. Daitch, M. Bernardo, D. Lossa, L. Friberg, U. Theuretzbacher, L. Leibovici, M. Paul, Y. Carmeli*

Session accepted as Paper Poster Session

Drug combinations: 1+1 does not equal 2

2270 **Colistin, turns active an otherwise ineffective rifampicin-linezolid combination in Gram-negatives**
E. Armengol Rivero (Barcelona, Spain), I. Perez-Guillen, M. Jorba, R. Herraez Moral, J. Sierra*

2644 **Pharmacodynamic analysis of meropenem in combination with a novel ß-lactamase inhibitor ANT2681 against New Dehli metallo ß-lactamase-producing *Escherichia coli***
A. Johnson (Liverpool, United Kingdom), L. Mcentee, N. Farrington, A. Kirby, R. Kolamunnage-Dona, M. Everett, M. Zalacain, C. Sable, L. Alibaud, N. Harper, S. Das, W. Hope*

2715 **Evaluation of omadacycline alone and in combination with rifampin against biofilm-producing *Staphylococcus aureus* and *Staphylococcus epidermidis***
T. Morrisette (Detroit, United States), K. Lev, R. Kebriaei, J. Abdul-Mutakabbir, M. Rybak*

3318 **Predicting antistaphylococcal effects of daptomycin and gentamicin combinations in an *in vitro* dynamic model using MICs determined at pharmacokinetically-derived concentration ratios**
M. Golikova, E. Strukova, Y. Portnoy, S. Zinner (Cambridge, United States), A. Firsov*

3357 **MPC-based prediction of anti-mutant effects of linezolid/daptomycin combinations against *Staphylococcus aureus*: a study in an *in vitro* dynamic model**
K. Alieva (Moscow, Russian Federation), M. Golikova, E. Strukova, Y. Portnoy, S. Zinner, A. Firsov*

3443 **Combined effect of fosfomycin and amikacin against fosfomycin-heteroresistant *Escherichia coli* isolates**
I. Portillo Calderón (Seville, Spain), M. Ortiz Padilla, B. De Gregorio-Iaria, V. Merino Bohórquez, J. Blazquez, J. Rodríguez-Baño, J. Rodriguez Martinez, A. Pascual Hernandez, F. Docobo Perez*

3514 **Imipenem/sulbactam, a repurposed drug combination for the treatment of MDR *Acinetobacter baumannii* infections**
M. Meiqi Tan, L. Phee, J. Standing, D. Wareham (London, United Kingdom)*

4639 **Activity of enmetazobactam in combination with cefepime in a murine urinary tract infection model challenged with an ESBL-producing isolate of *Escherichia coli***
C. Vingsbo Lundberg, A. Belley, P. Knechtle (St. Louis, France)*

4734 **Antibacterial activity of aztreonam-epigallocatechin gallate combinations versus multidrug-resistant strains of *Acinetobacter baumannii***
J. Betts, K. Lucassen, J. Salguero-Bodes, M. Hornsey, H. Seifert, R. La Ragione, P. Higgins (Cologne, Germany)*

4821 **Cannabidiol synergic antimicrobial activity combined with polymyxin B (PB) against PB susceptible and resistant Gram-Negative bacilli**
N. De Lima Martins Abichabki (Ribeirao Preto, Brazil), L. Zacharias, T. Ogasawara, F. Campioni, A. Seribelli, J. Falcão, A. Zuardi, J. Hallak, J. Crippa, A. Darini, L. Andrade*

4927 **Efficacy of ceftolozane-tazobactam in combination with colistin against extensively drug-resistant *Pseudomonas aeruginosa* including high risk clones, in an *in vitro* pharmacodynamic model**
M. Montero (Barcelona, Spain), S. Domene Ochoa, C. Lopez Causape, B. Vanscoy, S. Luque, L. Sorlí, A. Angulo, E. Padilla, N. Prim, V. Pomar, A. Rivera, N. Campillo, S. Grau, P. Ambrose, A. Oliver, J. Horcajada*

5263 **Antimicrobial combination activity of vancomycin and antimalarial quinacrine against methicillin-resistant *Staphylococcus aureus* isolated from infected diabetic foot ulcers**
A. Oliveira Da Silva (Vila Real, Portugal), D. Correia, V. Silva, J. Carvalho, A. Castro, G. Igrejas, R. Rego, P. Poeta*

5697 ***In vitro* activity of imipenem/relebactam among Gram-negative clinical isolates in two Spanish tertiary hospitals**
M. Peñuelas Martínez, C. García Salguero, M. Iñigo, F. Candel (Madrid, Spain), J. Del Pozo, E. Culebras*

6117 **Combinations activity of azidothymidine and colistin against colistin-resistant *Klebsiella pneumoniae* in a murine model of urinary tract infection**
R. Odedra, D. Corbett, A. Coates, D. Molnar, Y. Hu, P. Warn, P. Thommes (Cheshire, United Kingdom)*

6144 **Gliotoxin, a new candidate against methicillin-resistant *Staphylococcus aureus* showing synergistic effect with classical antimicrobial drugs in *Caenorhabditis elegans* infection model**
P. Esteban (Zaragoza, Spain), S. Redrado, L. Comas, C. Seral, J. Pardo Jimeno, M. Arias, E. Gálvez*

6482 **Evidence from *in vitro* pharmacokinetic/pharmacodynamic studies on polymyxin-based combination therapies to treat infections due to carbapenem-resistant Gram-negative bacteria**
M. Chiamenti (Mantova, Italy), D. Bragantini, L. Scudeller, L. Piddock, F. Franceschi, S. Ellis, M. Sanguinetti, G. Menchinelli, A. Savoldi, E. Righi, E. Tacconelli*

7987 **Pharmacodynamic properties of amoxicillin-clavulanic acid in a neutropenic mouse thigh infection model**
A. Muller (The Hague, Netherlands), W. Kloezen, B. De Winter, A. Van Der Meijden, H. Van Der Spek, M. Ten Kate, S. Van Den Berg, J. Meletiadis*

9223 **Tackling resistance to carbapenem and colistin in clinical isolates of *Acinetobacter baumannii***
R. Ravichandran, D. Machado (Lisbon, Portugal), M. Viveiros, C. Kroeger, M. Martins*

Session accepted as Paper Poster Session

Evaluating and improving antimicrobial drug prescription in inpatients

1057 **Impact of an antimicrobial stewardship team on the de-escalation of carbapenem use in a tertiary hospital**
M. Maeda (Tokyo, Japan), Y. Nagatomo, Y. Naito, E. Akima, K. Nakane, K. Ugajin, M. Yoshikawa, T. Takuma, I. Tokimatsu, Y. Niki*

1058 **Essential human resources for antimicrobial stewardship teams in Japan: estimates from a nation-wide survey**
M. Maeda (Tokyo, Japan), Y. Muraki, T. Kosaka, T. Yamada, Y. Aoki, M. Kaku, M. Seki, Y. Tanabe, N. Fujita, Y. Niki, K. Morita, K. Yanagihara, K. Yoshida, T. Kawaguchi*

1297 **Design and implementation of a Real-Time Carbapenem List (RTCL) using Electronic Patient Record (EPR) to enable Post Prescription Review and Feedback (PPRF) as a carbapenem stewardship strategy for resource-constrained antimicrobial stewardship team**
C. Hickey (Dublin, Ireland), M. Kelly, G. Courtney, K. Flannery, B. Boyle*

1452 **Mandatory computerised decision support system is necessary for sustained control of carbapenems and piperacillin-tazobactam usage in a multi-faceted hospital antimicrobial stewardship programme: interrupted time series with segmented regression analysis**
B. Chua (Singapore, Singapore), S. Heng, L. Ang, S. Tan, H. Tay, M. Yap, J. Quek, C. Teng, B. Young, R. Lin, B. Ang, T. Lee, D. Lye, T. Ng*

2148 **Multidisciplinary treatment model led by infectious physician reduce the unreasonable use of antibiotics and improve the efficacy in the treatment of patients with diabetic foot infection**
L. Xiangyan (Beijing, China), X. Qi, S. Tian, S. Jiang, R. He*

2176 **Outcomes of the antibiotic stewardship programme in a teaching hospital of southern Italy : an interrupted time-series analysis**
M. Macera (Naples, Italy), F. Calò, L. Onorato, N. Coppola*

2225 **Impact of antibiotic stewardship programme in an intensive care unit in Brazil**
W. Freitas (Rio de Janeiro, Brazil), M. Silvana Alves, S. Nouer*

2649 **Epidemiology and management of pneumonia based on data entry in a computerised decision support system for antimicrobial prescriptions: a retrospective study**
G. Catho (Geneva, Switzerland), A. Ranzani, J. Stirnemann, V. Prendki, B. Huttner*

3107 **Adherence to antibiotic guidelines at a Danish university hospital, a quantitative and qualitative prospective study**
P. Rasmussen (Aalborg, Denmark), S. Sørensen, L. Mygind*

3160 **Implementing antibiotic stewardship in humanitarian contexts: MSF's experience**
A. Filali (Paris, France), R. Kanapathipillai, L. Noonan, B. Mollo, J. Michel, N. Hurtado, M. Nada, C. Mills*

3423 **Setting up antimicrobial stewardship programme in tertiary area hospitals in India**
K. Walia (New Delhi, India), V. Ramasubramanian, V. Ohri*

3499 **Improving the adequacy of empirical antimicrobial therapy at regional level in bacteraemia due to *Escherichia coli* of urinary source: an intervention of the VINCat programme (infection control and antimicrobial stewardship Catalonian programme)**
J. Horcajada (Barcelona, Spain), S. Hernández, I. Grau, R. Pérez-Vidal, L. Boix-Palop, J. Farguell, C. Valls, S. Gómez-Zorrilla, M. Quesada, H. Monzon, A. Jóver-Sainz, J. Tricas, J. Llaberia, D. Blancas, O. Gasch Blasi, E. Palau, S. Grau Cerrato*

3661 **Review of the hospital empiric antibiotic guideline in treating community-onset bloodstream infection in a Singapore tertiary hospital**
G. Foo (Singapore, Singapore), J. Somani, C. Teng, T. Tan, K. Chew*

4018 **Patient level predictors of vancomycin never events**
J. Liu (Downers Grove, United States), N. Mercuro, S. Davis, P. Yarnold, T. Patel, L. Petty, G. Pais, K. Kaye, M. Scheetz*

4025 **The antimicrobial stewardship in surgery (ASCHI) project: long-term follow-up**
A. Chiesa (Brescia, Italy), A. Zoncada, N. Brianese, E. Van Hauwermeiren, A. Ferraresi, S. Lorenzotti, C. Fornabaio, P. Lanza, A. Patroni, C. Tinelli, N. Pasquali, M. Rovatti, M. Martinotti, A. Pan*

4085 **Increase of parenteral antibiotic use in Japan could be explained by the society aging**
R. Koizumi (Tokyo, Japan), Y. Kusama, Y. Gu, M. Ishikane, Y. Muraki, D. Yamasaki, M. Tanabe, N. Ohmagari*

4371 **Persuading the prescriber: the impact of prospective audit with feedback on hospital antibiograms**
M. Chatzopoulou (Larissa, Greece), A. Kyriakaki, L. Reynolds*

4914 **Transforming care through data transparency: impact on cellulitis therapy standardisation**
S. Minor (Maitland, United States), N. Sankar, J. Burns, K. Calise, V. Herrera*

5056 **Infectious disease consultation reduces time to appropriate antimicrobial treatment in Gram-negative bacteraemia: data from an area of high prevalence of antibiotic resistance**
V. Da Prat (Milan, Italy), L. Galli, M. Moro, P. Cichero, B. Castiglioni, C. Oltolini, C. Tassan Din, A. Poli, C. Ossi, A. Andolina, A. Ambrosio, A. Lazzarin, A. Castagna, P. Scarpellini, M. Ripa*

5426 **Prospective observational study of antimicrobial stewardship programmes in Brazil: preliminary results**
R. Menezes, M. Gonçalves, M. Costa, E. Krummenauer, C. Reuter, J. Renner, M. Carneiro (Santa Cruz do Sul, Brazil)*

5779 **Antibiotic use indicators: which and how? Pilot study of 3 indicators in French hospitals**
M. Coppry Marries Firpionn (Bordeaux, France), M. Péfau, A. Jouzeau, L. Dugravot, A. Chabaud, E. Couve-Deacon, C. Martin, M. Ploy, O. Ali-Brandmeyer, J. Claver, R. Gauzit, C. Rabaud, L. Simon, A. Rogues, C. Dumartin*

6116 **The appropriateness of prescribing antimicrobials in an infectious emergency outpatient department**
M. Logar (Ljubljana, Slovenia), I. Korpar, M. Uršič*

6442 **Personal experience and availability of surveillance data, diagnostics and therapeutics are the main drivers for treating carbapenem-resistant Gram-negative bacteria infections**
A. Savoldi (Verona, Italy), E. Carrara, L. Piddock, F. Franceschi, S. Ellis, E. Tacconelli*

6712 **Quality of documentation on antibiotic treatment in medical records: evaluation of the long-term impact of an antimicrobial stewardship intervention**
C. Vercheval (Liege, Belgium), P. Damas, F. Frippiat*

7102 **Impact of the inpatient infectious disease consultations at a tertiary care university hospital**
J. Choucair (Beirut, Lebanon), D. Jaafar, M. Chedid, E. Haddad, G. Saliba, R. Waked*

7176 **Implementing an antibiotic stewardship programme without increasing the surgical site infection rate in a highly antibiotic-resistant setting**
W. Harb, F. Mansour, J. Mourad, M. Trelles, A. Williams (Luxembourg, Luxembourg)*

7257 **Persuasive antimicrobial stewardship intervention in the context of a KPC outbreak: a controlled interrupted time-series analysis**
N. Rocha Pereira (Porto, Portugal), P. Figueiredo, S. Correia, S. Shahriari, J. Neves, J. Teixeira, J. Paiva, C. Alves, A. Azevedo*

7554 **Monitoring of interactions with clarithromycin: evaluation of routinely performed drug interaction checks**
A. Weber (Munich, Germany), J. Jung, R. Draenert*

7559 **SAVE: Stewardship Antibiotica VErona: a new model of stewardship to reduce antimicrobial overuse in a setting with high levels of antimicrobial resistance rates**
E. Carrara, M. Sibani (Verona, Italy), L. Barbato, F. Mazzaferri, N. Salerno, F. Soldani, G. Lo Cascio, P. Minuz, O. Olivieri, V. Di Francesco, L. Bissoli, C. Bovo, E. Tacconelli*

7639 **Antimicrobial stewardship in oral and maxillofacial surgery: melting the iceberg**
I. Joost (Düsseldorf, Germany), M. Kempe, L. Schorn, C. Mackenzie*

7640 **Implementation of a homegrown electronic antimicrobial prescribing authorisation process at King Abdulaziz Medical City (KAMC) in Saudi Arabia**
N. Shamas (Riyadh, Saudi Arabia), M. Al Ahmadi, A. Alsaedi, D. Naeem, D. Aljefri, M. Aseeri, M. Alshamrani*

7701 **Digital antimicrobial dashboard facilitates antimicrobial stewardship in a large London teaching hospital**
L. Whitney, M. Gilchrist (London, United Kingdom), A. Chavda, A. Kinderlerer, S. Mookerjee, A. Holmes*

8203 **The role of co-morbidities in the prescription of carbapenemes**
A. Makina (Athens, Greece), G. Poulakou, E. Liakopoulou, A. Makina, A. Papadopoulos, L. Sybardi*

8358 **The case for infectious disease-centered antimicrobial stewardship: a 10-year experience at Saint George Hospital**
S. Saliba (Beirut, Lebanon), O. Zmerli, A. Chamieh, C. Afif, E. Azar*

8426 **Antimicrobial stewardship practices in Brazil: where are we?**
R. Menezes, M. Gonçalves, M. Costa, E. Krummenauer, J. Renner, C. Reuter, M. Carneiro (Santa Cruz do Sul, Brazil)*

9412 **A critical appraisal of the new antibiotic prescription chart using HAPPI (Hospital Antibiotic Prudent Prescribing Indicators) in a large UK district hospital**
A. Liu (Cheltenham, United Kingdom)*

9575 **Clinical and financial impact of an empiric antibiotic prescribing policy: single department experience**
L. Melo, M. Barosa, R. Marques (Amadora, Portugal), J. Delgado Alves*

9596 **eHealth-based antimicrobial stewardship programme focused on individual prescriptions assessment: sustainability at 4 years**
C. Palos (Loures, Portugal), L. França, P. Rodrigues, R. Tavares, A. Silva*

Session accepted as Mini-oral ePoster Session

From new TDM technology to optimised dosing

318 **Renal function and albumin are drivers for exposure of flucloxacillin in critically ill patients**
N. Jager (Amsterdam, Netherlands), R. Van Hest, R. Brüggemann, J. Lipman, J. Roberts*

1153 **Continuous infusion and outpatient parenteral antimicrobial therapy with ceftazidime-avibactam: evaluation of efficacy based on therapeutic drug monitoring**
V. Goncette, N. Layios, F. Frippiat (Liège, Belgium)*

1334 **Administration of ceftazidime to patients undergoing haemodialysis: are trough levels consistently above the EUCAST breakpoints for *Enterobacterales* and *Pseudomonas* ?**
A. Tamigniau, D. Govaerts, B. Guillaume, S. Treille, S. Cherifi, C. Lelubre, I. Delattre, P. Tulkens, D. Remy (Brussels, Belgium)*

1419 **Dose optimisation of cefotaxime in critically ill patients: a population pharmacokinetic study**
E. Roelofsen (Zuid Holland, Netherlands), B. De Winter, A. Abdulla, H. Endeman, A. Dijkstra, A. Muller, B. Koch*

4034 **Alternative, cost-effective dosage regimens of ceftolozane/tazobactam in patients with renal impairment: a simulation analysis**
L. Dheyriat, L. Bourguignon, M. Leroy, T. Ferry, S. Goutelle (Lyon, France)*

4087 **Therapeutic drug monitoring of levofloxacin using a mobile microvolume-UV/VIS spectrophotometer and derivative spectroscopy**
J. Alffenaar (Sydney, Australia), E. Jongedijk, C. Van Winkel, M. Sariko, S. Heysell, S. Mpagama, D. Touw*

4855 **Pharmacokinetic variability and target attainment of meropenem in critically ill patients undergoing extracorporeal membrane oxygenation: a matched-cohort analysis**
M. Gijsen (Leuven, Belgium), E. Dreesen, Y. Debaveye, J. Wauters, I. Spriet*

7597 **Continuous infusion of cefoxitin is associated with higher probability of target attainment in patients infected with ESBL-producing *Enterobacteriaceae***
P. Benoit (Paris, France), A. Mizrahi, A. Le Monnier, N. El Helali*

7734 **Development of a dried blood spot assay to quantify levofloxacin drug concentrations for personalised dose adjustment in multidrug-resistant tuberculosis in endemic settings**
S. Mohamed (Charlottesville, United States), S. Stroup, M. Sariko, E. Jongedijk, D. Touw, P. Mbelele, S. Mpagama, J. Alffenaar, S. Heysell*

Session accepted as 2-Hour Oral Session

Hospital antimicrobial stewardship interventions: models, tools, experience, impact!

1625 **Effects of prospective review and feedback and mandatory computerised decision support system for carbapenems and piperacillin-tazobactam on other broad-spectrum antibiotic use: interrupted time series with segmented regression analysis**
B. Chua (Singapore, Singapore), S. Heng, L. Ang, S. Tan, H. Tay, M. Yap, J. Quek, C. Teng, B. Young, R. Lin, B. Ang, T. Lee, D. Lye, T. Ng*

1904 **The positive impact of infectious diseases consultation on antimicrobial appropriateness in hospitalised patients with antimicrobial stewardship oversight: a propensity-score matched study**
J. Bork (Baltimore, United States), K. Claeys, E. Heil, M. Banoub, S. Leekha, J. Sorkin, M. Kleinberg*

2695 **Impact of a restrictive antibiotic policy on the emergence of extended-spectrum ß-lactamase producing *Enterobacteriaceae* in the intensive care unit: a quasi-experimental observational study**
C. Le Terrier (Geneva, Switzerland), M. Vinetti, R. Richard, B. Jarrige, S. Breurec, M. Carles, G. Thiéry*

3978 **Effects of fluoroquinolone-sparing empiric therapy guideline implementation in a collaborative hospital network**
E. Dodds Ashley (Durham, United States), T. Jones, M. Johnson, A. Davis, A. Dyer, A. Nelson, D. Anderson, R. Moehring*

4290 **An antibiotic stewardship intervention in the emergency department leads to improved antibiotic prescription especially during normal working hours and among younger faculty**
M. Demichel, S. Horster, J. Jung, A. Weber, A. Lechner, R. Draenert (Munich, Germany)*

4822 **Use of antimicrobial stewardship smartphone applications by physicians and appropriate prescribing in hospitals: a systematic review**
R. El Helou (Amsterdam, Netherlands), D. Foudraine, G. Catho, A. Peyravi Latif, N. Verkaik, A. Verbon*

5663 **An interoperable informatics application for the workflow improvement of an antimicrobial stewardship programme in a tertiary hospital**
M. Alaguero, M. Telenti, E. Garcia-Prieto, E. Garcia, T. Suarez-Zarracina, C. Calzón, L. Forcelledo Espina, L. López-Amor, E. Salgado, L. Villa, L. Fernandez-Hernandez, E. Llaneza, M. Sánchez-Núñez, J. Fernández (Oviedo, Spain)*

6336 **Effectiveness and cost-effectiveness of antimicrobial stewardship programmes in French acute care hospitals**
A. Perozziello (Paris, France), X. Lescure, S. Deuffic-Burban, L. Kardas-Sloma, L. Binh Luong Nguyen, Y. Yazdanpanah, J. Lucet*

9558 **Comparative effectiveness of stewardship interventions in reducing *Clostridioides difficile* infection incidence**
K. Brown (London, United Kingdom), K. Schwartz, B. Langford, C. Diong, G. Garber, N. Daneman*

Session accepted as Mini-oral ePoster Session

Hot news from clinical trials

771 **RESTORE-IMI 2: randomised, double-blind, phase III trial comparing efficacy and safety of imipenem/cilastatin (IMI)/relebactam (REL) versus piperacillin/tazobactam (PIP/TAZ) in adult patients with hospital-acquired or ventilator-associated bacterial pneumonia (HABP/VABP)**
I. Titov, R. Wunderink, A. Roquilly, D. Rodriguez Gonzalez, A. David-Wang, H. Boucher, K. Kaye (Ann Arbor, United States), M. Losada, J. Du, R. Tipping, M. Rizk, M. Patel, M. Brown, N. Kartsonis, J. Butterton, A. Paschke, L. Chen*

1192 **Meropenem-Vaborbactam (VABOREM) in treatment of patients with hospital- and ventilator-acquired pneumonia (HABP/VABP) and bacteraemia due to carbapenem-resistant *Enterobacteriaceae***
M. Bassetti, F. Menichetti, G. Daikos, S. Cammarata, K. Fusaro, D. Zinzi (Pomezia, Italy)*

1594 **Ceftobiprole compared with vancomycin plus aztreonam in the treatment of acute bacterial skin and skin-structure infections: results of a phase III, randomised, double-blind trial (TARGET)**
J. Overcash, C. Kim, R. Keech, I. Gumenchuk, B. Ninov, Y. Gonzalez-Rojas, M. Waters, S. Simeonov, M. Engelhardt, M. Saulay, D. Ionescu, J. Smart, M. Jones, K. Hamed (Basel, Switzerland)*

2792 **Empowering nurses to assess patient-reported antibiotic allergies: a pilot implementation study of a validated antibiotic allergy assessment tool**
M. Devchand (Heidelberg, Australia), E. Cohen, S. Walker, K. Chua, N. Holmes, S. Bury, K. Garrett, J. Trubiano*

4174 **Fosfomycin for the treatment of neonatal sepsis**
P. Williams (Clovelly, Australia), J. Berkley, O. Christina, S. Murunga, A. Walker, B. Nyaoke, R. Omollo, S. Ellis, E. Correia, M. Sharland*

6791 **Pharmacokinetics and pharmacodynamics of dalbavancin in the clinical setting**
G. Stroffolini (Turin, Italy), S. Biffi, A. De Nicolò, A. Barco, S. Bonora, G. Di Perri, M. Antonucci, A. Briozzo, V. Avataneo, G. Cariti, A. D'Avolio*

7976 **Risk factors (derived from host, pathogen and disease) did not affect the efficacy of delafloxacin monotherapy in acute bacterial skin and skin structure infections trials**
B. Pizà Vallespir, S. Biliotti, A. Nizzardo, A. Nuti, S. Cammarata, D. Zinzi (Pomezia, Italy)*

Session accepted as Paper Poster Session

Innovative PK/PD studies

1607 **Evaluating prophylactic post cardiac transplantation amphotericin B treatment by simulation**
C. Mane (Toulouse, France), V. Duhalde, I. Labadens, O. Cointault, D. Concordet, P. Gandia*

2252 **Influence of inflammation on pharmacokinetics and protein binding of tedizolid in healthy volunteers**
B. Wulkersdorfer (Vienna, Austria), C. Schörgenhofer, P. Matzneller, V. Al Jalali, M. Bauer, E. Lackner, F. Kees, C. Dorn, B. Jilma, M. Zeitlinger*

2271 **Pharmacokinetic/pharmacodynamic analysis of tedizolid phosphate compared to linezolid for the treatment of infections caused by Gram-positive bacteria**
A. Aguirre Quinonero (Vitoria, Spain), A. Rodríguez, M. Solinís, A. Canut*

2592 **A mechanism-based pharmacokinetic/pharmacodynamic model based on pharmacokinetic and static time-kill data alone can predict the *in vitro* bacterial regrowth of 3 fluoroquinolone-resistant *Escherichia coli* strains after dynamic exposure**
R. Michelet (Berlin, Germany), J. Seeger, C. Kloft*

4112 **Rifampicin reduces tedizolid concentrations in healthy volunteers**
S. Lee (Singapore, Singapore), D. Hee*

4780 **Current evidence on dose reduction of antibiotics in patients with impaired renal function: a systematic review**
S. De Vroom (Amsterdam, Netherlands), F. Van Daalen, S. Zieck, R. Mathôt, R. Van Hest, S. Geerlings*

5292 **Systematic review on estimated rates of nephrotoxicity and neurotoxicity in patients treated with polymyxins**
F. Wagenlehner (Giessen, Germany), E. Lucenteforte, F. Pea, J. Pogue, A. Soriano, L. Tavoschi, V. Steele, A. Henriksen, C. Longshaw, D. Manissero, R. Pecini*

5349 **Frequency and impact of differences across Chronic Kidney Disease Epidemiology Collaboration (CKD-EPI) and Cockcroft-Gault (C/G) estimations of glomerular filtration rate on antimicrobial dosing**
D. Francis, B. Potoski (Gibsonia, United States)*

7542 **Posaconazole therapeutic drug monitoring in high-risk haematology patients receiving antifungal prophylaxis (SAPHIR-study)**
C. Padoin (Bobigny, France), J. Gangneux, M. Michallet, E. Saillio, A. Kumichel, P. Regis, P. Ceballos, T. Gastinne, A. Pigneux*

7776 **Model-informed exposure response analyses for ceftazidime and levofloxacin against *Klebsiella pneumoniae* and *Pseudomonas aeruginosa* in murine thigh infection models**
Y. Jiao, K. Lin, D. Sutaria, J. Chia, D. Nicole Griffith, C. Chiang, Y. Yeh, J. Chien, J. Lo, N. Shah, X. Tao, L. Miesel, J. Bulitta (Orlando, United States)*

8224 **Population pharmacokinetics and pharmacodynamics of colistin A and B in the murine thigh infection model with *Pseudomonas aeruginosa*: an integrated experimental and modelling approach**
Y. Jiao, J. Chia, K. Lin, D. Nicole Griffith, D. Sutaria, C. Chiang, Y. Yeh, J. Chien, J. Lo, N. Shah, X. Tao, L. Miesel, J. Bulitta (Orlando, United States)*

Session accepted as 2-Hour Oral Session

Innovative PK/PD tools optimise drug development and patient care

3070 **Exploring the utility of optimised meropenem exposures against carbapenem-resistant *Escherichia coli* with and without KPC**
C. Jones, E. Kline, A. Iovleva, Y. Doi, R. Shields (Pittsburgh, United States)*

4816 **Pharmacodynamic properties of minocycline monotherapy and combined with polymyxin B in a lung model in neutropenic mice**
H. Van Der Spek, W. Kloezen, A. Van Der Meijden, M. Ten Kate, J. Mouton, A. Muller, J. Meletiadis, S. Van Den Berg (Rotterdam, Netherlands)*

4886 **The predictive performance of a model averaging approach is superior over using distinct population pharmacokinetic models in model-informed precision dosing of vancomycin**
D. Uster (Hamburg, Germany), S. Stocker, J. Carland, R. Day, S. Wicha*

5129 **Optimising pharmacokinetics/pharmacodynamics of β-lactam/β-lactamase inhibitor combinations against high inocula of extended-spectrum β-lactamase-producing bacteria**
V. Tam (Houston, United States), H. Abodakpi, W. Wang, K. Ledesma, P. Merlau, K. Chan, R. Altman, A. Sofjan, T. Tran, M. Nikolaou*

5421 **Vancomycin for patients with MRSA bloodstream infections (BSIs) is nephrotoxic even within the recommended area under the curve (AUC) therapeutic exposure range**
T. Lodise (Watervliet, United States), M. Scheetz, J. Carreno, T. Holland*

8194 **Sulbactam-durlobactam (ETX2514) activity against carbapenemase-producing *Acinetobacter baumannii* in the presence or absence of imipenem or meropenem using an *in vitro* hollow-fibre infection model**
Y. Jiao, A. Tanudra, J. Bulitta, J. O'Donnell (Waltham, United States)*

8958 **Which dosage of amoxicillin in infective endocarditis? Development of a simple predictive medicine tool for adaptation**
A. Rambaud (Nantes, France), B. Gaborit, D. Colin, P. Le Turnier, R. Lecomte, N. Asseray Madani, A. Leroy, G. Deslandes, E. Dailly, P. Jolliet, D. Boutoille, R. Bellouard, M. Grégoire*

Session accepted as Mini-oral ePoster Session

Is your drug where it should be? Target-site pharmacokinetics

4865 **Comparative protein binding *in vitro* and *in vivo*: quantitative insights into binding dynamics by pharmacometrics**
S. Wicha (Hamburg, Germany), B. Wulkersdorfer, E. Kurdina, P. Matzneller, V. Al Jalali, M. Vossen, S. Riesenhuber, E. Lackner, C. Dorn, F. Kees, M. Zeitlinger*

5022 **Cefazolin meningeal diffusion compared to cloxacillin for the treatment of methicillin-susceptible *Staphylococcus meningitis***
P. Le Turnier, M. Grégoire, G. Deslandes, K. Lakhal, D. Colin, R. Lecomte, J. Talarmin, V. Dubee, R. Bellouard, D. Boutoille, A. Leroy, B. Gaborit (Nantes, France)*

5369 **Characterisation of ceftobiprole's cerebrospinal fluid penetration in patients with external ventricular drainage**
M. Castaldello (Brescia (Italy), Italy), M. Malla, V. Avataneo, M. Antonucci, A. De Nicolò, A. Librizzi, L. Guadrini, F. Turla, A. Di Paolo, F. Ceccherini, L. Galeotti, L. Signorini, A. D'Avolio, F. Rasulo, N. Latronico, S. Piva*

5733 **Ceftriaxone penetration into epithelial lining fluid: are dosing regimens sufficient for severe community-acquired pneumonia?**
A. Motos (Barcelona, Spain), R. Amaro, G. Li Bassi, F. Pagliara, M. Yang, H. Yang, J. Bobi, L. Fernandez Barat, E. Aguilera Xiol, M. Rigol, D. Nicolau, J. Kuti, A. Torres*

6348 **Probability of target attainment by conventional pharmacokinetic/pharmacodynamic targets is overestimated in obese patients receiving linezolid and meropenem**
D. Busse (Berlin, Germany), L. Ehmann, P. Simon, D. Petroff, N. Hartung, R. Michelet, W. Huisinga, H. Wrigge, C. Kloft*

7844 **Comparison of patients' brain microdialysate and cerebrospinal fluid concentrations versus time profiles of cefotaxime and metronidazole as representative antibiotic substrates or not of efflux transport systems**
A. Chauzy (Poitiers, France), S. Bouchene, N. Gregoire, W. Couet, O. Mimoz, S. Marchand, C. Dahyot-Fizelier*

Session accepted as Paper Poster Session

Linking antibiotic use with resistance

195 **Implementation and one-year results of antimicrobial stewardship programme in a tertiary reference hospital in San Jose, Costa Rica**
M. Ramirez-Cardoce (San Rafael, Costa Rica), C. Fernandez-Barrantes, E. Segura-Retana, E. Avendano-Fernandez*

245 **Carbapenem antimicrobial stewardship programme**
J. García-Rodríguez (Ferrol (Spain), Spain), B. Bardán-García, P. Juiz González, H. Álvarez-Díaz, A. Mariño-Callejo*

588 **Correlation between antibiotic resistance of main Gram-negative pathogens and antibiotic consumption in a general hospital of China**
Y. Cai (Beijing, China)*

1781 **Association between susceptibility to quinolones in *Escherichia coli* and tetracycline use in the community: analysis of 9 communities with a single model**
M. Vibet, F. Javaudin, M. Low, B. Gottesman, J. López-Lozano, E. Montassier, E. Batard (Nantes, France)*

2623 **Ten years of antimicrobial stewardship in a tertiary care hospital in northern Italy**
R. Aschbacher, C. Vedovelli, G. Spoladore, R. Binazzi, M. Falciani, P. Santa, E. Pagani, L. Pagani (Bolzano, Italy)*

3216 **Antibiotic utilisation and *Clostridoides difficile* rate: a 12-year time series and cross-correlation analysis**
D. Lye (Singapore, Singapore), S. Heng, L. Ang, S. Tan, H. Tay, M. Yap, B. Chua, J. Quek, T. Ng, T. Lee*

3502 **Antibiotic utilisation and carbapenem-resistant *Acinetobacter baumannii*: a 12-year time series and cross-correlation analysis**
T. Lee, S. Heng, L. Ang, S. Tan, H. Tay, M. Yap, B. Chua, J. Quek, T. Ng, D. Lye (Singapore, Singapore)*

3591 **Antibiotic utilisation and incidence rate of extended-spectrum beta-lactamases: a 12-year time series and cross-correlation analysis**
T. Lee (Singapore, Singapore), S. Heng, L. Ang, S. Tan, H. Tay, M. Yap, B. Chua, J. Quek, T. Ng, D. Lye*

4088 **Effect of short-term carbapenem restriction on the antimicrobial susceptibility of multidrug-resistant Gram-negative bacilli in an intensive care unit in Brazil**
R. Bandeira (Belo Horizonte, Brazil), M. Melo, B. Couto, G. Dias, L. Cardoso, A. Dornas*

4284 **Impact of antimicrobial stewardship and infection control programmes on the incidence of carbapenem-resistant *Pseudomonas aeruginosa*: a non-linear time-series analysis**
M. Meschiari (Modena, Italy), C. Nebot, A. Beyaert, M. Sarti, C. Venturelli, G. Orlando, J. Lopez Lozano, C. Mussini*

5122 **The impact of shortening antibiotic treatment duration on antimicrobial resistance carriage: a modelling study**
Y. Mo (Singapore, Singapore), M. Oonsivilai, C. Lim, A. Hernandez-Koutoucheva, R. Leon-Sampredo, J. Tosanguan, R. Niehus, B. Cooper*

6788 **Emergence of resistance in Gram-negative bacteria and correlation with antibiotic use in 52 Swiss intensive care units**
S. Barnsteiner (St. Gallen, Switzerland), F. Baty, W. Albrich, B. Babouee Flury, C. Pluess-Suard, A. Kronenberg, M. Schlegel, P. Kohler*

6866 **Antibiotic use and antimicrobial resistance in Northwestern China in 2017**
F. Liu (Xian, China), Y. Suo, J. Wang, W. Zingg*

7005 **Long-term impact of an antimicrobial stewardship programme implemented in a tertiary care Greek hospital on antibiotics consumption and on the incidence of carbapenem-resistant Gram-negative pathogens: an interrupted time-series analysis**
A. Markogiannakis, M. Samarkos, M. Gamaletsou (Athens, Greece), I. Deliolanis, N. Pantazis, F. Ntziora, M. Psichogiou, G. Rentziou, E. Malliarou, D. Bassoulis, E. Iliadi, N. Sypsas*

7313 **Impact of antibiotic stewardship strategies for *Clostridioides difficile* infection**
V. Bérot (Paris, France), P. Choinier, L. Drieux-Rouzet, J. Robert, H. Junot, A. Bleibtreu*

7637 **Ranking antibiotic classes by their potential impact on in-hospital selection of resistance: an ecological approach**
J. Shapiro (Lyon, France), L. Gilles, A. Myard-Dury, P. Girardo, A. Luzzati, M. Mary, J. Sauzon, B. Lafay, O. Dauwalder, F. Laurent, G. Lina, C. Chidiac, S. Couray-Targe, F. Vandenesch, F. Jean Pierre, J. Rasigade*

Session accepted as Paper Poster Session

More (on) OPAT

1388 **Results of an outpatient parenteral antimicrobial therapy programme in Spain**
J. Rodriguez Prida, S. Santos Seoane, C. Aparicio, J. Cueto-Felgueroso, C. Helguera, C. Martinez-Mugica, J. Moris, A. Rodriguez-Guardado (Oviedo, Spain)*

1563 **Risk factors for readmission among OPAT patients in the Netherlands**
S. Douiyeb (Amsterdam, Netherlands), J. De La Court, R. Schade, T. Minderhoud, F. Sombogaard, D. Lammers, K. Sigaloff*

1614 **Suitability of citrate buffered piperacillin/tazobactam via continuous infusion in outpatient parenteral antimicrobial chemotherapy (OPAT)**
F. Drummond, C. Jamieson (Birmingham, United Kingdom), L. Ozolina, A. Wilkinson*

3199 **From OPAT to COpAT in a regional New Zealand hospital**
M. Giola (Tauranga, New Zealand), J. Meyer, M. Addidle, V. Sathyendran, J. Chua*

3364 **Incidence of venous thromboembolism among patients receiving outpatient parenteral antimicrobial therapy at Sheffield Teaching Hospitals NHS Foundation Trust, UK: an observational study**
A. Keeley (London, United Kingdom), C. Keil, H. Hiles, N. Hopka, C. Durojaiye, K. Cartwright*

3889 **Dalbavancin: to OPAT or not to OPAT**
A. Richards (Beverley, United Kingdom), L. Maclachlan, M. Ivan, G. Barlow, K. Adams, P. Lillie, L. Cullen, K. O'Keeffe*

4095 **Multidisciplinary engagement improves monitoring of Outpatient Parenteral Antimicrobial Therapy (OPAT) in solid tumour patients at a comprehensive cancer centre**
A. Robins (Houston, United States), N. Dailey Garnes, P. Mcdaneld, M. Rowan, J. Bartek*

4275 **Suitability of ceftazidime for continuous infusion in outpatient parenteral antimicrobial therapy**
F. Drummond, C. Jamieson (Birmingham, United Kingdom), L. Ozolina, A. Wilkinson*

7259 **Suitability of ceftolozane/tazobactam (ZERBAXA) via continous infusion in outpatient parenteral antimicrobial chemotherapy (OPAT)**
F. Drummond, C. Jamieson (Birmingham, United Kingdom), L. Ozolina, A. Wilkinson*

9020 **The impact of antimicrobial stewardship for outpatient parenteral antimicrobial therapy**
A. Vivero Larraza (Barcelona, Spain), N. Sopena, M. Bonet, E. De Felipe, L. Mateu Prunonosa, E. Reynaga Sosa, H. Manjón Navarro, J. Joseph Vilaplana, A. Arguedas Hernandez, G. Bonet*

Session accepted as Paper Poster Session

New drug development and emerging clinical data

846 **Outcomes in ventilated patients with hospital-acquired/ventilator-associated bacterial pneumonia (HABP/VABP) treated with imipenem/cilastatin (IMI)/relebactam (REL) versus piperacillin/tazobactam (PIP/TAZ): subgroup analysis of the RESTORE-IMI 2 randomised, controlled trial**
A. Roquilly, I. Titov, D. Rodriguez Gonzalez, A. David-Wang, R. Wunderink, H. Boucher, K. Kaye, M. Losada, J. Du, K. Mahoney, M. Patel, M. Brown, J. Butterton, A. Paschke, L. Chen (Kenilworth, NJ, United States)*

1190 **Systematic evaluation of development pathways of centrally-approved antibiotics in Europe including an innovative graphical illustration method**
A. Jorda (Vienna, Austria), M. Zeitlinger*

1610 **An international quality control pilot programme for the measurement of antimicrobial drugs**
E. Wallenburg (Nijmegen, Netherlands), R. Brüggemann, A. Harteveld, L. Wisselo, E. Franssen, R. Aarnoutse*

1843 **Is it realistic to offer an antibiotic susceptibility bonus to developers?**
C. Morel (Geneva, Switzerland), O. Lindahl, S. Harbarth, M. De Kraker, S. Edwards, A. Hollis*

2497 **Comparison of 28-day mortality rates of recently completed prospective, randomised treatment studies of adult patients with carbapenem-resistant Gram-negative bacterial infections**
T. Lodise (Watervliet, United States), M. Bassetti, R. Ferrer, T. Naas, Y. Niki, D. Paterson, M. Zeitlinger, G. Tillotson, R. Echols*

2544 **Evaluation of difficult-to-treat resistant Gram-negative bacilli from European respiratory isolates: SIDERO-WT-2014–2018**
M. Soriano (Seattle, United States), S. Nguyen, M. Hackel, D. Sahm, R. Echols, M. Takemura, Y. Yamano*

2550 ***In vitro* antibacterial activity of cefiderocol against a multinational collection of difficult-to-treat resistant Gram-negative bacteria from respiratory and bloodstream infections: SIDERO-WT-2014–2018**
S. Nguyen (Carrollton, United States), M. Soriano, M. Hackel, D. Sahm, R. Echols, M. Takemura, Y. Yamano*

2557 ***In vitro* antibacterial activity of cefiderocol against a multinational collection of Gram-negative bacteria from urinary isolates: SIDERO-WT-2014–2018**
R. Pecini (Harrison, United States), S. Nguyen, M. Hackel, D. Sahm, R. Echols, M. Takemura, Y. Yamano*

2560 ***In vitro* activity of cefiderocol against *Stenotrophomonas maltophilia* clinical isolates in Europe and North America: multinational surveillance SIDERO-WT-2018 study**
N. Ishibashi (Toyonaka, Japan), M. Hackel, H. Maki, T. Satou, R. Echols, D. Sahm, Y. Yamano*

2567 ***In vitro* activity of cefiderocol against carbapenem non-susceptible *Enterobacterales* from multiple countries in Europe and North America: multinational surveillance SIDERO-WT-2018 study**
N. Kohira (Osaka, Japan), M. Hackel, H. Maki, T. Satou, R. Echols, D. Sahm, Y. Yamano*

2577 ***In vitro* and *in vivo* antimicrobial activity of cefiderocol and comparators against *Stenotrophomonas maltophilia***
R. Nakamura, M. Oota, T. Yoshitomi, T. Satou, Y. Yamano (Osaka, Japan)*

2700 **Study of the *in vitro* activity of cefiderocol in comparison to other antimicrobial agents against a collection of *Acinetobacter baumannii* clinical isolates from different geographical locations**
L. Muñoz, C. Ballesté (Barcelona, Spain), I. Roca, J. Vila Estape*

4557 **Antibacterial activity of the novel compound [Mn(bpen-cholamide)(CO)3]Br versus methicillin-resistant *Staphylococcus aureus***
J. Betts, P. Roth, A. Liakopoulos (Leiden, Netherlands), U. Schatzschneider, R. La Ragione*

5210 **Antibiotic-metal complexes: where microbiology meets bio-physics**
M. Ferreira, L. Bessa, F. Campanile, D. Bongiorno, S. Stefani, P. Gameiro (Porto, Portugal)*

7037 **Efficiency of phototherapy as a non-conventional antimicrobial strategy against selected Gram-negative bacteria in planktonic and biofilm models**
H. Kamal (Cairo, Egypt), N. Farag, S. Tammam, M. El-Azizi*

7320 **Antimicrobial activity, synergy and toxicity of a new gold(III) complex (AuC2) against multidrug-resistant pathogens with no detectable resistance**
C. Ratia, V. Cepas Lopez, R. Soengas, Y. López Cubillos, M. Velasco De Andrés, M. Iglesias, F. Lozano, F. López-Ortiz, S. Soto (Barcelona, Spain)*

7998 ***In vitro* comparative activity of cefepime/taniborbactam against metallo-beta-lactamase-producing *Pseudomonas aeruginosa* and *Klebsiella pneumoniae* isolates**
P. Paranos, P. Georgiou (Athens, Greece), S. Antonopoulou, A. Michelaki, E. Vagiakou, S. Vourli, S. Pournaras, J. Meletiadis*

8241 **Antibacterial and anti-biofilm activity of colistin-loaded nanoparticles against *Acinetobacter baumannii***
R. Awad (Poitiers, France), F. Tewes, S. Marchand, W. Couet, M. Nasser*

8915 **Bacterial iron-uptake pathways: gates for the transport of antibiotics**
Q. Parraud, S. Laurence, G. Mislin, I. Schalk (Illkirch, France)*

9098 ***In vitro* anti-biofilm and immunomodulatory effects of functionalised magnetite nanoparticles**
A. Holban (Bucharest, Romania), A. Grumezescu, H. Basil, C. Iordache, L. Ditu, M. Denisa, B. Ghita, B. Vasile, V. Lazar, E. Andronescu*

Session accepted as 1-Hour Oral Session

New drugs and generics: initiatives to make them available or reliable

275 **Assessment of the quality of data supporting the efficacy of new antibiotics for multidrug-resistant bacteria**
D. Yahav, N. Tau, D. Shepshelovich (Petah-Tikva, Israel)*

6899 **A real-world review on QIDP designation: what lessons can we learn?**
A. Kukreja (Gurugram, India), N. Antunes, W. Hui, D. Holman*

7173 **Therapeutic equivalence between brand name antibiotics versus generics: a systematic review and meta-analysis**
A. Cotia (São Paulo, Brazil), I. Boszczowski, J. Matuoka, M. Barbosa, H. Oliveira*

7660 **Pilot study of reimbursement model to ensure access to new critical antibiotics in Sweden**
J. Hellman (Solna, Sweden), C. Edlund, T. Jamtehov, F. Robertsson, A. Ternhag*

9361 **Sub-standard and falsified antibiotics: a systematic review**
G. Zabala (London, United Kingdom), K. Bellingham, V. Vidhamaly, P. Boupha, K. Boutsamay, P. Newton, C. Caillet*

Session accepted as 2-Hour Oral Session

New drugs and new targets for highly resistant bacteria

2631 **Validation and exploration of HldE: a promising target for antibiotic potentiation in Gram-negative bacteria**
S. Silve, Y. Cherrak, J. Hansen, T. Vermat, M. Mourez, E. Bacqué, F. Jeannot, S. Coyne (Marcy l'étoile, France)*

2679 **ART24, a novel live biotherapeutic product, in development for the prevention of *Clostrioides difficile* infection spares gut commensal species *in vitro* and allows for expansion of beneficial bacteria**
M. O'Donnell, B. Healy, C. Hill, P. Ross, M. Rea, R. Farquhar, L. Chesnel (Concord, United States)*

3245 **Efficacy of cefiderocol against carbapenem-resistant *Acinetobacter baumannii* in ventilator-associated pneumonia mouse model**
K. Ota (Nagasaki, Japan), N. Kaku, N. Uno, K. Sakamoto, Y. Morinaga, H. Hasegawa, T. Miyazaki, K. Izumikawa, H. Mukae, K. Yanagihara*

3926 **Oral immunotherapy with secretory IgA improves survival in the hamster model of *Clostrioides difficile* infection**
W. Weiss (Fort Worth, United States), M. Simon, S. Kiessing, E. Chiari, M. Pulse, S. Brown, C. Von Eichel-Streiber, H. Gerding, M. Mandago*

5956 ***In vitro* activity of cefepime-taniborbactam (VNRX-5133) against genetically-diverse, largely multidrug-resistant, *Pseudomonas aeruginosa* clinical isolates**
R. Shields (Pittsburgh, United States), C. Jones, E. Kline, A. Rubio, Y. Doi*

7192 **Plazomicin activity against carbapenemase-producing *Enterobacterales* carrying aminoglycoside-modifying enzymes from European and United States hospitals**
M. Castanheira (North Liberty, United States), T. Doyle, R. Mendes, J. Gogtay, H. Sader*

Session accepted as 1-Hour Oral Session

New insights on the therapeutic potential of bacteriophages

984 **Genomic and proteomic analysis of 42 bacteriophages located in the genomes of 17 clinical strains of *Klebsiella pneumoniae* resistant to carbapenems**
I. Bleriot Rial (A Coruña, Spain), F. Fernández-Cuenca, L. Blasco, R. Trastoy Pena, A. Ambroa Abalo, L. Fernandez Garcia, E. Perez-Nadales, J. De La Torre Cisneros, J. Oteo, F. Navarro, E. Miró, A. Pascual Hernandez, G. Bou Arevalo, L. Martinez-Martinez, M. Tomas*

1669 **First report of the discovery of amurin peptides: direct lytic agents with broad activity against carbapenem-resistant *Enterobacteriaciae*, *Acinetobacter*, and *Pseudomonas*, including colistin-resistant strains**
K. Sauve, J. Oh, A. Watson, D. Lehoux, C. Cassino, R. Schuch (Yonkers, United States)*

5238 **Phage susceptibility testing with lensless imaging technique**
P. Perlemoine (Grenoble Cedex 9, France), P. Marcoux, E. Picard, A. Maire, M. Zelsmann, E. Hadji, E. Lacot*

5785 **Phago-antibiogram**
A. Khalid (Westmead, Australia), A. Petrovic Fabijan, C. Venturini, S. Maddocks, R. Lin, J. Iredell*

Session accepted as Paper Poster Session

New therapeutic compounds and strategies

907 **Using mechanisms of action to assess new antibiotics against Gram-negative bacteria**
Y. Tsai, C. Liou, J. Lin, C. Fung, F. Chang, L. Siu (Miaoli, Taiwan)*

1367 **Gentamicin-intercalated smectite as a new therapeutic agent against *Helicobacter pylori* infection and faecal microbiome analysis after eradication in mouse model**
S. Jeong (Seoul, South Korea), K. Lee, K. Jie Hyun, S. Park, Y. Song*

1823 **Marine organisms from Yucatán Peninsula (México) as a potential natural source of new antimicrobial compounds against multidrug-resistant pathogens**
C. Lasarte (A Coruña, Spain), M. Martínez Guitián, D. Pech Puch, M. Pérez Povedano, J. Vazquez-Ucha, G. Bou Arevalo, J. Rodríguez González, C. Jiménez González, A. Beceiro*

1826 **Respiratory ß-2-microglobulin exerts direct antimicrobial activity**
A. Holch, R. Bauer, J. Münch, L. Ständker, A. Rodriguez, S. Wiese, P. Walther, Y. Ruiz Blanco, E. Sanchez-Garcia, B. Spellerberg (Ulm, Germany)*

2330 **Antibiotic with novel lipid a pathway target shows activity against Gram-negative bacteria**
E. Siegwart (Saffron Walden, United Kingdom), J. George, A. Mistry, T. Raynham*

2337 **Drug repositioning as a possible strategy to combat bacterial infections: evaluation of non-antibiotic human therapeutics as quorum-sensing inhibitors**
M. Gajdács (Szeged, Hungary), G. Spengler*

2603 **ART24, a novel live biotherapeutic product, in development for the prevention of *Clostrioides difficile* infection (CDI) recurrence is effective in a mouse model of CDI infection**
C. Murphy, T. Murphy, R. Farquhar, L. Chesnel (Concord, United States)*

2650 **Safety characterisation of ART24, a novel live bio-therapeutic product, in development for the prevention of *Clostridiodes difficile* infection, by *in silico* and *in vitro* testing**
M. O'Donnell (Cork, Ireland), C. Walsh, R. Mendes, C. Hill, P. Ross, M. Rea, R. Farquhar, L. Chesnel*

2691 **ART24, a novel live biotherapeutic product, in development for the prevention of *Clostrioides difficile* infection is bactericidal against *C. difficile* and degrades toxins A and B *in vitro***
M. O'Donnell, J. Hegarty (Cork, Ireland), S. Schulz, R. Jacobson, C. Hill, P. Ross, M. Rea, R. Farquhar, L. Chesnel*

2710 **ART24, a novel live biotherapeutic product, in development for the prevention of *Clostrioides difficile* infection is active against a broad range of *C. difficile* ribotypes *in vitro***
James Hegarty (Cork, Ireland), M. O'Donnell, B. Healy, C. Hill, P. Ross, M. Rea, R. Farquhar, L. Chesnel*

2726 ***In vitro* activity of lefamulin against isolates commonly causing community-acquired pneumonia collected during the SENTRY surveillance programme 2015–2019 in Europe**
S. Paukner (Vienna, Austria), S. Gelone, S. Arends, H. Sader*

2937 **Dihydropyridine-class antihypertensive drugs exhibit strong bactericidal activities against *Helicobacter pylori* and significantly reduce gastric colonisation in mice**
A. González Rodríguez (Zaragoza, Spain), J. Casado, E. Chueca, S. Salillas, A. Velázquez-Campoy, V. Espinosa Angarica, L. Benejat, J. Guignard, A. Giese, J. Sancho, P. Lehours, A. Lanas*

3212 ***In vitro* activity of eravacycline and comparators against 931 non-fastidious and 323 fastidious clinical isolates from China**
Y. Yang (Shanghai, China), Q. Shi, Y. Sun, Y. Zheng, D. Dong, Y. Guo, D. Zhu, F. Hu*

3489 **Assesment of ceragenin CSA-131-poloxamer for treatment of *Stenotrophomonas maltophilia* infections as a potential antimicrobial agent**
Ö. Oyardı (Istanbul, Turkey), C. Bozkurt Guzel, P. Savage, E. Demir, Z. Erturan*

3764 ***In vitro* activity of carbapenemase-producing *Enterobacterales* to mecillinam**
F. Fuchs (Cologne, Germany), A. Hamprecht*

3777 **Impact of suppression of envelope stress responses on bacterial sensitisation to antimicrobial agents**
E. Recacha (Seville, Spain), S. Díaz Díaz, J. Machuca Bárcena, A. García-Duque, F. Docobo Perez, A. Pascual Hernandez, J. Rodriguez Martinez*

3857 **Analysis of the microbiological data from the delafloxacin (DLX) phase III community-acquired bacterial pneumonia (CABP) trial using European analysis sets**
S. Mccurdy, L. Lawrence, S. Cammarata, A. Nuti, D. Zinzi (Pomezia, Italy)*

4125 **Assessment of antimicrobial molecules and bacteriocins isolated from *Pseudomonas* species for activity against multidrug-resistant bacteria**
S. Adufa-Appeagyei (London, United Kingdom), P. Wilson, S. Ali, S. Yui*

4720 **Antimicrobial activity of enacyloxin IIa and gladiolin against the urogenital pathogens *Neisseria gonorrhoeae* and *Ureaplasma* species**
N. Heath, R. Rowlands, G. Webster, E. Mahenthiralingam, M. Beeton (Cardiff, United Kingdom)*

4843 **Novel small-molecule inhibitors of bacterial lipoprotein transport against *Enterobacteriaceae***
E. Breidenstein (Cambridge, United Kingdom), O. Abdulle, T. Avis, C. Charrier, C. Coward, T. Duffy, G. Dharmalingam, N. Khan, C. Mason, P. Meo, N. Nagalingam, D. Powell*

4937 **Rifaximin leads to eradication of KPC *Klebsiella pneumoniae* gut colonisation in a mice model**
E. Xenofontos, G. Renieris, D. Droggiti, K. Synodinou, L. Sabrakos, E. Giamarellos-Bourboulis (Chaidari, Greece)*

5167 **Omadacycline in a comparative analysis of *in vitro* activity on *Clostridioides difficile* isolates from Stockholm, Sweden**
A. Camporeale (Stockholm, Sweden), C. Tellapragada, C. Nord, C. Giske*

5483 **Molecular characterisation of *Fusarium oxysporum* species complex isolates from the United States and susceptibility profile of the investigational antifungal olorofim**
H. Badali (San Antonio, United States), C. Gibas, H. Patterson, C. Sanders, J. Mele, H. Fan, N. Wiederhold*

5509 **Comparison *in vitro* activity of ceragenins for treatment of *Burkholderia cepacia* complex infections**
E. Demir (istanbul, Turkey), Ö. Oyardı, O. Altay, P. Savage, C. Bozkurt Guzel*

5572 **Effectiveness of ceftazidime-avibactam in a tertiary hospital of Spain**
M. Aguirregabiria, N. Antona Urieta, L. Lopez Soria, J. Goikoetxea, M. Castaño Lopez, J. Barrios Andrés (Barakaldo, Spain)*

5881 **Evaluation of *in vitro* activity of new polymyxin B analog SPR206 against clinical multidrug-, colistin- and tigecycline-resistant Gram-negative bacilli**
Y. Zhang (Beijing, China), C. Zhao, Q. Wang, X. Wang, H. Chen, H. Li, F. Zhang, H. Wang*

6231 **Screening research of antibacterial potential of selected released-active forms of antibodies**
N. Petrova (Moscow, Russian Federation), E. Don, A. Emelyanova, E. Kardash, S. Tarasov*

6897 **Synthesis and antibacterial evaluation of 9-substituted palmatine analogues as a novel class of anti-*H. pylori* agents targeting urease**
W. Yanxiang (Beijing, China), J. Pang, T. Fan*

7264 **A broad-spectrum bacterial gyrase inhibitor with a novel scaffold**
A. Vassort (Marcy l'Etoile, France), D. Kohnhaeuser, M. Broenstrup, A. Kirschning, K. Cirnski, J. Herrmann, R. Mueller, M. Mourez, D. Corbett, S. Sordello*

7461 **The antimicrobial role of a commonly used mucolytic agent in *Chlamydia pneumoniae* infection**
D. Kókai, D. Paróczai, D. Virok, V. Endresz, K. Burian (Szeged, Hungary)*

7942 **Drug repurposing as an effective strategy to treat multidrug-resistant infections: teaching old drugs new tricks**
D. Alves Ferreira (Dublin, Ireland), C. Roma-Rodrigues, P. Baptista, A. Fernandes, M. Martins*

8046 **SOS response to a novel inhibitor of DNA replication**
S. Renard (Lyon, France), V. Bazin, F. Davy*

8078 **Next-generation sequencing for the research and development of novel antibiotics**
C. Monlong, A. Delherme, M. Deuez, C. Taillier, T. Vermat, M. Mourez, S. Coyne, E. Lessoud (Marcy l'etoile, France)*

8424 ***In vitro* antimicrobial activity of liposomal ceftriaxone and liposomal amoxicillin and clavulanic acid against clinical strains isolated from companion animals with urinary tract infections**
M. Ogren (Carcavelos, Portugal), M. Gaspar, S. Gil, M. Ferreira, C. Carneiro, M. Oliveira, L. Tavares, F. Aires Da Silva, S. Aguiar*

8429 **Dananase: discovery of a novel *Pseudomonas aeruginosa* active polyketide type-1 synthetase**
D. Knapl (Vienna, Austria), G. Mitulovic, P. Pichler, T. Reiter, L. Wagner, W. Winnicki*

Session accepted as Paper Poster Session

News in beta-lactamase inhibitors

1853 **Activity of the β-lactamase inhibitor LN-1-255 against plasmid-mediated Class C cephalosporinases enzymes from *Enterobacteriaceae***
J. Vazquez-Ucha (A Coruña, Spain), C. Lasarte, M. Martínez Guitián, J. Arca Suárez, C. Gonzalez-Bello, G. Bou Arevalo, A. Beceiro*

2113 **Activity of novel β-lactamase inhibitor QPX7728 combined with various β-lactams against *Enterobacterales* collected from urinary tract infections, including β-lactamase-producing isolates**
M. Castanheira (North Liberty, United States), J. Lindley, H. Becker, R. Mendes, O. Lomovskaya*

2206 **Development of novel inhibitors of metallo-β-lactamases in carbapenem-resistant Gram-negative pathogens**
V. Savage (Macclesfield, United Kingdom), N. Ooi, A. Wilkinson, R. Newman, V. Lee, K. Maskew, N. Chalam-Judge, D. Orr, A. Bunt, S. Lee, D. Lindsay, I. Cooper*

2249 **Complementary inhibition of penicillin binding proteins by cefepime and zidebactam in presence of VIM-1 results in potent *in vitro* and *in vivo* bactericidal action against metallo-β-lactamase producing *Pseudomonas aeruginosa***
B. Moya, S. Bhagwat, G. Cabot (Palma, Spain), G. Bou Arevalo, M. Patel, A. Oliver*

2397 **Meso-2,3-dimercaptosuccinic acid in combination with a carbapenem against metallo-β-lactamase-producing *Escherichia coli* in murine peritonitis: a proof-of-concept**
G. Cheminet (Paris, France), V. De Lastours, N. Kieffer, F. Chau, K. Peoc'H, L. Massias, B. Fantin, P. Nordmann*

3643 ***In vitro* study of TEM inhibition by the nanobody cAbTEM-1 in view to a potential way out of the bacterial resistance**
F. Cawez (Liège, Belgium), F. Kerff, R. Herman, M. Vandevenne, P. Mercuri, M. Galleni*

3855 **Beta-lactam exposures to methicillin-resistant *Staphylococcus aureus* involve cell membrane and surface adaptation for daptomycin synergy**
C. Lew (Madison, United States), N. Mishra, S. Farah, B. Zapata, A. Bayer, W. Rose*

3959 **Activity of the β-Lactamase inhibitor LN-1-255 against ceftazidime-resistant AmpC-hyperproducing *Pseudomonas aeruginosa***
C. Lasarte (A Coruña, Spain), J. Vazquez-Ucha, J. Arca Suárez, G. Torrens, C. Juan Nicolau, A. Oliver, G. Bou Arevalo, C. Gonzalez-Bello, A. Beceiro*

4144 ***In vitro* activities of β-lactam antibiotics alone and in combination with sulbactam against *Acinetobacter baumannii***
L. Wang, R. Han, Y. Chen, Z. Huang, X. Zhang, F. Hu, F. Yang (Shanghai, China)*

5174 **Combination testing of avibactam against multidrug-resistant Gram-negative bacteria**
R. Chen (Vienna, Austria), M. Kussmann, M. Obermüller, M. Karer, R. Kriz, W. Ruppitsch, H. Burgmann, H. Lagler*

5230 **Activity of ANT2681, a Novel metallo-beta-lactamase inhibitor in Combination with meropenem against metallo-beta-lactamase-positive *Enterobacterales* collected from hospitals world-wide in 2018**
I. Morrissey (Monthey, Switzerland), T. Valmont, C. De Piano, N. Sprynski, C. Sable, M. Everett, M. Zalacain*

5727 **Tricyclic boronates inhibit carbapenemases**
A. Parkova, K. Calvopiña (Bristol, United Kingdom), P. Schneider, C. Schofield*

8199 **Comparison of the preclinical renal effects of piperacillin/tazobactam and imipenem-cilastatin/relebactam in combination with vancomycin**
M. Pai (Ann Arbor, United States), M. He, A. Matvekas, E. Souza*

Session accepted as Paper Poster Session

Opportunities and tools to change prescribing behaviour

932 **Antibiotic prescribing decisions in intensive care: a qualitative study**
A. Pandolfo (London, United Kingdom), R. Horne, Y. Jani, N. Bidad, S. Brett, T. Reader, D. Brealey, V. Enne, D. Livermore, V. Gant*

1635 **Feasibility studies of the WHO practical toolkit for antimicrobial stewardship programmes in healthcare facilities in low-and middle-income countries**
G. Maki (Detroit, United States), I. Smith, S. Paulin, W. Kasambara, P. Chuki, P. Rupali, L. Barrow, E. Johnson, D. Bajracharya, D. Singh, T. Prentiss, L. Kaljee, M. Zervos*

1668 **Development of a user-friendly clinical decision support system (TREAT-Essential) for antimicrobial stewardship**
M. Mogensen (Aalborg, Denmark), L. Ward, P. Leutscher, H. Schønheyder, M. Ludwig, C. Madsen, S. Andreassen*

2340 **Antimicrobial use for asymptomatic bacteriuria: first, do no harm**
Y. Shpunt, I. Estrin, H. Saadon, G. Ben-Yossef, L. Goldstein, D. Klafter, Y. Levi, S. Zilberman-Itskovich, D. Katz, T. Lazarovitch, R. Zaidenstein, D. Marchaim (Beer Yaacov, Israel)*

3707 **An opportunity for antimicrobial stewardship in urinary tract infections using rapid tests directly on urine samples**
A. Alvarez-Uria (Madrid, Spain), A. Burillo, L. Jiménez-Navarro, N. Perez, C. Sánchez-Sánchez, M. Palomo, M. Olmedo Samperio, P. Muñoz, E. Bouza*

3844 **Understanding antibiotic prescribing behaviours among hospital physicians and exploring strategies currently used by infectious diseases physicians to influence change: a qualitative interview study**
V. Zanichelli (Ottawa, Canada), C. Nott, J. Grimshaw, J. Squires, J. Presseau, K. Suh*

5116 **Characterising the patients with negative blood cultures as a potential target for stewardship (NOBACT project): predictors for mortality in patients with obtained blood cultures**
J. Girón Ortega (Seville, Spain), R. Fernández Guerrero, C. Sánchez Tembleque, M. Montes De Oca, E. Morte Romea, P. Luque Gómez, M. De Cueto-López, L. Suardi, F. Guerrero-Sanchez, Z. Palacios Baena, S. Jiménez-Jorge, J. Rodríguez-Baño, P. Retamar Gentil*

5985 **Antimicrobial stewardship opportunities at discharge: current prescribing at Boston Medical Centre**
N. Rebold (Boston, United States), K. Brade*

6021 **Adequacy of antibiotic treatment in patients with negative blood cultures: identifying a novel target for antimicrobial stewardship (NOBACT study)**
R. Fernández Guerrero (Seville, Spain), J. Girón Ortega, E. Morte Romea, P. Luque Gómez, C. Sánchez Tembleque, M. Montes De Oca, F. Guerrero-Sanchez, M. De Cueto-López, L. Suardi, Z. Palacios Baena, S. Jiménez-Jorge, J. Rodríguez-Baño, P. Retamar Gentil*

7888 **Why don't hospital prescribers stop antibiotics when it would be safe to do so? Results of a discrete choice experiment**
L. Roope, J. Buchanan, E. Morrell, K. Pouwels, K. Sivyer, F. Mowbray, L. Abel, E. L.A. Cross, L. Yardley, T. Peto, A. Walker, M. Llewelyn (Brighton, United Kingdom), S. Wordsworth*

8590 **Hospital physicians' perspective on antibiotic prescribing and antimicrobial resistance: a qualitative study**
I. Christensen (Sarpsborg, Norway), J. Haug, J. Vildershøj Bjørnholt, D. Berild, B. Skodvin, L. Jelsness-Jørgensen*

9160 **Assessment of de-escalation of empirical antimicrobial therapy in medical wards with high rates of multidrug-resistant bacteria: a multi-centre prospective cohort study**
G. Poulakou (Athens, Greece), V. Rapti, K. Leontis, A. Kakasis, S. Pagoni, I. Tsimbos, K. Masgala, L. Sybardi, N. Alexiou, V. Apostolopoulos, C. Giannopoulos, K. Arvaniti, C. Trakatelli, A. Prionas, M. Samarkos, S. Tsiodras, H. Giamarellou*

9494 **Knowing local cumulative antibiogram: does it matter?**
S. Carvalho, J. Caldas, R. Duro, C. Alves, N. Rocha Pereira (Porto, Portugal)*

9642 **Systematic blood culture testing identifies a large proportion of patients in whom antibiotics could be safely discontinued: hospital-associated infections in a tertiary care hospital in Ethiopia**
M. Semret (Montreal, Canada), W. Taye, L. Kong, T. Alemayehu, T. Beyene, M. Libman, W. Degu, O. Johansen, G. Gebretekle, D. Seifu, C. Yansouni*

Session accepted as Mini-oral Flash Session

Optimised prescribing through diagnostics

1822 **T2 magnetic resonance technology in the diagnosis of sepsis and clinical impact in patient management**
R. Paggi (Perugia, Italy), G. De Socio, A. Belati, F. Allegrucci, A. Repetto, E. Cenci, A. Mencacci*

2189 **Is it safe to use rapid molecular tests for the detection of microorganisms in blood to optimise antimicrobial therapy in septic patients?**
C. Rodrigues (Sao Paulo, Brazil), T. Varejao Strabelli, R. Focaccia Siciliano, R. Zeigler, L. Hajjar, A. Matos Porto*

2925 **Decrease in antibiotic days of therapy after notification of *Clostridioides difficile* carriage status: an interventional study**
M. Gilboa (Ramat-Gan, Israel), E. Meltzer, L. Maizels, S. Raibman-Spector, A. Segev, G. Rahav, G. Smollan, A. Leibowitz, G. Regev-Yochay*

3461 **Impact of restricting procalcitonin measurements on antibiotic use, clinical outcomes and costs in a Swiss tertiary care hospital: an interrupted time-series analysis**
M. Abbas (Geneva, Switzerland), N. Vernaz, E. Von Dach, N. Vuilleumier, S. Harbarth, B. Huttner*

3778 **High clinical impact on antimicrobial stewardship using multiplex PCR syndromic panels for severe community-acquired infections: a real-life experience**
A. Alvarez-Uria (Madrid, Spain), M. Valerio Minero, M. Kestler Hernandez, C. Sánchez-Sánchez, S. De La Villa Martinez, M. Veintimilla Yanez, M. Machado, P. Muñoz, E. Bouza*

4712 **Impact of diagnostic and antimicrobial stewardship on time-to-appropriate therapy and clinical outcomes in infections caused by carbapenem-resistant Gram-negative organisms**
K. Mccrink, K. Deronde, A. Jimenez, G. Rosello, Y. Natori, K. Claeys, O. Martinez, B. De Pascale, A. Perez-Cardona, L. Abbo, A. Vega (Miami, United States)*

4967 **Communication of rapid identification results from positive blood cultures decreases time to effective therapy**
R. Haj, L. Taggart, J. Forbes, E. Leung, J. Wu, R. Fattouh, L. Matukas (Toronto, Canada)*

7484 **Evaluation of a new tool in diagnostic process of sepsis: reporting results to a smartphone**
N. Zurita Cruz (Madrid, Spain), A. Fraile Torres, T. Soler Maniega, L. Fontan, S. Gómez De Frutos, A. Yarci Carrión, E. Navarro Lara, M. De Las Cuevas, L. Cardeñoso*

Session accepted as Paper Poster Session

PK/PD studies and applications

24 **High-dose ceftaroline fosamil recommendations for paediatric patients with *Staphylococcus aureus* complicated skin and soft-tissue infections using an extrapolation approach**
P. Chan (Sandwich, United Kingdom), M. Mcfadyen, A. Quaye, H. Leister-Tebbe, V. Hendrick, J. Hammond, S. Raber*

519 **Interim pharmacokinetic analysis of a multi-centre randomised open label phase IIb study in neonates to validate the meta-analysis population pharmacokinetic model used to simulate an optimised dosing regimen in neonates and infants aged < 90 days: the NeoVanc trial**
L. Hill (London, United Kingdom), E. Jacqz-Aigrain, V. Elie, W. Zhao, M. Clements, M. Turner, I. Lutsar, P. Heath, E. Roilides, S. Walker, M. Sharland*

979 **Globally intravenous dosing of antibiotics in infants and children clusters around a small number of strategies but is not completely uniform**
M. Clements (London, United Kingdom), J. Bielicki, S. Gastine, Y. Hsia, N. Russell, J. Standing, S. Walker, M. Sharland*

1207 **Probability of target attainment analyses inform ceftolozane/tazobactam dosing regimens in hospital-acquired pneumonia/ventilator-associated pneumonia patients with end-stage renal disease on intermittent haemodialysis**
H. Feng (Kenilworth, United States), Y. Patel, Z. Zhang, J. Fiedler-Kelly, C. Bruno, E. Rhee, C. De Anda, W. Gao*

1220 **Cost-benefit analysis comparing trough, two-Level AUC, and Bayesian AUC dosing for vancomycin**
B. Lee (Los Angeles, United States), G. Fong, M. Bolaris, M. Neely, E. Minejima, A. Kang, G. Lee, C. Gong*

1277 **Population pharmacokinetic modelling and simulations to support ceftazidime-avibactam dose selection for paediatric patients with nosocomial pneumonia**
M. Mcfadyen (Kent, United Kingdom), M. Vourvahis, M. Lovern, R. Franzese, T. Riccobene, T. Carrothers, M. Tawadrous*

1296 **Development of intravascular microdialysis as a tool for therapeutic drug monitoring and intensive PK studies in children**
V. Al Jalali (Vienna, Austria), B. Wulkersdorfer, P. Matzneller, E. Lackner, S. Poschner, W. Jaeger, M. Zeitlinger*

1587 **The pharmacodynamics of omadacycline against *Escherichia coli* and *Acinetobacter baumannii* studied in an *in vitro* pharmacokinetic model of infection**
A. Noel, M. Attwood, K. Bowker, A. Macgowan (Bristol, United Kingdom)*

1693 **Imipenem/relebactam pharmacokinetic/pharmacodynamic analyses from an *in vivo* neutropenic murine thigh infection model**
M. Patel (Kenilworth, United States), N. Daryani, H. Feng, D. Hilbert, M. Melchers, E. Mavridou, K. Young, M. Rizk*

1716 **Ceftobiprole and daptomycin concentrations in valve tissue in a patient with aortic native valve endocarditis**
S. Boni, M. Antonucci, V. Avataneo, A. De Nicolò, L. Martinelli, S. Artioli, G. Di Perri, A. D'Avolio (Turin, Italy)*

1834 **Vancomycin pharmacokinetics in patients undergoing extracorporeal membrane oxygenation after 48 hours of treatment**
L. Herrera-Hidalgo, M. Munoz-Burgos, J. Laimerao, M. Mejias-Trueba, A. Garcia-Avello, J. Martinez, L. Lopez-Cortes (Seville, Spain), M. Gil-Navarro*

2050 **Pharmacokinetic model for intravenous vancomycin in pregnant rats and pups**
M. Pham (Omaha, United States), S. Avedissian, G. Pais, M. Joshi, B. Griffin, J. Chang, K. Hlukhenka, W. Prozialeck, M. Scheetz*

2086 **Imipenem/relebactam pharmacokinetic/pharmacodynamic analyses from an *in vivo* neutropenic mouse delayed lung infection model**
N. Daryani (Kenilworth, United States), M. Patel, A. Flattery, K. Young, M. Rizk*

2368 **Prolonged versus intermittent infusion of beta-lactam antibiotics: a systematic review and meta-regression of bacterial killing in preclinical infection models**
S. Dhaese (Ghent, Belgium), A. Heffernan, D. Liu, M. Abdul Aziz, V. Stove, V. Tam, J. Lipman, J. Roberts, J. De Waele*

2776 **Comparison of intermittent versus continuous infusion vancomycin therapy for severe patients in intensive care unit**
C. Yamada, J. Telles (Sao Paulo, Brazil), D. Santos, J. Cieslinski, V. Stadler Tasca Ribeiro, J. Gasparetto, F. Tuon*

2782 **Amikacin probability of target attainment in critically ill oncological patients: results from a prospective observational cohort**
O. Borges, K. Migotto, J. Souza Framil, M. Campos, P. Caruso, J. Telles (Sao Paulo, Brazil), I. Leonardo França Jr*

2927 **Effect of augmented renal clearance on the extended-interval dosing of aminoglycosides in critically ill paediatric patients**
N. Rhodes (Downers Grove, United States), S. Avedissian, A. Hadid, J. Bradley, J. Le*

3146 **Extracorporeal membrane oxygenation does not impact the pharmacokinetics of liposomal amphotericin B**
C. Mane (Toulouse, France), S. Ruiz, C. Monchaud, D. Concordet, G. Bernard, P. Gandia*

3342 **Amikacin initial dosing in emergency surgery: pharmacokinetics and determinants of optimal dose**
S. Goutelle (Lyon, France), G. Fritsch, M. Leroy, C. Piron, C. Salvez, A. Friggeri*

3588 **Pharmacodynamics of amikacin and fosfomycin combination therapy in neonatal sepsis modelled in a hollow fibre infection model**
C. Darlow (Stockport, United Kingdom), F. Docobo Perez, N. Farrington, A. Johnson, L. Mcentee, A. Jimenez-Valverde, J. Unsworth, R. Da Costa, S. Ellis, F. Franceschi, M. Sharland, L. Piddock, S. Das, W. Hope*

4482 **Does cefepime require dose adjustments in critically ill patients on extracorporeal membrane oxygenation? A pharmacokinetic study**
V. Cheng (Brisbane, Australia), K. Shekar, M. Abdul Aziz, H. Buscher, A. Corley, E. Gilder, A. Diehl, I. Lye, S. Mcguinness, R. Parke, C. Reynolds, S. Welch, J. Fraser, J. Roberts*

4499 **Treatment of urinary tract infections in haemodialysis patients: the controversy about antimicrobial urine concentration**
W. El Nekidy (Abu Dhabi, United Arab Emirates), A. Eshbair, M. Mooty, N. Attallah, A. Cherfan, F. Hijazi, I. Ghazi*

4520 **Investigating dynamic protein binding of clindamycin *in vivo* by means of intravasal microdialysis in healthy volunteers**
B. Wulkersdorfer (Vienna, Austria), S. Wicha, E. Kurdina, P. Matzneller, V. Al Jalali, M. Vossen, S. Riesenhuber, E. Lackner, C. Dorn, F. Kees, M. Zeitlinger*

4568 **PK/PD of intravenous and oral fosfomycin in neonates with presumed serious bacterial Infection**
Z. Kane (London, United Kingdom), S. Gastine, P. Williams, J. Berkley, S. Ellis, E. Correia, C. Darlow, W. Hope, M. Sharland, J. Standing*

5008 **Exploring minocycline pharmacodynamics against *Acinetobacter baumannii* and *Staphylococcus aureus* in a lung model in neutropenic mice: clinical implications on optimal dosing regimens**
A. Van Der Meijden, W. Kloezen, H. Van Der Spek, M. Ten Kate, J. Mouton, A. Muller, J. Meletiadis, S. Van Den Berg (Rotterdam, Netherlands)*

5312 **Impact of alternative dosing infusions of ceftolozane-tazobactam monotherapy against extremely-resistant *Pseudomonas aeruginosa* sequence type 175 isolates with different susceptibility profile ranging from 2 to 16 mg/L in a hollow-fibre infection model**
M. Montero (Barcelona, Spain), S. Domene Ochoa, C. Lopez Causape, B. Vanscoy, S. Luque, L. Sorlí, A. Angulo, E. Padilla, N. Prim, V. Pomar, A. Rivera, N. Campillo, S. Grau, P. Ambrose, A. Oliver, J. Horcajada*

5807 **Simulated exposures of oritavancin in *in vitro* PK/PD models select for MRSA with reduced susceptibility to oritavancin but minimal cross-resistance or seesaw effect with other antimicrobials**
B. Werth (Seattle, United States), N. Ashford, I. Barreras Beltran, K. Penewit, E. Holmes, A. Waalkes, S. Salipante*

5888 **Population pharmacokinetics of cefazolin in paediatric patients undergoing cardiac surgery**
S. Parker (Brisbane, Australia), G. Moloney, B. Bierbach, J. Ungerer, J. Suna, N. Alphonso, J. Roberts*

6421 **Beyond the minimal inhibitory concentration: novel pharmacokinetic/pharmacodynamic metrics quantify the exposure-effect relationship of levofloxacin- against fluoroquinolone-resistant *Escherichia coli* based on *in vitro* infection models**
J. Seeger (Berlin, Germany), R. Michelet, S. Guenther, C. Kloft*

6709 **Cefepime 2g plus enmetazobactam 0.5g administered IV q8h achieves high probability of target attainment in patients with complicated urinary tract infections**
J. Vollmer, M. Machacek, A. Belley, P. Knechtle (St. Louis, France)*

6985 **Influence of extracorporeal membrane oxygenation on the pharmacokinetics of ceftolozane/tazobactam**
C. Mane (Toulouse, France), C. Delmas, J. Porterie, P. Verwaerde, G. Jourdan, D. Concordet, B. Marcheix, G. Bernard, S. Ruiz, P. Gandia*

7218 **Obesity affects interstitial space fluid of subcutaneous adipose tissue concentrations of meropenem after single application: a controlled clinical trial**
P. Simon, D. Busse (Berlin, Germany), D. Petroff, C. Dorn, J. Heyne, A. Dietrich, S. Stehr, M. Zeitlinger, F. Kees, C. Kloft, H. Wrigge*

7358 **Caco-2 permeability assessment and *in vivo* pharmacokinetics of VRT001-C (oral ceftriaxone)**
S. Chaudhary (Panchkula (Haryana), India), D. Roy, A. Sachdeva, A. Payasi, A. Aggarwal*

7400 **Pharmacokinetics of amikacin and gentamicin in the setting of burn patients with Gram-negative bacterial infections**
S. Corcione (Turin, Italy), A. De Nicolò, A. Pensa, F. Segala, G. Di Perri, M. Stella, A. D'Avolio, F. De Rosa*

7642 **Amikacin nomogram for treatment of adult cystic fibrosis exacerbations based on an external evaluation of a population pharmacokinetics model**
V. Pasche (Montréal, Canada), D. Thirion, E. Matouk, A. Marsot*

7943 **Identification and quantification of microdialysis variability using an integrated *in vitro*, *ex vivo* and *in silico* approach**
L. Ilia (Berlin, Germany), D. Busse, L. Ehmann, P. Simon, R. Michelet, C. Kloft*

8017 **Urine alkaline pH effect on ciprofloxacin and fosfomycin efficacy in a murine urinary tract infection model by *Escherichia coli***
M. Carretero Ledesma (Seville, Spain), T. Cebrero Cangueiro, G. Labrador Herrera, Y. Smani, J. Cisneros Herreros, J. Pachon-Diaz, J. Blazquez, E. Cordero Matias, M. Pachon-Ibáñez*

8335 **Inoculum effect of OXA-48-like-producing *Enterobacteriaceae* against ceftazidime-avibactam**
L. Chat, J. Nguyen Van, B. Pilmis, F. Caméléna, A. Le Monnier, B. Bercot, H. Jacquier, A. Mizrahi (Paris, France)*

8622 **Implementation of model-based therapeutic drug monitoring of vancomycin**
R. Garreau, M. France, L. Chatel, D. Leclercq, N. Montmartin, L. Bourguignon, S. Goutelle (Lyon, France)*

9210 **Pharmacodynamics of common antibiotics against uropathogenic *Escherichia coli* revealed significant antibiotic tolerance and persistence of intracellular bacteria**
I. Kerkez (Tartu, Estonia), M. Putrins, P. Tulkens, T. Tenson, F. Van Bambeke*

9506 **CSF diffusion of cefotaxime following high-dose administration in central nervous system infections: a multi-centre retrospective study (DIFCEFO study)**
M. Grégoire (Nantes, France), N. El Helali, R. Guilhaumou, J. Scala-Bertola, V. Dubee, J. Talarmin, A. Charmillon, J. Schmit, S. Kerneis, J. Mootien, F. Bani Sadr, X. Duval, M. Revest, F. Lemaitre, P. Benoit, P. Le Turnier*

Session accepted as Paper Poster Session

Stewardship driven by medical professions

807 **Impact of pharmacist-driven antimicrobial stewardship interventions on multicomponent patient outcomes**
E. Beasley, C. Georgescu, G. Suleyman, K. Cole (Sylvania, United States)*

1042 **Survey of attitudes, beliefs, and knowledge of community pharmacists in the United States on antimicrobial stewardship**
D. Bowers (Yakima, United States), C. Bran Morales, C. Daly, D. Jacobs*

2344 **Organisation of an ID consultation: are medical reports more important than patients?**
J. Tschopp (Lausanne, Switzerland), B. Guery*

3180 **Aims and challenges of founding a national network of young clinical microbiologists: a French experience**
G. Theo (Paris, France), J. Bigot, A. Gaymard, S. Marot, A. Muggeo, M. Paluch, T. Poncin, J. Sevestre, D. Yann, M. Pichon, S. Dellière*

4109 **Outcomes of a pharmacist-led antimicrobial stewardship programme within a family medicine resident clinic**
L. Dumkow (Belmont, United States), L. Westerhof, T. Hanrahan, S. Mcpharlin, N. Egwuatu*

4642 **Mapping the implementation of a clinical pharmacist-driven antimicrobial stewardship programme at a tertiary care centre in India**
V. Nampoothiri (Kochi, India), S. Sudhir, M. Varsha, Z. Mohamed, V. Menon, E. Charani, S. Singh*

6423 **Two in three final-year veterinary students demand improved education in rational antimicrobial use**
C. Espinosa-Gongora (Frederiksberg, Denmark), L. Jessen, O. Dyar, B. Beovic, A. Bousquet-Melou, B. Gonzalez-Zorn, P. Nebbia, R. Odore, C. Pulcini, G. Re, S. Sacristán, S. Schwarz, D. Timofte, P. Toutain, L. Guardabassi*

8517 **Half of prescribed antibiotics are not needed: a pharmacist-led antimicrobial stewardship intervention and clinical outcomes in a referral hospital in Ethiopia**
M. Semret (Montreal, Canada), G. Gebretekle, C. Yansouni, M. Libman, W. Taye, T. Alemayehu, W. Degu, A. Mulu, D. Haile Mariam*

Session accepted as Paper Poster Session

Your daily clinical experience with antibiotics

1203 **Real-world experience of dalbavancin use for the treatment of Gram-positive infections**
N. Spernovasilis (Heraklion, Greece), A. Mathioudaki, P. Ioannou, A. Gikas, G. Samonis, D. Kofteridis*

1899 **De-escalation of carbapenems to ciprofloxacin in the treatment of bacteraemia caused by extended spectrum beta-lactamase-producing *Enterobacteriaceae***
J. Lim, W. Tong, J. Seah, H. Shafi (Singapore, Singapore), C. Teng*

3172 **Efficacy of temocillin versus carbapenems for the treatment of extended spectrum beta-lactamase-producing *Enterobacteriaceae* urinary tract infections: a case control study**
S. Gravier (Colmar, France), T. Delory, D. Le Puart, G. Gaube, S. Siméon, B. Davido, S. Lejeune, E. Piet, R. Lepeule, P. Lesprit, M. Lafaurie*

3775 **Treatment of bacteraemia caused by *Enterobacter* spp.: should the potential for AmpC induction dictate therapy?**
G. Drozdinsky (Petah-Tikva, Israel), A. Neuberger, M. Paul, D. Yahav*

3954 **Efficacy of temocillin against multidrug-resistant *Enterobacterales*: a retrospective cohort study**
F. Leysour De Rohello, M. Etienne, S. Dahyot, I. Tiret, M. Pestel-Caron, F. Caron, K. Alexandre (Rouen, France)*

4854 **Real-life dalbavancin use in acute bacterial skin and skin-structure infections and bone and joint infections: clinical experience at Florence university hospital (Italy)**
N. Di Lauria (Florence, Italy), F. Bartalesi, D. Bartolozzi, M. Cecchi, P. Corsi, A. Ipponi, F. Lagi, E. Mantengoli, A. Bartoloni*

5826 **Retrospective analysis of intravenous fosfomycin use at Florence University Hospital, Italy: clinical and microbiological analysis**
N. Di Lauria (Florence, Italy), E. Mantengoli, N. Aiezza, A. Antonelli, S. Bresci, T. Giani, F. Lagi, K. Kaye, P. Patel, G. Rossolini, A. Bartoloni*

7724 **A multi-centre study of dalbavancin use in Italy (DALBITA Study): which could be the appropriate place for this easy-to-manage antibiotic to treat Gram-positive infections?**
C. Aldieri (Milan, Italy), F. Bai, F. Raumer, E. Di Meco, A. Cattelan, M. Moioli, P. Morelli, M. Rizzi, F. Castelli, M. Guglielmo, B. Menzaghi, G. Rizzardini, A. Saracino, A. Cascio, M. Puoti, A. D'Arminio Monforte, G. Marchetti*

8415 **The 2020 Dutch working party on antibiotic policy guideline for empirical antibacterial therapy of sepsis in adults**
E. Sieswerda (Amsterdam, Netherlands), H. Bax, J. Hoogerwerf, M. De Boer, M. Boermeester, M. Bonten, D. Dekker, R. Gerth Van Wijk, N. Juffermans, M. Kuindersma, P. Van Der Linden, D. Melles, P. Pickkers, J. Schouten, J. Rebel, A. Van Zanten, J. Prins, J. Wiersinga*

8693 **Trimethoprim-sulfamethoxazole as de-escalation agent in bloodstream infections due to *Enterobacter* spp, *Serratia marcescens* and *Citrobacter freundii***
A. Sousa (Vigo, Spain), M. Pérez-Rodríguez, M. Suárez, P. Diéguez, O. Lima, A. Cabaleiro, A. Otero, F. Vasallo Vidal, R. Longueira, A. Nodar, M. Crespo*

8771 **Optimising antimicrobial stewardship: an evaluation of temocillin in the treatment of Gram-negative bacteraemia**
L. Cottom (Glasgow, United Kingdom), L. Bagrade, R. Dhillon, J. Gillies, B. Jones*

Abstract Programme

6. Fungal infection & disease

- Fungal disease epidemiology
- Diagnostic mycology (incl molecular)
- Antifungal drugs & treatment (incl clinical trials)
- Antifungal resistance & susceptibility testing (incl surveillance)
- Other

Session accepted as Paper Poster Session

Antifungal stewardship, therapeutic drug monitoring and pharmacokinetics

931 **A multi-site evaluation of antifungal prescribing and the use of fungal diagnostics in critical care**
C. Logan (London, United Kingdom), C. Hemsley, A. Fife, J. Edgeworth, D. Wyncoll, P. Hopkins, T. Bicanic*

986 **Development of an antifungal stewardship programme at a London teaching hospital**
L. Whitney, R. Wilson (London, United Kingdom), F. Davies, M. Coleman, J. Woo, R. Palanicawandar, M. Gilchrist*

1702 **Evaluation of voriconazole therapeutic drug monitoring practice: experience of a tertiary referral centre**
Y. Kwang, A. Netluch, T. Lai, S. Chen, H. Kim (Sydney, Australia), I. Sandaradura, J. Alffenaar*

1765 **Clinical feasibility of simultaneous microdialysis of voriconazole and its *N*-oxide metabolite at target site demonstrated by *in vitro* investigations**
J. Schulz (Berlin, Germany), R. Michelet, F. Kluwe, C. Kloft*

1929 **Antifungal cost in the patients with febrile neutropaenia episodes due to haematological malignancies**
H. Gedik (Istanbul, Turkey)*

2533 **The cost-effectiveness of isavuconazole compared to voriconazole, the standard of care in the treatment of patients with invasive fungal infection prior to differential pathogen diagnosis in Spain**
J. Azanza, S. Grau Cerrato, L. Vázquez, P. Rebollo, C. Peral, L. Alejandra, V. Lopez Gomez (Alcobendas, Spain)*

3709 **Posaconazole versus voriconazole as antifungal prophylaxis for invasive fungal diseases in patients with haematological malignancies**
R. Almutairy (Jeddah, Saudi Arabia), M. Khan, M. Shamrani, H. Almarhabi, M. Aseeri, D. Naeem*

4311 **Isavuconazole for the treatment of invasive fungal infection in solid organ transplant recipients: experience from a referral centre**
M. Ruiz-Ruigómez (Madrid, Spain), L. Corbella Vazquez, I. Rodriguez Goncer, J. Sequeira, M. Hernandez Jimenez, F. Lopez-Medrano, R. San Juan Garrido, J. Aguado Garcia, M. Fernandez Ruiz*

5009 **Pharmacokinetic variability and target attainment of fluconazole in critically ill patients**
R. Van Daele (Leuven, Belgium), J. Wauters, R. Brüggemann, R. Denooz, M. Hayette, Y. Debaveye, I. Spriet*

5180 **A new *Lichtheimia corymbifera* mouse model close to human pathophysiology to test antifungal drugs**
K. Brunet (Poitiers, France), J. Martellosio, F. Arrivé, T. Brunet, I. Lamarche, S. Marchand, B. Rammaert*

5566 **Serum concentrations of intravenously administered posaconazole in critically ill patients**
W. Heinz (Weiden, Germany), D. Wichmann, H. Klinker, S. Kluge*

5831 **Safety and efficacy of triazole use for prophylaxis and treatment of invasive fungal diseases in patients receiving gilteritinib, a novel tyrosine kinase Inhibitor for the treatment of acute leukaemias**
M. Aleissa (Boston United States), M. Luskin, B. Alshehri, H. Leblebjian, A. Mcdonnell, F. Marty*

6803 **Frequency and severity of potential drug-drug interactions before, during and after an antifungal stewardship pilot project**
S. Lachenmayr (Munich, Germany), A. Gretler, D. Strobach, H. Mannell, K. Berger, H. Ostermann*

6969 **Experience of 319 post-surgical abscesses: focus on empiric antifungal therapy**
E. Taddei (Roma, Italy), F. Giovannenze, E. Birocchi, R. Murri, L. Cerolini, F. Taccari, R. Cauda, M. Fantoni*

7211 **Plasma exposures following posaconazole injection and delayed-release tablet**
Y. Wang, S. Tsai, Y. Fu, P. Chen, S. Lin, Y. Chen, Y. Chen, S. Lin (Taipei, Taiwan)*

9280 **Chitosan-coated magnetite nanoparticles as a biocompatible nystatin carrier: physicochemical characterisation and *in vitro* fungicidal determination**
S. Yazdanpanah (Shiraz, Iran), K. Zomorodian, H. Veisi, H. Veisis*

Session accepted as Paper Poster Session

Aspergillus infections: not always the same!

975 **Invasive pulmonary aspergillosis after heart transplantation**
K. Monosova (Saint Petersburg, Russian Federation), M. Simonenko, Y. Sazonova, K. Zagorodnikova, L. Vasiljeva, R. Vadim, M. Bortsova, P. Fedotov*

980 **The Danish nationwide surveillance of azole-resistance in *Aspergillus fumigatus:* data from the first nine months**
M. Risum (Copenhagen, Denmark), R. Krøger Hare, J. Gertsen, L. Kristensen, F. Rosenvinge, S. Sulim, E. Marmolin, B. Røder, J. Bangsborg, E. Dzajic, M. Pedersen, K. Astvad, S. Andersen, M. Arendrup*

3256 **Relevance of EORTC-MSG criteria in invasive fungal infections in lung transplant recipients**
L. Martin (Bordeaux, France), E. Blanchard, H. Roze, F. Gabriel, V. Servant, X. Demant, H. Nivet, M. Tunon De Lara, J. Jougon, C. Raherison-Semjen, F. Laurent, C. Dromer*

3382 **Invasive aspergillosis by cryptic *Aspergillus* species in a 700-bed third level hospital**
M. Fernandez (Barcelona, Spain), I. Alejo, E. Rubio Garcia, C. Cardozo, P. Puerta, M. Garrido, M. López, A. Alastruey-Izquierdo, C. Pitart, C. Garcia Vidal, F. Marco Reverte*

4002 **Aspergillosis complicating severe respiratory syncytial virus in intensive care unit patients: a retrospective cohort study**
H. Nam (Chicago, United States), M. Ison*

4246 **Epidemiology of respiratory colonisations and infections caused by *Aspergillus* and non-*Aspergillus* moulds in lung transplant patients**
M. Helary, C. Godet, G. Jebrak, S. Houze, H. Mal, C. Bonnal (Paris, France)*

4385 **Emergence of cryptic *Aspergillus* species infection and importance of antifungal susceptibility testing**
J. Tang (Hong Kong, Hong Kong), C. Tsang, H. Ye, F. Xing, S. Lo, C. Xiao, A. Wu, A. Ngan, K. Law, Y. To, D. Sze, T. Hui, T. Zhu, C. Yao, B. Tse, S. Lau, P. Woo*

4866 **Invasive aspergillosis and influenza virus infection: an accidental relationship?**
M. Machado (Madrid, Spain), H. Guillén Zabala, M. Valerio Minero, A. Galar Recalde, M. Kestler Hernandez, P. Catalán, B. Padilla, J. Peral, E. Reigadas Ramirez, J. Guinea Ortega, P. Escribano, R. Alonso, E. Bouza Santiago, P. Muñoz*

4939 **Clinical, microbiological and molecular studies of invasive pulmonary aspergillosis caused by *Aspergillus lentulus* in China**
S. Yu (Beijing, China), M. Zhou, Y. Xu*

5520 **Prevalence of azole resistance in clinical *Aspergillus fumigatus* isolates in Greece**
M. Siopi (Athens, Greece), O. Rivero-Menendez, A. Chatzimoschou, A. Velegraki, A. Alastruey-Izquierdo, E. Roilides, G. Vrioni, S. Pournaras, J. Meletiadis*

6557 **Antifungal susceptibility of *Aspergillus* section *Flavi* clinical isolates in France**
E. Djenontin (Créteil, France), J. Costa, A. Benmostefa, B. Mousavi, N. Lin, C. Guillot, N. Ait-Ammar, J. Guillot, L. Delhaes, F. Botterel, E. Dannaoui*

6944 **Invasive CNS aspergillosis in non-neutropenic patients: a review of nine cases from North India**
N. Gupta (Manipal, India), A. Mittal, P. Kodan, N. Mundadan, R. Kumar, T. Kumar, G. Singh, D. Xess, P. Ramteke, M. Soneja*

8144 **Invasive aspergillosis caused by *Aspergillus* non-fumigatus in children and adults after haematopoietic stem cell transplantation (HSCT) & chemotherapy**
M. Popova, Y. Rogacheva (Saint Petersburg, Russian Federation), A. Volkova, I. Markova, A. Shvetcov, I. Nikolaev, O. Pinegina, S. Ignatyeva, T. Bogomolova, A. Siniaev, A. Gevorgian, O. Paina, T. Bykova, E. Darskaya, O. Goloshapov, M. Vladovskaya, S. Bondarenko, I. Moiseev, L. Zubarovskaya, N. Klimko, B. Afanasyev*

8257 **Invasive *aspergillosis* in solid organ transplantation: changes in epidemiology, therapy and prognosis: a national cohort (DIASPERTOS Study)**
J. Fortun Abete (Madrid, Spain), L. Corbella Vazquez, E. Filigheddu, M. Ras, E. Vidal, M. Montejo Baranda, M. Machado, A. Fernandez-Cruz, F. Lopez-Medrano, J. Aguado Garcia, S. Pérez, N. Sabe, L. Lopez Soria, P. Muñoz, S. Rodriguez-Fernandez, E. Reigadas Ramirez, P. Martín-Dávila*

8473 **Limitations of the diagnostic criteria for invasive aspergillosis in solid organ transplantation: a national cohort (DIASPERTOS study)**
J. Fortun Abete (Madrid, Spain), L. Corbella Vazquez, E. Filigheddu, M. Ras, E. Vidal, M. Montejo Baranda, M. Machado, A. Fernandez-Cruz, M. Fernandez Ruiz, J. Aguado Garcia, N. Sabe, R. Rodríguez, P. Muñoz, M. Valerio, L. Linares, P. Martín-Dávila*

8681 **Keep the attention high on Putative Invasive Pulmonary Aspergillosis (PIPA) in medical wards and intensive care units: a four-year retrospective analysis**
T. Lupia, S. Raviolo, A. Trentalange, A. Curtoni, R. Cavallo, F. De Rosa, S. Corcione (Turin, Italy)*

8803 **The emerging non-conventional invasive aspergillosis: 5-year experience**
M. Machado (Madrid, Spain), M. Valerio Minero, M. Olmedo Samperio, A. Alvarez-Uria, E. Reigadas Ramirez, J. Guinea Ortega, A. Vena, R. Alonso, A. Burillo, E. Bouza Santiago, P. Muñoz*

9599 **The burden of chronic pulmonary aspergillosis on the respiratory service at a district general hospital**
F. Maghrabi (Manchester, United Kingdom), R. Cade, C. Kosmidis, R. Sundar, D. Denning*

Session accepted as Paper Poster Session

Candida and *Cryptococcus*: treatment options and novel agents

988 **Clinical experience of oral ibrexafungerp for treatment of four patients with invasive candidiasis from the FURI study**
J. Prattes (Graz, Austria), C. Zurl, N. Azie, D. Angulo Gonzalez, R. Krause*

1211 ***Candida* spp. in the respiratory tract secretions of critically ill patients and the impact of antifungal treatment**
N. Spernovasilis (Heraklion, Greece), A. Vouidaski, C. Alexopoulou, A. Papazachariou, E. Paraschou, A. Achyropoulou, S. Maraki, D. Ierodiakonou, G. Samonis, D. Kofteridis*

1354 **Treatment status and prognosis of 203 cryptococcosis in non-human immunodeficiency virus-infected and nontransplant patients**
S. Yi (Shanghai, China), B. Hu*

2516 **Empiric treatment with fluconazole, as compared to echinocandins or amphotericin B, was associated with lower mortality among intensive care unit patients with sepsis due to candidaemia**
M. Papadimitriou Olivgeris (Lausanne, Switzerland), A. Spiliopoulou, F. Kolonitsiou, A. Lambropoulou, V. Karamouzos, A. Georgakopoulou, I. Spiliopoulou, F. Fligou, M. Marangos, M. Christofidou*

3034 **Synthesis of nano-capsulated caprylic acid: evaluation of antifungal activity and its effect on *EFG1* gene expression in *Candida albicans***
M. Roudbary (Tehran, Iran), S. Roudbarmohammadi, R. Zarimeidani, S. Mardani*

3924 **Severe cryptococcal meningoencephalitis with large vessel vasculopathy and multi-territory cerebral infarcts**
C. Sun (Adelaide, Australia), M. Kernich, N. Chia, R. Nelson*

4116 **Progressive disseminated histoplasmosis in a population with HIV/AIDS in the Colombian coffee triangle**
J. Hoyos Pulgarin (Medellin, Colombia), A. Alzate, G. Moreno, J. Sierra, A. Jaramillo Torres*

4333 **Chronic mucocutaneous candidiasis in children in Saint Petersburg, Russia**
O. Kozlova, E. Frolova, T. Bogomolova, E. Suspitsin, T. Gabrusskaya, E. Dosovitskay, N. Klimko (Saint Petersburg, Russian Federation)*

4729 **Personalised prediction with machine learning approach to predict candidaemia in medical wards**
A. Ripoli, E. Sozio, F. Sbrana, G. Bertolino, C. Pallotto, S. Meini, B. Viaggi, G. Cardinali, C. Tascini (Naples, Italy)*

5135 ***In vitro* activity of novel biofilm-disrupting agents against *Candida auris* and other *Candida* species**
J. Vazquez (Augusta, United States), S. Wakade, E. Manavathu, M. Bogacz, M. Myntti, S. Thompson*

5627 **A five-year survey of *Candida* spp. bloodstream infections in a French university hospital (2014 - 2018): relevance and adaptation time of antifungal treatments**
S. Emery, M. Vannini, V. Mondain, N. Retur, R. Collomp, L. Hasseine, F. Lieutier-Colas (Strasbourg, France)*

5926 **Analysis of outcomes by geographic region of enrolment in STRIVE, the phase II of rezafungin for the treatment of candidaemia and invasive candidiasis**
J. Fortun Abete (Madrid, Spain), A. Skoutelis, R. Viani, T. Sandison*

6254 **Early empirical anidulafungin therapy reduces the prevalence of invasive candidiasis in critically ill sepsis patients: a retrospective study**
M. Hasan (Dhaka, Bangladesh), S. Neelotpol, R. Rabbani*

6502 **Clinical outcome of early central venous catheter removal in children with candidaemia : a retrospective multi-centre study**
N. Poey (Paris, France), M. Caseris, A. Faye, S. Bonacorsi, M. Lorrot, J. Toubiana, P. Mariani*

7119 ***In vitro* activity of novel propionohydrazide derivatives BG-354 and KTU-341 against multidrug-resistant *Candida auris***
P. Kavaliauskas (New York, United States), B. Grybaite, K. Anusevicius, V. Mickevicius, R. Plančiūnienė, R. Grigaleviciute, T. Walsh, R. Petraitiene, V. Petraitis*

7388 **Echinocandin blood and peritoneal concentration in patients with *Candida* peritonitis**
J. Fortun Abete (Madrid, Spain), A. Gomez Lopez, F. Gioia, M. Buitrago*

7523 **Evaluation of the efficacy of rezafungin in the treatment of *Candida albicans* endophthalmitis using a rabbit model**
L. Long, J. Herrada, D. Caley, G. Munguba, R. Sherif, K. Bartizal, M. Ghannoum (Cleveland, United States)*

8284 **Effect of nikkomycin Z and caspofungin upon *in vitro* induction of echinocandin resistance by *Candida tropicalis***
A. Silva, J. Branco (Porto, Portugal), I. Miranda, A. Rodrigues, S. Costa-De-Oliveira*

8536 **Pharmacokinetic, efficacy and safety of micafungin administered at high doses to neonates suffering from invasive candidiasis: results from a phase II study**
C. Auriti (Rome, Italy), B. Goffredo, I. Bersani, F. Piersigilli, A. Santisi, S. Cairoli, A. Dotta, P. Bagolan*

8965 **Impact of time to central venous catheter removal on the mortality of adults with non-severe catheter-related candidaemia**
C. Agnelli Bento (São Paulo , Brazil), M. Valerio Minero, M. Machado, J. Guinea Ortega, A. Vena, E. Bouza, P. Muñoz*

9305 **The polymorphism rs2305619 of Pentraxin 3 is associated with susceptibility of non-HIV-related cryptococcosis in a Chinese Han population**
W. Zhang (Chengdu, China), Q. Liao, Y. Liu, S. Wu, M. Kang*

9320 **Screening the antifungal activities of monoterpenes and their isomers against *Candida* species**
K. Zomorodian (Shiraz, Iran), A. Iraji, S. Yazdanpanah*

Session accepted as Paper Poster Session

Diagnostic mycology: biomarkers / antibodies

314 **Fully automatic (1-3)-β-D-glucan test for the invasive fungal detection**
L. Alana (Chengdu, China), L. Han*

1317 **Rapid detection of fungal feet infection by LED-UV light**
E. Fusté, G. Jimenez Galisteo, M. Sanchez, M. Aguilar, T. Vinuesa (L'Hospitalet de Llobregat, Spain)*

2444 **Clinical evaluation of a novel chemiluminescent microparticle immunoassay of *Aspergillus* galactomannan in diagnosis of invasive aspergillosis**
H. Wang (Beijing, China), C. Liu, Y. Zhang, K. Sun, J. Du, Y. Su, Z. Zhou*

2494 **Clinical performance of a novel Point-of-Care testing automation of fungus (1-3)-β-D-glucan assay**
H. Wang (Beijing, China), B. Wang, Y. Fu, Y. Zhang, J. Du, Y. Su, Z. Zhou*

3113 **Application of peptides as a novel method to enrich and identify of *Candida* species**
M. Vatanshenassan (Utrecht, Netherlands), C. Brouwer, T. Boekhout, M. Ríos Carrasco, F. Hagen*

3444 **Comparison of the performance of two galactomannan detection tests: Platelia Galactomannan (Bio-Rad) and Galactomannan Virclia (Vircell)**
E. Bouza Santiago, R. Alonso (Madrid, Spain), M. Montero Vega, M. Alguacil, M. Machado, I. Gadea Girones, R. Fernández Roblas, P. Muñoz, J. García Rodríguez, A. Leyva*

3906 **Performance of the sōna *Aspergillus* galactomannan lateral flow assay from serum samples for the diagnosis of invasive aspergillosis in patients after haematopoietic stem cell transplantation**
T. Erb, R. Meyer, E. Kotter, H. Bertz, J. Held (Erlangen, Germany)*

4440 **Comparison between visual reading, smartphone image and digital scanner interpretation of lateral flow device result for detecting *Aspergillus*-specific IgG**
B. Wilopo (Manchester, United Kingdom), E. Hunter, P. Goodwin, E. Phillips, G. Platt, M. Richardson, D. Denning*

4875 **Evaluation of two lateral-flow assays with galactomannan in BAL fluids for the detection of invasive pulmonary aspergillosis: a retrospective two-centre study**
U. Scharmann, H. Verhasselt, L. Kirchhoff, P. Rath, J. Steinmann, K. Ziegler (Nuremberg, Germany)*

5493 **Interest of immunoblotting with *Aspergillus fumigatus* western blot IgE assay for the differential diagnosis of IgE sensitisation and allergic broncho pulmonary aspergillosis**
R. Piarroux (Lyon, France), S. Ranque, J. Vitte*

6056 **Basophil activation test use for identification of fungal sensitisation in severe asthma patients**
Y. Kozlova, E. Frolova, A. Uchevatkina, L. Filippova, O. Aak, G. Solovjeva, V. Kuznetsov, N. Vasilyeva, N. Klimko (Saint Petersburg, Russian Federation)*

6119 **Diagnostic value of the IMMY *Aspergillus* LFA on bronchoalveolar lavage fluid of intensive care patients**
A. Dunbar, T. Mercier (Leuven, Belgium), V. Veldhuizen, B. Rijnders*

6251 **Bismethylgliotoxin is detected in serum from oncohaematological neutropaenic paediatric patients: presentation of two cases of probable IPA with negative galactomanan and positive bmGT**
M. Domingo, P. Esteban, S. Redrado, C. Lopez, L. Roc Alfaro, Y. Aguilar, O. Algara, A. Milagro, C. Calvo, J. Pardo Jimeno, A. Rezusta (Zaragoza, Spain), E. Gálvez*

9040 **Comparison of diagnostic performance of two *Aspergillus* antigen ELISAs**
K. Hoffmann (Lübeck, Germany), V. Borchardt-Lohölter, P. Rosenstock, K. Dichtl, U. Seybold, S. Ormanns, H. Horns, J. Wagener*

Session accepted as Paper Poster Session

Diagnostic mycology: culture / mass spectrometry

1250 **Comparison of three chromogenic agars for the detection of *Candida auris***
M. Bruins (Zwolle, Netherlands), M. Wolfhagen*

2011 **Evaluation of sample preparation method by the liquid nitrogen for identification of *Aspergillus fumigatus* and *Schizophyllum commune* in matrix-assisted laser desorption ionisation-time of flight mass spectrometry analysis**
N. Abe (Nara, Japan), M. Komatsu, K. Nakanishi, G. Matsumoto, Y. Ohno, H. Matsutani, S. Fukuda, M. Shimada, S. Matsuo*

2373 **Can MALDI-TOF MS provide enough discrimination between *Aspergillus fumigatus* sensu stricto and cryptic species?**
E. Zvezdanova, P. Escribano, J. García Rodríguez, J. Lozano-Serra, R. Jimenez Barrena, I. Guerrero Lozano, C. Castro, V. Sánchez Hellín, P. Muñoz, J. Guinea Ortega, B. Rodriguez-Sanchez (Madrid, Spain)*

3330 **Clinical evaluation of the ID-fungi plates for direct identification of dermatophytes on nail, hair and skin samples by MALDI-TOF MS**
R. Sacheli (Liege, Belgium), S. Winandy, A. Adjetey, R. Darfouf, Q. Legras, C. Meex, L. Marechal, J. Arrese, M. Hayette*

4177 **Direct identification of *Candida* species from positive blood culture by MALDI-TOF MS using a commercial pre-treatment kit**
Y. Yamagishi (Aichi, Japan), T. Mouri, H. Suematsu, A. Masuya, K. Ashizawa, Y. Shimpo, H. Mikamo*

4370 **Species delimitation of clinically challenging fungi by Orbitrap ultra high-resolution mass spectrometry: a case study in *Mucor*, *Rhizopus* and *Lichtheimia***
I. Moser, A. Jamalian (Landsmeer, Netherlands), B. Stielow, J. Knuuttila, A. Giraldo Lopez, S. De Hoog, J. Freeke*

5414 **Comparative evaluation of the Bruker Biotyper and Vitek MS MALDI-TOF MS systems for identification of non-albicans *Candida* and uncommon yeast isolates**
L. Teke (Istanbul, Turkey), B. Bayraktar, A. Baris*

5551 **Rapid diagnostic test: identification of *Candida* spp. directly from the blood culture bottle using short-term subculture incubation and MALDI-TOF MS in a routine microbiology laboratory**
Â. Celestino De Souza, P. Barth (Porto Alegre, Brazil), P. De Souza Sampaio, L. Lutz, V. Aquino, E. Wurdig Roesch, D. Castro Pereira*

5763 **Optimisation of culture protocol for the recovery of fungal pathogens from expectorated sputum of cystic fibrosis patients**
W. Memon (Baltimore, United States), R. Abellera, S. Zhang, R. Marayan*

6058 **Evaluation of the performance of Vitek MS and Bruker MS on the identification of *Candida haemulonii* species complex**
X. Hou (Beijing, China)*

6477 ***Candida auris* species and lineage identification from plate and blood cultures applying Orbitrap ultra high-resolution mass spectrometry**
A. Jamalian (Landsmeer, Netherlands), J. Freeke, B. Stielow, I. Moser, A. Giraldo Lopez, H. Friedrich, J. Meis, S. De Hoog*

7250 **Ultra high-resolution mass spectrometry database improves identification of clinical yeasts from blood cultures by the Acrion system**
A. Jamalian (Landsmeer, Netherlands), J. Freeke, I. Moser, H. Friedrich, J. Knuuttila, A. Rantakari, J. Salo, K. Haapasalo-Tuomainen, B. Stielow, S. De Hoog*

7619 **High-resolution mass spectrometry database (Acrion) improves identification of clinical yeasts**
J. Freeke (Vantaa, Finland), A. Jamalian, I. Moser, A. Giraldo Lopez, J. Knuuttila, O. Niiranen, B. Stielow, S. De Hoog*

Session accepted as Paper Poster Session

Diagnostic mycology: molecular methods

329 **Rapid semi-quantitative format PCR for the detection of *Pneumocystis jirovecii* replacing the direct examination**
A. Coste, R. Brouillet, J. Diserens, M. Moraz, F. Lamoth, P. Hauser, G. Greub, K. Jaton (Lausanne, Switzerland)*

505 **Potential value of qPCR for the early detection of *Mucorales* in high-risk patients**
D. Schmidt (Essen, Germany), U. Scharmann, J. Buer, P. Rath*

873 **Development of a routine laboratory test enabling the detection of dermatophytes as well as the identification of *Trichophyton rubrum* by means of duplex real-time PCR from mycological samples and cultures**
T. Pablo, F. Decruyenaere, M. Meo, A. Mzabi (Dudelange, Luxembourg), M. Perrin*

1779 **Cross-platform comparison of one qPCR assay with four leading technologies and six master mixes for the detection of *Pneumocystis jirovecii***
S. Dellière (Paris, France), M. Gits-Muselli, S. Bretagne, A. Alanio*

2399 **Examining discordance in blood culture and T2 positivity in the detection of candidaemia: modelling the odds of blood culture and T2 discordance as a function of candidaemia risk factors**
A. Vahia (Detroit, United States), G. Alangaden, G. Suleyman*

3518 **Evaluation of two *Aspergillus* PCR assays testing of bronchoalveolar lavage fluid and serum for diagnosis of chronic pulmonary aspergillosis**
Z. Li (Guangzhou, China), P. Zeng, S. Li, Z. Wang, F. Ye*

3620 **Commercial real-time PCR implementation for rapid diagnosis of onychomycosis: a new workflow in a clinical laboratory**
A. Blanco Suárez (Viladecavalls, Spain), E. Cuchí Burgos, R. Rubio Casino, M. Ballestero Tellez, P. Perez*

3864 **Development and validation of a specific real-time PCR assay for the rapid detection of *Candida auris***
A. Ibrahim, S. Baron, H. Yousfi, R. Lalaoui, L. Hadjadj, S. Morand, J. Rolain (Marseille, France), F. Bittar*

4424 **Comparison of two commercially available qPCR kits for the detection of *Candida auris***
A. Brunke (Cologne, Germany), J. Sattler, G. Plum, P. Wiegel, O. Kurzai, J. Meis, A. Hamprecht*

4460 **Primary evaluation of three *Aspergillus* PCRs compared to galactomannan assay**
L. Verdurme (Saint-Ouen-l'Aumône, France), M. Gama, E. Hedbaut*

4719 **Rapid diagnostics of *Pneumocystis jirovecii*: so far not good enough**
A. Sand (Oslo, Norway), A. Ingebretsen, J. Vildershøj Bjørnholt*

5530 **Cycle of quantification (Cq) does not differentiate colonisation from *Pneumocystis jirovecii* pneumonia, using real-time PCR**
P. Basazemajja, T. Schuurs, A. Stellingwerff, A. Al Moujahid (Leeuwarden, Netherlands)*

6065 **Presence and distribution of fungal species and dermatophytes in nail and skin samples**
L. Marki, A. Brachner, B. Ronacher, H. Enroth (Skövde, Sweden)*

6106 **Diagnosis of deep cutaneous mycoses in kidney transplant recipients by clinical metagenomics approach**
E. Sitterlé, G. Gricourt, D. Vanessa, A. Scemla, J. Pawlotsky, M. Bougnoux, C. Rodriguez (Creteil, France)*

6272 **Evaluation of the combined use of galactomannan antigen and *Aspergillus* DNA real-time PCR detection in laboratory diagnosis of invasive aspergillosis among haematological patients**
G. Vrioni (Athens, Greece), C. Tsiamis, M. Mavrouli, K. Theodoridou, V. Kapsimali, A. Tsakris*

7227 **Development of two new techniques based on real-time PCR for the detection of *Candida auris* in clinical settings**
L. Bernal Martinez (Madrid, Spain), A. Mesa, L. De Francisco, A. Gomez Lopez, M. Buitrago*

7273 **Comparison of *Candida* PCR and blood culture results in high-risk patients with candidaemia in the intensive care unit**
T. Simsek Bozok, F. Kuscu, T. Bozok, S. Komur, A. Ulu, A. Inal, B. Kurtaran, F. Kibar, Y. Tasova (Adana, Turkey)*

7284 **An evaluation to assess the performance of the Fungiplex Aspergillus real-time PCR and the Fungiplex Aspergillus Azole-R IVD real-time PCR Kits following the implementation of an extraction control**
J. Green (Glasgow, United Kingdom)*

7550 **Evaluating the extraction and molecular detection of *Candida auris* strains using commercial kits**
J. Green (Glasgow, United Kingdom)*

7692 **Development of an extraction control in Fungiplex Candida IVD real-time PCR Kit**
J. Green (Glasgow, United Kingdom), C. Dalton*

7719 **A real-time PCR for the detection of *Mucormycetes*: Fungiplex Mucorales**
J. Green (Glasgow, United Kingdom), K. Dempsey*

8179 **Diagnostic approach for *Aspergillus* infection: performance evaluation of a new molecular assay for detection and quantification of *Aspergillus* spp. in clinical samples**
R. Tedeschi (Pordenone, Italy), P. Stano, L. Pagani, G. Lorenzi, G. Ciganotto, P. Zigante, A. Camporese*

8321 **Detection of *Aspergillus* spp. in bronchoalveolar lavage fluid of haematological and non-haematological patients with invasive aspergillosis by real-time PCR**
S. Ignatyeva (Saint Petersburg, Russian Federation), T. Bogomolova, V. Spiridonova, O. Shadrivova, N. Vasilyeva, E. Desyatik, Y. Borzova, N. Klimko*

8616 **Comparison of six simple methods for ribosomal DNA extraction directly from nail sample suspected to onychomycosis for PCR-based assay**
M. Motamedi (Shiraz, Iran), M. Mahmoudi, S. Yazdanpanah*

8654 **Comparison of the performances of three commercial real-time PCR kits with an in-house real-time PCR assay for the diagnosis of invasive aspergillosis**
C. Dulac, A. Bourguignon, L. Mollier-Pierret, D. Dupont, M. Wallon, M. Rabodonirina, F. Persat, J. Menotti (Lyon, France)*

Session accepted as 2-Hour Oral Session

Different diagnostic tools for different fungal infections

1036 **Accuracy and clinical impact of fungal cell-free DNA PCR panel on plasma for diagnosis of invasive fungal infection**
F. Senchyna (Palo Alto, United States), C. Hogan, D. Ho, A. Subramanian, I. Budvytiene, S. Gombar, H. Costa, M. Budvytis, N. Banaei*

1103 **Improved molecular diagnosis of dermatomycosis**
L. Berlinger (Lucerne 6, Switzerland), R. Lombriser, A. Gisler, S. Steiner, S. Pranghofer, M. Altwegg*

2416 **Clinical evaluation of a novel rapid test for *Aspergillus* galactomannan**
H. Wang (Beijing, China), J. Peng, Y. Zhang, K. Sun, J. Wen, Y. Su, Z. Zhou*

2929 **Serum (1-3)-ß-D-glucan has suboptimal performance for the diagnosis of *Pneumocystis jirovecii* pneumonia and correlates poorly with respiratory burden measured by quantitative PCR in patients with cancer**
A. Szvalb (Houston, United States), A. Malek, Y. Jiang, D. Kontoyiannis*

3014 **Quantitative PCR detection of circulating DNA for the diagnosis of mucormycosis: prospective evaluation in the ModiMucor study**
L. Millon (Besançon, France), D. Caillot, A. Berceanu, H. Gbaguidi-Haore, V. Letscher-Bru, F. Dalle, B. Denis, S. Bretagne, A. Alanio, D. Boutoille, F. Morio, F. Lanternier, M. Bougnoux, F. Botterel, C. Cordonnier, T. Chouaki, A. Charbonnier, F. Ader, D. Dupont, S. Rocchi, E. Scherer, R. Herbrecht*

3573 **Serum lateral flow tests for invasive aspergillosis: a prospective cohort study**
T. Mercier (Leuven, Belgium), E. Guldentops, K. Lagrou, J. Maertens*

5432 **Evaluation of the performance of the Dynamiker Fungus (1-3)-β-D-glucan assay for the diagnosis of invasive aspergillosis in high-risk patients with haematological malignancies**
M. Siopi (Athens, Greece), M. Krmelj, S. Karakatsanis, C. Roumpakis, E. Eldeik, K. Korantanis, H. Sambatakou, P. Tsirigotis, M. Pagoni, N. Sypsas, S. Pournaras, J. Meletiadis*

5965 **The diagnostic accuracy of cryptococcal antigen detection in serum and cerebrospinal fluid in HIV patients with suspected cryptococcal meningitis: systematic review and meta-analysis**
E. Temfack (Douala, Cameroon), J. Bigna Rim, R. Spinnaker, A. Loyse, T. Chiller, P. Pappas, J. Perfect, T. Sorrell, T. Harrison, J. Cohen, O. Lortholary*

7133 **Diagnostic performance of two novel semi-quantitative cryptococcal antigen assays**
C. Skipper (Minneapolis, United States), K. Tadeo, E. Martyn, D. Meya, B. Kafufu, J. Rhein, D. Boulware*

7142 **Usefulness of serum as a non-invasive sample for the detection of *Histoplasma capsulatum*: comparative analysis of different diagnostic techniques**
L. Bernal Martinez, P. De La Cruz, S. Gago, L. Alcazar-Fuoli, M. Buitrago (Madrid, Spain)*

Session accepted as Paper Poster Session

Fungi and antifungal drugs: a complex relationship

45 ***In vitro* activity of manogepix (APX001A) and comparators against 1294 fungal isolates collected worldwide during the SENTRY surveillance programme (2018)**
M. Huband (North Liberty, United States), M. Pfaller, R. Flamm, P. Bien, M. Castanheira*

708 **Detection of echinocandin resistance in *Candida glabrata* in the microbiology laboratory using commercial methods: interpret with caution!**
P. Escribano (Madrid, Spain), L. Alguacil, J. Diaz-Garcia, C. Sanchez Carrillo, P. Muñoz, J. Guinea Ortega*

1358 **Antifungal susceptibility profiles of olorofim (formerly F901318), and currently available systemic antifungals against mould and yeast phases of *Talaromyces marneffei***
J. Zhang, H. Liu, L. Xi, Y. Chang, K. Kwon-Chung, S. Seyedmousavi (Bethesda, United States)*

1926 **Spectrophotometric MICs reading of azoles and amphotericin B shows high agreement with visual reading MIC interpretation using EUCAST 9.3.1 methodology**
J. Serrano Lobo, P. Escribano, J. Diaz-Garcia, W. Sanchez-Yebra Romera, L. Lopez Soria, M. Fajardo, B. Lorenzo, F. Sánchez Reus, I. Vidal Catala, M. Fernandez Torres, I. Sanchez-Romero, C. Ruiz De Alegría-Puig, J. Del Pozo, P. Munoz, J. Guinea Ortega (Madrid, Spain)*

2096 **Occurrence, susceptibility profiles, evaluation of synergistic activity of isavuconazole or voriconazole plus anidulafungin and genetic characterisation of *Candida auris* detected in a surveillance programme**
M. Castanheira (North Liberty, United States), L. Deshpande, P. Rhomberg, E. Utt, S. Messer, M. Pfaller*

2106 **Application of whole genome sequencing analysis to detect the azole-resistance mechanisms in *Aspergillus fumigatus* in a global surveillance programme**
M. Castanheira (North Liberty, United States), A. Davis, L. Deshpande, P. Rhomberg, M. Pfaller*

2614 ***In vitro* synergy of isavuconazole in combination with colistin against *Candida auris***
P. Schwarz (Marburg, Germany), A. Bidaud, E. Dannaoui*

3218 ***In vitro* activity of ibrexafungerp in pH 7.0 and pH 4.5 testing environments against 187 fluconazole-susceptible and -resistant *Candida* species from vulvovaginal candidiasis patients**
J. Sobel (Detroit, United States), S. Barat, K. Borroto-Esoda, N. Azie, D. Angulo Gonzalez*

3659 **Antifungal susceptibility description in *Candida parapsilosis* bloodstream infection: is there a change in the last years?**
A. Ferre Beltran (Palma de Mallorca, Spain), A. Olmos Torres, H. Vilchez Rueda, F. Fanjul Losa, E. Alcoceba, A. Oliver, J. Murillas Angoiti, M. Riera*

4266 **Impact of proposed revised EUCAST breakpoints on susceptibility classification of contemporary Danish mould isolates**
K. Jørgensen (Copenhagen, Denmark), R. Datcu, R. Krøger Hare, M. Arendrup*

4369 **Antifungal susceptibility testing practices in mycology laboratories in France, 2018**
A. Bellanger, F. Persat, F. Foulet, C. Bonnal, F. Botterel, E. Dannaoui (Paris, France)*

5558 **Antifungal susceptibility patterns among clinical isolates of *Aspergillus fumigatus* from paediatric cystic fibrosis patients in Greece: a laboratory-based study with focus on azole resistance**
M. Siopi (Athens, Greece), A. Stathi, H. Kirikou, L. Zachariadou, S. Pournaras, J. Meletiadis*

6173 **Novel qPCR demonstrates azole-resistant TR34/L98H and TR46/Y121F/T289A *Aspergillus fumigatus*, in air spore-samplings around Danish agricultural fields**
R. Krøger Hare (Copenhagen, Denmark), T. Heick, L. Jørgensen, M. Arendrup*

6505 **Comparison of antimycotic activity against clinical isolates of *Candida albicans* and *Candida glabrata* of originator and generics of voriconazole and anidulafungin**
A. Nussbaumer-Pröll (Vienna, Austria), S. Eberl, B. Selitsch, C. Dorn, F. Kees, T. Gasperetti, J. Marx, R. Welte, R. Bellmann, M. Zeitlinger*

6610 **Spectrophotometric detection of azole-resistant *Aspergillus fumigatus* clinical isolates with EUCAST broth microdilution method. Is it time for automating EUCAST antifungal susceptibility testing of *Aspergillus* spp.?**
I. Efstathiou, H. Van Der Lee, M. Arendrup, P. Verweij, J. Meletiadis (Athens, Greece)*

6658 **Role of TAC1 orthologs in *Candida auris* azole resistance**
J. Li (Lausanne, Switzerland), A. Coste, D. Bachmann, D. Sanglard, F. Lamoth*

7376 **Impact of calmodulin inhibition by fluphenazine on susceptibility, biofilm formation and pathogenicity of caspofungin-resistant *Candida glabrata***
A. Ceballos, D. Amado, E. Robert, C. Parra Giraldo, P. Lepape (Nantes, France)*

7647 **Whole genome sequencing (WGS) and antifungal susceptibility testing of *Candida glabrata (C. glabrata)* reveals new associations of antifungal resistance (AFR) with gene variants**
I. Stefanini, E. Stoakes, H. Wu, L. Mccrae, A. Hussain (Birmingham, United Kingdom), J. Moat1, C. Dowson, M. David, C. Constantinidou*

7902 **Exploring posaconazole pharmacodynamics against *Candida krusei* isolates: determination of EUCAST PK/PD susceptibility breakpoints**
M. Beredaki (Athens, Greece), M. Arendrup, S. Pournaras, J. Meletiadis*

7975 **Early (within 7h) phenotypic detection of fluconazole-resistant *Candida glabrata* isolates**
P. Georgiou (Athens, Greece), M. Arendrup, S. Pournaras, J. Meletiadis*

Session accepted as Mini-oral ePoster Session

Improving diagnostics in the fungal field

216 **Evaluation of newly formatted *Aspergillus* lateral flow assay for IgG antibody detection in chronic pulmonary aspergillosis**
Anna Yang (Tianjin, China), Y. Wang, B. Lu*

2745 **The accuracy of β-D-glucan and *Aspergillus* DNA detection by PCR in serum and bronchoalveolar lavage fluid for the diagnosis of pulmonary aspergillosis in critically ill patients with suspected ventilator associated pneumonia**
L. Loughlin (Belfast, United Kingdom), T. Hellyer, P. White, D. Mcauley, R. Posso, M. Richardson, D. Denning, J. Simpson, R. Mcmullan*

3083 **Usefulness of anaerobic blood culture vials for the microbiological diagnosis of candidaemia**
E. Farfour (Suresnes, France), C. Le Brun, A. Mizrahi, T. Guillard*

3479 **Differentiation at species level of the members of the PSC complex (*Pseudallescheria boydii* / *Scedosporium apiospermum*) involved in cystic fibrosis by MALDI-TOF MS**
V. Monnin (La Balme Les Grottes, France), L. Picoulet, D. Giraud, S. Arend, B. Celliere, P. Courault, D. Pincus, G. Durand, V. Girard*

3805 **18F-fluorodeoxyglucose positron emission tomography: computed tomography is a better tool for chronic disseminated candidiasis follow-up than conventional imaging**
B. Rammaert (Poitiers, France), C. Maunoury, T. Rabeony, C. Elie, P. Bakouboula, S. Alfandari, P. Berger, M. Rubio, T. Braun, J. Correas, F. Montravers, O. Lortholary*

4367 **Orbitrap ultra high-resolution mass spectrometry proteomics data mirrors clinically relevant functional associations of black dematiaceous hyphomycetes (black yeast-like fungi)**
S. De Hoog (Utrecht, Netherlands), A. Giraldo Lopez, I. Moser, J. Knuuttila, J. Freeke, A. Jamalian, B. Stielow*

5226 **Conserved host transcriptomic responses to acute infection are observed in the presence of multiple fungal pathogens**
J. Steinbrink (Durham, United States), A. Zaas, M. Johnson, E. Tsalik, B. Alexander, C. Woods, M. Mcclain*

7705 **Multi-centre validation of a EUCAST method for the antifungal susceptibility testing of microconidia-forming dermatophytes**
M. Arendrup (Copenhagen, Denmark), K. Jørgensen, J. Guinea Ortega, K. Lagrou, E. Chryssanthou, M. Hayette, F. Barchiesi, C. Lass-Flörl, P. Hamal, E. Dannaoui, A. Chowdhary, J. Meletiadis*

Session accepted as Paper Poster Session

Mucormycosis and uncommon fungi

118 **Olorofim for a case of severe disseminated *Lomentospora prolificans* infection**
S. Tio (Parkville, Australia), K. Thursky, G. Ng, J. Rex, D. Carney, M. Slavin*

335 **Risk factors for mortality in patients with pulmonary mucormycosis**
H. Son (Seoul, South Korea), J. Song, S. Choi, J. Jung, M. Kim, Y. Chong, S. Lee, S. Choi, Y. Kim, J. Woo*

663 **Matched-paired analysis of patients treated for invasive mucormycosis with isavuconazole versus standard treatment**
D. Seidel (Cologne, Germany), O. Cornely, M. Vehreschild, P. Köhler, H. Bertz, N. Klimko, M. Hoenigl, R. Herbrecht, H. Wisplinghoff, F. Barmaki-Rad, M. Saulay, M. Engelhardt, K. Hamed*

1272 **The guideline compatibility of mucormycosis management: a retrospective review of the case reports from European quality (EQUAL) score perspective**
H. Koc, G. Metan (Ankara, Turkey)*

2585 **A case of *Lomentospora prolificans* (LoPro) treated with the novel antifungal olorofim**
S. Chen, N. Joshi Rai, S. Cunneen, K. Cornelissen, J. Rex, C. Heath, E. Harvey (Manchester, United Kingdom)*

3907 **The trend of changes in paranasal computed tomography of patients with haematologic malignancies and febrile neutropaenia**
S. Shokouhi (Tehran, Iran), I. Alavidarazam, S. Shabani, D. Jalalvand, R. Jamily*

4206 **Successful salvage therapy for mucormycosis with isavuconazole in paediatric patients: cases series**
L. Ashkenazi-Hoffnung (Petah Tikva, Israel), E. Bilavski, G. Grisaru, E. Sadot, I. Levy, S. Fischer, E. Nahum, O. Scheuerman*

5106 **Polyethylene glycol (15)-hydroxystearate enhances amphotericin B activity against *Mucorales***
K. Brunet (Poitiers, France), A. Chauzy, N. Gregoire, F. Tewes, W. Couet, S. Marchand, B. Rammaert*

9016 **Urinary tract infection and fungaemia due to *Saprochaete capitata* in a patient with acute myeloid leukaemia**
A. Birinci (Samsun, Turkey), T. Avan, E. Tanyel, D. Gur Vural, K. Bilgin, Y. Tanriverdi Cayci*

Session accepted as Paper Poster Session

Mycology - ecology, mycobiome and immunology

948 **The influence of delivery mode in the oral mycobiome: from childhood to adulthood**
M. Maia Azevedo (Porto, Portugal), P. Campos, M. Pereira, R. Araújo, C. Ramalho, E. Zaura, B. Sampaio-Maia*

2241 **Isoquinolinesulfonamide H89 reduces the intestinal inflammation and promotes *Candida albicans* clearance from the gut**
C. Dumortier, R. Charlet (Lille, France), B. Sendid, A. Bettaieb, S. Jawhara*

3527 **Inhibition of *Candida albicans* biofilms by Gram-negative bacteria and their cell-free supernatants**
Ö. Oyardı (Istanbul, Turkey), M. Hacioglu*

3656 **The Mycosands initiative: exploring fungal contamination in the sand and water around the Mediterranean Sea and other water bodies of Europe: relevance to human health and well-being**
J. Brandao, J. Gangneux, E. Segal (Tel Aviv, Israel)*

6177 **Comparison of *in vivo* pathogenicity of four *Candida auris* clades in a neutropenic bloodstream infection murine model**
Z. Tóth (Debrecen, Hungary), L. Forgács, A. Borman, A. Szekely, S. Lockhart, R. Ben-Ami, G. Kardos, F. Nagy, B. Balázs, R. Kovács, L. Majoros*

6323 **Investigation of skin microbiota reveals *Mycobacterium ulcerans-Aspergillus* sp. trans-kingdom communication**
N. Hammoudi (Marseille, France), C. Carole, M. Million, S. Ranque, M. Drancourt, O. Kabore, D. Zingue, A. Bouam*

6324 **Hepatic phaeohyphomycosis due to *Pleurostoma hongkongensis*, a novel species**
K. Chan (Hong Kong, Hong Kong), C. Tsang, J. Chan, A. Ngan, W. Chan, S. Lau, P. Woo*

7139 **A comparative phenotypic study of aggregate versus non-aggregate *Candida auris* isolates**
P. Lepape (Nantes, France), J. Rodríguez, E. Robert, I. Ourliac Garnier, M. Albassier, P. Bonnet, A. Ceballos, C. Parra Giraldo, C. Alvarez*

7855 **The role of complement and diabetes in invasive candidiasis**
V. Harpf, R. Würzner (Innsbruck, Austria)*

9004 **Evaluation of potential implication of the wastewater microbiome in fungal pathogens spreading using next-generation sequencing technology**
H. Yousfi (Yerres, France), M. Loic, G. Anne, P. Karima, L. Karine, L. Arnaud, P. Jean-Jacques, S. Abdelghani*

9296 **Morphogenesis and pathogenesis regulation of *Candida albicans* by probiotic bacterium: *Pediococcus acidilactici***
Z. Zare Shahrabadi, K. Zomorodian (Shiraz, Iran), K. Pakshir, S. Rezaie*

9351 **BCR1-independent biofilm formation of outbreak related *Candida parapsilosis* isolates from nosocomial bloodstream infections**
S. Shafeeq (Stockholm, Sweden), S. Pannanusorn, J. Morschhäuser, U. Römling*

Session accepted as 2-Hour Oral Session

Optimising antifungal treatment in different clinical settings

331 **Systemic antifungal therapy (AFT) with isavuconazonium sulfate (ISAVUSULF) or other AFT in adults with invasive mucormycosis (IM) or invasive aspergillosis (IA) caused by a non-*fumigatus* species (IA-nf): A multi-centre, non-interventional registry study**
G. Thompson, J. Garcia-Diaz, M. Miceli, M. Nguyen, L. Ostrosky-Zeichner, J. Young, C. Fisher, N. Clark, R. Greenberg, A. Spec, L. Kovanda, R. Croos-Dabrera, D. Kontoyiannis (Houston, United States)*

1191 **An open-label, phase I, multi-centre study to evaluate the pharmacokinetic, safety and tolerability profile of oral isavuconazonium sulfate in paediatric patients**
A. Arrieta (Orange, United States), M. Neely, J. Day, S. Rheingold, P. Sue, W. Muller, L. Danziger-Isakov, J. Chu, I. Yildirim, G. Mccomsey, H. Frangoul, T. Chen, V. Statler, W. Steinbach, D. Yin, K. Hamed, C. Lademacher, A. Desai, J. Akin, D. Leiva Phillips, L. Kovanda, T. Walsh*

1580 **Optimising the use of triazole therapeutic drug monitoring using quality improvement methodology**
R. Wilson (London, United Kingdom), F. Davies, R. Palanicawandar, K. Mcdonough, M. Coleman, J. Woo, C. Parkinson, L. Whitney, M. Gilchrist*

2611 **Evaluation of targeted antifungal prophylaxis after liver transplantation: are echinocandins the optimal choice?**
M. Rinaldi (Bologna, Italy), M. Bartoletti, A. Ferrarese, E. Franceschini, C. Campoli, S. Coladonato, S. Ambretti, A. Siniscalchi, M. Morelli, M. Cescon, P. Burra, C. Mussini, R. Lewis, P. Viale, M. Giannella*

3189 **Caspofungin weight-based dosing supported by a population pharmacokinetic model**
A. Märtson (Groningen, Netherlands), K. Van Der Elst, A. Veringa, J. Zijlstra, A. Beishuizen, T. Van Der Werf, J. Kosterink, M. Neely, J. Alffenaar*

5086 **Clinical efficacy of echinocandins in the treatment of candidiasis in cirrhotic patients: retrospective multi-centre study**
Z. Pasquini (Ancona, Italy), M. Bartoletti, M. Rinaldi, L. Scudeller, S. Piano, D. Giacobbe, A. Maraolo, L. Bussini, F. Del Puente, P. Angeli, M. Giannella, P. Caraceni, M. Morelli, I. Gentile, M. Bassetti, P. Viale*

5459 **Candidaemia management: can we do better?**
J. Calderón (madrid, Spain), J. Herraiz Jimenez, A. Ramos Martínez, E. Muñez Rubio, A. Callejas, A. Díaz De Santiago, I. Sanchez Romero, M. Lopez Dosil, A. Fernandez-Cruz*

6987 **Clinical outcomes in patients receiving high vs standard dose caspofungin in the treatment of *Candida* intravascular infections**
G. Clous (Columbus, United States), K. Coe, L. Wardlow, C. Hanks, Z. El Boghdadly, E. Reed*

8845 **Analysis of early outcomes in the STRIVE Trial of rezafungin once-weekly treatment of candidaemia and invasive candidiasis**
G. Thompson, J. Vazquez (Augusta, United States), P. Merino-Amador, A. Das, R. Viani, T. Sandison, P. Pappas*

Session accepted as 1-Hour Oral Session

Pharmacokinetic considerations in fungal infections

2953 **Posaconazole dosing and association with therapeutic drug levels in allogeneic cell transplant recipients**
M. Kraljevic (Basel, Switzerland), N. Khanna, M. Medinger, J. Passweg, Y. Chalandon, S. Masouridi Levrat, N. Mueller, U. Schanz, C. Van Delden, D. Neofytos*

3221 **Using saliva for precision dosing of antifungal drugs: saliva population pharmacokinetic model**
H. Kim (Sydney, Australia), A. Märtson, E. Dreesen, I. Spriet, S. Wicha, A. Mclachlan, J. Alffenaar*

4800 **Pharmacokinetic evaluation of micafungin prophylaxis for invasive mould disease in childhood acute lymphoblastic leukeamia: part of the OPTIMA study**
D. Bury (Utrecht, Netherlands), R. Ter Heine, W. Tissing, E. Muilwijk, T. Wolfs, R. Brüggemann*

7419 **Therapeutic drug monitoring of isavuconazole in patients undergoing antifungal therapy in Denmark**
R. Jørgensen (Copenhagen, Denmark), M. Risum, M. Arendrup*

Session accepted as Mini-oral ePoster Session

Population and pathogenesis in fungi

1775 ***NDT80* transcription factor acts as a repressor of *Candida parapsilosis* virulence attributes**
J. Branco (Porto, Portugal), C. Cruz, L. Rodrigues, T. Gonçalves, I. Miranda, A. Rodrigues*

1879 **Prevention of pneumocystis pneumonia by Ibrexafungerp in a murine prophylaxis model**
S. Barat, K. Borroto-Esoda, A. Ashbaugh, D. Angulo Gonzalez (Jersey City, NJ, United States), M. Cushion*

1935 **Differential innate immune responses of human macrophages and bronchial epithelial cells against *Talaromyces marneffei***
C. Tsang (Pokfulam, Hong Kong), Y. Tan, K. Kok, S. Lau, P. Woo*

2065 **Mycobiome-microbiome cross-talk analysis during acute pulmonary exacerbation: focus on climax-attack model in cystic fibrosis**
F. Lussac-Sorton, S. Imbert, P. Sorret, L. Vandenborght, F. Francis-Oliviero, R. Enaud, M. Alvalos-Fernandez, T. Schaeverbeke, P. Berger, M. Fayon, R. Thiebaut, L. Delhaes (Bordeaux, France)*

5014 **Mycobiome sequencing reveals a high fungal diversity in patients with severe atopic dermatitis**
B. Schmid (Zurich, Switzerland), E. Bersuch, A. Künstner, A. Fähnrich, H. Busch, M. Glatz, P. Bosshard*

6617 **Understanding the pathogenicity of *Scedosporium* species, the emerging cystic fibrosis pathogens**
M. Homa (Szeged, Hungary), C. Szebenyi, O. Jáger, C. Vágvölgyi, T. Papp*

8567 **Polyclonal antibody anti-CR3-RP Ab inhibits biofilm of *Candida albicans* and decreases an expression of the genes related to biofilm-formation and cell surface hydrophobicity**
J. Dekkerova (Bratislava, Slovakia), H. Bujdáková, S. Kendra*

Session accepted as Paper Poster Session

Rare fungi: are they really so rare?

295 **Characterisation of airborne fungi present in two hospitals in Kabale District, Uganda**
A. Odebode (Akoka, Nigeria), G. Niwamanya*

1137 **Prospective survey of mucormycosis in Israel**
Y. Shachor-Meyouhas (Haifa, Israel), I. Oren, G. Rahav, M. Korem, N. Eliakim-Raz, L. Ashkenazi-Hoffnung, R. Ben-Ami, L. Nesher, M. Weinberger, R. Cohen, A. Stern, Z. Gazit, S. Amit, H. Ben Zvi, T. Lazarovitch, Y. Geffen, N. Keller, J. Bishara, I. Levy, I. Kassis, Y. Maor, A. Novikov, N. Mizrahi*

1217 **Genotyping, phylogenetic analysis and *in vitro* antifungal susceptibility profile of clinical isolates of *Neoscytalidium* species**
M. Hedayati (Sari, Iran), S. Heidari, M. Gheisari, M. Abastabar, M. Poorabdollah, M. Mirenayat, N. Basharzad, S. Ansari, V. Mortezaee, S. Seyedmousavi, A. Alastruey-Izquierdo*

1723 **Risk factors and mortality in invasive *Rasamsonia* spp. infection: an analysis of cases in the FungiScope registry and from the literature**
J. Stemler (Cologne, Germany), J. Salmanton-Garcia, D. Seidel, B. Alexander, H. Bertz, M. Hoenigl, R. Herbrecht, L. Meintker, A. Meißner, S. Mellinghoff, E. Sal, M. Zarrouk, P. Köhler, O. Cornely*

2429 **The clinical and economic burden of mucormycosis in Japan**
R. Ueno (Tokyo, Japan), S. Nishimura, G. Fujimoto, D. Ainiwaer, S. Kim*

2501 **MixinYeast: a multi-centre survey on mixed yeast infections**
N. Medina (Guatemala, Guatemala), J. Soto-Debrán, D. Seidel, A. Perez De Ayala Balzola, A. Chakrabarti, C. Cassagne, C. Garcia Vidal, E. Roilides, E. Dannaoui, G. Lo Cascio, H. Badali, H. Zarrinfar, I. Akyar, J. Guitard, J. Steinmann, R. Stauf, J. Meletiadis, J. García Rodríguez, L. Trovato, M. Ruíz-Pérez De Pipaón, P. Munoz, P. Hamal, S. Khodavaisy, S. Bretagne, T. Pelaez Garcia, T. Jagielski, E. Ochman, I. Żak, Y. Cag, C. Lass-Flörl, S. Arikan-Akdagli, A. Alastruey-Izquierdo*

3183 **Neuroparacoccidioidomycosis: analysis of 10 cases observed in an endemic area in Argentina**
P. Villalba, G. Mendez, C. Niveyro (Posadas, Argentina), V. Sosa*

4003 **Prevalence and risk factors for *Histoplasma Capsulatum* infection amongst HIV patients attending the Buea Regional Hospital using the *Histoplasma* urine antigen detection enzyme immunoassay**
K. Marius Paulin (Buéa, Cameroon), D. Denning, C. Mandengue, N. Raymond*

4093 **Identification, antifungal susceptibility profile, and biofilm formation of *Rhodotorula mucilaginosa* in China (August 2010 to July 2015): a multi-centre study**
J. Huang (Beijing, China), M. Xiao*

4269 **Respiratory co-infections by *Pneumocystis jirovecii* and other pathogens in non-HIV immunosuppressed patients: a retrospective review**
B. Dietl (Barcelona, Spain), L. Boix-Palop, C. Cardozo, J. Aguilar Company, A. Rial-Villavecchia, P. Puerta, M. Martin, P. Perez, I. Ruiz-Camps, C. Garcia Vidal, E. Calbo Sebastian*

4814 **Molecular genetic analysis of population of dermatophyte fungus *Trichophyton rubrum***
I. Pchelin, D. Azarov, M. Churina, S. Romanyuk, Y. Mochalov, G. Chilina, S. Apalko, N. Vasilyeva (St. Petersburg, Russian Federation), A. Taraskina*

5356 **Epidemiology and antifungal susceptibility of *Rhodotorula* spp. in a tertiary care hospital**
I. Costales (Oviedo, Spain), C. Castelló-Abietar, H. Lorenzo Juanes, A. Templado-Barroso, A. Ramirez, M. Sandoval, T. Pelaez Garcia*

5712 **Twenty-seven years of chromoblastomycosis in Martinique**
Y. Le Govic (Fort-de-France, Martinique), N. Berrette, E. Baubion, E. Amazan, G. Ferrati-Fidelin, C. Miossec, S. De Hoog, N. Desbois-Nogard*

6028 **Epidemiological and clinical characteristics among HIV adults with invasive fungal infections in north-eastern Mexico**
G. Aguirre García (monterrey, Mexico), J. Cázares González, M. Martínez-Reséndez, R. Lara-Medrano, C. Alfaro-Rivera, N. Gaona Chavez, J. Rodríguez, H. Villanueva-Lozano*

6304 **The epidemiology, genotypes, antifungal susceptibility of *Trichosporon* species, and impact of voriconazole therapy on outcome of *Trichosporon* fungaemia**
K. Shin-Huei (Kaohsiung, Taiwan), P. Lu, Y. Chen, M. Ho, C. Lee, S. Lin*

6320 **An updated analysis of the burden of fungal diseases in Uganda**
F. Bongomin, B. Kirenga, R. Kwizera, D. Meya, D. Denning (Manchester, United Kingdom)*

6556 ***Saccharomyces cerevisiae* fungaemia: a 10-year review in the CHU of Liege (Belgium)**
C. Diop (Liege, Belgium), J. Descy, C. Meex, R. Sacheli, M. Hayette*

6624 **Species distribution and antifungal susceptibility profile of the emerging yeast pathogen *Blastobotrys***
H. Badali, C. Gibas, H. Patterson, D. Mccarthy, J. Mele, H. Fan, N. Wiederhold (San Antonio, United States)*

6821 **Can FT-IR spectroscopy reasonably type *Saprochaete clavata* isolates? A comparison with whole genome sequencing and MALDI-TOF MS approaches for outbreaks' investigation**
E. De Carolis (Rome, Italy), L. Maccacaro, A. Sorrentino, B. Posteraro, A. Urbani, G. Lo Cascio, M. Sanguinetti*

6836 **Fungal disease burden: an underestimated health challenge in Cote d'Ivoire**
D. Koffi (Abidjan, Côte d'Ivoire), B. Ira, O. Toure, R. Jambou, D. Denning*

7471 **Evaluation of fungi isolates from cystic fibrosis adult patients in a tertiary hospital of Madrid, Spain**
A. Fraile Torres (Madrid, Spain), L. Fontan, S. Gómez De Frutos, T. Soler Maniega, T. Alarcon Cavero, R. Girón, L. Cardeñoso, B. Buendia*

7694 **Clinical and laboratory study on invasive infections due to *Fusarium* species in critically ill adult and paediatric patients in Serbia: ten years' experience of National Laboratory for Medical Mycology**
V. Arsic Arsenijevic (Belgrade, Serbia), S. Otasevic, A. Tortorano, D. Ivanovic, J. Kolarovic, L. Paripovic*

7997 **Serum galactomannan antigenaemia of HIV-positive patients in an endemic area for *Talaromyces marneffei***
Y. Huang (New Taipei, Taiwan), C. Liao, C. Yang*

8006 **Pulmonary mucormycosis: a large French survey**
A. Coste (Brest, France), A. Conrad, S. Poirée, R. Porcher, F. Ader, M. Bougnoux, S. Ansart, G. Guillerm, V. Letscher-Bru, D. Boutoille, F. Morio, P. Peterlin, C. Defrance, G. Melica, F. Botterel, O. Lortholary, R. Herbrecht, F. Lanternier*

8979 ***Lichtheimia corymbifera* cutaneous infection**
O. Sabalza (Valencia, Spain), N. Lozano Rodríguez, M. Garrido Jareño, R. Chouman Arcas, E. González-Barberá, J. Sahuquillo-Arce, J. Peman Garcia, J. López-Hontangas*

9571 **Trichomonadine association with *Pneumocystis jirovecii*: a retrospective study**
S. Mille, D. Toubas, F. Foudrinier, D. Jerôme, A. Huguenin (Reims, France)*

Session accepted as 1-Hour Oral Session

Resistance in fungi

1142 **Comparative variant analysis of *Aspergillus fumigatus* genomes for identification of novel mutations in candidate genes possibly be involved in mediation of azole resistance**
B. Spiess (Mannheim, Germany), T. Boch, M. Mossner, D. Nowak, J. Skladny, C. Lass-Flörl, O. Bader, T. Miethke, J. Steinmann, P. Rath, A. Dietz, N. Merker, V. Nowak, W. Hofmann, D. Buchheidt*

1383 **Whole genome sequencing and comparative analysis of echinocandin susceptible and resistant sequential *Candida glabrata* clinical isolates**
A. Albarrag (Riyadh, Saudi Arabia), K. Alzahrani*

6600 **Mechanisms of resistance and virulence of azole-resistant *Aspergillus flavus* clinical isolates**
E. Djenontin (Créteil, France), B. Mousavi, N. Lin, L. Lachaud, M. Cornet, J. Guillot, L. Delhaes, F. Botterel, E. Dannaoui*

8058 **Mutations in *Aspergillus fumigatus hmg1* confer increased expression of ergosterol biosynthesis and efflux pump encoding genes**
J. Rybak (Memphis, United States), W. Ge, N. Wiederhold, V. Bruno, P. Rogers, J. Fortwendel*

8132 **Prevalence and clonal distribution of azole-resistant *Candida parapsilosis* isolates causing human bloodstream infections in a tertiary Italian hospital**
C. Martini (Rome, Italy), M. Cacaci, R. Torelli, E. De Carolis, T. De Groot, F. Bugli, M. Sanguinetti, B. Posteraro, J. Meis*

Session accepted as 2-Hour Oral Session

The changing fungal landscape

896 **Nationwide azole resistance survey in clinical *Aspergillus fumigatus* isolates: a snapshot of the situation at 30 Spanish hospitals**
J. Diaz-Garcia (Madrid, Spain), P. Escribano, J. Serrano, B. Rodriguez-Sanchez, E. Zvezdanova, M. Martin Gomez, E. Ibañez Martinez, M. Rodriguez Mayo, T. Pelaez Garcia, E. García G. De La Pedrosa, R. Tejero-García, J. Marimon, E. Reigadas Ramirez, A. Rezusta, C. Labayru Echeverría, A. Perez De Ayala Balzola, J. Ayats, F. Cobo, M. Pazos Pacheco, P. Muñoz, J. Guinea Ortega*

1186 **Needles in a haystack: ultra-orphan invasive fungal infections reported in FungiScope: global registry for emerging fungal infections**
J. Salmanton-Garcia (Cologne, Germany), P. Köhler, S. Mellinghoff, H. Wisplinghoff, O. Cornely, D. Seidel*

4156 **30-day mortality among neonates with candidaemia in a high azole resistance setting, South Africa, 2012-2017**
L. Shuping (Johannesburg, South Africa), N. Govender*

4414 **Risk factors for intra-abdominal candidiasis in intensive care units: results from EUCANDICU study**
M. Bassetti, A. Vena (Madrid, Spain), D. Giacobbe, C. Trucchi, F. Ansaldi, M. Antonelli, V. Adamkova, C. Alicino, M. Almyroudi, E. Atchade-Thierry, A. Azzini, P. Brugnaro, N. Carannante, A. Carnelutti, S. Corcione, A. Cortegiani, G. Dimopoulos, S. Dubler, J. Garcia Garmendia, M. Girardis, O. Cornely, S. Ianniruberto, B. Kullberg, K. Lagrou, C. Lebihan, R. Luzzati, M. Malbrain, M. Merelli, A. Marques, I. Martin-Loeches, A. Mesini, J. Paiva, M. Peghin, S. Raineri, R. Richardson, J. Schouten, H. Spapen, P. Tassioudis, J. Timsit, V. Tisa, M. Tumbarello, C. Van Den Berg, B. Veber, M. Venditti, G. Voiriot, J. Wauters, N. Zappella, P. Montravers*

4592 **Genotyping and antifungal susceptibility of *Candida albicans* isolates from vaginal samples: are the genotypes different from blood?**
A. Mesquida (Madrid, Spain), J. Diaz-Garcia, T. Vicente, E. Reigadas Ramirez, M. Palomo, P. Muñoz, J. Guinea Ortega, P. Escribano*

7946 **Histoplasmosis epidemiology in Costa Rica**
J. Villalobos, J. Castro, C. Ramírez (San Jose, Costa Rica), L. Villalobos González*

7983 **Outcome and characteristics of invasive fungal infections in critically ill burn patients: a multi-centre retrospective study**
V. Maurel, M. Camby, A. Alanio, M. Lagrange, C. De Tymowski, M. Legrand, B. Denis (Paris, France)*

8864 **Species distribution and antifungal susceptibility of *Candida* spp. causing candidaemia in China: an update from the CHIF-NET study**
M. Xiao (Beijing, China), S. Chen, F. Kong, Y. Xu*

Session accepted as Paper Poster Session

The changing scenario of *Candida* infections

350 **Significance of candidaemia causing neonatal sepsis and efficacy of caspofungin therapy**
S. Seal (Kolkata, India)*

895 **Species identification and antifungal resistance of yeasts causing fungaemia at a tertiary care hospital in Madrid, Spain: the coast is clear**
J. Diaz-Garcia (Madrid, Spain), C. Sanchez Carrillo, E. Reigadas Ramirez, P. Muñoz, P. Escribano, J. Guinea Ortega*

1366 **Epidemiology of nosocomial candidaemia in paediatrics: a multi-centre study in Iran**
F. Ahangarkani (Sari, Iran), M. Rezai, T. Shokohi, S. Khodavaisy, M. Ilkit, R. Alizadeh Navai, Z. Abtahian, J. Meis, H. Badali*

1453 **Development and implementation of an electronic admission-screening tool for *Candida auris* at a large healthcare system in Miami, Florida**
A. Jimenez (Miami, United States), K. Sposato, G. Rosello, D. De Pascale, A. Flanagan Giroud, L. Abbo*

1501 **HIV is a risk factor for death among persons with candidaemia in South Africa**
N. Govender (Johannesburg, South Africa), J. Todd, C. Cohen*

1651 **CANDIMAD study: a prospective multi-centre laboratory based survey of antifungal resistance in *Candida* spp. causing invasive candidiasis in Madrid**
J. Diaz-Garcia (Madrid, Spain), A. Mesquida, M. Meléndez Carmona, F. González-Romo, C. Maria Soledad, N. Zurita Cruz, M. Muñoz Algarra, M. Garcia, A. Sánchez, I. Quiles, M. Duran-Valle, C. Sanchez-Carrillo, P. Muñoz, P. Escribano, J. Guinea Ortega*

1969 ***Candida parapsilosis*..not so "candid"! The burden of *Candida parapsilosis* bloodstream infections and azole-resistance pattern in a tertiary care university hospital**
C. Sarda (Pavia, Italy), R. Bruno, B. Mariani, A. Muzzi, A. De Silvestri, A. Morea, C. Cavanna, F. Lallitto, E. Seminari*

2608 **Not all candidaemias are the same: utility of a rapid identification**
C. Leli, L. Di Matteo, S. Busso, V. Cavallo, A. Rocchetti (Alessandria (AL), Italy)*

2755 **Risk factors for candidaemia in hospitalised patients with liver cirrhosis: a multi-centre case-control-control study**
M. Bartoletti (Bologna, Italy), M. Rinaldi, Z. Pasquini, L. Scudeller, S. Piano, D. Giacobbe, A. Maraolo, F. Del Puente, P. Angeli, M. Giannella, P. Caraceni, L. Bussini, M. Morelli, C. Campoli, I. Gentile, M. Bassetti, P. Viale*

2982 **Severe candidaemia in a tertiary care hospital**
M. Vaquero-Herrero (Salamanca, Spain), S. Ragozzino, M. Siller Ruiz, M. Marcos, H. Ternavasio De La Vega*

4158 **Emergence of another truly multidrug-resistant yeast pathogen, *Candida kefyr*, in Kuwait**
S. Ahmad (Safat, Kuwait), Z. Khan, N. Al-Sweih, W. Alfouzan, L. Joseph, M. Asadzadeh*

4977 **Epidemiology and antifungal susceptibility patterns of invasive fungal infections from 2012 to 2014 in a teaching hospital in central China**
S. Yu (Beijing, China), M. Zhou, Y. Xu*

4996 **Prevalence of haematogenous seeding at distant sites in patients with *Candida* bloodstream infections**
N. Castillo Almeida (Rochester, United States), P. Gurram, C. Grimont, M. Mahmood, L. Baddour, M. Sohail*

5945 **Clonality of regional *Candida auris* isolates identified by whole genome sequencing**
S. Roberts (Chicago, United States), E. Ozer, C. Qi*

6072 **Species distribution and antifungal susceptibility of yeast bloodstream isolates in adult patients at three university hospitals in South Korea**
Y. Jeong (Incheon, South Korea), S. Kim*

6226 **Investigation of *Candida parapsilosis* outbreaks by microsatellite genotyping and emergence of clonal antifungal drug-resistant strains in a multi-centre surveillance in China**
Z. Li (Beijing, China), S. Yu, S. Chen, M. Xiao, F. Kong, Y. Xu*

6953 **Evolution of candidaemia epidemiology and outcomes over the last 10 years: a single-centre study**
J. Battistolo (Lausanne, Switzerland), E. Glampedakis, L. Damonti, J. Poissy, T. Calandra, J. Pagani, P. Eggimann, P. Bochud, O. Marchetti, F. Lamoth*

7905 **Changes in epidemiology, treatment and outcomes of candidaemia at a tertiary care children's hospital**
A. Arrieta (Orange, United States), N. Ashouri, D. Nieves, S. Osborne*

8048 **Candidaemia: a decade-long experience from India**
R. Adhikary (Bangalore, India), B. Mv, S. Joshi, B. Hb, A. A*

8085 **Epidemiology of candidaemia in Swiss tertiary care hospitals: a 15-Year Study 2004 to 2018**
K. Adam (Basel, Switzerland), M. Osthoff, A. Conen, V. Erard, K. Boggian, P. Schreiber, F. Lamoth, S. Zimmerli, P. Bochud, D. Neofytos, H. Fankhauser, R. Frei, K. Mühlethaler, J. Schrenzel, R. Zbinden, N. Vernaz, O. Marchetti, N. Khanna*

8155 **The impact of candidaemia management on mortality: a 4-year retrospective study from a tertiary care hospital**
A. Martins (Porto, Portugal), C. Silva, J. Caldas, E. Alves Branco, S. Almeida Lacerda Pereira, B. Prista Leão, R. Filipe, S. Magalhães, M. Pinheiro, A. Silva-Pinto, A. Sarmento, L. Santos*

8235 **Characterisation of a Portuguese population with candidaemia in a tertiary care hospital**
C. Silva (Santa Maria da Feira, Portugal), J. Caldas, A. Martins, S. Almeida Lacerda Pereira, E. Alves Branco, R. Filipe, B. Prista Leão, S. Magalhães, M. Pinheiro, A. Silva-Pinto, A. Sarmento, L. Santos*

9159 **Surveillance for control of antifungal resistance in *Candida* bloodstream infections fails to inform antifungal stewardship in European countries**
L. Galia, A. Callegari (Spresiano, Italy), E. Carrara, N. Babu Rajendran, M. Compri, E. Tacconelli*

9390 **Update on *Candida auris* in Russia**
N. Barantsevich (Saint-Petersburg, Russian Federation), O. Orlova, L. Ivanova, I. Churkina, Y. Belsky, S. Andrey, A. Vetokhina, E. Barantsevich*

Session accepted as Paper Poster Session

Treatment options in aspergillosis

624 **Clinical experience with isavuconazole in Chinese healthy volunteers and Chinese patients with invasive aspergillosis**
J. Zhang (Shanghai, China), Y. Zhang, D. Wu, G. Cao, K. Hamed, A. Desai, J. Aram, X. Guo, R. Fayyad, O. Cornely*

1720 **Current use of baseline chest CT in haematology patients at high risk for invasive fungal infection**
J. Stemler (Cologne, Germany), C. Bruns, S. Mellinghoff, P. Köhler, O. Cornely*

1844 **Clinical and laboratory features of mixed invasive mycoses in adult haematologic patients with invasive aspergillosis**
O. Shadrivova, S. Khostelidi, Y. Borzova, E. Desyatik, J. Chudinovskikh, O. Uspenskaya, M. Popova, A. Volkova, T. Shneyder, T. Bogomolova, S. Ignatyeva, L. Zubarovskaya, B. Afanasyev, N. Vasilyeva, N. Klimko (Saint Petersburg, Russian Federation)*

2919 **Salvage treatment of invasive pulmonary aspergillosis with isavuconazole and caspofungin combination in a lung transplant recipient**
P. Pavone (Rome, Italy), C. Carillo, Y. Pecoraro, F. Venuta, C. Mastroianni, G. Russo*

3887 **A surgical take on broncho-pulmonary *Aspergillus*: 20 years of experience**
L. Bertrand (Munich, Germany)*

4722 **Proposition of a uniform methodological approach to attribution of invasive aspergillosis as a cause of death**
R. Van Grootveld (Leiden, Netherlands), R. Van De Peppel, H. Jolink, P. Von Dem Borne, A. Bernards, M. Van Der Beek, M. De Boer*

4818 **Pharmocogenetic approach to the antifungal drug administration: clinical case**
A. Taraskina, Y. Borzova, E. Desyatik, D. Vera, N. Regina, N. Vasilyeva (St. Petersburg, Russian Federation)*

8013 **Evaluation of the efficacy of combination of antifungals against invasive aspergillosis in an invertebrate animal model**
S. Jemel (Créteil, France), V. Jullien, E. Billaud, J. Guillot, F. Botterel, E. Dannaoui*

8676 **Allergic bronchopulmonary aspergillosis (ABPA) complicating chronic obstructive pulmonary disease (COPD) without asthma: responses to antifungal therapy**
S. Aggarwal (Manchester, United Kingdom), C. Kosmidis*

9427 **Diagnostics and treatment of invasive aspergillosis in B-cell lymphoma patients after cytostatic chemotherapy and autologous stem cell transplantation**
J. Chudinovskikh, T. Semiglazova, M. Popova, O. Shadrivova, E. Frolova, T. Bogomolova, S. Ignatyeva, I. Zyuzgin, L. Filatova, J. Oleinik, N. Klimko (Saint Petersburg, Russian Federation)*

9449 **Incidence, risk factors and clinical impact of invasive pulmonary aspergillosis in patients hospitalised with influenza infection**
V. Bellelli (Rome, Italy), G. Siccardi, L. Celani, P. Vassalini, E. Congeduti, C. Borrazzo, M. Venditti, G. D'Ettorre*

Session accepted as Mini-oral Flash Session

Yeast wars: the rise of *auris*

246 **Delineation of the direct impact of *Candida auris ERG11* mutations on clinical triazole resistance**
J. Rybak (Memphis, United States), C. Sharma, L. Doorley, G. Palmer, P. Rogers*

3356 **Differential resistance of *Candida auris* biofilms against surface disinfectants commonly used in the hospital**
B. Zatorska, M. Diab-Elschahawi (Vienna, Austria), D. Moser, E. Presterl*

3612 **Hospital lanyards: a potential resevoir for *Candida auris* and other *Candida* species identified in a hospital outbreak**
C. Patterson (London, United Kingdom), H. Mitchell, W. Newsholme, D. Wyncoll, H. Winteridge, Y. Ceesay, M. Chand, A. Patel, J. Edgeworth*

3646 **Ibrexafungerp demonstrates potent and consistent *in vitro* activity against >400 global *Candida auris* isolates, including isolates with elevated MIC's to echinocandins**
S. Barat, K. Borroto-Esoda, D. Angulo Gonzalez (Jersey City, NJ, United States)*

3958 ***In vitro* evolution reveals mutations in *Candida auris ERG6* to confer high level amphotericin B resistance**
J. Rybak (Memphis, United States), K. Barker, J. Parker, Y. Li, J. Mũnoz, G. Palmer, C. Cuomo, S. Kelly, P. Rogers*

4126 ***Candida auris* in a large healthcare system in South Florida: importance of active surveillance testing to prevent spread**
A. Jimenez (Miami, United States), K. Sposato, G. Rosello, D. De Pascale, J. Cardozo, O. Orozco, B. De Pascale, O. Martinez, V. Salazar, K. Deronde, A. Vega, L. Abbo*

7239 ***Candida auris* compared to other *Candida* spp. candidaemia: a two-year experience in a Spanish tertiary hospital**
J. Mulet (Valencia, Spain), N. Tormo, C. Salvador, R. Guna, M. Martínez-Serrano, R. Olmos, B. Fuster, M. Belda, C. Gimeno Cardona*

9313 **Echinocandin resistance in emerging multidrug-resistant yeast *Candida auris* and investigation into the mechanism of resistance**
D. Sharma (Chandigarh, India), R. Paul, S. Rudramurthy, S. Paul, H. Prakash, S. Bhattacharya, A. Chakrabarti*

9353 **Rapid identification of *Candida auris* from direct blood culture positive samples by MALDI-TOF MS from patients with candidaemia in a tertiary care hospital**
R. Marak (Lucknow, India), S. Yadav, A. Dixit*

9422 **Molecular and epidemiological characterisation of an outbreak of *Candida auris* in a Spanish hospital**
E. Cortes-Acosta, I. Sigona-Giangreco, A. Ruiz (Valencia, Spain), A. Martínez-Martínez, E. Valentin, J. Peman*

Abstract Programme

7. Parasitic diseases & International health

- Diagnostic parasitology
- Antiparasitic susceptibility & resistance
- Antiparasitic drugs & treatment
- Parasitic disease epidemiology
- Travel medicine & migrant health
- Food & water safety and environmental health
- International & public health
- Other

Session accepted as 1-Hour Oral Session

Chagas disease: more than meets the eye

2052 **Screening and management of Chagas disease in at-risk blood donors in a non-endemic country: experience of a north-western tertiary care centre in Italy**
G. Sarteschi (Genoa, Italy), L. Nicolini, P. Stura, R. Pincino, M. Soracco, P. Tatarelli, L. Magnasco, M. Bassetti*

3862 **Chagas disease diagnosis: performance of a new automated native antigen technique**
J. Wang Wang (Barcelona, Spain), B. Rivaya Sanchez, G. Fernández Rivas, N. López González, L. Valerio, L. Matas Andreu*

6722 **Prevalence of positive serology for *Trypansoma cruzi* in a sample population of migrants from El Salvador and Honduras living in the Metropolitan Area of Milan (MAM)**
R. Grande (Milan, Italy), A. Villa, M. Gismondo, L. Galimberti, A. Piliafas, A. Rizzo, S. Fadelli, R. Cimmino, E. Ciriaco, C. Fiammanti, S. Antinori*

8673 **Neurologic complications in Chagas disease: results from a systematic review of published literature**
L. Lepore (Rome, Italy), M. Giancola, D. Checchi, F. Caldara, T. Ascoli Bartoli, A. D'Abramo, L. Scorzolini, G. Ippolito, K. Puchner, E. Nicastri*

9420 **Evaluation of salivary protein rTiSP14.6 as a marker of exposure to the bite of the insect *Triatoma infestans*, vector of *Trypanosoma cruzi***
A. Moreno, I. Martin, E. García, J. Nieto, M. Flores-Chavez (Madrid, Spain)*

Session accepted as Mini-oral Flash Session

Exotic diseases around the world

859 **Deaths of emerging and re-emerging infectious diseases outbreaks, epidemics and pandemic in the last 10 years: a systematic review**
T. Quynh (Ho Chi Minh, Vietnam), H. Le, A. Zayan, G. Abdel-Samea, E. Othman, H. Le, T. Hoang, K. Le, M. Hashizume, K. Hirayama, N. Huy*

1403 **Toxocariasis in children in south Russia: epidemiological and laboratory features**
L. Ermakova, Y. Kiosiva, A. Andreeva, N. Golovchenko, T. Tverdokhlebova, A. Shirinyan, N. Pshenichnaia (Moscow, Russian Federation), A. Grekova*

1713 **Mass PCR testing and targeted treatment for malaria in a low transmission area in Amazonia, French Guiana**
E. Mosnier (Cayenne, French Guiana), F. Djossou, R. Priam, M. Demar, L. Epelboin, M. Douine, M. Nacher, A. Carbunar, M. Gaillet, J. Landier, Y. Lazrek, L. Musset*

3962 **High prevalence of *Plasmodium falciparum* and non-falciparum infections in asymptomatic adults in forest Ghana**
M. Heinemann (Hamburg, Germany), R. Phillips, C. Vinnemeier, C. Rolling, E. Tannich, T. Rolling*

6044 **Evaluation of cystic echinococcosis prevalence in an endemic region of Kazakhstan**
A. Mustapayeva (Almaty, Kazakhstan), G. D'Alessandro, G. Doszhanova, A. Colpani, N. Sadybekov, Z. Baimakhanov, E. Assanov, S. Salybekov, S. Kaniyev, E. Serikuly, L. Tagabayeva, C. Budke, A. Vola, M. Mariconti, Z. Zholdybay, A. Katarbayev, Z. Zhakenova, E. Brunetti, K. Juszkiewicz, A. Duisenova, T. Manciulli*

6938 **Oral Chagas disease outbreak in the Brazilian Amazon: first report of an outbreak related to patauà fruit**
M. Miguel (Madrid, Spain), J. De Oliveira Guerra, P. Bonates Bessa, K. Couceiro, M. Hossanah, A. Storino, D. Nahmias, J. López, K. Lopez, D. Raysa Teixeira, J. Ortiz, M. Vale Barbosa Guerra.*

7321 **The 2017 epidemic of pulmonary plague in Madagascar**
J. Ratomaharo (Athis-Mons, France), R. Andriamihaja, L. Razafindrakoto, R. Rakotoarivelo, M. Randria, D. Vololontiana*

7766 ***Plasmodium ovale* curtisi and wallikeri infections in imported malaria: a 2013-2018 retrospective study from the French National Malaria Reference Centre**
V. Joste (paris, France), J. Bailly, V. Hubert, E. Kendjo, N. Argy, S. Houze*

8741 **Leptospirosis in hospitalised patients in Ambatondrazaka, Madagascar: incident cases and exposure factors**
M. Nadal (Paris, France), V. Raharimanga, A. Rahanitraharinivo, N. Rabenindrina, Z. Randriamanantany, L. Randrianasolo, E. Cardinale, J. Heraud, C. Filippone, C. Marino, P. Bourhy, I. Vigan-Womas, H. Guis, L. Baril*

Session accepted as Paper Poster Session

Focus *Leishmania*

101 **A new nano-sized formulation of amphotericin B-loaded chitosan with remarkable improved antileishmanial effects for the treatment of *Leishmania major***
T. Zadeh Mehrizi, M. Haji Molla Hoseini, N. Mosaffa, M. Shafiee Ardestani, A. Khamesipour, M. Banifazl, H. Ebrahimi Shahmabadi, A. Ramezani (Tehran, Iran)*

208 **Antileishmanial effects of amphotericin B-chitosan, amphotericin B-dendrimer, betulinic acid-chitosan and betulinic acid-dendrimer in the treatment of *Leishmania major*: real-time PCR assay plus**
T. Zadeh Mehrizi, M. Shafiee Ardestani, M. Haji Molla Hoseini, A. Khamesipour, N. Mosaffa, M. Banifazl, H. Ebrahimi Shahmabadi, A. Ramezani (Tehran, Iran)*

2004 ***In vitro* efficacy of miltefosine on chronic cuteneous leishmaniasis compared to meglumine antimoniate**
V. Tunali (MUGLA, Turkey), I. Cavus, A. Yıldırım, O. Zorbozan, M. Harman, C. Gündüz, A. Özbilgin, N. Turgay*

2870 **Difficult-to-treat mucocutaneous leishmaniasis in an elderly Italian traveller returning from Argentina resolved with combination treatment**
G. Basile (Florence, Italy), G. Cristofaro, L. Locatello, I. Vellere, M. Piccica, S. Bresci, G. Maggiore, O. Gallo, S. Fallani, A. Novelli, G. Gaiera, T. Di Muccio, M. Gramiccia, L. Gradoni, A. Bartoloni, L. Zammarchi*

3001 **Genetic polymorphism of metabolic enzymes of *Leishmania* spp. parasites isolated from different clinical types of cutaneous leishmaniasis patients**
M. Nateghi Rostami (Tehran, Iran), M. Hosseini, F. Darzi*

4845 **Visceral leishmaniasis burden in Bologna province, Italy**
G. Fornaro (Bologna, Italy), G. Bonati, E. Vanino, I. Zaghi, M. Rinaldi, S. Coladonato, A. Cascavilla, M. Bartoletti, A. De Pascali, S. Varani, L. Attard, P. Viale*

6200 **Comparative inflammatory cytokines gene expression in culture of human macrophages infected with *Leishmania tropica* and *Leishmania major* parasites**
F. Darzi (Tehran, Iran), M. Nateghi Rostami, R. Davoodian*

6907 **Leishmaniasis in immunocompromised individuals without HIV: not so different. A comparative analysis of 60 patients**
C. Tortajada (Valencia, Spain), L. Castellano, E. Calabuig, C. Carratala, A. Farga, M. Fernandez, J. Flores*

8220 **Hunt for *Leishmania* RNA Virus (LRV) in transcriptome database of *Leishmania* species: which is best for bioinformatic analysis?**
D. Kaya (Istanbul, Turkey), O. Ozcan, O. Kurt, U. Sezerman*

8665 **Genotypic investigation of *Leishmania* spp. in dog population of northern Greece**
A. Papoutsi (Thessaloniki, Greece), G. Chatzisimeonidis, N. Vastarouchas, A. Karamitros, N. Zoumpoulidis, U. Giannakou, E. Andreadou, T. Lialiaris*

9029 **The impact of war on cutaneous leishmaniasis disease transmission and its control in Syria**
R. Allan (Haywards Heath, United Kingdom), G. Muhjazig*

Session accepted as Mini-oral Flash Session

Food, water and environmental safety

933 **Resistant bacteria in retail meat**
S. Malig (Odense, Denmark), E. Knudsen, S. Hoegh, U. Justesen*

5083 **Colistin-resistant bacteria in indian raw food samples**
K. Abdul Ghafur (Chennai, India), G. Palani, T. Ma, N. Sethuraman, P. Kumar S, P. Selvakumaar, S. Nagusah, R. Antony*

5423 **Botulism early recovery: one-decade experience in a referral centre**
F. Hatami, I. Alavidarazam (Tehran, Iran), S. Shokouhi, M. Mardani Dashti*

6404 **Investigation of waterborne outbreaks due to drinking water consumption in Greece, 2004-2019 (1st semester): time to learn our lessons**
K. Mellou, M. Tzani, T. Sideroglou, A. Chrysostomou, T. Georgakopoulou, S. Tsiodras (Athens, Greece)*

6904 **Mass visitation of show caves as a threat to human health**
R. Tomazin (Ljubljana, Slovenia), T. Matos, J. Mulec*

8447 **Detection of *Legionella* spp. and *Legionella pneumophila* in environmental samples using culture and live/dead-qPCR**
M. Zamfir (Munich, Germany), S. Walser-Reichenbach, S. Heinze, C. Herr*

Session accepted as Mini-oral ePoster Session

Leishmania in the spotlight

1901 **Evaluation of rapid extraction methods coupled with recombinase polymerase amplification assay for point-of-need diagnosis of post-kala-azar dermal leishmaniasis**
R. Chowdhury (Dhaka, Bangladesh), P. Ghosh, M. Khan, F. Hossain, K. Faisal, R. Nath, J. Baker, A. Wahed, S. Maruf, P. Nath, D. Ghosh, M. Rashid, M. Duthie, D. Mondal*

2043 **Effective control strategies for cutaneous leishmaniasis after Syrian influx in Turkey**
G. Ünüvar (Kayseri, Turkey), S. Topluoglu, T. Kayman, H. Ilter, F. Kara, E. Alp Mese*

2641 ***Leishmania* species diagnosed in European specialised treatment centres in the period 2014-2019**
G. Van Der Auwera, R. Guery, L. Davidsson, S. Karlsson Sobirk, S. Van Henten, R. Wampfler, M. Gramiccia, T. Di Muccio, P. Chiodini, S. Walker, C. Chicharro, A. Bart (Amsterdam, Netherlands), S. Varani, G. Harms, H. Brekke, F. Robert-Gangneux, S. Cortes, E. Nicastri, P. Buffet, J. Blum*

3850 **Leishmanial Localised Lymphadenopathy (LLL) by *Leishmania infantum*: a benign disease different from visceral leishmaniasis**
J. San Martin (Fuenlabrada, Spain), J. Ruiz-Giardin, L. Horrillo, A. Castro, I. Garcia Arata, J. García-Martínez, J. Jaqueti, L. Molina, B. Matia*

3866 **Visceral leishmaniasis by *Leishmania infantum* in immunocompetent adults: update of the leishmaniasis outbreak in Madrid (Spain)**
J. San Martin (Fuenlabrada, Spain), J. Ruiz-Giardin, A. Castro, L. Horrillo, L. Molina, J. Jaqueti, J. García-Martínez, I. Garcia Arata, B. Matia*

3872 **Biomarkers help to stop secondary prophylaxis on *Leishmania*-HIV co-infected patients**
J. San Martin (Fuenlabrada, Spain), J. Ruiz-Giardin, E. Carrillo, A. Castro, L. Botana, L. Molina, A. Ibarra-Meneses, J. Jaqueti, I. Garcia Arata, J. García-Martínez, F. Moreno Nuncio*

4955 **Diagnosis of cutaneous leishmaniasis through shotgun metagenomics**
C. Angebault (Creteil, France), C. Bernigaud, F. Foulet, T. Duong, D. Vanessa, L. Lachaud, C. Rodriguez, F. Botterel*

8290 **Identification of gene expression profiles of *Leishmania major* by integrated bioinformatics analyses**
O. Ulusan, A. Sadıqova, U. Mert, S. Öztürk, A. Caner (Izmir, Turkey)*

9035 **Worldwide diversity of tegumentary leishmaniasis and the risk of mucosal lesions: a clinical report in 459 European travellers**
R. Guery, S. Walker, G. Harms, A. Neumayr, P. Van Thiel, J. Gangneux, J. Clerinx, S. Karlsson Sobirk, L. Visser, L. Lachaud, M. Bailey, A. Bart, C. Ravel, E. Caumes, G. Van Der Auwera, J. Blum, D. Lockwood, P. Buffet (Paris, France)*

Session accepted as Paper Poster Session

Malaria News

643 **A systematic analysis of the direct antiglobulin test in post-artesunate delayed haemolysis during severe imported *Plasmodium falciparum* malaria: a multi-centre retrospective study**
O. Paccoud (Paris, France), X. Chamillard, K. Ndiaye, I. Vinatier, M. Khalloufi, C. Boulat, L. Surgers, B. Wyplosz, O. Bouchaud, S. Matheron, E. Caumes, S. Jauréguiberry*

1461 **Utility of multiplex PCR in the screening, diagnosis and follow-up of malaria in patients attended in a tropical medicine referral centre**
J. Sánchez López (Venturada, Spain), S. Chamorro, B. Comeche, B. Monge Maillo, F. Norman, J. Perez-Molina, R. López-Vélez, J. Chacon, M. Lanza Suárez, J. Rubio, O. Martin*

1591 **Global estimation of antimalarial drug effectiveness for the treatment of uncomplicated *Plasmodium falciparum* malaria, 1991–2019**
R. Giulia (Oxford, United Kingdom), S. Rumisha, T. Lucas, K. Twohig, A. Python, M. Nguyen, A. Nandi, S. Keddie, J. Rozier, K. Battle, P. Gething, D. Weiss*

2132 **Specific antibody responses to recombinant UB05 and MSP3 proteins displayed through the surface of Coliphage Qβ in mother-neonate couples**
A. Lissom (Yaounde, Cameroon), R. Megnekou, C. Sanders, J. Djontu, L. Ngu, A. Waffo, G. Nchinda*

2527 **Imported malaria: the innovative approach of machine learning on clinical management and severity prediction**
A. D'Abramo (Rome, Italy), F. Rinaldi, L. Lepore, A. Corpolongo, L. Scorzolini, N. Bevilacqua, A. Mariano, T. Ascoli Bartoli, C. Palazzolo, M. Giancola, G. Ippolito, E. Nicastri*

4231 **Nano chitosan effect on *Plasmodium falciparum in vitro***
F. Tabatabaie (Tehran, Iran), T. Elmi, Z. Zamani*

4660 **Presentation, outcomes and relapse rate of patients admitted with *Plasmodium vivax* malaria in Karachi, Pakistan**
F. Mahmood (Karachi, Pakistan), M. Hashmi, R. Ahmad, S. Shahid, A. Ahmed, S. Awan*

4683 **Patients presenting with malaria: are we missing opportunities to screen for other travel-associated infectious diseases?**
E. Mcguire (London, United Kingdom), J. Klein, A. Goodman*

5784 **Short-term prognosis and factors associated with acute kidney injury in imported severe malaria: results of a multi-centre retrospective study**
C. Pierre-Louis (Saint-Mandé, France), E. Gaudray, T. Martinez, M. Boutonnet, S. De Rudnicki, P. Pasquier, C. Ficko, E. Peytel, N. Libert*

6593 **A glance at the endothelial activation in complicated and uncomplicated malaria**
N. Makkar (Chandigarh, India), P. Malhotra, J. Ahluwalia, R. Singh, R. Sehgal*

6849 **Knowledge, attitude, and practice of Visiting Friends or Relatives (VFR) travellers towards prevention of malaria**
F. Heinrich (Hamburg, Germany), T. Brehm, M. Addo, T. Rolling*

7459 **Ugandan increase in malaria cases is reflected in imported cases to Norway of which surprisingly many have mixed infections identified by PCR**
H. Brekke (Oslo, Norway), C. Fladeby, G. Løvgården, F. Pettersen, L. Dedi, F. Müller*

7470 **Malaria outbreak response in a nomadic pastoralist setting, Kenya 2019**
R. Rono (Kabarnet, Kenya)*

7678 **Epidemiology and genetic diversity of *Plasmodium falciparum* in Kobeni, south-eastern Mauritania**
S. Diallo (Nouakchott, Mauritania), L. Basco*

8406 **Artesunate-containing therapies and abnormal haemoglobin: do we need to adapt the treatment?**
R. Jambou (Paris, France), E. Adji, A. Toure O, A. Gnondjui, S. Koui Tossea, L. Tiacoh, S. Assi, I. Sanogo*

9230 **Do we re-admit after outpatient artemether-lumefantrine? Evaluating the safety and efficacy of an ambulatory guideline for the treatment of uncomplicated *Plasmodium falciparum* malaria in a busy district general hospital in east London, UK**
W. Niven, J. Quinn, N. Studd, J. Healy, J. Abukar, A. Boyd, K. Woods (London, United Kingdom)*

9564 **Economic evaluations of malaria interventions: a systematic review**
A. Klicpera (Vienna, Austria), A. Banke-Thomas*

Session accepted as 2-Hour Oral Session

Malaria: still here?

306 **Genomic analysis and exploration of putative drug resistance loci in malaria parasites**
J. Han (Melbourne, Australia), J. Munro, M. Bahlo*

1465 ***Plasmodium vivax* diversity, population structuration and history of origin in Sudan**
M. Ali Albsheer (Khartoum, Sudan), E. Iyasu, D. Kepple, E. Lo, M. Ibrahim, M. Hamid*

1881 **Impact of chemoprophylaxis on the outcomes of *Plasmodium vivax* and *Plasmodium ovale* imported malaria cases among civilian travellers**
M. Le Goff (Brest, France), E. Kendjo, M. Thellier, R. Piarroux, P. Boelle, S. Jaureguiberry*

3909 **Failure of artemether-lumefantrine treatment for *Plasmodium falciparum* malaria imported from sub-Saharan Africa to the UK**
H. Adler (Liverpool, United Kingdom), J. Cruise, J. Jones, I. Slack, A. Neary, J. Van Aartsen, E. Carter, P. Hine, E. Okenyi, R. Taggart, D. Nolder, L. Stewart, C. Sutherland, S. Aston, T. Blanchard, T. O'Dempsey, M. Beadsworth, N. Beeching*

7308 **Post-artesunate delayed haemolysis presenting with positive direct antiglobulin test: are steroids a therapeutic option?**
T. Ascoli Bartoli (Rome, Italy), L. Lepore, A. D'Abramo, A. Corpolongo, A. Mariano, N. Bevilacqua, M. Giancola, C. Palazzolo, L. Scorzolini, P. Buffet, E. Nicastri*

8243 **Implementation of an antimalarial stewardship programme in a tertiary care hospital in south India**
S. Dorairajan (Chennai, India), S. Saravanakumar, A. S, P. Biji*

9334 **The first blood-stage controlled human malaria infection model in Europe for *Plasmodium vivax* vaccine efficacy testing**
A. Minassian (Oxford, United Kingdom), Y. Themistocleous, S. Silk, J. Barrett, C. Nielsen, D. Quinkert, I. Poulton, F. Ramos Lopez, C. Mitton, T. Rawlinson, N. Edwards, K. Ellis, M. Baker, R. Lopez Ramon, J. Cho, S. Hodgson, F. Bach, W. Nahrendorf, A. Lawrie, P. Spence, A. Blagborough, I. Taylor, F. Nugent, K. Johnson, A. Kemp, J. Rayner, W. Ros, J. Prachumsri, S. Biswas, S. Draper*

Session accepted as Mini-oral ePoster Session

Medications to fight parasites: what's new?

2017 **Miltefosine as a promising agent for chronic cutaneous leishmaniasis: an *in vivo* model**
V. Tunali (Mugla, Turkey), I. Cavus, A. Yıldırım, O. Zorbozan, M. Harman, C. Gündüz, A. Özbilgin, N. Turgay*

2069 **Safety and efficacy of fumagillin for the treatment of intestinal microsporidiosis: a French prospective cohort study**
A. Maillard (Paris, France), A. Scemla, B. Laffy, N. Mahloul, J. Molina*

2875 **Quinacrine is effective for treatment of resistant giardiasis**
K. Andersson Ydsten (Stockholm, Sweden), U. Hellgren, H. Ásgeirsson*

3316 **Leishmaniasis in Turkey: assessment of the efficacy of antimicrobial peptides against *Leishmania tropica in vitro***
N. Unubol, I. Cavus, Ö. Kurt (İstanbul, Turkey), A. Özbilgin, T. Kocagoz*

4749 ***In vitro* activity of beauvericin against *Sarcoptes scabiei*: may a mycotoxin help for the control of scabies?**
C. Al Khoury, N. Nemer, G. Nemer, M. Kurban, C. Bernigaud, K. Fischer, J. Guillot (Créteil, France)*

4770 **Lemongrass oil: a promising acaricidal and ovicidal agent against scabies?**
L. Meilin, L. Buming, C. Bernigaud, J. Guillot (Créteil, France), F. Fang*

7420 **Implementation of intravenous artesunate for severe malaria in France: analysis of outcome in 1391 patients**
C. Roussel, P. Ndour, E. Kendjo, S. Larréché, A. Taieb, B. Henry, B. Lebrun-Vignes, C. Chambrion, N. Argy, S. Houze, O. Mouri, D. Courtin, A. Angoulvant, H. Delacour, F. Gay, J. Siriez, M. Danis, F. Bruneel, O. Bouchaud, E. Caumes, R. Piarroux, M. Thellier, S. Jauréguiberry, P. Buffet (Paris, France)*

9600 **A systematic evaluation of the anti-plasmodial activity of low molecular weight heparin against human malaria parasite *Plasmodium falciparum***
M. Hmoud (Baghdad, Iraq), P. Horrocks*

Session accepted as Paper Poster Session

More on parasitic diseases epidemiology and management

1460 **Imported schistosomiasis in children: a French prospective multi-centre study of prevalence, clinical features and diagnostic methods**
C. Leblanc (Bondy, France), S. Brun, O. Bouchaud, A. Izri, M. Caseris, M. Husain, A. Bergevin, L. Pham, A. Paugam, L. Paris, S. Jauréguiberry, V. Levy, C. Bloch Queyrat, V. Ok, M. Boubaya, S. Escoda, F. Sorge, A. Mandelcwajg, A. Faye, P. Mariani, L. De Pontual*

1626 **Epidemiological aspects of ascariasis in the south of Russia**
M. Chernikova, I. Khutoryanina, L. Ermakova, N. Pshenichnaia (Moscow, Russian Federation)*

1758 **Is strongyloidiasis currently endemic in Croatia?**
M. Balen Topić (Zagreb, Croatia), E. Marjanović, D. Tomasovic, S. Mario*

2554 **Fatal babesiosis in a non-HIV immunocompromised host**
U. Schwab (Newcastle upon Tyne, United Kingdom)*

2668 **Frequency of *Toxoplasma gondii* infection in schizophrenic patients: a pilot study**
A. Pietrzyk, P. Smyk, P. Kochan, V. Lunde (Oslo, Norway), H. Rønneberg, K. Fus, B. Papir, A. Depukat, M. Bulanda*

3839 **Autochthonous human and canine *Strongyloides stercoralis* infection in Europe: a systematic review**
L. Ottino (Florence, Italy), D. Buonfrate, P. Paradies, Z. Bisoffi, A. Antonelli, G. Rossolini, S. Gabrielli, A. Bartoloni, L. Zammarchi*

3871 **Occurrence of sporadic human ascariasis in non-endemic regions: the importance of zoonotic transmission from swine**
T. Fritsche (Marshfield, United States), J. Meece, S. Meyer, K. Ortega, N. Wolff, M. Hall*

4258 **An outbreak of scabies in the north-east region of Ghana**
Y. Amoako (Kumasi, Ghana), R. Phillips, J. Arhtur, M. Abugri, E. Akowuah, K. Amoako, B. Marfo, S. Ravensbergen, Y. Stienstra*

4733 **First study on *Giardia intestinalis* assemblages in Algerian individuals**
S. Belkessa, D. Vincent Thomas López, H. Nielsen, K. Houali, F. Ghalmi, C. Stensvold (Copenhagen, Denmark)*

4948 **Strongiloidiasis in patients with Chagas disease in Barcelona**
E. Dopico (Barcelona, Spain), L. Solsona, M. Aguilar, Y. Rando-Matos, L. Guerrero, G. López De Egea, J. Mascort, E. Sulleiro*

5322 **Usefulness of qPCR for the assessment of vectorial competence of wild caught sand flies species: preliminary results**
L. Remadi (Monastir, Tunisia), N. Chargui, M. Jiménez, R. Molina, N. Haouas, E. González, H. Babba*

5942 **A rare case of paragonimiasis infected by *Paragonimus ohirai***
Y. Zhang (Shanghai, China), W. Jin, Q. Miao, J. Pan, B. Hu*

6095 **Prevalence and genetic diversity of *Blastocystis* in asymptomatic and symptomatic individuals from Puducherry, India**
S. Padukone (Puducherry, India), A. Selvarathinam, M. Kumar, J. Mandal, N. Rajkumari, B. Vishnu Bhat, R. Swaminathan, S. Parija*

7416 **Preliminary evidence of absence of cystic echinococcosis in the Dibrugarh district of Assam state, North-East India**
R. Taye Gam, I. Phukan, S. Deb, A. Saikia, P. Sharma, N. Nirmoliya, B. Rupali, T. Manciulli (Pavia, Italy)*

7638 **Estimation of cystic echinococcosis prevalence in an endemic region in Uzbekistan**
A. Colpani (Pavia, Italy), O. Achilova, G. D'Alessandro, C. Budke, M. Mariconti, T. Muratov, A. Vola, A. Mamedov, M. Giordani, E. Brunetti, U. Suvonkulov, T. Manciulli*

7707 **Distribution during 10 years of the genotypes A and B of *Giardia intestinalis* among the infected subjects attending to an Italian tertiary care hospital**
A. Calderaro, S. Montecchini (Parma, Italy), M. Buttrini, S. Rossi, F. Motta, G. Piccolo, M. Antonaci, M. Dell'Anna, M. Arcangeletti, C. Chezzi, F. De Conto*

7857 **Phenotypic and genotypic examination of *Dientamoeba fragilis* and *Blastocystis* isolates in patients with ulcerative colitis and irritable bowel syndrome**
T. Unalan-Altintop (Ankara, Turkey), C. Vahabov, K. Ergunay, O. Kurt, T. Kav, Y. Akyon, S. Erguven*

7889 **Outbreak of cryptosporidiosis among responders to a rollover of a truck carrying calves: Normandy, France, October 2019**
G. Gargala (Rouen, France), D. Dulieu, H. Razakandrainibe, D. Leméteil, V. Villier, D. Costa, L. Favennec*

7963 **Delayed diagnosis of neuroschistosomiasis in a non-endemic country: a tertiary referral centre experience**
A. De Wilton (London, United Kingdom), D. Aggarwal, P. Chiodini*

8744 **A case of cystic hydatid disease acquired in Ireland**
C. Grant (Dublin, Ireland), C. Conlon, C. Fleming, H. Tuite, E. Slattery*

9133 **Risk factors for epilepsy and cysticercosis in Abidjan, Ivory Coast: a case-control study**
M. Soumahoro (Abidjan, Côte d'Ivoire), J. Melki, Y. Kangah, A. Tanoh, N. Tano, M. Diomandé, M. Camara, M. Ngouan, T. Sonan, B. Assi, R. Jambou*

9362 **Study of brain-derived neurotrophic factor gene expression in brain tissue of rat infected to acute and chronic toxoplasmosis: a study in animal model**
M. Fallah (Hamadan, Iran), M. Matini, A. Maghsood, M. Arabestani, M. Shahbazi*

9538 **Genetic diversity of the *Plasmodium vivax* circumsporozoite protein in isolates from Brazilian Amazon rainforest and Rio de Janeiro Atlantic Forest**
N. Oliveira, R. Fernandes, L. Cury, A. Lavigne, A. Pina, D. Perce, M. Catanho, P. Brasil, C. Ribeiro, M. Ferreira Da Cruz (Rio de Janeiro, Brazil)*

Session accepted as Paper Poster Session

Parasitic Diseases: diagnosis and treatment

784 **Launch of a new faecal molecular external quality assessment scheme by UK NEQAS Parasitology**
J. Shrivastava (London, United Kingdom), A. Saez, P. Chiodini*

983 **New raw materials for serology immunoassay quality controls**
P. Monsbrot (Limoges, France), G. Champier, C. Dollack, T. Schumacher, M. Dardé, S. Hantz*

1925 **Preliminary results of microRNA expression profile in patients with cystic echinococcosis and identification of possible cellular pathways**
S. Orsten (Ankara, Turkey), T. Çiftçi, S. Yabanoğlu Çiftçi, A. Azizova, G. Yüce, E. Ünal, A. Doğrul, D. Akıncı, Y. Akyon, O. Akhan*

2163 **Chagas disease in Japan, 2012-2019: clinical presentation and diagnostic delay**
K. Imai (Saitama, Japan), N. Tarumoto, J. Sakai, T. Murakami, S. Maesaki, S. Miura, T. Maeda*

2482 **Molecular diagnosis of toxoplasmosis: impact of sample storage duration for five types of biological samples**
M. Brenier-Pinchart, E. Varlet, F. Robert-Gangneux, D. Filisetti, J. Guitard, Y. Sterkers, H. Yera, H. Pelloux (Grenoble, France), P. Bastien*

2863 **Clinical efficiency of anti-*Blastocystis* therapy in ulcerative colitis patients**
A. Toychiev (Tashkent, Uzbekistan), S. Osipova*

2867 **Evaluation of endoperoxides and tetrahydropyrans as potential anti-leishmanial drugs**
M. Ortalli, S. Varani (Bologna, Italy), G. Cimato, R. Veronesi, M. Lombardo, C. Trombini, M. Monari, A. Quintavalla*

3112 **Diagnostic value of the molecular detection of *Sarcoptes scabiei* from a skin scraping in patients with suspected scabies**
M. Bae (Seoul, South Korea), J. Kim, J. Park, S. Bae, J. Jung, H. Cha, N. Jeon, H. Lee, M. Kim, S. Chang, S. Kim*

3215 **Development of new bicyclic nitroimidazoles as antitubercular and antiparasitic agents**
C. Wei Ang, A. Jarrad, A. Debnath, L. Tan, M. Sykes, Y. Wang, M. Butler, P. Bernhardt, N. West, V. Avery, A. Popat, S. Franzblau, M. Cooper, M. Blaskovich (Brisbane, Australia)*

3501 **Pulmonary sparganosis: a case report with 20 months follow-up**
Z. Lei, J. Liu (Guangzhou, China), S. Zhu, Y. Pang, H. Ma, J. Zhu, L. Xu, B. Lin, Z. Gao*

3667 **A new rapid test on whole blood and on serum for the toxoplasmosis screening in pregnancy**
V. Meroni (Pavia, Italy), G. Ferrari, F. Genco, E. Dore, B. Mariani, M. Furione, M. Zavattoni, L. Scudeller, F. Peyron*

3767 **Diagnostic accuracy of toxoplasma Western blot test in suspected seroconversion in pregnancy : a multi-centre study**
V. Meroni (Pavia, Italy), A. Corcione, F. Genco, L. Scudeller, H. Pelloux, F. Hélène, M. Brenier-Pinchart, C. L'Ollivier, L. Paris*

3891 **Chagas disease diagnosis: comparison between two different native antigen assays**
J. Wang Wang (Barcelona, Spain), B. Rivaya Sanchez, G. Fernández Rivas, M. Navarro Albareda, S. Roure, L. Matas Andreu*

3936 **Diagnosis of amoebic liver abscess by detection of *Entamoeba histolytica* DNA in serum using quantitative PCR**
G. Theo (Paris, France), M. Gits-Muselli, N. Guigue, M. Picat, S. Hamane, S. Bretagne*

3997 **Association between the *Blastocystis* spp. load and patient's socio-demographic and clinical profile in the north-eastern area of Spain**
C. Matovelle Ochoa (Zaragoza, Spain), E. Rubio, P. Chueca, P. Goñi, A. Betran Rosel*

4201 **Diagnostic performance and validation of two ready-to-use real-time PCR assays for the detection of *Plasmodium* spp. and the principal species capable to infect human**
C. Escolar (Zaragoza, Spain), N. Martínez Cameo, M. Hernández, P. Egido, A. Milagro, A. Rezusta*

4530 **Comparison of the performance of hydatid fluid and the recombinant antigen recDipol in the diagnosis of cystic echinococcosis patients**
E. Akdur Öztürk (Izmir, Turkey), M. Akil, F. Bilgic, C. Sánchez Ovejero, R. Román, A. Casulli, M. Siles-Lucas, N. Altıntaş, A. Ünver*

4753 **Changes occurred in immunological and molecular determinations of toxoplasmosis in pregnancy and newborn children**
C. Istrate (Bucharest, Romania), C. Cretu, P. Mihailescu*

4971 **"Seek and ye shall find": endoscopic finding and molecular diagnosis of *Trichuris trichiura***
M. Peradotto (Turin, Italy), Z. Teresa, C. Serena, A. Bondi, B. Paolo, C. Costa, S. D'Amelio, R. Cavallo*

5394 **The necessity of testing for diarrhoea-causing intestinal parasites on broad indications**
G. Hartmeyer (Odense, Denmark), S. Hoegh, M. Kemp*

5403 **MoCaT as first option in the cystic echinococcosis treatment: what we have obtained**
C. Popa (Bucharest, Romania), C. Cretu, M. Petru Escu, L. Popa, C. Botezatu, P. Mihailescu, B. Mastalier*

5439 **Value of soluble programmed death-1 (sPD-1) and sPD-ligand-1 (sPD-L1) as early biomarkers for the post-surgical monitoring of cystic echinococcosis in Tunisian paediatric patients**
E. Ben Salah (Monastir, Tunisia), W. Sakly, C. Barrera, S. Mosbahi, R. Farhani, A. Bellanger, A. Ksia, B. Gottstein, A. Nouri, H. Babba, L. Millon*

6140 **Differentiation of *Blastocystis* subtypes by PCR and Sanger sequencing versus NGS-based total ribosomal DNA analysis**
K. Ascuña Durand, R. Salazar Sanchez, L. Andersen, J. Ballon Echegaray, C. Stensvold (Copenhagen, Denmark)*

6159 **Performance of a commercially available LAMP assay and RDT for diagnosing *Plasmodium falciparum* malaria at very low parasitemias in a controlled human malaria infection trial**
R. Payne (Sheffield, United Kingdom), N. Edwards, K. Ellis, Y. Themistocleous, S. Silk, J. Barrett, A. Flaxman, D. Bellamy, R. Morter, T. Rawlinson, S. Draper, A. Minassian*

6462 **Delayed haemolytic anaemia following artesunate treatment in a returning African traveller**
R. Oconnor, F. Carroll (Dublin, Ireland), C. Doyle, C. Merry, C. Bannan*

6532 **Comparison of native and a new recombinant fusion protein (AgB8/1+AgB8/2+Ag5) for serological diagnosis of cystic echinococcosis**
F. Bilgic (Izmir, Turkey), D. Dirim Erdoğan, C. Gündüz, E. Akdur Öztürk, M. Korkmaz*

6582 **Laboratory capacity for the diagnosis of leishmaniasis in Greece, 2018: a national surveillance study**
M. Tzani, K. Mellou, T. Sideroglou, A. Chrysostomou, A. Vakali, T. Georgakopoulou, D. Pervanidou, S. Tsiodras (Athens, Greece)*

6730 **Application of MALDI-TOF MS for identification of helminths in clinical samples**
I. Sy (Homburg/Saar, Germany), T. Wendel, M. Feucherolles, A. Nimmesgern, A. Stuermann, Y. Endriss, J. Utzinger, S. Poppert, S. Becker*

6815 **An unusual case of recurrent lymphocytic meningitis**
M. Raza (Milton Keynes, United Kingdom), P. Kapila, K. Omar, R. Randhawa*

6888 **Role of PRAS40/mTOR/Akt in the intracellular development of *Toxoplasma gondii* tachyzoites**
M. González-Del Carmen, V. Cortés Mollinedo (Cordoba, Mexico), G. Rojas García*

7282 **Genetic variability of *Trypanosoma cruzi*, in clinical samples from Latin American immigrant patients, living in Barcelona, Spain**
M. Tavares De Oliveira (Barcelona, Spain), E. Sulleiro Igual, A. Silgado Gimenez, M. De Lana, B. Zingales, J. Santana Da Silva, J. Marin-Neto, I. Molina*

7363 **Application of molecular techniques in the diagnosis and follow-up of patients with imported malaria in a non-endemic country**
I. Fradejas Villajos, M. Hernandez Jimenez, M. Pérez-Jacoiste Asín, J. Rubio, E. Trigo-Esteban, J. Ruiz-Giardin, M. Palanca-Giménez, J. Azcona-Gutierrez, M. Calderon, J. Cuadros, S. Garcia-Bujalance, J. Jaqueti, J. Cuenca, C. García-García, P. Martín-Rabadán, G. Rojo, I. Gonzalez-Azcarate, A. Perez De Ayala Balzola (Madrid, Spain)*

7422 **Comparison of PCR assays for detection of *Echinococcus multilocularis* from human formalin-fixed paraffin-embedded tissue preparations**
J. Knapp, F. Monnien, S. Felix, D. Florent, B. Heyd, C. Richou, S. Bresson Hadni, L. Millon (Besançon, France)*

7567 **Evaluation of a multiplex real-time PCR for the diagnosis of intestinal protozoa**
E. Oliva, A. Raglio (Bergamo, Italy), S. Varani, N. Menegotto, R. Gargiulo, A. Bruno, S. Cavallari, M. Coppola, C. Farina*

7645 **Performance of the Allplex Assay in comparison to microscopy and in-house real-time PCR for the detection of helminths in Tanzanian stool samples**
R. Wampfler, B. Barda, M. Ruf (Basel, Switzerland), J. Keiser*

7993 **Amphotericin B as rescue therapy for alveolar echinococcosis in patients with benzimidazole treatment failure or toxicity**
J. Bloehdorn, S. Burkert (Ulm, Germany), L. Peters, J. Schmidberger, A. Hillenbrand, T. Gräter, M. Furitsch, T. Barth, D. Henne-Bruns, W. Kratzer, N. Eberhardt, A. Beer, B. Grüner*

8019 **Genome sequencing of *Leishmania infantum* causing cutaneous leishmaniosis from a Turkish isolate: meta-analitic study for evaluation of proteins with polymorphism**
D. Guldemir (Ankara, Turkey), S. Nalbantoglu*

8143 **Role of glucose transporters in the intracellular proliferation of *Toxoplasma gondii***
T. Fernández Rebolledo (Veracruz, Mexico), W. Díaz Beltrán, M. González-Del Carmen*

8625 **Evaluation of the performance of a commercial rapid diagnostic test for cystic echinococcosis in a clinical setting**
A. Vola (Pavia, Italy), A. De Silvestri, M. Mariconti, R. Lissandrin, M. Maestri, A. D'Addiego, E. Brunetti, T. Manciulli*

Session accepted as Paper Poster Session

Public health in special/international settings

671 **Trachoma between schoolchildren: epidemiological situation in an endemic region of north-east Brazil**
R. Pires Neto (Fortaleza, Brazil), A. Maurício Silva Maciel, V. Da Silva Gomes, F. Brandao De Farias, J. Paulo De Sousa*

722 **A prospective cohort study of Malawian children presenting with fever**
A. De Wilton (London, United Kingdom), F. Howley*

898 **Aetiologies, management and outcome of non-traumatic coma in small children: a prospective study in Benin**
E. Kinkpe, L. Ayedadjou, F. Boumediene, D. Ajzenberg, A. Mowendabeka, T. Lathière, J. Alao, I. Dossou-Dagba, M. Cot, G. Bertin, A. Aubouy, S. Houze, J. Faucher (Limoges, France)*

1335 **Human dirofilariasis in a changing world, evolving zoonosis just under the skin**
G. Stroffolini, A. Calcagno, S. Scabini, T. Lupia, G. Di Perri, R. Angilletta (Turin, Italy), P. Caramello*

1671 **Imported malaria: overview of the diagnosed and suspected cases of malaria in a Spanish city (15 years of experience)**
J. Ruiz Giardin (Madrid, Spain), J. San Martin, I. Ayala Larrañaga, L. Rivas Prado, L. Carpintero Garcia, A. Hernandez Piriz, J. Jaqueti, I. Garcia Arata, L. Molina, J. García-Martínez, N. Cabello-Clotet*

3969 **Investigation of intestinal parasites in immunocompromised and immunocompetent patients with diarrhoea: what about *Blastocystis* and *Dientamoeba fragilis*?**
E. Kain (Istanbul, Turkey), N. Mansur, F. Önder, A. Uzay, S. Öktem Okullu, Ö. Kurt, A. Tözün*

5148 **Doctor i've been bitten: a smart phone application to identify arthropod bites and stings**
A. Kew (Nottingham, United Kingdom), V. Smith*

8170 **Neglected tropical diseases contribute to the number of years with civil war**
K. Last (Hamburg, Germany), C. Papan, S. Becker, N. Mutters*

8293 **Introduction of automated blood culture in a resource-limited setting in West Africa**
A. Von Laer (Berlin, Germany), M. N'Guessan, F. Sounan Touré, T. Eckmanns, K. Nowak, K. Groeschner, C. Akoua-Koffi*

8607 **Weekly surveillance of bacterial, viral and parasitic infections involving private and public medical analysis laboratories through 317833 diagnostic tests in the Provence-Alpes-Côte-d'Azur region, 2014-2019**
P. Colson (Marseille, France), J. Poveda, S. Trombert Paolantoni, A. Giraud-Gatineau, S. Haim-Boukobza, L. Verdurme, J. Rolain, H. Chaudet*

9017 **Impact of hand hygiene intervention on hand washing ability of school-aged children**
S. Khan (Karachi, Pakistan), H. Ashraf, S. Iftikhar, N. Baig-Ansari*

9166 **The bacterial gut microbiota during controlled human infection with *Necator americanus* larvae**
Q. Ducarmon, M. Hoogerwerf, J. Janse, A. Geelen, J. Koopman, R. Zwittink (Leiden, Netherlands), J. Goeman, E. Kuijper, M. Roestenberg*

Session accepted as 1-Hour Oral Session

Returned traveller: finally home but sick

2289 **Increasingly limited options for the treatment of enteric fever in travelers returning to England, 2014-2017**
M. Herdman (London, United Kingdom), B. Karo, J. Dave, P. Katwa, J. Freedman, G. Godbole, S. Balasegaram*

3351 **Incidence of Doxycycline Responding Illnesses (DRI) in returning travellers with fever**
D. Camprubí (Barcelona, Spain), J. Oteo, S. Santibañez Saenz, L. Romero-Acevedo, H. Martí-Soler, A. Portillo Barrio, C. Subirà, A. Almuedo-Riera, M. Martinez, N. Rodriguez-Valero, J. Navero-Castillejos, I. Losada Galvan, M. Pinazo, J. Muñoz*

5487 **The role of genomics in typhoid control: sentinel traveller surveillance, in-host evolution and transmission dynamics**
Z. Dyson (Cambridge, United Kingdom), V. Balaji, F. Qadri, T. Dallman, A. Pollard, G. Dougan, K. Holt*

6281 **First European outbreak of eosinophilic meningitis in travellers returning from Cuba**
S. Roure, G. Fernández Rivas (Badalona, Spain), B. Rivaya Sanchez, G. Lladós, L. Grau, L. Guarro, S. Poppert, M. Ruf, L. Valerio, B. Nickel, L. Matas Andreu*

9548 **Non-human primate injuries in returning travellers: implications for pre- and post-travel management**
T. Rampling (London, United Kingdom), S. Baljekar, M. Brodermann, M. Brown, N. Longley*

Session accepted as 2-Hour Oral Session

Taking care of immigrants

64 **Tuberculosis among migrant people in Sicily: a real-life report**
G. Pipitone (Palermo, Italy), T. Prestileo, A. Sanfilippo, F. Di Lorenzo, A. Ficalora, S. Corrao*

957 **Results of a schistosomiasis screening programme in an immigrant population**
L. Casado, J. Boga, M. Rodriguez-Perez, J. Fernandez-Suarez, A. Perez-Garcia, A. Garcia, C. Menendez, A. Rodriguez-Guardado (Oviedo, Spain)*

1789 **Results of a screening programme for Strongyloidiasis in HIV-positive immigrants**
A. Garcia, J. Boga, A. Perez-Garcia, C. Menendez, J. Fernandez-Suarez, M. Rodriguez-Perez, N. Moran, M. Martinez-Sela, A. Rodriguez-Guardado (Oviedo, Spain)*

2866 **A machine learning model for evaluating Chagas disease screening in immigrant populations**
J. Fernandez-Martinez, J. Boga, L. Casado, E. De Andres-Galiana, J. Fernandez-Suarez, M. Rodriguez-Perez, F. Vazquez, A. Garcia, C. Menendez, A. Rodriguez-Guardado (Oviedo, Spain)*

3104 **Should *Chlamydia trachomatis* be part of migrant screening?**
M. Bonneton (paris, France), L. Surgers, V. Lalande, N. Valin, K. Lacombe*

3506 **Clinical and economic impact of three different strategies for the management of schistosomiasis in Sub-Saharan immigrants to Italy**
A. Botta (Florence, Italy), M. Tilli, A. Bartoloni, L. Zammarchi, S. Boccalini*

3943 **Chronic schistosomiasis and strongyloidiasis amongst Ethiopian immigrants in Netanya**
T. Finn (Netanya, Israel), F. Babushkin, K. Geller, T. Grossman, R. Cohen*

4811 **Country-specific approaches to latent tuberculosis screening and its current effectiveness in migrants to Europe**
K. Rustage (London, United Kingdom), I. Margineanu, L. Nellums, Y. Stienstra, D. Goletti, T. Noori, D. Zenner, M. Pareek, K. Kristensen, J. Friedland*

7122 **An epidemiological overview of intestinal parasitoses in a non-endemic setting: a comparison between Italians and immigrants from developing countries during the years 2011-2018**
A. Calderaro (Parma, Italy), S. Montecchini, M. Buttrini, S. Rossi, F. Motta, G. Piccolo, M. Antonaci, M. Dell'Anna, M. Arcangeletti, C. Chezzi, F. De Conto*

Session accepted as Paper Poster Session

Travel medicine and migrant health

728 ***Ignatzschineria* bacteraemia following maggot wound infestation**
K. Nadrah (Ljubljana, Slovenia), U. Glinšek Biškup, B. Šoba, V. Cvitković Špik, M. Mueller-Premru*

1474 **Knowledge and awareness of inadvertent use of yellow fever vaccine among renal transplant recipients**
L. Cabral Miranda (São Paulo, Brazil), F. Agena, A. Sartori, L. Azevedo, E. David-Neto, L. Pierrotti*

1612 **Review of enquiries to the UK national travel advice line by healthcare professionals regarding immunocompromised travelers**
B. Merrick (London, United Kingdom), S. Kanagarajah, D. Patel*

2301 **Multiplex PCR for the detection of traveller's diarrhoea: a nested case-control study**
F. Schaumburg (Münster, Germany), C. Correa-Martinez, S. Niemann, R. Köck, K. Becker*

2398 **Outpatient clinic for tuberculosis screening: an opportunity to promote healthcare access among applicants for international protection**
J. Testa (Busto Arsizio, Italy), M. Pizzi, M. Farinazzo, B. Menzaghi, F. Franzetti*

2460 **Encephalitis in French travellers, 2016-2019**
A. Mailles (Saint-Maurice, France), M. Martinot, X. Argemi, F. Bourdain, P. Jaquet, J. Krause, E. Canoui, J. Stahl*

3162 **An unusual case of a Spanish traveller patient with chyluria and molecular diagnosis of schistosomiasis**
M. Sempere Alcocer (Nueva Andalucia, Spain), F. Jose M., C. Beatriz, H. Luis, J. Saugar, P. Fernández-Soto*

3628 **Imported leishmaniases in a Parisian hospital, France: a 6-year experience**
N. Aissaoui (Paris, France), S. Hamane, M. Gits-Muselli, N. Guigue, A. Petit, S. Delliere, A. Alanio, S. Bretagne*

3982 **Cognitive impairment following severe malaria in travellers**
A. Duvignaud (Bordeaux, France), B. Glize, H. Lemistre, P. Perreau, D. Nguyen, L. Martin, T. Pistone, A. Desclaux, D. Malvy*

5563 **Intestinal colonisation with extended-spectrum beta-lactamase-producing *Escherichia coli* after international trips in travellers attending a travel clinic in Rio de Janeiro**
S. Tufic, L. De Araújo Longo, G. Caramano De Oliveira, L. Cecílio Vilar, V. Brígido De Carvalho, B. Meurer Moreira, K. Rodrigues (Rio de Janeiro, Brazil)*

6368 **Yellow fever enquiries to a national telephone advice line regarding travellers who are pre-conception, pregnant or breastfeeding**
C. Patterson (London, United Kingdom), S. Kanagarajah, D. Patel*

7612 **Screening for latent tuberculosis infection among asylum seekers in Brescia, Italy: results from the E-DETECT Project**
V. Marchese (Brescia, Italy), P. Zanotti, B. Formenti, B. Rossi, E. Lovato, E. Girardi, L. Barcellini, G. Stancanelli, D. Cirillo, I. El Hamad, A. Matteelli*

7947 **Acquisition of antimicrobial resistance organisms by US international travellers**
G. Mellon (Boston, United States), S. Turbett, C. Worby, E. Oliver, P. Kelly, D. Leung, M. Knousse, S. Hagmann, A. Earl, E. Ryan, R. Larocque*

8069 **Travel health advice: do travellers follow the recommendations?**
M. Diaz-Menendez, V. Quesada Cubo, M. Arsuaga Vicente, F. De La Calle Prieto (Madrid, Spain), M. Ladrón De Guevara, M. Lago, P. Barreiro, E. Trigo Esteban*

8484 **Evaluating the healthcare utilisation of undocumented migrants in the Helsinki and Uusimaa hospital district, Finland: a protocol for a register-based cross-sectional study**
K. Rautila (Helsinki, Finland), O. Helve, P. Tiittala*

9183 **Travel-related meningitis: results from a thirteen-year retrospective study**
C. Pierre-Louis (Saint-Mandé, France), F. Charton, L. Labarbe, M. Cabon, M. Gominet, D. Andriamanantena, C. Ficko*

9201 **Travel patterns and knowledge of risk of infections during international travels in solid organ transplantation**
P. Martín-Dávila (Madrid, Spain), F. Norman, J. Fortun Abete, T. Ruiz Merlo, M. Fernandez Ruiz, J. Aguado Garcia, M. Farinas, C. González Rico, B. Mahillo, P. Parra, R. López-Vélez*

9232 **Imported dengue fever in French travellers: a multi-centre retrospective study**
C. Pierre-Louis (Saint-Mandé, France), C. Ficko, A. Perignon, C. Rapp, E. Caumes*

9360 **Sepsis caused by *Salmonella* Paratyphi B variant producing a *bla*OXA-48 in a traveller patient**
A. Balandraud, L. Hadjadj, G. Dubourg, J. Rolain, S. Baron (Marseille, France)*

9451 **Dengue fever in returning travellers: a retrospective study in London, UK**
A. Duret (London, United Kingdom), I. Suchett-Kaye, S. Adnan Aali, P. Papineni*

9527 **Microbiota modifications in travellers to tropical and subtropical areas**
C. Franch Serrano, D. Carmena Jiménez, L. Prieto-Pérez, M. Casapia, M. Linares, J. Cuadros, P. Carolina Köster, B. Bailo, M. Górgolas, J. Ramos Rincón, A. Cabello, R. Perez Tanoira (Madrid, Spain)*

Session accepted as 1-Hour Oral Session

Travellers as vehicles of AMR

2118 **ESBL-producing *Enterobacteriaceae* in patients with travellers' diarrhoea: a prospective cohort study**
O. Ljungquist (Skäret, Sweden), S. Nematzadeh, C. Giske, F. Resman, K. Riesbeck, J. Tham*

3675 **Does our microbiome travel well? Microbiome resilience and acquisition of multidrug-resistant bacteria in travellers**
M. Davies (Birmingham, United Kingdom), M. Arcilla, J. Van Hattem, C. Schultsz, M. De Jong, D. Melles, A. Mcnally, W. Van Schaik, P. Wolffs, J. Penders*

3769 **Real-time sampling of travellers to Laos: epidemiology of mobile genetic elements**
S. Dunn (Birmingham, United Kingdom), A. Snaith, A. Kantele, E. Kuenzli, J. Corander, A. Mcnally*

3966 **The colonisation of Czech travellers and expatriates living in the Czech Republic by colistin-resistant *Enterobacteriaceae* including *Escherichia coli* harbouring *mcr-1* genes on a plasmid or chromosome**
M. Krutova (Prague, Czech Republic), A. Baráková, E. Nycova, G. Tereza, R. Karpiskova, O. Nyc, P. Drevinek, J. Tkadlec*

8160 **The rise and fall of a resistome: travel returners shed light on the dynamics of ESBL-producing *Escherichia coli***
A. Mari (Basel, Switzerland), F. Bonfiglio, E. Kuenzli, D. Lang, D. Nogarth, H. Seth-Smith, A. Egli*

Abstract Programme

8. Healthcare-associated & Nosocomial Infections, Infection Control

- Intravascular catheter-related infections
- Other foreign-body and implant infections
- Surgical site infections
- Healthcare-associated pneumonia
- Nosocomial infection surveillance & screening methods
- Epidemiology and transmission (incl observational studies)
- Infection control interventional trials (incl. microbiota transplantation)
- Disinfection & biocides
- Other

Session accepted as Paper Poster Session

Advances in implant infection management

1295 **Transjugular intrahepatic portosystemic shunt and infections: a single-centre retrospective study**
A. Lombardi (Pavia, Italy), M. Sambo, M. Colaneri, A. Cambianica, P. Sacchi, V. Zuccaro, A. Di Matteo, P. Quaretti, L. Moramarco, N. Cionfoli, M. Mondelli, R. Bruno*

1430 **Outcome impact of a highly bactericidal scheme as initial treatment of acute staphylococcal PJI**
A. Auñon, M. Martin-Garcia, R. Parron, A. Blanco García, J. García Cañete, R. Fernández Roblas, I. Gadea Gironés, J. Esteban-Moreno (Madrid, Spain)*

1545 **Does iodine-impregnated incision drape prevent periprosthetic joint infection? One-year follow-up of 1187 patients in a randomised controlled trial**
A. Brun Hesselvig (Dyssegaard, Denmark), M. Arpi, T. Bjarnsholt, A. Odgaard*

2058 **Arthroscopic debridement, antibiotic and implant retention (DAIR) with local administration of Exebacase (Lysin CF-301) (LysinDAIR) followed by suppressive tedizolid as salvage therapy in elderly patients for relapsing multidrug-resistant *Staphylococcus epidermidis* prosthetic knee infection**
T. Ferry (Lyon, France), B. Cecile, C. Kolenda, C. Cassino, C. Chidiac, T. Perpoint, C. Le Corvaisier, J. Josse, A. Souche, S. Lustig, F. Laurent*

2268 **Prosthetic joint infections treated with two-stage revision procedure: a case series**
A. Saade-Antypas (Paris, France), J. Urvoy, D. Luque Paz, H. Common, P. Tattevin, A. Gougeon-Jolivet, C. Arvieux*

2400 **Appropriacy of empirical antibiotic therapy in percutaneous endoscopic gastrostomy site infection among head and neck cancer patients: a 15-year retrospective study**
S. Park (Seoul, South Korea), J. Oh, J. Kim, E. Joo, J. Lee*

2981 **Ultrasound-guided local administration of personalised cocktail of bacteriophages followed by suppressive antibiotherapy as salvage therapy in patients with relapsing total femur prosthetic joint infection (PJI)**
T. Ferry (Lyon, France), C. Kolenda, F. Craighero, S. Lustig, S. Gunst, C. Fevre, C. Petitjean, E. Fiaux, M. Etienne, C. Chidiac, L. Gilles, F. Laurent*

3224 **Risk factors for treatment failure of prosthetic joint infections: a multi-centre prospective cohort study**
L. Cardoso, J. Matos, L. Jorge, M. Carneiro, K. Morejon, B. Bassetti, M. Graf, C. Pilati, J. Rocha, R. Leme, M. Salles (Sao Paulo, Brazil)*

3312 **Exploration of the added value of rifampicin to antibiotic regimens for the management of *Cutibacterium* periprosthetic joint infection**
K. Kusejko, G. Scanferla, D. Pablo-Marcos, A. Auñon Rubio, J. Esteban-Moreno, M. Fernandez Sampedro, N. Gassmann, I. Waldmann, I. Uçkay, N. Benito, S. Corvec, M. Ferrari, T. Kramer, M. Wouthuyzen-Bakker, J. Lora-Tamayo, P. Vijayvargiya, R. Trebse, P. Morand, D. Slama, P. Sendi, V. Stadelmann, C. Strahm, M. Thurnheer, R. Kouyos, R. Patel, Y. Achermann (Zurich, Switzerland)*

4050 ***Pseudomonas aeruginosa* prosthetic joint infection: results from a prospective cohort**
H. Prié (Paris, France), V. Meyssonnier, Y. Kerroumi, B. Heym, O. Lidove, S. Marmor, V. Zeller*

4392 **Impact of multidisciplinary management on the outcome of aortic prosthetic vascular graft infections: a retrospective, single-centre experience**
M. Puges (Bordeaux, France), A. Cluzeaud, C. Cazanave, V. Brizzi, C. Caradu, E. Ducasse, X. Bérard*

4997 **Risk factors for treatment failure in patients with deep spinal SSI with foreign bodies treated with debridement, antibiotic and implant retention (DAIR): an international multi-centre retrospective cohort study**
R. Mens, M. Van Hoof, R. Kroeze, Y. Achermann, S. Maurer, R. Escudero Sánchez, J. Cobo Reinoso, P. Tattevin, D. Luque Paz, M. Salles, J. Lourtet Hascoet, T. Kramer (Berlin, Germany)*

5395 **Successful treatment of osteoarticular infections caused by quinolone-resistant Gram-negative bacilli with colistin plus β-lactams: preliminary results of a prospective multi-centre clinical study**
M. Mancheno-Losa (Madrid, Spain), J. Lora-Tamayo, E. Benavent Palomares, L. Sorlí, M. Riera Jaume, J. Cobo, N. Benito, L. Morata, A. Ribera, R. Rigo, S. Luque, A. Bahamonde, B. Sobrino, M. Del Toro, M. Fernandez Sampedro, J. Barbero Allende, E. Muñez Rubio, J. Esteban-Moreno, A. Oliver, I. García, F. Chaves, O. Murillo*

6759 **Features and outcomes of biliary tract-related bloodstream infections in patients with biliary prosthesis: results from the PROBAC study**
M. Mussa (Pavia, Italy), P. Pérez-Crespo, J. Lanz, L. Lopez-Cortes, P. Retamar Gentil, T. Marrodán-Ciordia, J. Fernandez-Suarez, E. Calbo Sebastian, L. Boix-Palop, J. Sanchez Calvo, J. Sevilla Blanco, J. Cuquet Pedragosa, A. Jóver-Sainz, C. Natera, A. Sousa-Dominguez, J. Goikoetxea, J. Reguera Iglesias, E. Leon, C. Armiñanzas Castillo, M. Ortega Lafont, F. Galan-Sanchez, A. Del Arco, A. Bahamonde, A. Smithson Amat, D. Vinuesa García, C. Herrero, A. Reyes Bertos, I. Perez-Camacho, A. Sánchez-Porto, M. Guzman, B. Becerril Carral, E. Merino De Lucas, J. Rodríguez-Baño*

7134 **Risk factors for prosthetic joint infections caused by Gram-negative bacteria: experience at an infectious disease referral centre**
S. Tedeschi (Bologna, Italy), L. Pancaldi, N. Rossi, E. Zamparini, M. Neri, M. De Paolis, A. Di Martino, P. Viale*

7507 **Fungal prosthetic vascular graft infections: beware of aorto-enteric fistulas!**
M. Puges (Bordeaux, France), X. Bérard, T. Caulier, L. Stecken, O. Leroy, E. Senneville, I. Accoceberry, F. Gabriel, O. Robineau, C. Cazanave*

8405 ***Enterococcus* species involvement in vascular graft infections**
J. Bauer (Tourcoing, France), O. Leroy, P. d'Elia, J. Sobocinski, O. Robineau, E. Senneville*

8833 **Optimising the microbiological diagnosis of prosthetic joint infection: a 5-year evaluation**
L. Cottom (Glasgow, United Kingdom), P. Wright*

9509 **Clinical predictors of peripheral vascular graft infection by *Staphylococcus aureus***
L. Castelo Corral (A Coruña, Spain), L. Ramos, A. Alonso Álvarez, A. Padin-Trigo, M. Rodriguez Mayo, F. Peña-Rodriguez, C. Suárez González, C. Sierra Freire, M. García López, E. Sánchez Vidal, E. Míguez Rey, D. Sousa*

9523 **Characteristics of vascular graft infection: a prospective single-centre cohort study**
D. Margaryan (Berlin, Germany), T. Tkhilaishvili, N. Cesta, M. De Masi, A. Trampuz*

Session accepted as 2-Hour Oral Session

Advances in understanding the epidemiology of HAI

260 **The role of food and environment in the transmission of *Clostridioides difficile***
S. Lim (Perth, Australia), P. Moono, D. Knight, T. Riley*

3694 **Differences in risk and outcomes for patients with *Clostridium difficile* toxin positive versus only cytotoxigenic culture positive faecal samples: results from COMBACTE-CDI case-control study**
K. Davies (Leeds, United Kingdom), V. Viprey, D. Ewin, A. Banz, W. Spittal, J. Vernon, A. Benson, G. Davis, P. Cleuziat, M. Wilcox*

3795 **Prevalence of *Clostridioides difficile* strains found in Texas soil**
A. Zeidan (San Antonio, United States), E. Young, R. Panchal, A. Yap, K. Reveles*

6453 **Potential impact of removing metronidazole from the treatment armamentarium for mild acute *Clostridioides difficile* infections**
S. Zilberman-Itskovich, I. Youngster, T. Lazarovitch, M. Bondorenco, L. Toledano, Y. Kachlon, B. Mengesha, R. Zaidenstein, D. Marchaim (Beer Yaacov, Israel)*

6844 **Current treatment pathways for *Clostridioides difficile* infection in Europe**
N. Petrosillo (Rome, Italy), G. Granata, M. Cataldo, K. Davies*

7856 **Changes in the laboratory diagnosis of CDI in Wales after the introduction of *C. difficile* toxin gene detection**
M. Perry (Cardiff, United Kingdom), T. Morris, S. Scotford, B. Anderson, S. Jones, S. Copsey, C. Davis, H. Hughes*

8620 ***Clostridioides difficile* infection incidence and consumption of selected antibiotics: EU/EEA countries 2008—2018**
P. Kinross (Stockholm, Sweden), L. Diaz Högberg, S. Tschudin-Sutter, K. Weist, C. Suetens*

8889 **Probiotics for recurrent *Clostridioides difficile* infection: a systematic review and meta-analysis**
S. George (Hamilton, Canada), N. Irfan, D. Mertz*

9292 **Microbiome changes among patients who transitioned from *Clostridioides difficile* negative to *C. difficile* positive using systematic screening tests**
L. Munoz-Price (Milwaukee, United States), S. Atkinson, A. Pan, K. Mai, V. Lam*

Session accepted as Mini-oral Flash Session

Better together: antibiotic stewardship and infection control

57 **Combined antibiotic stewardship and infection control measures to contain an outbreak of linezolid-resistant *Staphylococcus epidermidis* in an interdisciplinary intensive care unit**
C. Papan (Homburg, Germany), F. Berger, K. Last, M. Hoffmann, H. Knoll, M. Schröder, T. Volk, U. Schlotthauer, B. Gärtner, S. Becker*

657 **Feasibility, reproducibility and first results of a multimodal prevention approach for KPC-Kp in a high prevalence hospital setting**
V. Belvisi (Latina, Italy), C. Del Borgo, R. Marocco, S. Vita, P. Dolce, M. Meschiari, S. Parrocchia, L. De Marchis, L. Alibardi, M. Clores, A. Carraturo, G. Blanco, C. Cosentino, A. Melucci, E. Di Vincenzo, A. De Meo, A. Mecozzi, M. Aiuti, A. Pompucci, G. Visconti, A. Ianari, C. Mastroianni, C. Mussini, M. Lichtner*

4260 **Infection control, antimicrobial consumptions and incidence of hospital-acquired *Clostridiodes difficile* infection in acute care hospitals in Catalonia**
L. Boix-Palop (Terrassa, Spain), L. Castella, A. Hornero, N. Larrosa, P. Perez, N. Sopena, S. Grau, S. Hernández, A. Padulles, M. Gimenez, R. Ferrer, S. Melendo, J. Horcajada, E. Calbo Sebastian*

4325 **Impact of antimicrobial stewardship and infection control programmes on the incidence of carbapenem-resistant *Klebsiella pneumoniae*: a nonlinear time-series analysis**
M. Meschiari (Modena, Italy), C. Nebot, A. Beyaert, M. Sarti, A. Bedini, G. Orlando, J. Lopez Lozano, C. Mussini*

5385 **Impact of antimicrobial stewardship and infection prevention interventions on a cluster of VIM-producing *Pseudomonas aeruginosa* in a large, academic health system in Miami, Florida**
G. Rosello (Miami, United States), A. Jimenez, K. Deronde, A. Vega, O. Martinez, B. De Pascale, K. Sposato, A. Perez-Cardona, S. Marshall, M. Yasmin, R. Bonomo, L. Abbo*

5455 **Impact of early carbapenemase notification on infection control management and antimicrobial stewardship**
L. Perez (Porto Alegre, Brazil), C. Magagnin, C. Dias, G. Narvaez*

6349 **Exploring social links and networks of communication in relation to infection prevention and control and antibiotic stewardship across surgical specialties in South Africa**
C. Bonaconsa, O. Mbamalu (Cape Town, South Africa), A. Boutall, M. Hampton, A. Holmes, M. Mendelson, T. Pennel, E. Charani*

6708 **Mapping the roles and responsibilities for infection prevention and antibiotic prescribing along the surgical pathway in India and South Africa: case studies**
S. Singh, M. Mendelson, S. Surendran, C. Bonaconsa, O. Mbamalu (Cape Town, South Africa), V. Nampoothiri, A. Boutall, M. Hampton, P. Dhar, T. Pennel, C. Tarrant, A. Holmes, E. Charani*

7128 **Modulating the microbiota of the hospital environment by microbial cleaning: impact on infections and antimicrobial resistance**
M. D'Accolti, I. Soffritti, L. Lanzoni, M. Bisi, A. Volta, S. Mazzacane, E. Caselli (Ferrara, Italy)*

7621 **A combined strategy of antimicrobial stewardship and hospital-acquired infection control reduced the incidence of bacterial infection in a kidney transplantation programme (Hippomenes-PACTA-PROA study)**
J. Montoro, F. Lopez-Medrano (Madrid, Spain), M. Pérez-Jacoiste Asín, M. Fernandez Ruiz, J. Sequeira, R. San Juan Garrido, E. Gonzalez, A. Andres, J. Aguado Garcia*

Session accepted as Paper Poster Session

Burden of healthcare-associated infections and antimicrobial resistance

1449 **Do patients colonised by carbapenemase-producing *Klebsiella pneumoniae* have greater crude mortality? ANGEL-KpS Study**
Á. Cano Yuste (Cordoba, Spain), M. García, M. Gallo-Marín, I. Machuca, I. Gracia-Ahufinger, J. Torre-Giménez, A. Frutos, L. Kindelán-Segador, E. Perez-Nadales, A. M.Natera, J. Castón, J. Rodríguez-Baño, L. Martinez-Martinez, J. De La Torre Cisneros, B. Gutiérrez-Gutiérrez*

1854 **Infection and mortality rates due to carbapenem-resistant organisms in infants admitted to the neonatal unit**
R. Thomas (Johannesburg, South Africa), C. Ondongo-Ezhet, N. Motsoaledi, P. Jaglal, J. Wadula, F. Nakwa, S. Velaphi*

1897 **Excess length of acute inpatient stay attributable to acquisition of hospital-onset *Enterobacteriaceae* bloodstream infection with and without antimicrobial resistance: a multistate model analysis**
M. Goto (Iowa City, United States), H. Suzuki, R. Nair, D. Livorsi, E. Perencevich*

3567 **Is there any risk factor in terms of mortality in patients with nosocomial colistin-resistant *Klebsiella pneumoniae* infection?**
Ç. Ataman Hatipoğlu, F. Erdinç, G. Ertem, S. Cesur, E. Kaya Kılıç, Ş. Altun Demircan, K. Arslan, A. Buyukdemirci, N. Tulek (Ankara, Turkey), S. Kinikli*

4391 **Clinical impact of infections caused by carbapenemase-producing *Enterobacteriaceae***
L. Corbella Vazquez (Madrid, Spain), M. Fernandez Ruiz, M. Ruiz-Ruigómez, I. Rodriguez Goncer, J. Sequeira, F. Lopez-Medrano, M. Hernandez Jimenez, M. Lizasoaín, J. Villa, J. Aguado Garcia, R. San Juan Garrido*

4912 **A retrospective study to evaluate the epidemiology, standard of care, outcomes and resource utilisation in patients with confirmed or suspected infection by a carbapenem-resistant Gram-negative organism in Spain: the CARBAR study part 1, epidemiology of Gram-negative organisms**
J. Horcajada (Barcelona, Spain), M. Salavert, J. De La Torre Cisneros, I. Gracia-Ahufinger, J. Paño Pardo, H. Vilchez Rueda, N. Benito, A. Rivera, D. Sousa Regueiro, V. Estrada Perez, M. Ibarguren Pinilla, D. Manissero, C. Longshaw, K. Tone, S. Lopes*

4993 **The economic burden of carbapenem-resistant non-fermenting Gram-negative bacteria healthcare-associated infections**
Y. Cai (Singapore, Singapore), C. Wong, W. Lee, J. Teo, T. Lim, B. Tan, A. Kwa*

6109 **Healthcare-associated bacteraemic urinary tract infections: results of the prospective multi-centre ITUBRAS-2 project**
S. Gómez-Zorrilla (Barcelona, Spain), I. López Montesinos, F. Becerra, E. Ruiz, I. Grau, V. Pintado, B. Padilla, N. Benito, L. Boix-Palop, M. Gutierrez, M. Peñaranda Vera, M. Gamallo, J. Martinez Martinez, E. Morte, J. Del Pozo, X. Duran, J. Diaz-Regañon, D. Lopez, R. Canton Moreno, A. Oliver, P. Ruiz-Garbajosa, J. Horcajada*

6553 **Flat lining of nine-year deaths rate throughout various carbapenem-resistant Gram-negative outbreaks at Saint George Hospital, Lebanon**
A. Chamieh (Marseille, France), O. Zmerli, S. Saliba, C. Afif, G. Juvelekian, J. Rolain, E. Azar*

6847 **Epidemiology, risk factors and outcomes of infections caused by carbapenem-resistant Gram-negative bacteria in paediatric intensive care unit**
L. Celani, M. Ridolfi, C. Borrazzo, M. Trancassini, G. Antonelli, P. Papoff, C. Mastroianni, G. D'Ettorre, P. Pavone (Rome, Italy)*

7629 **Seasonal patterns in the burden of common bacterial pathogens in south-east Michigan post-acute care facilities**
M. Cassone (Ann Arbor, United States), J. Mantey, K. Gontjes, B. Lansing, K. Gibson, L. Mody*

9467 **Carbapenem-resistant *Enterobacteriaceae* infections: more could be worst?**
S. De Gregorio (Caba, Argentina), V. Tudanca, S. Repetto, L. Paravano, C. Rodriguez, M. Nastro, D. Stecher, C. Vay, A. Famiglietti, M. Foccoli*

Session accepted as Mini-oral ePoster Session

Clostridioides difficile: prevalence, diagnosis and outcomes

3194 **_Clostridioides difficile_ NAAT-positive with toxin-negative test results: impact of antibiotic treatment on clinical outcomes**
J. Haque (Milwaukee, United States), A. Dawson, K. Osinski, M. Thakkar, A. Yarur, L. Munoz-Price*

3234 **A phase II open-label clinical trial of investigational microbiota-based drug RBX2660 for prevention of recurrent _Clostridioides difficile_ infection: two-years evaluation of efficacy, durability, microbiome changes and participant demographics**
C. Reimer (Copenhagen, Denmark), R. Orenstein, L. Bancke, C. Gonzalez, K. Blount*

4221 **Microbiome analysis of faecal microbiota transplantation via lyophilised capsules for recurrent _Clostridiodes difficile_ infection**
L. Villar Gomara (Madrid, Spain), S. Vazquez Cuesta, N. Lozano, M. Olmedo Samperio, S. Rodriguez-Fernandez, M. Kestler Hernandez, L. Alcalá, M. Marín, P. Muñoz, E. Bouza, E. Reigadas Ramirez*

4239 **Economic burden of recurrent _Clostridium difficile_ infection (rCDI) in adult patients admitted in Spanish hospitals: multi-centre, retrospective, observational study**
E. Bouza (Madrid, Spain), J. Cobo Reinoso, M. Rodriguez Hernandez, M. Salavert, J. Horcajada, J. Iribarren Loyarte, E. Obi, V. Lozano, S. Maratia, M. Cuesta, E. Uría, E. Limón*

4863 **Microbiome characterisation of patients with _Clostridiodes difficile_ infection and colonised patients**
S. Vazquez Cuesta (Madrid, Spain), N. Lozano, L. Villar Gomara, L. Alcalá, M. Marín, P. Muñoz, E. Bouza, E. Reigadas Ramirez*

4910 **Community-acquired _Clostridioides difficile_ infection: a prospective study in an unselected population**
L. Villar Gomara (Madrid, Spain), S. Vazquez Cuesta, L. Alcalá, M. Marín, P. Muñoz, E. Bouza, E. Reigadas Ramirez*

4933 **Clinical and gut microbiome characterisation of _Clostridiodes difficile_ infection in immunosuppressed patients**
S. Vazquez Cuesta (Madrid, Spain), L. Villar Gomara, N. Lozano, L. Alcalá, M. Marín, P. Muñoz, E. Bouza, E. Reigadas Ramirez*

Session accepted as 1-Hour Oral Session

Do you really want to know what is in your hospital room?

2441 **Short-term environmental contamination with MRSA explained by in-room activity of MRSA-colonised patients**
A. Wolfensberger (Zürich, Switzerland), N. Mang, K. Gibson, M. Cassone, K. Gontjes, H. Sax, L. Mody*

3190 **Variable number tandem repeat analysis on patient _Pseudomonas aeruginosa_ (PsA) bacteraemia isolates and hospital shower water PsA strains to determine their links**
Ö. Yetiş (London, United Kingdom), P. Wilson, J. Turton, Z. Payne, S. Ali*

4300 **When cold water is too warm: healthcare-associated Legionnaires' disease associated with hot season**
F. Waldeck (St. Gallen, Switzerland), P. Kohler, M. Frischknecht, R. Kuhn, M. Von Kietzell, W. Albrich, M. Schlegel*

5914 **A simple cleaning intervention to prevent transmission of carbapenemase-producing _Enterobacterales_ from hospital sinks**
J. Kwong (Melbourne, Australia), M. Leroi, T. Bannam, D. Edmonds, E. Grabsch, S. Narayanasamy, J. Greenough, C. Lane, M. Easton, B. Howden, P. Johnson, M. Grayson*

Session accepted as Paper Poster Session

Environmental contamination and infection prevention

76 **Architecture fundamentally influences opportunity costs during an outbreak in a neonatology unit: real-life data and simulation of room designs**
S. Scheithauer (Göttingen, Germany), M. Kaase, D. Fenz, H. Küster, S. Horn, B. Sliwa*

433 **Risk factors of environmental dissemination of different multidrug-resistant organisms**
R. Saliba (Bobigny, France), D. Seytre, G. Theo, T. Delerue, F. Jaureguy, E. Carbonnelle, D. Karam Sarkis, T. Billard-Pomares, J. Zahar*

1119 **Inhibitory effect of whole blood on the antiseptic action of E-101 solution, a myeloperoxidase-mediated formulation, compared to conventional wound cleansers**
G. Denys (Indianapolis, United States), J. Carpenter, R. Allen, J. Stephens, Jr.*

1188 **UV-C light application after terminal disinfection for vancomycin-resistant enterococci: an additional safety?**
A. Portmann (Basel, Switzerland), M. Dangel, A. Büchler, A. Egli, A. Widmer*

1893 **Comparison of the microbiological efficacy of disinfection using ultraviolet and aerosolised hydrogen peroxide system for carbapenemase-producing _Enterobacteriaceae_ in a healthcare setting**
S. Park (Seoul, South Korea), J. Lee, E. Kim, S. Kwak, M. Hong, E. Kim, J. Jung, M. Kim, S. Kim*

2026 **The sink as source of transmission of VIM metallo-β-lactamase-producing _Pseudomonas aeruginosa_ in the intensive care unit**
V. Robin (Brussel, Belgium), D. De Geyter, I. Wybo, F. Crombe, D. Pierard*

2326 **Increases in environmental cleaning and reduction in in-hospital mortality in multi-patient rooms with single-use disinfection wipes hung at the patient bed: a prospective, crossover trial**
K. Chedid (Ann Arbor, United States), M. Dadon, I. Shaul, I. Katz, O. Greiver, M. Alfaro, L. Hod, T. Lazarovitch, H. Saadon, G. Ben-Yossef, S. Moscovich, A. Shorbaje, R. Zaidenstein, E. Martin, D. Marchaim*

2438 **Genomic and environmental investigation of hospital room occupied by an imported case of meningitis due to extensively drug-resistant (XDR) *Pseudomonas aeruginosa***
H. Baba (Sendai, Japan), H. Kanamori, M. Katsumi, T. Sato, K. Ishikawa, T. Chida, S. Ikeda, K. Tokuda*

3398 **Comparison of environmental *Legionella pneumophila* and *Legionella* spp. detection from water and swab samples by culture and qPCR**
S. Castriciano (Brescia, Italy), M. Savoldi Boles, C. Pilotti, M. Martinelli, R. Musumeci, C. Cocuzza*

3403 **Detection of transferable CTX-M-producing multidrug-resistant *Enterobacteriaceae* from public transportation in China**
X. Wen (Guangzhou, China), M. El-Sayed Ahmed, G. Chen, C. Shen, Z. Zhao, W. Liang, Y. Yang, G. Tian*

3458 **Adaptation to triclosan in carbapenemase-producing *Klebsiella pneumoniae* clinical isolates**
A. Gual-De-Torrella (Seville, Spain), P. Pérez-Palacios, M. Delgado-Valverde, J. Oteo, A. Pascual Hernandez, F. Fernández-Cuenca*

3544 **Dual-function antimicrobial laundry supplement and textile coating for the decontamination of healthcare laundry**
L. Owen (Leicester, United Kingdom), K. Laird*

3706 **Microbiological surveillance of duodenoscope reprocessing following an outbreak with OXA-48 producing *Klebsiella pneumoniae***
A. Kola (Berlin, Germany), K. Kelterborn, F. Schwab, P. Gastmeier*

3825 **Bacterial and fungal contamination and simultaneous analysis of chemical indoor air pollution in medical-social establishment and liberal healthcare offices**
J. Gangneux (Rennes, France), H. Guegan, A. Baudet, O. Blanchard, M. Guillaso, P. Le Cann, E. Baures, A. Florentin*

3881 **High occurrence of *Serratia* spp. in abiotic surfaces at hospital intensive care unit areas during non-outbreak situations**
S. Aracil-Gisbert (Madrid, Spain), N. Guerra-Pinto, A. Ortiz-Fernández, V. Fernandez Lanza, C. Soriano, M. Fernandez-De-Bobadilla, S. Gallego-Zarzosa, M. López-Olivencia, V. Quinteros-Fiel, P. Ruiz-Garbajosa, R. Canton Moreno, R. De Pablo, F. Baquero, T. Coque*

3888 **Influence of the Built Environment (BE) microbiota on the epidemiology of antimicrobial resistance at intensive care unit of a tertiary hospital**
S. Aracil-Gisbert (Madrid, Spain), N. Guerra-Pinto, A. Ortiz-Fernández, V. Fernandez Lanza, C. Soriano, M. Fernandez-De-Bobadilla, M. López-Olivencia, V. Quinteros-Fiel, S. Gallego-Zarzosa, P. Ruiz-Garbajosa, R. Canton Moreno, R. De Pablo, F. Baquero, T. Coque*

4136 **Control of hospital-wide outbreak of OXA-48-producing *Enterobacteriaceae* outbreak**
M. Ling (Singapore, Singapore), M. How, K. Tan, E. Lee, K. Ko, J. Sim*

4199 **Achieving sustained decolonisation of CPE in sinks**
G. Regev-Yochay (Ramat-Gan, Israel), G. Smollan, H. Jaber, C. Cohen, I. Tal, N. Pinas Zade, C. Rubin, S. Amit, E. Zimlichman, N. Keller*

5043 **Dynamics of *Staphylococcus* aureus in the hospital environment and in patients: is the environment identified as a reservoir?**
A. Van Der Schoor (Rotterdam, Netherlands), A. Voor In, T Holt, C. Klaassen, J. Severin, D. Gommers, M. Bruno, J. Hendriks, M. Vos*

5064 **Activity of peracetic acid against MDR *Enterococcus faecium* and non-typhoidal Salmonella from diverse epidemiological and genetic backgrounds**
A. Rebelo (Porto, Portugal), B. Duarte, A. Freitas, A. Callejón, L. Vieira Peixe, C. Novais, P. Antunes*

5665 **Take care of the cents and the euros look after themselves? Antimicrobial activity of European money**
J. Knobloch (Hamburg, Germany), C. Belmar Campos, E. Klupp, G. Franke*

5692 **Systematic review of *Legionella* amelioration systems in healthcare facilities**
J. Mcdanel, A. Marra, D. Diekema, E. Kiscaden, H. Healy, L. Herwaldt (Iowa City, United States)*

6037 **Environmental epidemiological survey of carbapenem-resistant *Klebsiella pneumoniae* in 5 intensive care unit**
Q. Shi (Shanghai, China), Y. Huang, W. Sun, Y. Cui, B. Hu, X. Gao*

6451 **Elevated tolerance to disinfectants in a carbapenemase-producing *Klebsiella pneumoniae* isolate obtained from a duodenoscopy-associated outbreak**
K. Konrat, M. Brunke (Berlin, Germany), Y. Pfeifer, L. Becker, C. Schaudinn, B. Piening, I. Schwebke, M. Arvand*

7200 **Dynamic interactions between methicillin-resistant *Staphylococcus aureus* and methicillin-sensibler *Staphylococcus aureus* contamination of the near patient and extended environment and patient colonisation revealed by whole genome sequencing in a tertiary referral hospital**
P. Kinnevey (Dublin, Ireland), A. Kearney, M. Earls, T. Poovelikunnel, G. Brennan, A. Shore, H. Humphreys, D. Coleman*

7316 **Assay for screening of *Enterococcus faecium* susceptibility to the disinfectant Sodium Dichloroisocyanurate plus detergent**
B. Skive (Frederiksberg, Denmark), A. Hammerum, H. Hasman, M. Pinholt, C. Jensen, I. Dahl Knudsen, A. Kjerulf, H. Ingmer*

7317 **The role of microbiological surveillance in ensuring the safety of endoscopes reprocessing**
B. Tuvo (Pisa, Italy), C. Bisordi, G. Arzilli, G. Scardina, G. Visi, V. Casigliani, L. Cosco, A. Baggiani, B. Casini*

8580 **Ultimate survival of *Serratia marcescens* in clorhexidine**
A. Delgado-Iribarren (Alcorcón, Spain), R. Barquero Jiménez*

9331 **Bacterial growth in antiseptics, disinfectants and soaps in a tertiary care hospital, Ouagadougou, Burkina Faso**
P. Lompo (Ouagadougou, Burkina Faso), M. Peeters, N. Ouédraogo, H. Kafando, A. Heroes, S. Yameogo, H. Tinto, L. Sangaré, J. Jacobs*

9629 **A point prevalence study of carbapenemase-producing *Enterobacteriaceae* colonisation of drains in a tertiary care hospital**
S. Woods (Dublin, Ireland), N. O Connell, L. Power*

Session accepted as Paper Poster Session

Epidemiology and surveillance of hospital-acquired infections

81 **A regional survey on the level of implementation of key infection prevention and control structures in acute-care hospitals in Crete, Greece**
E. Astrinaki, E. Kritsotakis, E. Bolikas, E. Panagiotaki, D. Christofaki, A. Chalkiadaki, A. Salvaraki, E. Ioannidou, E. Stamataki, G. Pavlidaki, E. Lagoudaki, M. Moustaki, V. Kataxaki, D. Stamataki, M. Katsidoniotaki, S. Karakonstantis (Heraklion, Greece), A. Gikas*

460 **Prevalence of device use and transmission-based precautions in nineteen large Australian acute care public hospitals: secondary outcomes from a national healthcare-associated infection point prevalence survey**
P. Russo (Melbourne, Australia), A. Stewardson, A. Cheng, T. Bucknall, B. Mitchell*

669 **Incidence rate of health care associated infection in tertiary care children's hospital in Ukraine**
A. Vodianyk (Kiev, Ukraine), K. Soiak, A. Aleksandrin*

994 **Prospective surveillance of health-care associated infections in residents in long term care facilities in Graz, Austria**
E. König (Graz, Austria), M. Haubenwallner, C. Pux, K. Prisching, W. Schippinger, E. Stoiser, R. Krause, I. Zollner-Schwetz*

1593 **Beyond the contact precaution: what does the surveillance culture tell us about multidrug-resistant microoganisms in critically ill patients? Data of the Public Hospital of São Paulo City, Brazil**
C. Abboud (Sao Paulo, Brazil), E. Evangelista De Souza, D. Feriani, L. Gordilho Mutti Carvalho, A. Santos Ibanes, E. Vasconcelos, V. Barros Barbosa, F. Inoue, J. Monteiro*

2634 **Prospective genomic surveillance of multidrug-resistant organisms in Vietnamese intensive care units**
L. Roberts (Cambridge, United Kingdom), F. Khokhar, N. Van Kinh, N. Vu Trung, G. Nguyen, D. Co, L. Hoi, H. Nguyen, T. Giang, C. Bui, H. Tran, J. Bryan, A. Herrick, B. Nadjm, H. Rogier Van Doorn, J. Parkhill, Z. Iqbal, E. Torok*

2647 **Adherence to an admission screening for multidrug-resistant organisms in a tertiary care hospital in Switzerland**
F. Waldeck (St. Gallen, Switzerland), P. Kohler, M. Schlegel, E. Lemmenmeier*

2658 **Multidrug-resistant organisms (MDRO) colonisation pattern, prevalence and acquisition in a neonatal intensive care unit, evidence for guiding active surveillance cultures: a 2-year experience active surveillance process at Saint Joseph Hospital, Jerusalem**
A. Sabateen (East Jerusalem, Palestine)*

3419 **Multilevel analysis of the regional variation in healthcare-associated infections and antimicrobial use prevalence in acute-care hospitals in Greece**
E. Kritsotakis, E. Astrinaki, T. Machaira, S. Karakonstantis (Heraklion, Greece), A. Gikas*

4250 **Healthcare associated infections and outcomes: changes between 2013 and 2018 in Turkey**
M. Aydin (Istanbul, Turkey), E. Azak, H. Bilgin, S. Menekse Yilmaz, A. Asan, H. Elmaslar Mert, Z. Yulugkural, L. Altunal, Ç. Ataman Hatipoğlu, G. Ertem, E. Altunok, M. Demirkaya, S. Alkan Ceviker, F. Akgul, Z. Memis, P. Konya, A. Azap, G. Aydin, D. Korkmaz, Z. Karakoç, D. Yapar, F. Karakecili, O. Gunal, Ş. Keske, M. Kapmaz, C. Kader, A. Demirel, Ö. Ergönül*

4457 **Hospital onset bloodstream infection (HOBSI) as a marker of the burden of hospital associated infection (HAI) at a tertiary care hospital in South India**
R. Iyer (Hyderabad, India), R. Jangam*

4789 **Active follow-up of patients colonised with highly-resistant microorganisms to discontinue isolation measures**
C. Haanappel (Rotterdam, Netherlands), A. Voor In, T. Holt, L. Bode, I. De Goeij, M. Vos*

4876 **Nosocomial bloodstream infection rates: exploration of a quality indicator for infection prevention**
B. Laan (Amsterdam, Netherlands), S. Geerlings, W. De Rond, I. Spijkerman*

5159 **Healthcare-associated infections, antibiotic use and resistance in Swiss long-term care facilities: a multi-centre point prevalence study**
D. Hequet, S. Seiffert, S. Kessler, G. Rettenmund, E. Lemmenmeier, L. Qalla-Widmer, N. Oliver, A. Egli, H. Seth-Smith, T. Münzer, M. Schlegel, C. Petignat, P. Kohler (St. Gallen, Switzerland)*

5199 **Automated detection of antimicrobial-resistant bacteria based on real-time microbiological data**
V. Schechner (Tel-Aviv, Israel), T. Grossman*

5715 **Impact of applying mucosal barrier injury laboratory-confirmed bloodstream infection criteria in patients with solid tumours and haematologic malignancies**
A. Puin, M. Fernandes Vieira, M. Freire, P. Bonazzi, K. Yaqub Ibrahim, M. Del Pilar, J. Pereira, V. Rocha, E. Abdala (São Paulo, Brazil)*

5760 **Mucosal barrier injury laboratory-confirmed bloodstream infection in oncology patients: descriptive analysis of epidemiological and laboratorial data**
A. Puin, M. Freire, P. Bonazzi, M. Fernandes Vieira, K. Yaqub Ibrahim, M. Del Pilar, J. Pereira, V. Rocha, E. Abdala (São Paulo, Brazil)*

6403 **Increasing trends of emerging extensively drug-resistant bacteria cases at Lyon University Hospital, 2015-2019**
E. Christelle (Lyon, France), D. Hilliquin, E. Munier-Marion, E. Kuczewski, C. Dananché, C. Barreto, S. Gardes, B. Grisi, S. Gerbier Colomban, G. Jacqueline, C. Dupieux-Chabert, P. Vanhems*

6431 **Polymerase chain reaction-based active surveillance of multidrug resistant pathogens in a paediatric intensive care unit: to screen or not to screen?**
Ó. Martínez Expósito, E. Morteruel Arizkuren, J. Barrios Andrés, F. Pilar Orive, M. Aranzamendi Zaldumbide (Barakaldo, Spain)*

6774 **Effectiveness of monitoring colonisation by multidrug-resistant bacteria in polytrauma patients: 7 years of experience**
S. Torri (Milan, Italy), A. Bielli, V. Cento, G. Colombo, O. Chiara, F. Sammartano, C. Vismara, C. Perno, E. Mazzola*

6876 **Evolution of multidrug-resistant organisms active surveillance strategy in a Portuguese acute care hospital, from 2015 to 2018**
D. Peres (Matosinhos, Portugal), A. Cipriano, V. Alves, F. Vieira, I. Devesa, I. Neves*

8721 **Computerised registry as a potential tool for surveillance and management of complex bone and joint infections in France**
A. Lemaignen (Tours, France), L. Grammatico-Guillon, P. Astagneau, S. Marmor, T. Ferry, S. Touchais, G. Le Moal, C. Arvieux, S. Ansart, P. Abgueguen, O. Lesens, J. Michon, P. Delobel, P. Pavese, B. Heym, J. Courjon, B. Brunschweiler, A. Roux, F. Dauchy, A. Baldolli, D. Mainard, J. Jenny, F. Laurent, A. Jolivet-Gougeon, E. Senneville, L. Bernard*

9378 **Incidence, risk factors and outcome determinants of healthcare-associated blood stream infection at a neonatal intensive care unit in North India**
K. Saigal (Delhi, India), A. K Achuthan, A. Ghosh, M. Jajoo*

Session accepted as 1-Hour Oral Session

Getting close to the elimination of SSI

1113 **Added value of throat and perineal *Staphylococcus aureus* screening, in addition to nasal screening, for identifying patients at risk of *S. aureus* surgical site infection**
C. Recanatini (Utrecht, Netherlands), D. Troeman, J. Hasan, F. Sifakis, H. Goossens, S. Malhotra-Kumar, D. Hazard, O. Ali, S. Harbarth, M. Bonten, C. van Werkhoven, J. Kluytmans*

2740 **Selective decontamination of the digestive tract prevents postoperative pneumonia and anastomotic leakage after esophagectomy**
R. Janssen (Nijmegen, Netherlands), F. Van Workum, N. Baranov, H. Blok, J. Ten Oever, E. Kolwijck, A. Tostmann, C. Rosman, J. Schouten*

2892 **Debridement And Implant Retention (DAIR) with local administration of personalised cocktail of bacteriophages (PhagoDAIR) followed by suppressive antibiotherapy as salvage therapy in patients with relapsing prosthetic knee infection (PKI)**
T. Ferry (Lyon, France), C. Kolenda, B. Cecile, C. Gustave, S. Lustig, C. Fevre, C. Petitjean, C. Chidiac, L. Gilles, F. Laurent*

4309 **Modelling the impact of antibiotic resistance on surgical site infections: the case of hip replacements**
S. Evans (London, United Kingdom), N. Naylor, K. Pouwels, T. Lamagni, K. Cooper, B. Muller-Pebody, J. Robotham*

4328 **Global outbreak of *Mycobacterium chimaera* infections in cardiac surgery patients: tracking risk through ongoing surveillance in the UK**
T. Lamagni (London, United Kingdom), A. Charlett, B. Mason, J. Wares, E. Davies, J. Mcmenamin, L. Doherty, G. Smith, M. Chand*

Session accepted as Paper Poster Session

Healthcare-associated pneumonia

107 **Risk factors for non-ventilator-associated hospital-acquired pneumonia in patients outside the intensive care unit**
V. Kachalov (Zurich, Switzerland), W. Jakob, S. Kuster, R. Kouyos, S. Balakrishna, A. Wolfensberger*

849 **Baseline microbiology, susceptibility, molecular characterisation, and emergence of non-susceptibility in a recent randomised, controlled trial (RESTORE-IMI 2) comparing imipenem/cilastatin (IMI)/relebactam (REL) versus piperacillin/tazobactam (PIP/TAZ) for hospital-acquired or ventilator-associated bacterial pneumonia (HABP/VABP)**
K. Young (Kenilworth, United States), A. David-Wang, A. Roquilly, D. Rodriguez Gonzalez, R. Wunderink, I. Titov, M. Hackel, K. Kazmierczak, M. Wise, A. Maniar, D. Hilbert, M. Losada, J. Du, M. Brown, A. Paschke, L. Chen*

1435 **Increased serum hydrogen sulfide as determinant of resolution of ventilator associated pneumonia caused by *P. aeruginosa***
G. Renieris (Athens, Greece), K. Katrini, E. Karakike, N. Antonakos, A. Karageorgos, L. Sabrakos, E. Giamarellos-Bourboulis*

1865 **Risk score for non-ventilator-associated hospital-acquired pneumonia (nvHAP)**
A. Wolfensberger (Zürich, Switzerland), V. Kachalov, W. Jakob, S. Kuster, S. Balakrishna, R. Kouyos*

2909 **Impact of early appropriate antimicrobial therapy on a new hierarchical endpoint for ventilator-associated bacterial pneumonia**
E. Weiss, S. Ruckly, C. Dupuis, J. Zahar, J. Timsit (Paris, France)*

3006 **Antimicrobial susceptibility and clinical characteristics of severe pneumonia due to *Haemophilus influenzae*: an observational study**
P. Danneels, M. Postorino, A. Strazzulla (Melun, France), A. Pitsch, S. Jochmans, M. Monchi, V. Dubee, S. Diamantis*

3027 **Effectiveness of trimetoprim-sulfametoxazole for treatment of ventilator-associated pneumonia: a cohort study**
A. Strazzulla (Melun, France), M. Postorino, A. Purcarea, C. Chakvetadze, A. De Pontfarcy, G. Tebano, A. Pitsch, L. Vong, S. Jochmans, C. Vinsonneau, M. Monchi, S. Diamantis*

3867 **Health economics of nosocomial pneumonia in UK intensive care units: an exploratory study**
A. Wagner, D. Turner, V. Enne (London, United Kingdom), R. Baldan, C. Russell, D. Livermore*

3915 **Epidemiological characteristics of *Stenotrophomonas maltophilia*-associated lower respiratory tract infection in Qatar: a one-year retrospective study**
A. Prabhakaran Nair, S. Sasi (Doha, Qatar), M. Abukhattab, K. Chacko, A. Rajan, A. Deshmukh, M. Abraham, M. Al-Maslamani*

4306 **Revision of clinical guidelines for hospital-acquired pneumonia led to a reduction in carabapenem prescriptions at a Swiss cantonal hospital**
F. Schefer, T. Fehr, F. Fleisch, A. Cusini (Chur, Switzerland)*

4616 **Clinical efficacy of ceftolozane-tazobactam versus other active agents for the treatment of bacteraemia and nosocomial pneumonia due to drug-resistant *Pseudomonas aeruginosa***
M. Bassetti, D. Giacobbe, E. Rizzo, N. Castaldo (Udine, Italy), C. Mussini, A. Cattelan, A. Russo, C. Mastroianni, A. Capone, M. Tumbarello, A. Vena*

5344 **A prediction model for identification of patients at high risk for *Staphylococcus aureus* intensive care unit pneumonia and implications for trial design**
C. Recanatini (Utrecht, Netherlands), F. Paling, D. Hazard, J. Hasan, O. Ali, F. Sifakis, H. Goossens, S. Malhotra-Kumar, W. Van Wamel, M. Wolkewitz, M. Bonten, J. Kluytmans*

5446 **Comparison of Hospital Resource Utilisation (HRU) among patients who received either ceftolozane-tazobactam (C/T) or meropenem in ASPECT-NP: a randomised, controlled, double-blind study of adult patients with Ventilated Nosocomial Pneumonia (V-NP)**
L. Puzniak (Kenilworth, United States), T. Lodise, J. Yang, R. Dillon, M. Kollef*

5611 **Role of multidrug-resistant bacteria on nosocomial pneumonia mortality**
A. Romero Paternina, M. Martinez-Abarca Marquez (Madrid, Spain), I. González Carrasco, I. Burruezo López, M. Paz Arias, A. Valcarcel, M. Fragiel Saavedra, C. Outón, E. Dubon Peralta, N. Cabello-Clotet, M. Nuñez, V. Estrada*

5628 **Preliminary results for the evaluation of the impact of syndromic lower respiratory tract panel on antimicrobial management and infection control**
R. Can Sarınoğlu (İstanbul, Turkey), E. Tukenmez-Tigen, H. Bilgin, B. Aksu, V. Korten, G. Soyletir*

5704 **Diagnostic test characteristics of radiographic keywords in the diagnosis of bacterial pneumonia**
O. Albin (Ann Arbor, United States), J. Pogue, L. Petty, J. Mills, K. Kaye*

5711 **Incidence of ventilator-associated pneumonia in children intubated in paediatric intensive care unit**
E. Maisonneuve (Grenoble, France), C. Masson, H. Terrisse, C. Richarme, I. Wroblewski, G. Mortamet, C. Landelle*

5772 **Double carbapenem therapy for isolated pneumonia in carbapenem-resistant *Klebsiella* spp. and *Acinetobacter* spp.**
D. Akyol (Izmir, Turkey), S. Chousein Memetali, M. Demir, G. Guliyeva, U. Onal, H. Sipahi, S. Ulusoy, O. Sipahi*

6185 **Impact of the Spanish *Neumonía Zero* project on ventilator-associated pneumonia rates**
S. Carvalho Brugger (Lleida, Spain), M. Miralbés, B. Balsera, S. Rodriguez, M. Vallverdú, J. Caballero*

7146 **The burden of nosocomial pneumonia caused by *Pseudomonas aeruginosa* and *Staphylococcus aureus* for ventilated patients in European intensive care units: a weighted multi-state analysis**
M. Von Cube (Freiburg, Germany), T. Bluhmki, K. Kaier, F. Sifakis, O. Ali, J. Hasan, F. Paling, J. Kluytmans, S. Malhotra-Kumar, J. Beyersmann, M. Wolkewitz*

Session accepted as 1-Hour Oral Session

Interventions to reduce HAI

1574 **Nontoxigenic *Clostridioides difficile* strains against *C. difficile* colonisation: an experimental study**
J. Couturier (Paris, France), L. Franconeri, C. Janoir, L. Ferraris, S. Hoys, J. Aires, F. Barbut*

5734 **The effects of antibiotic cycling and mixing on acquisition of antibiotic-resistant bacteria in the intensive care unit: a post-hoc analysis of a prospective cluster-randomised crossover study**
P. Van Duijn (Groningen, Netherlands), W. Verbrugghe, P. Jorens, F. Spoehr, D. Schedler, M. Deja, D. Annane, C. Lawrence, M. Jereb, K. Seme, F. Sifrer, V. Tomic, F. Esteves, J. Carneir, S. Harbarth, M. Bonten*

7083 **Changing the hospital microbiome: a cluster-randomised controlled trial to analyse the influence of environmental cleaning on hospital-acquired infections using disinfectant, soap or probiotic agents**
R. Leistner (Berlin, Germany), B. Kohlmorgen, J. Golembus, D. Gruhl, E. Lemke, B. Raguse, G. Zakonsky, P. Gastmeier*

7607 **Impact of selective decolonisation of critically ill extreme elderly patients using invasive devices with chlorhexidine 2% daily bath on healthcare-associated infection rates**
J. Delgado Correal (Rio de Janeiro, Brazil), R. Rufino, M. Fornasari, C. Alburquerque, M. Martins, D. Santos, P. Damasco*

7631 **Participatient: Patient Engagement Counter Catheter-associated urinary tract infections with an App (PECCA)**
R. Bentvelsen (Leiden, Netherlands), B. Laan, S. Geerlings, N. Chavannes, K. Veldkamp*

Session accepted as Paper Poster Session

Intravascular and urinary catheters -related infection

419 **Is it cost effective to use a 2% chlorhexidine gluconate wipes bath to reduce primary bloodstream infection? A quasi-experimental study experience**
C. Abboud (Sao Paulo, Brazil), D. Feriani, L. Gordilho Mutti Carvalho, A. Santos Ibanes, E. Vasconcelos, V. Barros Barbosa, E. Evangelista De Souza*

1569 **Effectiveness of chlorhexidine-impregnated dressing and a bundle of interventions for prevention of central line-associated bloodstream infections**
B. Madran (Istanbul, Turkey), Ş. Keske, V. Bakır, Ö. Ergönül*

1743 **Risk for antibiotic resistance in patients hospitalised with urinary tract infection: a matched case-control study using the French health insurance database**
M. Opatowski (PAris, France), C. Brun-Buisson, M. Touat, J. Salomon, D. Guillemot, P. Tuppin, L. Watier*

1768 **Prevalence and risk factors of inappropriate use of intravenous and urinary catheters in surgical and medical patients**
B. Laan (Amsterdam, Netherlands), M. Vos, J. Maaskant, M. Van Berge Henegouwen, S. Geerlings*

2419 **Impact of a continuous improvement programme on central venous catheter care in reducing the incidence of primary bloodstream infection in neonatal intensive care unit**
R. Cantarim Inacio (São Paulo, Brazil), E. Medeiros*

3163 **Short-term peripheral venous catheter-related bloodstream infections**
T. Vu, J. Goritsas, H. Torres Diaz, K. Reveles, C. Dickerson, J. Cadena-Zuluaga (San Antonio, United States)*

3311 **Utility of central venous catheter cultures in predicting blood culture susceptibilities in catheter-related bloodstream infections due to *Staphylococcus spp*.**
H. Nomoto (Tokyo, Japan), M. Ishikane, K. Mezaki, N. Ohmagari*

3438 **Ultrasound guidance and risk for intravascular catheter-related infections among peripheral arterial catheters. A *post hoc* analysis of two large randomised controlled trials**
N. Buetti (Paris, France), S. Ruckly, J. Lucet, L. Bouadma, C. Schwebel, O. Mimoz, J. Timsit*

3929 **Peripheral venous catheter-related bloodstream infection in hospitalised children: the role of Gram-negative bacteria**
I. Berger (Herzliya, Israel), T. Cohen, E. Rahmani, I. Levy, A. Lowenthal, L. Goldberg, Y. Levinsky, H. Ben Zvi, O. Scheuerman*

4041 **Effectiveness of chlorhexidine dressings to prevent catheter-related infections: Does one size fit all? A systematic literature review and meta-analysis**
M. Puig-Asensio (Iowa City, United States), A. Marra, C. Childs, E. Perencevich, M. Schweizer*

4166 **Differences in clinical characteristics and causative pathogens between central line-associated bloodstream infections and catheter-related bloodstream infections using modified definition in medical intensive care unit**
J. Hyun, J. Yeom, J. Choi, N. Ku, S. Jeong, J. Ahn (Seoul, South Korea)*

5496 **Urinary catheter use in university hospital: a prospective intervention study**
I. Voita, M. Bojāre, U. Dumpis, A. Vilde (Riga, Latvia)*

6149 **Catheter-associated bloodstream infections: Empirical antibiotic recommendations based on microbiological data**
C. Collado Giner (Palma De Mallorca, Spain), M. García-Gasalla, M. Arrizabalaga Asenjo, L. Ventayol-Aguiló, M. Perez-Seco, M. Gallegos Alvarez, A. Payeras*

6186 **The risk of microbial contamination associated with nine different needle-free connectors**
Q. Shi (Shanghai, China), Y. Cui, W. Sun, Y. Shen, X. Chen, J. Lin, B. Hu, X. Gao*

6635 **An outbreak of *Ralstonia pickettii* bloodstream infection among paediatric leukaemia patients**
T. Bedir Demirdag, A. Parlakay, F. Bayrakdar, B. Gulhan, S. Kanik, S. Süzük, I. Mumcuoglu (Ankara, Turkey), B. Dinc, N. Yarali*

8018 **Catheter-associated urinary tract infections in patients hospitalised in intensive care unit**
M. Hamidi (Algiers, Algeria), H. Belekhal, S. Yahi, D. Bougdal, S. Sadat, K. Guenane, M. Denia*

8369 **Serum Galectin-3 status in hospitalised patients with catheter-associated asymptomatic bacteriuria**
S. Iftimie, A. Hernández-Aguilera, L. Ana Felisa, I. Pujol, F. Ballester, A. Castro, J. Camps (Reus, Spain)*

9314 **Successful reduction of urinary catheter days and inadequate catheterisation after introduction of a prevention bundle**
M. Cipriani (St. Gallen, Switzerland), M. Schlegel, M. Schwark-Bähler, P. Kohler, W. Albrich*

Session accepted as Mini-oral ePoster Session

IVC infections: where we stand

831 **Correlation of central line-associated bloodstream infections with employee turnover: continuity in nursing staff matters!**
S. Kuster, M. Dunic, C. Falk, H. Sax, P. Schreiber (Zurich, Switzerland)*

2809 **Nation-wide survey of catheter-related bloodstream infections in medical, surgical and intensive care settings, 2019**
M. Decalonne, F. Goube, R. Gimenes, A. Petiteau, A. Berger-Carbonne, S. Le Vu, N. Van Der Mee-Marquet (Tours, France)*

2985 **Short-term peripheral venous catheter-related bloodstream infections in French healthcare settings, 2019**
M. Decalonne, R. Gimenes, F. Goube, A. Petiteau, A. Berger-Carbonne, S. Le Vu, N. Van Der Mee-Marquet (Tours, France)*

3378 **Local signs at insertion site and prediction of catheter-related infections in short-term central venous and arterial catheters in the intensive care unit: individual findings from four multi-centre randomised controlled trials**
N. Buetti (Paris, France), S. Ruckly, J. Lucet, L. Bouadma, M. Garrouste-Orgeas, C. Schwebel, O. Mimoz, B. Souweine, J. Timsit*

4285 **Surveillance of central venous catheter bloodstream infections in critical care units in England: April 2017-March 2019**
S. Gerver (London, United Kingdom), A. Zaidi, P. Wilson, R. Hope*

5984 **Impact of the Spanish Bacteraemia Zero project on central line-associated bloodstream infection rates**
S. Carvalho Brugger (Lleida, Spain), M. Vallverdú, M. Miralbés, B. Balsera, S. Rodriguez, S. Iglesias, J. Caballero*

6797 **Indwelling time of peripherally inserted central catheters and incidence of bloodstream infections in haematology patients: a cohort study**
N. De Jonge (Amsterdam, Netherlands), M. Caris, H. Punt, D. Salet, B. Lissenberg-Witte, S. Zweegman, C. Vandenbroucke-Grauls, M. Van Agtmael, J. Janssen*

7969 **Impact of different components of a national intervention on CLABSI rates**
D. Ben-David (Tel Aviv, Israel), A. Vaturi, E. Solter, E. Temkin, Y. Carmeli, M. Schwaber*

8576 **Comparing ethanol lock therapy versus vancomycin lock on a salvation strategy for totally implantable vascular access device infections due to coagulase-negative staphylococci (the ETHALOCK study): a prospective randomised clinical trial**
C. Theis (Clermont-Ferrand, France), M. Vidal, N. Mrozek, D. Martineau, B. Pereira, O. Lesens*

Session accepted as 2-Hour Oral Session

Linking advanced molecular diagnosis with infection control: is that effective?

1526 **Impact of unrestricted movement of carbapenemase-producing *Enterobacteriales* (CPE) carriers on transmission of CPE in nursing homes: a prospective cohort study**
K. Linn (Singapore, Singapore), P. Hon, H. Xiaowei, S. Syed Husen, L. Chan, J. Ng, O. Ng, S. Vasoo, M. Ling, D. Fisher, K. Marimuthu*

3412 **MRSA transmission and hospital-acquired bacteraemia in a neonatal intensive care unit in Greece**
G. Kalogeras, M. Militsopoulou, E. Bouzavoutoglou, A. Doudoulakakis, N. Giormezis (Patras, Greece), A. Nika, A. Papaioannou, M. Tsolia, I. Spiliopoulou, E. Lebessi*

5376 **Endemic extended-spectrum beta-lactamase-producing *Klebsiella pneumoniae* ST48 in a hospital setting and genomic plasticity driven by transposable elements**
M. Nguyen Ngoc (Antwerp, Belgium), F. Maechler, J. Rodriguez Ruiz, B. Xavier, C. Lammens, H. Goossens, P. Gastmeier, S. Malhotra-Kumar*

5935 **Clinical implementation of routine whole genome sequencing for hospital infection control of multidrug-resistant pathogens**
P. Harris (Herston, Australia), B. Forde, A. Jennison, K. Hajkowicz, G. Playford, J. Clark, S. Beatson, D. Paterson*

6179 **Population structure of extended spectrum beta-lactamase-producing *Escherichia coli* and *Klebsiella pneumoniae* from anthropogenic environment and food in five European cities**
D. Martak (Besançon, France), J. Dick, T. Verschuuren, N. Conzelmann, S. Bunk, E. Salamanca, A. Meunier, M. Riccio, C. Brossier, I. Autenrieth, S. Harbarth, J. Rodríguez-Baño, E. Tacconelli, A. Fluit, J. Kluytmans, S. Peter, D. Hocquet*

6339 **Whole genome sequencing of bloodstream isolates of *Staphylococcus aureus* reveals prolonged transmission chains within neonatal intensive care units**
C. Goswami, S. Fox, M. Holden, A. Leanord, T. Evans (Glasgow, United Kingdom)*

6380 **Household transmission of ESBL-producing *Escherichia coli* and *Klebsiella pneumoniae* after hospital discharge of an ESBL carrier**
M. Riccio (Geneva, Switzerland), T. Verschuuren, N. Conzelmann, S. Bunk, D. Martak, E. Salamanca, J. Dick, C. Brossier, R. Martischang, G. Renzi, I. Autenrieth, S. Peter, J. Kluytmans, A. Fluit, E. Tacconelli, D. Hocquet, J. Rodríguez-Baño, S. Harbarth*

6724 **Variation in strain types of extended spectrum beta-lactamase-producing *Enterobacteriaceae* in long-term care facilities: a multi-centre, prospective cohort study**
S. Goepel (Tübingen, Germany), S. Bunk, N. Conzelmann, P. Beryl, J. Dick, F. Hölzl, D. Martak, E. Salamanca, T. Verschuuren, J. Kluytmans, D. Hocquet, I. Autenrieth, S. Peter, J. Rodríguez-Baño, E. Tacconelli*

8999 **Modelling pathogen transmission in intensive care units by integrating screening and antibiogram data**
T. Pham (Utrecht, Netherlands), M. Kretzschmar, X. Bertrand, M. Bootsma*

Session accepted as 2-Hour Oral Session

Meeting the challenges of implant infections' diagnosis and management

1160 **Streptococcal and *Staphylococcus aureus* prosthetic joint infections: are they really different?**
Y. Kherabi (Paris, France), V. Zeller, Y. Kerroumi, V. Meyssonnier, B. Heym, O. Lidove, S. Marmor*

3004 **A second surgical debridement for acute periprosthetic joint infections should not be discarded**
M. Wouthuyzen-Bakker (Groningen, Netherlands), C. Löwik, J. Ploegmakers, B. Knobben, B. Dijkstra, A. De Vries, G. Mithoe, G. Kampinga, W. Zijlstra, P. Jutte*

3176 **Retrospective study of nosocomial infections in patients with extracorporeal membrane oxygenation therapy in a coronary unit**
S. Mornese Pinna (Torino, Italy), M. Valerio Minero, I. Sousa Casasnovas, A. Galar Recalde, M. Olmedo Samperio, C. Devesa, A. Alvarez-Uria, M. Machado, M. Martinez-Selles, E. Bouza, F. Fernandez-Aviles, P. Muñoz*

5378 **Epidemiological and clinical characteristics and outcomes of cardiovascular-implantable electronic devices (CIED) infective endocarditis (IE): 40-year single-centre retrospective cohort study (1979-2018)**
M. Hernández-Meneses (Barcelona, Spain), J. Tolosana, J. Llopis, C. Falces, B. Vidal, D. Fuster, E. Quintana, A. Perissinotti, M. Almela, J. Ambrosioni, M. Moreno Camacho, J. Miro*

5656 **Analysis of treatment failures of haematogenous prosthetic joint infections: new infections occur more often than infection persists or relapses**
N. Renz (Berlin, Germany), A. Rakow, C. Perka, A. Trampuz*

7236 **Nasal colonisation with *Staphylococcus aureus* is a risk factor for ventricular assist device infection in the first year after implantation: a single-centre cohort study**
D. Nurjadi (Heidelberg, Germany), K. Last, S. Klein, S. Boutin, B. Schmack, F. Mueller, K. Heeg, A. Ruhparwar, A. Heininger, P. Zanger*

8571 **Tolerance of prolonged oral tedizolid (TDZ) antibiotic therapy for peri-prosthetic joint infections (PJIs): results of a pilot multi-centre French study**
E. Senneville (Tourcoing, France), A. Dinh, T. Ferry, O. Robineau*

8656 **Diagnostic accuracy of synovial cell count at reimplantation in periprosthetic knee infection undergoing two stage procedure**
T. Ascione (Naples, Italy), P. Pagliano, M. Mariconda, A. Baldini, G. Balato*

9537 **Spinal implant-associated infections: results from a four-year prospective cohort study**
D. Margaryan (Berlin, Germany), N. Renz, P. Vajkoczy, A. Trampuz*

Session accepted as Paper Poster Session

Multimodal approaches to reduce AMR transmission

1376 **Nasal colonisation by *Staphylococcus aureus* in nursing home residents in Crete, Greece**
K. Moschou, P. Ioannou (Heraklion, Greece), E. Moraitaki, D. Stafylaki, E. Boutakoglou, V. Koutsouroumpi, S. Maraki, G. Samonis, D. Kofteridis*

1416 **Hospital organisation, management and implementation of culture of excellence in infection control and prevention of hospital-acquired infections at Ziv medical centre, Israel**
J. Tarabeia (Zefat, Israel), S. Edelstein, M. Sudri, H. Ben-Amram, S. Zarka*

2402 **Rethinking the involvement of patients in infection prevention and control and antimicrobial stewardship**
H. Seale (Sydney, Australia)*

3242 **Effective utilisation of limited isolation rooms to provide safe patient care and staff safety in lower/middle-income country**
R. Roshan (Karachi, Pakistan), Z. Rafique*

3697 **An agent-based model to simulate the transmission of glycopeptide-resistant enterococci in hospital according to several control strategies**
S. Deboscker, T. Lavigne (Strasbourg, France), F. Severac, C. Ménard, N. Meyer, J. Gaudart*

4387 **Evaluation in general practice of the patient's feelings about a recent hospitalisation and isolation for a multidrug-resistant infection**
O. Hereng, A. Dinh, S. Bessis, S. Siméon, M. Matt, B. Davido (Garches, France)*

4645 **Presence of multidrug-resistant bacteria on uniforms of healthcare professionals in healthcare settings in Cyprus: implications for targeted infection control interventions**
P. Lena, S. Karageorgos, D. Lamnisos, P. Papageorgis, C. Tsioutis (Nicosia, Cyprus)*

5007 **Nurse density matters in antimicrobial resistance: A 30-country observational modeling study**
H. Kaba, E. Kuhlmann, S. Scheithauer (Göttingen, Germany)*

5223 **Interest of a systematic surgical mask wearing policy to decrease nosocomial flu burden at hospital**
V. Forget, S. Gros, E. Barneoud-Rousset, M. Demange, M. Ravry, A. Fourneret-Vivier, M. Poggio, L. Combrie, J. Grosjean, A. Pellicier, C. Dumollard, A. Wielandts, I. Guinot, E. Forestier (Chambéry, France)*, *F. Mallaval*

6507 **Omitting the nightly dose of selective digestive tract decontamination provides equally effective decontamination of potential pathogenic bacteria: a cost reducing and sleep-promoting intervention**
J. De La Court (Amsterdam, Netherlands)*, *T. Groot, K. Sigaloff, H. Van Der Spoel, R. Schade*

8016 **Predict to prevent: system dynamic modeling for healthcare-associated influenza**
M. Sansone (Gothenburg, Sweden)*, *L. Andersson, J. Westin, R. Norden*

9205 **Relevance of intra-hospital patient movements for the spread of healthcare-associated infections: a mathematical modelling study**
H. Tahir (Utrecht, Netherlands)*, *L. Lopez-Cortes, A. Kola, D. Yahav, A. Karch, H. Xia, J. Horn, K. Sakowski, M. Piotrowska, L. Leibovici, R. Mikolajczyk, M. Kretzschmar*

9260 **The dissemination and reservoirs of ESBL-producing *Escherichia coli* in intensive care unit**
L. Baomo (Guangzhou, China)*, *C. Zhuo, Y. Guo*

9364 **Patient perceptions of antimicrobial resistance: are we getting the right messages across?**
J. Doukrou Calsina, T. Planche, C. Suarez (London, United Kingdom)*

Session accepted as Paper Poster Session

Outbreaks' epidemiology and management

508 **Investigation of an *Enterobacter cloacae* OXA-436 carbapenemase outbreak: when everything goes down the drain**
A. Holm (Odense, Denmark)*, *A. Toft, M. Nordestgaard, A. Hammerum, H. Hasman, M. Kemp, U. Justesen*

2616 **Challenges in investigation and control of invasive group A *Streptococcus* outbreaks associated with community health services delivered at home**
L. Nabarro (London, United Kingdom)*, *C. Brown, D. Ready, R. Mearkle, E. Robinson, S. Balasegaram, V. Decraene, J. Elston, A. Popay, P. Hoffman, B. Patel, P. Harrington, S. Hopkins, T. Lamagni*

3336 **Outbreak of an uncommon rifampicin-resistant *bla*NDM-1 *Citrobacter amalonaticus* strain in a digestive rehabilitation centre: the putative role of rifaximin**
G. Royer (Créteil, France)*, *F. Fourreau, C. Gomart, A. Maurand, B. Hacquin, D. Ducellier, F. Cizeau, S. Lo, C. Cordonnier Jourdin, M. Darty, J. Decousser*

4233 **Adenovirus-associated epidemic keratoconjunctivitis outbreak in a tertiary hospital**
E. Miró (Barcelona, Spain)*, *M. Del Cuerpo, C. Berengua, P. Marin, J. Vela, V. Pomar, N. Rabella*

4472 **Epidemiology of nosocomial highly resistant microorganism outbreaks in the Netherlands**
A. Reuland (Utrecht, Netherlands)*, *A. Schoffelen, P. Bijkerk, P. Bergervoet, S. De Greeff, C. Vandenbroucke-Grauls*

5154 **Investigating a cluster of community-acquired methicillin-resistant *Staphylococcus aureus* infections in a school in Eastern Switzerland**
F. Waldeck (St. Gallen, Switzerland)*, *N. Oliver, S. Manser, D. Reinholz, A. Walt, M. Schlegel, S. Seiffert, C. Kahlert*

5603 **A leak in compliance with ventilation system maintenance instructions resulted in an aspergillosis outbreak**
G. Dizman, G. Metan (Ankara, Turkey)*, *D. Gülmez, Z. Bastug, Ö. Dizdar, S. Arikan-Akdagli, S. Unal*

6034 **Partnering with bedside nurses: questionnaire-based approach during an outbreak of carbapenem-resistant *Acinetobacter baumannii* in two separate intensive care units**
S. Kim, H. Seo, S. Oh, Y. Seo, B. Lee, B. Eun, J. Chae, K. Lee, T. Kim (Ulsan, South Korea)*

6212 **Outbreaks of multidrug-resistant *Klebsiella pneumoniae* in neonatal intensive care units in Ghana: a case for improved surveillance and infection control**
A. Labi (Accra, Ghana)*, *K. Nielsen, R. Marvig, S. Bjerrum, C. Enweronu-Laryea, M. Newman, P. Ayibor, L. Percival Andersen, J. Kurtzhals*

6717 **Identifying nosocomial transmission of influenza and associated deaths: a prospective, observational study**
L. Snell (London, United Kingdom)*, *J. Vink, H. Mitchell, C. Beviz, M. Kabia, J. Edgeworth, G. Nebbia*

7208 **Long-lasting outbreak of *Serratia marcescens* in a veterinary hospital due to contaminated chlorhexidine**
N. Keck, A. Dunié-Mérigot, M. Dazas, E. Hirchaud, S. Laurence, B. Gervais, J. Madec, M. Haenni (Lyon, France)*

7451 **Prospective surveillance of multidrug-resistant Gram-negative bacteria in a UK intensive care unit using whole genome sequencing**
H. Wilson (Cambridge, United Kingdom)*, *F. Khokhar, B. Warne, R. Carpenter, J. Bryan, P. Polgarova, N. Brown, D. Enoch, C. Summers, G. Dougan, J. Parkhill, E. Torok*

8566 **Hospital outbreak of carbapenem-resistant *Enterobacteriaciae* associated with an OXA-48 plasmid hosted mainly by *Escherichia coli* ST399**
A. Ledda, R. Manuel (London, United Kingdom)*, *H. Ciesielczuk, H. Dolphin, D. Barry, J. Summerville, D. Wareham, B. Cherian, J. Paul, C. Rosmarin, M. Cummins*

Session accepted as Paper Poster Session

Prevention and management of post-surgical infection

1096 **Antimicrobial prophylaxis administration after umbilical cord clamping in caesarean section does not increase risk for surgical site infection: a prospective analytic study with 55,901 patients**
R. Sommerstein (Bern, Switzerland), J. Marschall, A. Atkinson, D. Surbek, M. Dominguez, N. Troillet, A. Widmer*

1251 **Implementation of appropriate antibiotic prophylaxis in surgery: high benefit with no risk**
B. Madran (Istanbul, Turkey), Z. Akbulut, S. Tanju, Ş. Keske, S. Erus, M. Kapdağlı, S. Pala, Ş. Dilege, Ö. Ergönül*

1773 **Multiple evaluation of surgical antimicrobial prophylaxis in Japanese university hospitals**
H. Morioka (Nagoya, Japan), H. Ohge, M. Nagao, H. Kato, R. Kokado, K. Yamada, T. Yamada, N. Shimono, Y. Nukui, S. Yoshihara, I. Sakamaki, K. Nosaka, Y. Kubo, H. Kawamura, Y. Fujikura, T. Kitaura, M. Sunakawa, T. Yagi*

2068 **Effects of a strict postoperative glycaemic control on surgical site infection's incidence following liver transplantation: a randomised clinical trial**
R. Oliveira (São Paulo, Brazil), J. Mancero, J. Tanner, V. Brito Poveda*

2564 **Single dose cefazolin is feasible in orthopaedics: behavioural change success with collaborative working**
F. Erdinç, N. Tülek (Ankara, Turkey), B. Alemdaroğlu, S. Iltar, G. Ertem, S. Kinikli, Ç. Ataman Hatipoğlu*

2768 **Efficacy of fosfomycin-trometamol versus fluoroquinolone single-dose as prophylaxis for trans-rectal ultrasound-guided prostate biopsy**
T. Delory (Paris, France), A. Goujon, A. Masson-Lecomte, P. Arias, E. Mayet, T. Sophie, B. Bercot, J. Molina, P. Mongiat-Artus, M. Lafaurie*

2841 **Bacterial contamination of collagen membranes in dental surgery**
A. Rachkov (Minsk, Belarus), T. Shevela*

2850 **Improvement of infection rates and hand hygiene adherence in pre-post comparison after introduction of an infection-prevention-measures-bundle implemented by an infection prevention link physician**
M. Neuwirth (Cologne, Germany), F. Mattner, R. Galante, I. Dombrowski, R. Otchwemah*

3168 **Impact of beta-lactam allergy label on preoperative antibiotic prophylaxis**
C. Nguyen (Chicago, United States), K. Petrucci, E. Daily, A. Brown, J. Pisano, N. Pettit*

3714 **Current practices and evaluation of barriers and facilitators to surgical site infection prevention measures in Jimma, Ethiopia**
A. Lang (Rochester, United States), L. Berman, B. Gelana, D. Yilma, D. Siraj, D. Shirley*

4029 **Social and physical opportunities to improve surgical antimicrobial prophylaxis prescribing: utilisation of the behaviour change wheel**
C. Ierano, A. Rajkhowa, K. Thursky (Melbourne, Australia), C. Marshall, T. Peel, D. Ayton*

4444 **Epidemiology of cardiac surgical site infection in England, 2018/19**
T. Lamagni (London, United Kingdom), K. Cooper, C. Wloch, P. Harrington*

4549 **Assessing the impact of interventions designed to reduce the rate of postoperative sternal wound infection at a tertiary cardiothoracic centre**
T. Locke (Sheffield, United Kingdom), H. Parsons, N. Briffa, T. De Silva, T. Darton*

5166 **Prophylactic antibiotics administration in low- and middle-income countries: what are the consequences on antibiotic resistance? A systematic review**
L. Rambliere (Paris, France), D. Guillemot, E. Delarocque-Astagneau, H. Bich-Tram*

5350 **Successful introduction of a bundle of measures to reduce surgical site infection by *Staphylococcus aureus* in patients undergoing coronary artery bypass grafting**
E. Evangelista De Souza, L. Gordilho Mutti Carvalho, D. Feriani, A. Santos Ibanes, V. Barros Barbosa, E. Vasconcelos, C. Abboud (Sao Paulo, Brazil)*

6244 **A systems thinking methodology for evaluating interventions to optimise antibiotic use along the surgical pathway and minimise AMR**
F. Edathadathil (Kochi, India), M. Lebcir*

6418 **Efficacy of a carbapenem-sparing regimen for treating post-surgical intra-abdominal infections: a case-control study**
F. Giovannenze (Rome, Italy), E. Taddei, R. Murri, L. Cerolini, E. Birocchi, F. Taccari, R. Cauda, M. Fantoni*

7474 **Mediastinitis: an incidence study and case series in an elderly adult centre**
J. Alonso Torres (Buenos Aires, Argentina), F. Mesplet, N. Diaz, L. Zubeldía Brenner, G. Vinicoff, M. Aguirre, M. Ezcurra, M. Ruiz, S. Arriola, M. Viteri, L. Cusmano, C. Valdiviezo, E. Schimank, A. Terusi*

7661 **Prospective evaluation of bacteraemia rates and infectious complications among patients undergoing endoscopic retrograde cholangiopancreatography**
Ş. Altun Demircan, N. Tulek (Ankara, Turkey), S. Kinikli, E. Yuksekkaya, F. Erdinç, G. Ertem, Ç. Ataman Hatipoğlu, M. Kekilli*

8746 **Risk factor for nosocomial and surgical site infection after cardiac surgery**
M. Pérez-Rodríguez (Vigo, Spain), B. Vilas, A. Sousa, J. Lugo, M. Pereira, O. Lima, A. Nodar, R. Longueira, V. Del Campo, J. Legarra, M. Crespo*

8797 **Early onset post-sternotomy mediastinitis (PSM): a diagnostic challenge (1998-2018)**
F. Nacinovich (Buenos Aires, Argentina), P. Fernandez Oses, N. Spinelli, M. Viruel, F. Piccinini, M. Camporrotondo*

8872 **Airborne antibiotic-resistant *Staphylococcus epidermidis* in inpatient wards linked to deep surgical site infections**
A. Johansson (Umeå, Sweden), M. Widerstrom, T. Monsen, A. Larsen, M. Stegger*

9194 **Validation of a semi-automated surveillance of surgical site infections: improving exhaustiveness, representativeness and efficiency**
R. Malheiro (Porto, Portugal), N. Rocha Pereira, R. Duro, C. Pereira, C. Alves, S. Correia*

9337 **Surgical site infections in orthopaedic surgery: a retrospective analysis of the risks associated with multi-drug resistant bacteria isolation**
M. De Masi (Rome, Italy), L. Campogiani, E. Teti, V. Malagnino, L. Ferrari, N. Cesta, A. Di Marcantonio, P. Farsetti, U. Tarantino, M. Andreoni, L. Sarmati*

9563 **Antimicrobial stewardship and perioperative antimicrobial prophylaxis: results of an educational intervention**
F. Segala (Rome, Italy), R. Murri, E. Taddei, F. Giovannenze, P. Del Vecchio, E. Birocchi, F. Taccari, R. Cauda, M. Fantoni*

Session accepted as Mini-oral ePoster Session

Remaining vigilant and applying new tools for infection surveillance

2387 **Built environment microbiological surveillance in a large intensive care unit revealed abiotic reservoirs of highly persistent clones of *Klebsiella* species (*K. pneumoniae, K. oxytoca, K. variicola*)**
S. Aracil-Gisbert (Madrid, Spain), N. Guerra-Pinto, A. Ortiz-Fernández, V. Fernandez Lanza, C. Soriano, M. Fernandez-De-Bobadilla, Â. Novais, V. Quinteros-Fiel, S. Gallego-Zarzosa, M. López-Olivencia, L. Vieira Peixe, R. Canton Moreno, R. De Pablo, F. Baquero, T. Coque*

3546 **Automated surveillance of urinary tract infections in a tertiary care hospital in Stockholm**
S. Van Der Werff (Stockholm, Sweden), E. Thiman, H. Tanushi, J. Karlsson Valik, A. Henriksson, M. Alam, H. Dalianis, A. Ternhag, P. Naucler*

3868 **Intestinal colonisation by carbapenemase-producing *Enterobacteriaceae* detected by polymerase chain reaction in patients with negative cultures: do they really have an increased risk of infection?**
A. Rearte (Buenos Aires, Argentina), F. Herrera, J. Nievas, D. Sanchez Thomas, R. Rojas, F. Nicola, M. Relloso, J. Smayevsky, E. Temporiti, F. Gauna, W. Alcalá, A. Oviedo, F. Bues, S. Zerboni, P. Bonvehi*

4038 **Minimizing pseudo-cluster suggestions in infection control surveillance using pathogen DNA sequencing and artificial intelligence**
D. Chen, Md, R. Sussner, Bsn, Rn, Cic, M. Quinn, Bsn, Rn, Cic, G. Wang, M. Chanza, Ba, W. Huang, C. Scurlock, Md, Mba, C. Becker, Md, Phd, J. Fallon, Md, Phd, K. Hansen, Phd, Ms, D. Holler, Bs, Emt, J. Ashworth, Mscs, Mt(Ascp), M. Fortunato-Habib, Dnp, Ms, Bs, Rn, J. Carmona, B. Gross (Cambridge, United States)*

4091 **Shared hospital epidemiology of respiratory viruses: a 3-year analysis using multiplex PCR in a university hospital**
A. Valdes, B. Visseaux (Paris, France), D. Bouzid, N. Fidouh, D. Descamps, D. Van-Gysel, F. Lenne, V. Goldstein, J. Lucet*

5969 **The epidome: a species-specific approach to quantify population dynamics and heterogenicity of *Staphylococcus epidermidis* colonisation and infection in primary samples**
A. Rendboe, T. Johannesen, E. Månsson, S. Iversen, S. Baig, J. Jensen, B. Söderquist, P. Andersen, M. Stegger (Copenhagen, Denmark)*

8052 **Active surveillance mitigates the risk of donor-derived infections in solid organ transplant recipient: the role of infection control**
M. Campanella (Palermo, Italy), A. Medaglia, E. Conoscenti, S. Caruso, G. Panarello, V. Lamonaca, F. Barbera, F. Monaco, A. Pasquariello, F. Cardinale, D. Di Carlo, P. Conaldi, P. Grossi, A. Mularoni*

8253 **Performance of a computerised decision support system for the semi-automated detection of healthcare associated infections: an explorative pilot study**
A. Ranzani (Milano, Italy), G. Catho, A. Metsini, W. Zingg, B. Huttner*

Session accepted as Paper Poster Session

Studies on AMR risk factors

248 **Stay in the emergency department increases the risk of colonisation by carbapenem-resistant *Enterobacteriaceae* in the intensive care unit**
M. Salomão, M. Freire (Sao Paulo, Brazil), I. Boszczowski, S. Raymundo, A. Guedes, A. Shafferman Levin*

2449 **Risk factors for healthcare-associated infections caused by cefepime resistant *Pseudomonas aeruginosa* in a tertiary care hospital in Serbia**
I. Petrovic (Kragujevac, Serbia), Z. Djordjevic, M. Folic, S. Jankovic*

3993 **Predictors of vancomycin-resistant enterococci gut microbiome colonisation among patients with *Clostridioides difficile* infection 6.4.1**
E. Zasowski (Vallejo, United States), M. Ali, A. Anugo, K. Dotson, B. Endres, K. Garey*

4226 **Risk factors for colonisation with carbapenemase-resistant *Acinetobacter baumanii* in hospital**
M. Meschiari (Modena, Italy), K. Shaniko, S. Selmi, M. Sarti, G. Orlando, M. Menozzi, C. Mussini*

4335 **Risk factors associated with carbapenemase-producing *Enterobacteriaceae* infection**
L. Corbella Vazquez (Madrid, Spain), M. Fernandez Ruiz, M. Ruiz-Ruigómez, J. Sequeira, I. Rodriguez Goncer, M. Hernandez Jimenez, F. Lopez-Medrano, J. Villa, J. Aguado Garcia, R. San Juan Garrido*

4632 **Epidemiology and dissemination of multidrug-resistant *Pseudomonas aeruginosa* colonisation in an intensive care unit**
M. Portillo (Pamplona, Spain), J. Lobo, A. Bacaicoa, J. Oteo, A. Navascués Ortega, C. Ezpeleta Baquedano*

4867 **Stigma in MDRO carriers exposed to isolation precautions: an exploratory quantitative questionnaire study**
R. Wijnakker (Leiden, Netherlands), M. Lambregts, B. Rump, K. Veldkamp, R. Reis, L. Visser, M. De Boer*

5806 **Gastrointestinal colonisation by vancomycin-resistant enterococci and carbapenem-resistant Gram-negative bacteria in an endemic setting: prevalence, risk factors, and outcomes**
A. Vasilakopoulou, P. Karakosta, S. Vourli, A. Tarpatzi, A. Papadomanolaki, P. Varda, M. Kostoula, A. Antoniadou, S. Pournaras (Athens, Greece)*

6043 **Hospital related factors associated with multidrug-resistant organism acquisition: a multilevel case control study**
N. Nasir (Karachi, Pakistan), S. Khan, S. Rozi, N. Baig-Ansari, N. Khan, N. Rehmani, R. Roshan, B. Jamil, F. Mahmood*

6301 **The impact of medical drugs on the acquisition of ESBL-producing *Enterobacterales:* a matched case-control study**
P. Klauke (Berlin, Germany), F. Schwab, P. Gastmeier, F. Maechler*

7560 **Gut colonisation with carbapenemase-producing *Enterobacterales:* predicting factors for prolonged colonisation among adults**
L. Dortet, L. Escaut, G. Cuzon, I. Bukreyeva, N. Fortineau, T. Naas (Le Kremlin Bicêtre, France)*

7787 **Invasive *Acinetobacter baumannii* infections in paediatric infectious disease intensive care unit**
L. Stemberger Maric (Zagreb, Croatia), N. Krajcar, N. Papic, I. Butic, G. Tesovic*

8497 **Identifying drivers of acquisition of extended-spectrum beta-lactamase producing *Enterobacterales* in Malawi using whole genome sequencing and mathematical modelling**
J. Lewis (Liverpool, United Kingdom), M. Mphasa, R. Banda, E. Smith, C. Jewell, B. Faragher, N. Thomson, N. Feasey*

8939 **Risk factors for mortality in bloodstream infections in cancer patients**
A. Ulu, S. Komur, F. Kuscu, A. Inal (Adana, Turkey), B. Kurtaran, Y. Tasova*

Session accepted as Mini-oral ePoster Session

Understanding risk factors for HAI to tailor infection control

592 **Identification of individual risk factors for acquisition of vancomycin-resistant *Enteroccocus faecium* (VRE) during an outbreak in an university hospital and implication in prevention strategies**
T. Abrassart (Mons, Belgium), H. Strale, D. Martiny, B. Byl*

935 **Is there an increased risk for *Clostridium difficile* infection months after hospitalisation in a room occupied previously by a patient with *C. difficile*?**
H. Zayyad (Yafia, Israel), A. Peretz, S. Cohn, K. Labay*

1216 **What is the role of colonisation by carbapenem-resistant *Enterobacteriaceae* in older people who live in nursing homes? A multi-centre study**
P. Favier (Buenos Aires, Argentina), N. Carrión, R. Martins, E. Serio, M. Gallino, D. Torres, C. Raffo*

1855 **Colonisation and infection with ESBL-producing and carbapenem-resistant *Enterobacteriaceae* in kidney transplant recipients: risk factors, impact on renal graft function and use of hospital resources**
E. Salsi, A. Palmisano, D. Simonetti (Parma, Italy), M. Cotrufo, P. Fenaroli, U. Maggiore, E. Fiaccadori, C. Ferrari, A. Degli Antoni*

2335 **Antibiotic exposure and the risk of CRE acquisition**
N. Hassoun Kheir (Haifa, Israel), K. Hussein, M. Saffuri, S. Badaan, S. Peleg, Y. Geffen, M. Paul*

4762 **Relationship between local-area socioeconomic status and rates of bloodstream infection and *Clostridioides difficile* infection**
S. Thelwall (London, United Kingdom), R. Hope, S. Hopkins*

6032 **Gram-negative screening the neonatal unit: can we predict bloodstream infections?**
V. Price (Birmingham, United Kingdom), J. Swindells*

6267 **Risk factors for colonisation with multiple species of extended-spectrum beta-lactamase producing *Enterobacteriales*: a case-case-control study**
I. Vock (Basel, Switzerland), L. Aguilar Bultet, A. Egli, P. Tamma, S. Tschudin-Sutter*

6420 **Infections in patients colonised with extended-spectrum beta-lactamase-producing *Enterobacteriales*: a retrospective cohort study**
I. Vock (Basel, Switzerland), L. Aguilar Bultet, A. Egli, P. Tamma, S. Tschudin-Sutter*

Session accepted as Paper Poster Session

Update on *Clostridioides difficile* infection

288 **Patient transfers as a risk factor for *Clostridioides difficile* infection: a case-control study**
J. Edman-Wallér (Gothenburg, Sweden), S. Suominen, M. Werner*

602 **Faecal microbiota transplantation in the treatment of *Clostridioides difficile* infection**
R. Stebel (Brno, Czech Republic), L. Vojtilova, R. Svačinka, P. Husa*

1503 **Efficacy of pulsed xenon ultraviolet disinfection of multidrug-resistant bacteria and *Clostridioides difficile* spores**
H. Kitagawa (Hiroshima, Japan), K. Tadera, T. Hara, S. Kashiyama, H. Ohge*

1662 **Approaches to identify new onset diarrhoea among hospitalised patients and the frequency of stool sample collection for *Clostridioides difficile* infection: a pilot for the CLOUD Louisville study**
S. Furmanek, S. Pena-Oliva, R. Carrico, E. Gonzalez, K. Ford (Collegeville, United States), S. Gray, J. Ramirez*

1851 **An ultrasensitive test for the detection of *Clostridiodes difficile* toxins in stool samples using a single-molecule counting method**
D. Straus (Chelmsford, United States), A. Zuniga, A. Garces, A. Tempesta, A. Williams, B. Lauzier, J. Hickey, S. Gite, S. Clancy, Y. Rosario, J. Bowers*

2128 **Incidence and economic burden of *Clostridioides difficile* infections in inpatient settings of the German health care system: preliminary results of the IBIS study**
Y. Khodamoradi (Frankfurt, Germany), R. Cruz Aguilar, T. Schmidt-Wilcke, E. Schalk, S. Schmiedel, I. Wieters, C. Lübbert, A. Stallmach, W. Holtmeier, S. Graefe, A. Ullah, M. Vehreschild*

2279 **Evaluation of faecal calprotectin as a predictor of severity and relapse in *Clostridioides difficile* infection**
J. Origüen Sabater (Madrid, Spain), M. Agreda, M. Fernandez Ruiz, L. Corbella Vazquez, P. Parra, J. Villa, M. Orellana Miguel, T. Ruiz Merlo, M. Ruiz-Ruigómez, I. Rodriguez Goncer, F. Lopez-Medrano, R. San Juan Garrido, M. Lizasoaín, J. Aguado Garcia*

2624 ***Clostridioides difficile* burden of disease in adults: early experiences of a prospective population-based surveillance study of hospitalised CDI cases in the inpatient module of the City of Louisville Diarrhoea (CLOUD) study**
S. Pena-Oliva, S. Furmanek, R. Carrico, J. Zamparo, E. Gonzalez (Collegeville, United States), J. Ramirez*

2829 **Factors associated with the recurrence of *Clostridiodes difficile* infection in a university hospital**
J. Rodriguez Prida, S. Santos Seoane, M. Izquierdo, P. De La Iglesia, A. Perez-Garcia, C. Helguera, C. Menendez, A. Garcia, J. Boga, J. Moris, A. Rodriguez-Guardado (Oviedo, Spain)*

3115 **Impact of a dedicated *Clostridiodes difficile* infection isolation ward on clinical outcomes**
M. Varadarajan (Orpington, United Kingdom), G. Barlow*

3490 **Heterogeneity of *Clostridiodes difficile* infection testing and the impact on missed diagnoses: results from COMBACTE-CDI**
V. Viprey, D. Ewin, W. Spittal, J. Vernon, A. Benson, G. Davis, M. Wilcox, K. Davies (Leeds, United Kingdom)*

3529 **Healthcare resource utilisation for treatment of *Clostridioides difficile* infection across 12 European countries: health economic results of COMBACTE-CDI**
S. Wingen-Heimann (Cologne, Germany), L. Lurienne, K. Davies, A. Benson, G. Davis, V. Viprey, M. Wilcox, M. Bonten, O. Cornely, J. Vehreschild*

3676 **Effectiveness and safety of utilising oral vancomycin as prophylaxis for *Clostroidioides difficile* infections in high-risk patients**
A. Casapao (Jacksonville, United States), L. Nilles, C. Sothoron, C. Tucker, A. Pirasteh*

3744 **Key differences between community and in-patient *Clostridium difficile* infection: results from COMBACTE-CDI case-control study**
K. Davies (Leeds, United Kingdom), V. Viprey, D. Ewin, W. Spittal, J. Vernon, A. Benson, G. Davis, M. Wilcox*

3942 ***Clostridiodes difficile* ribotypes 001 and 176 with reduced susceptibility to moxifloxacin are the main cause of healthcare-associated *C. difficile* infections in Slovakia**
A. Plankaova, A. Šoltésová, J. Skálová, P. Drevinek, V. Čapek, M. Krutova (Prague, Czech Republic)*

4059 **Antimicrobial use correlates with *Clostridioides difficile* incidence across the departments of an academic centre**
N. Wassilew (Bern, Switzerland), A. Zehnder, A. Atkinson, A. Kronenberg, J. Marschall*

4280 **Characterisation and comparison of farm animal and human *Clostridioides difficile* isolates in Italy**
P. Spigaglia (Rome, Italy), F. Barbanti, M. Vescovi, R. Ceruti, C. Gaspano, S. Faccini, M. Merenda, C. Rosignoli*

4282 **Real-life experience with bezlotoxumab for the prevention of recurrent *Clostridioides difficile* infection**
J. Cobo Reinoso, R. Escudero Sánchez (Madrid, Spain), M. Ruiz-Ruigómez, J. Fernandez Fradejas, Á. Cano Yuste, A. Valencia Alijo, B. Díaz-Pollán, M. Muñóz Burgos, E. Merino De Lucas, O. Martín Segarra, C. Sáez, C. Armiñanzas Castillo, D. Rodríguez-Pardo, J. De La Torre Cisneros, F. Lopez-Medrano*

4453 **An outbreak of *Clostridioides difficile* infections due to a 027-like PCR ribotype 181**
M. Kachrimanidou (Thessaloniki, Greece), A. Baktash, D. Dimoglou, F. Netsika, O. Tsachouridou, D. Papadopoulou, E. Protonotariou, L. Skoura, M. Symeon, E. Kuijper*

4859 **Current diagnosis, management and control strategies for *Clostridioides difficile* infection in Europe**
M. Cataldo (Rome, Italy), G. Granata, N. Petrosillo, K. Davies*

4861 **Faecal microbiota transplantation via lyophilised capsules in primary episodes of *Clostridioides difficile* infection: preliminary results from a randomised clinical trial (EudraCT 2017-003147-38)**
E. Bouza (Madrid, Spain), M. Olmedo Samperio, M. Kestler Hernandez, S. Vazquez Cuesta, S. Rodriguez-Fernandez, L. Villar Gomara, L. Alcalá, M. Marín, P. Muñoz, E. Reigadas Ramirez*

5182 **Impact of immunosuppression on *Clostridioides difficile* infection**
E. Kampouri (Lausanne, Switzerland), M. Papadimitriou Olivgeris, T. Galperine, E. Chavan, A. Croxatto, B. Guery*

5313 **Predicted risk and observed occurrence of *Clostridioides difficile* infection in patients with community-acquired bacterial pneumonia treated with omadacycline or moxifloxacin**
M. Rodriguez (San Antonio, United States), K. Wright, B. Noble*

5461 **Epidemiology and outcomes of *Clostridioides difficile* infections among allogeneic haematopoietic cell transplant recipients in Switzerland: 2009-2019**
S. Ragozzino, S. Tschudin-Sutter, J. Passweg, N. Mueller, A. Müller, D. Neofytos, C. Van Delden, S. Masouridi Levrat, Y. Chalandon, N. Khanna (Basel, Switzerland)*

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5567 **Outcome of *Clostridioides difficile* infection in patients that are PCR positive: comparison of toxin positive with toxin negative cases**
C. Johnston (Swansea, United Kingdom), B. Carter, S. Weinberg, A. Holborow, A. Bone, I. Blyth, J. Walters, M. Perry, T. Morris, H. Hughes, J. Hargreaves, C. Richards, J. Harris, B. Healy*

5615 **European and national *Clostridioides difficile* infection surveillance**
K. Vendrik (Leiden, Netherlands), T. Van Der Kooi, V. Viprey, K. Davies, E. Kuijper*

5689 **Possibilities of implementation of lactobacilli's antagonistic properties for *Clostridiodes difficile* growth supression**
M. Sukhina, A. Safin (Moscow, Russian Federation), A. Zagaynova*

5886 **Risk factors for *Clostridioides difficile* infection among hospitalised patients in Brazilian centres: a multi-centre prospective study**
E. Girão (Fortaleza, Brazil), B. Tavares, C. Costa, D. Viana, G. Maciel, J. Romão, G. Gamarra, C. Rizek, T. Orsi, S. Santos, L. Perdigao Neto, I. Boszczowski, F. Piastrelli, H. Paz Morales, K. Nogueira, A. Maestri, R. Ruedas Martins, G. Brito, S. Figueiredo Costa*

6354 **Faecal microbiota transfer in real-life is more effective for recidivant *Clostiodioides difficile* infection than for highly resistant bacteria decolonisation**
P. Choinier (Paris, France), H. Sadou-Yaye, G. Monsel, E. Haddad, É. Vallet, J. Robert, A. Bellanger, L. Drieux-Rouzet, E. Caumes, N. Kapel, A. Bleibtreu*

6626 **Association between first episode *Clostridioides difficile* infection management and recurrence in a tertiary hospital**
L. Alvarez Paredes, M. Andrés Franch, C. Labayru Echeverría, M. Mantecón (Burgos, Spain), C. Losa Pérez, M. Ortega Lafont, E. Coletta, G. Megias Lobon*

6680 **Changing epidemiology of *Clostridioides difficile* infection in a French university hospital**
N. Khanafer (Lyon, France), L. Oltra, V. Pergay, O. Dauwalder, F. Vandenesch, P. Vanhems*

6695 **Oral vancomycin prophylaxis for primary and secondary prevention of *Clostridioides difficile* infection in patients treated with systemic antibiotic therapy: a systematic review and meta-analysis**
A. Maraolo (Naples, Italy), E. Zappulo, R. Scotto, G. Granata, R. Andini, E. Durante Mangoni, N. Petrosillo, I. Gentile*

6713 **A comparative study to assess the prevalence and risk factors for *Clostridioides difficile* infection in patients with and without inflammatory bowel disease in a tertiary care hospital in northern India**
U. Ghoshal (Lucknow, India), N. Tejan, R. Singh, A. Pandey, U. Ghoshal*

7095 **Is there any association between microbiological variables and toxigenic *Clostridioides difficile* infection (CDI) in a tertiary hospital?**
L. Alvarez Paredes, C. Labayru Echeverría, M. Andrés Franch, M. Mantecón (Burgos, Spain), C. Losa Pérez, M. Ortega Lafont, E. Coletta, G. Megias Lobon*

7112 **Bezlotoxumab in real-life treatment of *Clostridioides difficile* infections in a tertiary centre in Spain**
M. Olmedo Samperio, M. Kestler Hernandez (Madrid, Spain), M. Valerio Minero, M. Machado, A. Alvarez-Uria, B. Padilla, P. Muñoz, E. Bouza*

7116 **Clinical outcomes in oncological patients with *Clostridioides difficile* infection in Catalonia: a cohort study**
E. Calbo Sebastian (Barcelona, Spain), G. Carvalho Rodrigues, N. Sopena, S. Hernández, L. Castella, R. Pérez-Vidal, J. Cuquet, A. Conde, M. Marimón, J. Espinach, M. Andrés-Santamaria, P. Martos, E. Limón*

7495 **Predictors of asymptomatic *Clostridiodes difficile* colonisation on admission: prospective cohort study in a French university hospital**
N. Khanafer (Lyon, France), S. Bennia, G. Martin-Gaujard, L. Juillard, T. Rimmelé, L. Argaud, O. Martin, P. Cassier, F. Vandenesch, P. Vanhems*

7509 **Local and national diagnostic and typing capacity for *Clostridioides difficile* infection, Europe, 2018**
S. Rada, E. Kanitz (Vienna, Austria), D. Schmid, E. Kuijper, C. Suetens, P. Kinross*

7613 **Delafloxacin activity against moxifloxacin-resistant *Clostridioides difficile* clinical isolates**
S. Rodríguez-Pallarés (Cádiz, Spain), F. Galan-Sanchez, J. Arca Suárez, F. Cano, M. Rodriguez-Iglesias*

7667 **Does the new recommendations of treatment for non-severe *Clostridiodes difficile* -associated diarrhoea ensure a better outcome?**
M. Lupse (Cluj-Napoca, Romania), I. Darau, C. Diaconu, K. Komlodi, K. Momani, M. Flonta, N. Todor*

7840 **The association of antibiotics and *Clostridioides difficile* infections in allogeneic stem cell recipients**
C. Jakob (Cologne, Germany), M. Vehreschild, U. Holtick, C. Scheid, A. Walker, N. Jazmati, O. Cornely, J. Vehreschild*

8468 **Faecal lactoferrin is associated with severity at presentation but not relapse risk in *Clostridioides difficile* infection**
J. Origüen Sabater (Madrid, Spain), M. Agreda, M. Fernandez Ruiz, L. Corbella Vazquez, P. Parra, J. Villa, M. Orellana Miguel, M. Ruiz-Ruigómez, T. Ruiz Merlo, I. Rodriguez Goncer, M. Lizasoaín, R. San Juan Garrido, F. Lopez-Medrano, J. Aguado Garcia*

8591 **An intervention bundle to improve compliance with clinical guidelines for *Clostridioides difficile* infection: a quasi-experimental study**
J. Origüen Sabater (Madrid, Spain), M. Agreda, M. Fernandez Ruiz, L. Corbella Vazquez, T. Ruiz Merlo, P. Parra, M. Orellana Miguel, J. Villa, F. Lopez-Medrano, I. Rodriguez Goncer, M. Ruiz-Ruigómez, R. San Juan Garrido, M. Lizasoaín, J. Aguado Garcia*

8726 ***Clostridioides difficile* infection in haematological patients: a 14-year experience**
S. Vazquez Cuesta, A. Estévez Prieto, S. Monsalvo, L. Villar Gomara (Madrid, Spain), L. Alcalá, M. Marín, P. Muñoz, E. Bouza, E. Reigadas Ramirez*

8730 **Epidemic *Clostridioides difficile* isolates are signifcantly more lethal and persist at higher rates than non-epidemic isolates in hamsters following vancomycin treatment**
M. Pulse (Fort Worth, United States), J. Vitucci, W. Weiss, J. Simecka*

8754 **Epidemiology and risk factors for *Clostridioides difficile* at a referral cancer centre in Mexico: a case-control study**
F. Rivera (Tlalpan, Mexico), D. De-La-Rosa-Martinez, E. Rivas-Pichon, B. Garcia-Pineda, P. Cornejo, D. Vilar*

8794 **Prevalence and outcome of *Clostridioides difficile* infection in a multi-centre study in Southern Brazil**
A. Maestri, S. Raboni, H. Paz Morales, L. Ferrari, F. Tuon, A. Losso, C. Marcon, K. Nogueira (Curitiba, Brazil)*

8947 **National reporting of severe *Clostridioides difficile* infections in Germany between 2014 and 2018**
N. Schmidt (Berlin, Germany), A. Reuss, D. Altmann, M. Diercke, T. Eckmanns*

Session accepted as Paper Poster Session

Update on surveillance of Gram-positive bacteria

843 **Impact of coagulase-negative staphylococci positive blood culture occurring in early postoperative cardiac surgery**
M. Thy (Paris, France)*

1078 **Rapid detection of methicillin-resistant *Staphylococcus aureus* in patients with late hospital-acquired/ventilator-associated pneumonia**
L. Bussini (Bologna, Italy), C. Monari, R. Pascale, M. Rinaldi, S. Iannіruberto, E. Rosselli Del Turco, S. Ambretti, M. Giannella, P. Viale*

1285 **Epidemiology typing and molecular analysis of vancomycin-resistant *Enterococcus faecium* in haemato-oncological patients**
M. Bezdíček (Brno, Czech Republic), M. Nykrynova, K. Dufkova, K. Plevová, I. Kocmanová, M. Lengerova*

2291 **Rapid molecular screening for vancomycin-resistant *Enterococcus faecium* (VRE) allows to expedite evaluation of VRE-exposed patients and is cost saving**
A. Büchler (Basel, Switzerland), S. Ragozzino, D. Goldenberger, M. Wicki, A. Egli, A. Widmer*

2324 **Modelling the impact of antibiotic use and infection control agents on the incidence of methicillin-resistant *Staphylococcus aureus* incidence rates in hospital, informed by identifying antibiotic usage thresholds utilising non-linear time series analysis**
S. Gardner (Northern Ireland, United Kingdom), P. Mccarron, G. Conlon-Bingham, D. Farren, M. Scott, K. Burnett*

2547 ***Staphylococcus aureus* intestinal colonisation in patients undergoing bowel preparation for colonoscopy**
J. Gagnaire (Saint-Etienne, France), L. Rinaldi, F. Grattard, A. Carricajo, E. Del Tedesco, N. Williet, J. Rigaill, E. Botelho-Nevers, X. Roblin, P. Verhoeven, P. Berthelot*

3528 **Interpretation of WGS data for surveillance of vancomycin-resistant *Enterococcus faecium* in an endemic setting: challenges and limitations**
V. Eichel (Heidelberg, Germany), S. Klein, U. Frank, K. Heeg, S. Boutin, D. Nurjadi*

3549 **Management of a vancomycin-resistant *Enterococcus faecium* outbreak in the haematology unit of an Italian hospital**
S. Mondino (Vicenza, Italy), V. Manfrin, M. Rassu, R. Cazzaro, M. Ruggeri, G. Cavaliere, A. Diquigiovanni, D. Brodesco, S. Zanovello, M. Zanon, S. Barra*

4241 **Investigation of a vancomycin-resistant enterococci outbreak at a cardiothoracic-surgery department: new insights from next-generation sequencing**
M. Van Den Nest (Vienna, Austria), M. Diab-Elschahawi, G. Dechat, A. Bilc, L. Segagni Lusignani, E. Presterl*

5721 **Molecular epidemiology of methicillin-resistant *Staphylococcus aureus* infections during 7 years in a regional hospital in Israel**
R. Cohen (Netanya, Israel), T. Finn, F. Babushkin, K. Geller, C. Alexander, M. Afraimov, S. Cohen, S. Paikin, E. Anuka, M. Baum, A. Rokney*

5851 **Outcomes of scaling down vancomycin-resistant *Enterococcus* surveillance in a tertiary hospital in Singapore**
I. Low, E. Yeo, H. Chan, R. Sridhar, D. Fisher, N. Bagdasarian (Singapore, Singapore)*

6192 **Uncovering cryptic clusters of Group B streptococcal infant disease in the UK and Ireland through genomic analysis**
S. Collin, N. Groves, C. O'Sullivan, E. Jauneikaite, R. Cunney, M. Meehan, A. Smith, D. Lindsay, R. Campbell, L. Doherty, V. Chalker, P. Lamb, B. Afshar, S. Balasegaram, J. Coelho, D. Ready, C. Brown, K. Le Doare, S. Sriskandan, P. Heath, T. Lamagni (London, United Kingdom)*

7825 **Evaluation of FT-IR spectroscopy in vancomycin-resistant enterococcal nosocomial outbreak investigation**
S. Vandamme (Edegem, Belgium), J. Coppens, S. Van Koeveringe, K. Loens, H. Goossens, V. Matheeussen, H. Jansens*

9355 **Adaptation and validation of a quantitative *vanA/vanB* PCR on a high-throughput PCR system**
A. Both (Hamburg, Germany), L. Berneking, B. Berinson, H. Rohde, M. Lutgehetmann*

9630 **Comparison of the Panther Fusion MRSA assay with conventional culture for patient swabs in Amies transport medium with charcoal**
N. Otten, R. Jansen, D. Kwa, T. Van De Laar (Amsterdam, Netherlands)*

Session accepted as Paper Poster Session

What is new about hand hygiene?

951 **Computerised Tomography (CT) as a risk factor for the acquisition of carbapenem-resistant *Acinetobacter baumannii***
Z. Dadon, E. Ben-Chetrit (Jerusalem, Israel), M. Dahan, O. Benjaminov, P. Levin*

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1204 **A multi-modal intervention to improve hand hygiene compliance in peripheral wards of a tertiary care university centre: a cluster randomised controlled trial**
S. Aghdassi (Berlin, Germany), P. Gastmeier, C. Schröder, M. Behnke, P. Fließ, J. Wenk, C. Plotzki, T. Kramer*

4980 **Location and numbers of handrub dispensers in Swiss hospitals: a representative survey to establish a national minimal standard**
S. Kuster (Basel, Switzerland), J. Roth, M. Dangel, D. Pittet, A. Widmer*

5177 **Compliance to the WHO moment 2 in German hospitals: first evaluation of detailed hand hygiene before aseptic tasks and procedures in national surveillance module HAND KISS**
J. Walter, K. Bunte, C. Schröder, S. Hansen, M. Behnke, P. Gastmeier, T. Kramer (Berlin, Germany)*

5448 **Improvement of self efficacy and problem solving abilities in infection prevention staff, link nurses and physicians. Evaluation of a national workshop tour by the national hand hygiene campaign "AKTION SAUBERE HAENDE" in Germany**
K. Bunte, J. Walter, F. Schwab, A. Gropmann, P. Gastmeier, T. Kramer (Berlin, Germany)*

5939 **An agent-based simulation of hand hygiene and contact precautions for the control of *Clostridioides difficile* in an intensive care unit setting**
M. Rubin (Salt Lake City, United States), M. Leecaster, W. Ray, K. Khader, D. Toth*

7047 **Dispersal of microbes to hospital surfaces following two hand drying methods: paper towels or a jet air dryer**
I. Moura (Leeds, United Kingdom), D. Ewin, M. Wilcox*

7291 **Comparative evaluation of the effectiveness of prophylactic agents based on bacteriophages, liquid soap and skin antiseptics for hand disinfection**
N. Krivonosov (Moscow, Russian Federation), I. Grigoryan, A. Gordeev, A. Melkumyan, P. Tatiana*

7369 **Impact of a multimodal intervention on non-sterile glove use in the intensive care unit**
L. Cadenau (Amsterdam, Netherlands), M. Dekker, R. Van Mansfeld*

7561 **What are the reasons behind high handrub consumption? A national in-depth qualitative assessment**
D. Berthod (Paris, France), A. Perozziello, D. Alvarez, J. Lucet*

8524 **Chlorhexidine resistance of bacterial flora of HCWs' hands: is there any impact related to the routine use for hand hygiene?**
I. Boszczowski, W. Kazumassa, M. Baraldi, A. Luiz Pires Maciel, C. Schmitt, A. Marchi, S. Santos, M. Rufino Zani, N. Soares De Souza, L. Muniz De Souza, S. Figueiredo Costa (São Paulo, Brazil)*

Abstract Programme

9. Experimental Microbiology, Microbial Pathogenesis & Biofilm

- Microbial pathogenesis & virulence
- Host-pathogen interaction
- Preclinical biofilm studies
- Experimental and cellular microbiology
- Other

Session accepted as Paper Poster Session

Antibiofilm strategies

218 **Binding interference between *Bartonella* adhesin A and fibronectin as a novel therapeutic concept to treat bacterial infections**
D. Vaca, A. Thibau, J. Malmström, L. Happonen, V. Kempf (Frankfurt, Germany)*

1571 **Effect of hybrid organo-inorganic sol-gel coating loaded with antifungals on *Candida* strains**
D. Romera, J. Aguilera-Correa, A. Garcia-Casas, B. Toirac, A. Jimenez-Morales, J. Esteban-Moreno (Madrid, Spain)*

1795 **Anidulafungin-loaded hybrid organo-inorganic sol-gel coating can prevent the prosthetic joint infections provoked by *Candida albicans***
H. Garlito-Diaz, B. Toirac, A. Garcia-Casas, A. Jimenez-Morales, J. Esteban-Moreno (Madrid, Spain), J. Aguilera-Correa*

2193 **Proof of concept: efficacy of surgical titanium implants coated with linear gentamicin against osteomyelitis in pigs**
M. Riou (Nouzilly, France), A. Voisin, N. Kasal-Hoc, C. Barc, C. Rossignol, H. Adriaensen, J. Delaval, A. Lainé, S. Mélo, M. Foulc*

2256 **Polyarginine nanocapsules carry and deliver genetic material inside bacteria**
L. Alvarez-Fraga, J. Crecente-Campo, K. Conde (A Coruña, Spain), A. Cés-Martínez, J. Vazquez-Ucha, A. Beceiro, G. Bou Arevalo, M. Alonso, M. Poza Dominguez*

2286 **Destruction of *Staphylococcus aureus* biofilm matrix by innovative combination therapies between antibiotic and non-antibiotic substances**
J. Liu (Toulouse, France), A. Bousquet-Melou, J. Madec, M. Haenni, A. Ferran*

2790 **Evaluation of biofilm formation and removal efficacy of three medical-device detergents by bacterial and yeast species**
K. Park (Songpa-Gu, South Korea), K. Hur, H. Sung, M. Kim*

2880 **Nonsteroidal anti-inflammatory drugs as a promising alternative to antibiotics to combat methicillin-resistant *Staphylococcus aureus* biofilms**
V. Silva (Vila Real, Portugal), J. Pereira, L. Maltez, J. Capelo, G. Igrejas, P. Poeta*

3009 **Activities of eight antifungal agents against *Candida auris* biofilms**
A. Chatzimoschou, J. Meis (Nijmegen, Netherlands), E. Roilides*

3341 **Miconazole/domiphen bromide: a fungicidal combination treatment against biofilms of various azole-sensitive and azole-resistant *Candida* spp.**
J. Tits (Heverlee, Belgium), F. Cools, P. Cos, K. Verbruggen, J. Berman, B. Cammue, K. Thevissen*

3526 **Unravelling the anti-biofilm mechanism of action of an antimicrobial peptide: an atomic force microscopy study**
A. Silva Herdade (Lisbon, Portugal), S. Dias, S. Pinto, A. Coutinho, M. Castanho, A. Veiga*

3896 **Microbial biosurfactants: a new approach for the control of polymicrobial biofilm development on biomedical materials**
C. Ceresa (Novara, Italy), E. Fedeli, F. Tessarolo, D. Maniglio, E. Tambone, M. Rinaldi, I. Banat, M. Diaz De Rienzo, L. Fracchia*

4296 **Rhamnolipid coating reduces formation of *Candida albicans-Staphylococcus aureus* mixed biofilm on titanium implants: an *in vitro* study**
E. Tambone, C. Ceresa, D. Maniglio, F. Piccoli, I. Caola, G. Nollo, P. Ghensi, P. Caciagli, L. Fracchia, F. Tessarolo (Trento, Italy)*

4983 **Vaccinium macrocarpon urine metabolites inhibit *Candida albicans* adhesion and biofilm formation**
E. Ottaviano (Milan, Italy), G. Baron, L. Fumagalli, P. Allegrini, A. Riva, G. Morace, G. Aldini, E. Borghi*

6351 **Polyphasic validation of a nisin-biogel aiming at the control of canine periodontal disease**
E. Cunha (Lisbon, Portugal), F. Bernardino De Freitas, B. São Braz, J. Moreira, L. Tavares, A. Veiga, M. Oliveira*

6643 **Local anti-*Pseudomonas* IgY therapy prevents pyelonephritis in a novel murine experimental *Pseudomonas aeruginosa* urinary tract infection model**
M. Pals Bendixen (Copenhagen, Denmark), F. Schwartz, S. Baekdahl, L. Christophersen, I. Bull Rasmussen, M. Joergensen, C. Johann Lerche, K. Thomsen, N. Høiby, C. Moser*

7925 **Cationic antimicrobial polymers as new anti-biofilm agents**
R. Garcia Maset (Coventry, United Kingdom), F. Harrison, S. Perrier*

8269 **Prevented ciprofloxacin resistance development in *Pseudomonas aeruginosa* by immunomodulatory S100A8/A9 in a murine biofilm wound model**
A. Laulund (Søborg, Denmark), F. Schwartz, L. Christophersen, K. Thomsen, O. Ciofu, H. Trøstrup Pedersen, N. Høiby, C. Moser*

8763 **Human milk oligosaccharides exhibit biofilm inhibition and eradication activity against biofilms formed by yeast isolated from cystic fibrosis patients**
S. Jarzynka (Warsaw, Poland), A. Bialkowska, B. Garczewska, E. Augustynowicz Kopeć, G. Olędzka*

9413 **Adequate exposure time of cold atmospheric pressure plasma on *Staphylococcus aureus* biofilms**
F. Fahmide (Tehran, Iran), P. Ehsani, S. Atyabi*

9534 **Ability of antibiotic-loaded bone cement to prevent bacterial adhesion, biofilm formation and selection of resistance**
A. Bidossi (Milan, Italy), M. Bottagisio, E. De Vecchi*

Session accepted as 1-Hour Oral Session

Bacteria dwelling in cystic fibrosis lungs

509 **Trophic cooperation promotes *Pseudomonas aeruginosa* and *Staphylococcus aureus* survival in cystic fibrosis patients**
L. Camus (Lyon, France), B. Paul, S. Bastien, A. Doleans, S. Elsen, F. Vandenesch, K. Moreau*

3453 **_Staphylococcus aureus_ pathogenicity in cystic fibrosis patients: virulence genes, phylogeny and horizontal gene transfer**
J. Lange (Münster, Germany), K. Heidenreich, K. Higelin, K. Dyck, V. Marx, C. Reichel, D. Görlich, B. Kahl*

3582 **Sputum iron metabolism in patients with cystic fibrosis as a marker of infectious complications**
A. Kozlov (Samara, Russian Federation), A. Lyamin, O. Gusyakova, O. Kondratenko, D. Ismatullin, A. Khaliulin*

6692 **An _ex vivo_ pig lung model demonstrates potential to distinguish key aspects of chronic and acute infection in the cystic fibrosis lung**
E. Sweeney (Coventry, United Kingdom), N. Harrington, B. Crealock-Ashurst, F. Allen, F. Harrison*

Session accepted as Paper Poster Session

Biofilm mechanisms and effects

614 **Ursolic acid and its amide derivatives disrupt clinical _Acinetobacter baumannii_ isolates and biofilm formation**
A. Ahmed (Karachi, Pakistan), Y. Usmani, S. Simjee, S. Faizi*

687 **Role of deoxyribonucleic acid content in the composition of microbial biofilm in the pathogenesis of severe respiratory infections**
V. Ziamko (Vitebsk, Belarus), V. Okulich, A. Dzyadzko*

1432 **Antimicrobial susceptibility of _Cutibacterium avidum_ isolated from prosthetic joint infections: differences between biofilms and planktonic bacteria**
L. Salar Vidal, Y. Achermann, R. Trebse, M. Rak, M. Wouthuyzen-Bakker, J. Aguilera-Correa, J. Esteban-Moreno (Madrid, Spain)*

1804 **Comparison of _Cutibacterium acnes_ biofilm formation between strains isolated from prosthetic join infection and healthy skin microbiota**
L. Salar Vidal, J. Aguilera-Correa, Y. Achermann, D. Salmon-Ceron, P. Morand, M. Fernandez Sampedro, D. Pablo-Marcos, R. Trebse, M. Rak, S. Corvec, L. Happi, M. Wouthuyzen-Bakker, N. Benito, A. Ribera, J. Esteban-Moreno (Madrid, Spain)*

1970 **The role of _Staphylococcus aureus_ surface protein G (_sasG_) and its allelic variants in biofilm formation**
A. Carrera-Salinas (L'Hospitalet de Llobregat, Spain), A. González Díaz, D. Vázquez-Sánchez, M. Camoez, J. Niubò, S. Marti, M. Domínguez Luzon*

2707 **Biofilm formation of methicillin-resistant _Staphylococcus aureus_: does it varies with the type of infection?**
V. Silva (Vila Real, Portugal), L. Almeida, S. Hermenegildo, N. Cerca, J. Capelo, G. Igrejas, P. Poeta*

3134 **Anti-biofilm and antibacterial properties of cationic amphipatic AMP mimics**
C. Forestier (Clermont Ferrand, France), N. Charbonnel, R. Shyam, C. Taillefumier, S. Faure*

3537 **Antibacterial and anti-biofilm activities of mucolytics, alone and in combination with antibiotics against Gram-negative pathogens**
F. Yılmaz (istanbul, Turkey), S. Dosler*

3811 **Anti-biofilm activity of ozenoxacin against methicillin-resistant _Staphylococcus aureus_ strains**
Y. López Cubillos (Barcelona, Spain), I. Zsolt, J. Vila Estape*

4209 **Validation of new anti-staphylococcal compounds within a group of potential sortase A inhibitors**
O. Moshynets (Kiev, Ukraine), G. Volynets, T. Baranovskyi, G. Nitulescu, M. Denisa, A. Ungurianu, V. Bdzhola, G. Nitulescu, S. Yarmoluk*

4754 **Characterisation of relationships between _Staphylococcus aureus_ and _Escherichia coli_, _Acinetobacter baumannii_ and _Candida auris_ and their implications for survival and persistence in the dry environment**
N. Amaeze (Abuja, Nigeria), G. Ramage, W. Mackay, C. Williams, R. Kean*

5317 **Antibiotic penetration and bioavailability of vancomycin alone and in combination with rifampin in _Staphylococcus epidermidis_ biofilms**
E. O'Neill (Cranston, United States), E. Piehl, K. Daffinee, G. Williams, K. Laplante*

7247 **Delivering antibiotics locally to biofilms by targeted drug delivery and prodrug therapy**
R. Meyer (Aarhus, Denmark), R. Walther, S. Nielsen, P. Andersen, L. Hansen, R. Christiansen, H. Quang, J. Kjems, A. Zelikin*

8987 **Plant-based biomolecules against antibiotic-resistant microbes in skin infections and diseases**
J. Aguilera-Correa, S. Fernández López, T. J. Kinnari, R. Puupponen-Pimiä, A. Hanna-Leena, L. Nohynek, J. Esteban-Moreno, M. Górgolas, R. Perez Tanoira (Madrid, Spain)*

9091 **Metabolomic comparison of biofilm matrix of six species of _Candida_**
I. Sigona-Giangreco, M. Garcia-Hita, V. Garcia Bustos, A. Ruiz (Valencia, Spain), E. Cortes-Acosta, J. Peman, E. Canton, E. Valentin*

9235 **Graphene oxide sheets affect expression of biofilm formation key genes in _Escherichia coli_**
C. Vuotto (Rome, Italy), L. Pappalardo, G. Donelli, I. Francolini*

9285 **Multi-omics approaches to understand the regulation of biofilm formation in high biofilm-forming clinical isolate of _Candida parapsilosis_**
S. Shafeeq (Stockholm, Sweden), B. Sennblad, M. Grabherr, U. Römling*

Session accepted as Mini-oral Flash Session

Biofilm-associated infections

2617 **Biofilm production by Gram-negative bacilli isolated from periprosthetic joint infections**
A. Macias-Valcayo (Madrid, Spain), J. Aguilera-Correa, J. Esteban-Moreno*

3456 **Interleukin 1-α and vascular endothelial growth factor support the growth and persistence of biofilm-growing *Cutibacterium acnes* in individuals with acne**
I. Cavallo (Rome, Italy), F. Sivori, G. D'Agosto, G. Prignano, F. Pimpinelli, B. Capitanio, F. Ensoli, E. di Domenico*

4494 **Biofilms and catheter-related bloodstream infections: a tale of two kingdoms**
V. Borges, S. Wenner, I. Nogueira, I. Faria, M. Pessanha, C. Verissimo, R. Sabino, J. Rodrigues, R. Matias, F. Martins, P. Carvalho, J. Gomes, L. Jordao (Lisboa, Portugal)*

5412 **Microbial aetiology of prosthetic joint infections: what's growing in the cultures?**
E. Piehl (Providence, United States), V. Lopes, A. Caffrey, K. Laplante*

6142 **Intracellular persistence of uropathogenic *Escherichia coli* is undetectable in urinary bladders from mecillinam-treated pigs**
K. Stærk (Odense, Denmark), R. Grønnemose, Y. Palarasah, H. Kolmos, L. Lund, T. Andersen*

7585 **Development of *in vitro* and *ex vivo* wound biofilm models for the assessment of wound dressings**
K. Tiirik (Tartu, Estonia), L. Preem, K. Sagor, M. Putrins, T. Tenson, K. Kogermann*

8242 **Within-host genetic diversity of *Staphylococcus epidermidis* in prosthetic joint infections: consequences for microbiological diagnosis**
M. Widerstrom (Umeå, Sweden), M. Stegger, A. Johansson, A. Larsen, T. Monsen*

9556 **Adaptation to host of a *Staphylococcus schleiferii* responsible of an elbow prosthetic infection**
A. Bidossi, M. Bottagisio, E. De Vecchi (Milan, Italy)*

Session accepted as Paper Poster Session

Escherichia coli and *Salmonella* pathogenicity and virulence

571 **Proton pump inhibitors increase the digestive carrying of OXA-48-producing *Enterobacteriaceae* in a mouse model**
F. Javaudin (Nantes, France), Q. Le Bastard, M. Dion, Y. Bezabih, E. Montassier, E. Batard*

1161 **ESBL-producing *Escherichia coli* causing community-onset bloodstream infection and the association of bacterial clones and virulence genes with septic shock**
I. Fröding (Stockholm, Sweden), B. Hasan, I. Sylvin, P. Naucler, C. Giske*

1485 **Comparison of β-lactamase-producing *Escherichia coli* ST131 C1-M27 and ST131 non-C1-M27 by whole genome analysis using next-generation sequencing in Japan**
N. Noguchi (Tenri, Japan), A. Nakamura, M. Komatsu*

2007 **Association of the prophage BTP-1 with anti-virulence of *Salmonella typhimurium* sequence type 313**
A. Herrero (Copenhagen, Denmark), M. Spiegelhauer, P. Guerra, J. Olsen*

2030 **Microbiological factors of *Escherichia coli* from adult patients with bacteraemia and sepsis/septic shock from 21 hospitals in Spain: PROBAC-EC study**
N. Maldonado (Seville, Spain), I. López-Hernández, L. González-Rivas, L. Lopez-Cortes, P. Pérez-Crespo, J. Lanz, Á. Pulido Navazo, A. Del Arco, F. Barcenilla Gaite, M. Mantecón, A. Sousa-Dominguez, J. Fernandez-Suarez, T. Marrodán-Ciordia, A. Smithson Amat, C. Armiñanzas Castillo, E. Leon, J. Reguera Iglesias, C. Natera, I. Gea-Lázaro, J. Sanchez Calvo, A. Bahamonde, E. Calbo Sebastian, A. Reyes Bertos, F. Galan-Sanchez, I. Perez-Camacho, A. Pascual Hernandez, J. Rodríguez-Baño*

2325 **Insights into reservoir and pathogenicity of *Escherichia coli* ST83: role of haemolysin A operon duplication in severity of urinary tract infections**
M. Ksiezarek (Porto, Portugal), Â. Novais, H. Felga, F. Mendes, M. Escobar, L. Vieira Peixe*

2648 **Novel putative AHL-lactonases widely distributed across diverse carbapenemase-producing *Enterobacteriaceae***
M. Lopez (A Coruna, Spain), N. Ellaby, N. Woodford, M. Ellington, M. Tomas*

4390 **Mouse colonisation by multidrug-resistant *Escherichia coli* in the absence of antibiotic selection**
C. Connor (Birmingham, United Kingdom), A. Zucoloto, I. Yu, B. Mcdonald, A. Mcnally*

4701 **Contribution of microbial virulence factors on mortality in adult patients with bacteraemia due to *Escherichia coli* presenting with sepsis/septic shock: exploratory analysis of the PROBAC-EC cohort**
N. Maldonado (Seville, Spain), I. López-Hernández, L. González-Rivas, L. Lopez-Cortes, P. Pérez-Crespo, J. Lanz, J. Cuquet Pedragosa, J. Goikoetxea, A. Del Arco, F. Barcenilla Gaite, M. Mantecón, A. Sousa-Dominguez, J. Fernandez-Suarez, T. Marrodán-Ciordia, A. Smithson Amat, C. Armiñanzas Castillo, E. Leon, J. Reguera Iglesias, C. Natera, I. Gea-Lázaro, J. Sanchez Calvo, A. Bahamonde, E. Calbo Sebastian, A. Reyes Bertos, F. Galan-Sanchez, I. Perez-Camacho, A. Pascual Hernandez, J. Rodríguez-Baño*

5340 **TLR4-independent effects of LPS identified using longitudinal serum proteomics**
E. Harberts (Baltimore, United States), T. Liang, S. Yoon, B. Opene, D. Goodlett, R. Ernst*

6456 **Genetic architecture of interspecies hybrids**
K. Bartke (Uppsala, Sweden), L. Garoff, D. Huseby, G. Brandis, D. Hughes*

7006 **Genome wide mutations in a clinical *Escherichia coli* isolate with a DNA mismatch repair gene defect after exposure to remnants of a phagemid-containing *Escherichia coli***
J. Stohr (Breda, Netherlands), M. Kluytmans - Van Den Bergh, C. Verhulst, J. Rossen, J. Kluytmans*

7165 **Within host genetic comparison of *Escherichia coli* strains isolated from patients with urosepsis**
A. Cuénod (Basel, Switzerland), J. Agnetti, H. Seth-Smith, O. Grüninger, J. Reist, S. Tschudin-Sutter, S. Bassetti, N. Thomson, A. Egli*

7712 **Microbial predictive virulence factors for pyelonephritis caused by extended-spectrum beta-lactamase-producing *Escherichia coli* in children harbouring such strains in their gut microbiota**
B. Philippe (Paris, France), A. Birgy, C. Levy, F. Madhi, E. Sobral, R. Cohen, S. Bonacorsi*

8862 **Depicting the pathogenicity and genomics traits of hypermucoviscous *Enterobateriaceae* clinical isolates**
N. Rodriguez Medina (Cuernavaca, Mexico), U. Garza-Ramos, H. Valdovinos-Torres*

8892 **Octenidine: new insights in the detailed killing mechanism on Gram-negative bacteria at a cellular and molecular level**
N. Malanovic (Graz, Austria), A. Oen, G. Pabst, K. Lohner*

Session accepted as Paper Poster Session

Gram-Positives: Pathogenicity, identification and treatment

902 **Characterisation and virulence of fibronectin-binding protein of *Streptococcus intermedius***
M. Sasaki (Shiwagun, Japan), Y. Kodama, T. Ishikawa, Y. Shimoyama*

1876 **Reduced production of bacterial membrane vesicles predicts mortality in ST45/USA600 methicillin-resistant *Staphylococcus aureus* bacteraemia**
S. dey (detroit(Michigan), United States), S. Gudipati, C. Giuliano, M. Zervos, J. Monk, R. Szubin, S. Jorgensen, G. Sakoulas, A. Berti*

2448 **Characterisation of a fibronectin binding protein in the virulence of *Streptococcus parasanguinis* FW213**
Y. Chen (Taoyuan, Taiwan)*

2912 ***esp17* and its importance in dry stress resistance**
N. Kordzakhia (Tbilisi, Georgia)*

3492 **Combined inhibition of CD14 and C5 in *Escherichia coli* and Group B streptococci induced inflammation in human cord blood**
A. Bjerkhaug (Tromsø, Norway), H. Granslo, P. Cavanagh, J. Ludviksen, Å. Bjørnerem, T. Mollnes, C. Klingenberg*

3851 **Inter- and intra-clonal diversity in *Staphylococcus epidermidis* prosthetic joint infection**
A. Both (Hamburg, Germany), J. Huang, M. Qi, S. Weisselberg, H. Buettner, C. Lausmann, M. Alawi, P. Haffke, H. Rohde*

4066 **Platelet trends early during *Staphylococcus aureus* bacteraemia are predictive of persistence and mortality**
B. Lee (Los Angeles, United States), C. Kelsom, K. Tan, A. Wong-Beringer*

4131 **The type I histidine triad protein HtpsA contributes to the capsule development and virulence of *Streptococcus suis* serotype 2**
X. Pan (Nanjing, China), Z. Shao, M. Li, H. Ni*

4680 **Characterisation of biofilm formation by *Staphylococcus pseudintermedius* on a variety of medical devices**
C. Pesset, M. Antunes, C. Fonseca, M. Ferreira, I. Teixeira, E. De Oliveira Ferreira, B. Penna (Rio de Janeiro, Brazil)*

4761 **Exfoliative toxin A-producing *Staphylococcus aureus* clonal complex 8 strains causing staphylococcal scaled skin syndrome in newborns**
I. Abaev (Obolensk, Russian Federation), Y. Skryabin, N. Fursova, I. Dyatlov*

4943 ***Staphylococcus aureus* bacteraemia during a 2-year period in a tertiary university hospital: outcome and correlations to host- and pathogen-related characteristics**
H. Wächter (Münster, Germany), E. Yörük, D. Görlich, K. Becker, B. Kahl*

5017 **Fibronectin binding protein plays pivotal role in development of central nervous system complication of *Staphylococcus aureus* bacteraemia**
C. Kim (Seoul, South Korea), K. Song, C. Kang, E. Kim, J. Bae, H. Choi, Y. Jung, W. Park, N. Kim, M. Oh, H. Kim*

7300 **Bacteriocin production in *Staphylococcus aureus* CC398 and CC130 lineages, potential strategies to antimicrobial resistance**
R. Fernández Fernández, P. Gómez, L. Ruiz, M. Zarazaga, C. Torres (Logroño, Spain)*

7573 ***In vitro* evaluation of barrier function against foodborne bacteria and oral streptococci on polytetrafluoroethylene membranes**
G. Begić, O. Cvijanović Peloza, S. Mahmutovic Vranic (Sarajevo, Bosnia and Herzegovina), M. Blaskovic, Z. Peric Kacarevic, I. Gobin*

7575 **Comparison of rifampin synergy in high versus low biofilm-forming *Staphylococcus epidermidis***
E. Piehl (Providence, United States), E. O'Neill, K. Daffinee, K. Laplante*

8096 ***Staphylococcus aureus* dampen autophagy flux to survive inside a model of keratinocytes mimicking *S. aureus* nasal colonisation**
E. Audoux (St-Etienne, France), R. Caire, J. Josse, C. Dupieux-Chabert, P. Berthelot, F. Laurent, P. Verhoeven*

8770 **Developing a molecular toolbox for *Staphylococcus haemolyticus*: mimicry-by-methylation**
H. Venter (Tromsø, Norway), J. Cavanagh, C. Johnston*

Session accepted as Mini-oral ePoster Session

Identification and characterisation of bacterial virulence strategies

221 **Identification of novel pathogenicity factors in *Bartonella bacilliformis***
A. Dichter, S. Torres, S. Becker, M. García Quintanilla, V. Kempf (Frankfurt, Germany)*

4409 **Transcriptional and phenotypic responses to multidrug resistance plasmid acquisition are strain-specific in *Escherichia coli***
S. Dunn (Birmingham, United Kingdom), L. Carrilero, M. Brockhurst, A. Mcnally*

4436 **Elucidating the role of the essential operon *yajC-secD-secF* in *Burkholderia* spp.: a possible new target for new antimicrobial molecules**
E. Perrin (Sesto Fiorentino, Italy), M. Fonai, R. Fani, A. Mengoni*

4570 **Genome-wide transcriptional responses of *Escherichia coli* with different levels of zinc tolerance to zinc chloride exposure**
V. Johanns, S. Wolf, L. Epping, A. Lübke-Becker, T. Semmler, B. Walther (Berlin, Germany), L. Wieler*

5035 ***Klebsiella pneumoniae* type VI secretion system allows the implantation and survival of the pathogen within the intestinal microbiota**
T. Merciecca, L. Nakusi, S. Bornes, C. Besnard, E. Rifa, S. Theil, C. Forestier, S. Miquel (Clermont-Ferrand, France)*

5184 **Acylated homoserine lactone- (AHL) mediated quorum sensing in dental plaque: an opportunity for novel antimicrobial treatment of oral diseases**
A. Muras, P. Otero-Casal, A. Otero (Santiago de Compostela, Spain)*

5257 **A widespread toxin-antitoxin system exploiting growth control via alarmone signalling**
S. Alves Oliveira (Tartu, Estonia), S. Jimmy, C. Kumar, A. Garcia Pino, T. Kurata, A. Koh, A. Cepauskas, H. Takada, T. Tenson, H. Strahl, C. Stavropoulos, V. Hauryliuk, G. Atkinson*

6300 **A high-throughput real-time liquid-based *Caenorhabditis elegans* model for assessing the virulence of clinical encapsulated multidrug-resistant *Klebsiella pneumoniae* isolates**
A. Gancz (Ariel, Israel), D. Cohen-Eli, S. Navon-Venezia*

7061 **Meningococcal disease-associated prophage-like elements are present in *Neisseria gonorrhoeae* and some commensal *Neisseria* sp.**
B. Al Suwayyid, D. Speers, M. Wise, G. Coombs, C. Kahler (Perth, Australia)*

Session accepted as Paper Poster Session

Klebsiella genomes and phenotypes

2696 **Genome-based analyses of *Klebsiella pneumoniae* to detect possible host-associations, host-adaptation and effects on virulence**
K. Klaper (Wernigerode, Germany), L. Heinrich, R. Gerlach, S. Fuchs, Y. Pfeifer, G. Werner*

3657 **A novel chaperone-usher pili system associated to the worldwide-disseminated high-risk clone *Klebsiella pneumoniae* ST-15**
E. Gato (A Coruña, Spain), B. Rodiño-Janeiro, M. Pérez-Vázquez, A. Romero, G. Bou Arevalo, A. Pérez*

4950 **Food and clinical human isolates of *Klebsiella pneumoniae*: is there correlation between multidrug resistance and biofilm formation capacity?**
D. Díaz-Jiménez, A. Muras, J. Fernández, A. Parga, L. Leston, A. Otero, A. Mora Gutiérrez (Lugo, Spain)*

5930 **Influence of biofilm formation on clinical outcome and their associated genetic virulence factors in *Klebsiella pneumoniae* bloodstream infections in India**
D. Naveen Kumar (Sheffield, United Kingdom), K. Asokan, K. Vasudevan, D. Murugan, E. Karunakaran, P. Monk, V. Balaji*

6013 **Effect of the capsule exchange between serotype K1 and K20 *Klebsiella pneumoniae* on serum killing, neutrophil phagocytosis and mice lethality**
E. Liu, J. Chang, J. Lin, F. Chang (Taipei, Taiwan)*

6228 **Prevalence of virulence factors in colonising and infecting *Klebsiella pneumoniae* isolates obtained from a German multi-centre surveillance study**
K. Lucassen (Cologne, Germany), K. Xanthopoulou, J. Wille, A. Walker, Y. Stelzer, V. Persy, H. Seifert, P. Higgins*

6978 **Characterisation of virulence in KPC-2-producing *Klebsiella pneumoniae* CG258 from an outbreak in high complexity hospital in Brazil**
T. Rezende (São Paulo, Brazil), C. Morais, J. Monteiro, C. Abboud, J. Setubal, A. Pignatari, C. Kiffer*

8050 **Diversity of capsular switch among carbapenemase-producing *Klebsiella pneumoniae***
A. Chiarelli (Paris, France), N. Cabanel, R. Bonnin, P. Glaser*

8449 **Contrasting molecular epidemiology of *Klebsiella* spp. and *Escherichia coli* bloodstream infections in Oxfordshire (UK) 2009-2017**
S. Lipworth (Oxford, United Kingdom), K. Vihta, J. Kavanagh, L. Barker, K. Chau, S. George, A. Vaughan, D. Griffiths, M. Morgan, M. Andersson, K. Jeffery, T. Peto, D. Crook, N. Stoesser, A. Walker*

8764 **Genomic characterisation and pathogenicity determination of the classical, hypermucoviscous and hypervirulent *Klebsiella pneumoniae* isolates in Mexico**
U. Garza-Ramos (Morelos, Mexico), J. Rodríguez-Santiago, A. Sagal-Prado, J. Silva-Sanchez*

9052 ***In vivo* virulence of different clones of OXA-48-producing *Klebsiella pneumoniae* in *Galleria mellonella* infection model**
A. Leal, L. Forcelledo Espina, A. Rodriguez-Guardado, F. Vazquez, M. Rodicio, J. Fernández (Oviedo, Spain)*

9477 **Do we need to screen the colibactin genomic island (CGI) for diagnosis of colorectal cancer? Paradigm of *Klebsiella pneumoniae***
M. Ben Khedher, S. Khabthani, R. Ruimy, J. Rolain, S. Diene (Marseille, France)*

9480 **Co-aggregation of uropathogenic *Klebsiella oxytoca* with *Klebsiella pneumoniae* and probiotic *Escherichia coli* on the cell line**
A. Giliazeva (Senftenberg, Germany), J. Noack, A. Mardanova*

Session accepted as Paper Poster Session

Novel biofilm models and methods

454 **Combined effects of low incubation temperature, minimal growth medium and low hydrodynamics optimise *Acinetobacter baumannii* biofilm formation**
E. Eze (Kwazulu-Natal, South Africa)*

2048 **Formation of enterobacterial aggregates in presence of bovine synovial fluid**
A. Macias-Valcayo (Madrid, Spain), J. Aguilera-Correa, A. Staats, T. Gupta, D. Dusane, P. Stoodley, J. Esteban-Moreno*

2894 **Detection of microorganisms in sonicated titanium screw model after *in vitro* biofilm production using culture, MALDI-TOF MS and qPCR**
J. Cieslinski, V. Stadler Tasca Ribeiro, L. Kraft, P. Suss, E. Rosa, L. Morello, M. Pillonetto, J. Telles (Sao Paulo, Brazil), F. Tuon*

3450 **It's a trap! The development of a versatile drain biofilm model**
K. Ledwoch (Cardiff, United Kingdom), J. Maillard, P. Norville*

3583 ***Galleria mellonella* as a novel *in vivo* drug discovery platform using bioluminescent KAPE pathogens**
V. Francis (Exeter, United Kingdom), A. Smith, C. Kemmer, V. Trebosc, B. Schellhorn, R. Titball, O. Champion*

3723 **The efficiency of antimicrobial coatings in whole blood: development of a realistic *in vitro* model**
J. Valtin (Dresden, Germany), C. Werner*

3845 **A five-species biofilm model for confirming the potential of a nisin-biogel aiming at canine periodontal disease control**
E. Cunha (Lisbon, Portugal), S. Rebelo, L. Tavares, M. Carreira, M. Oliveira*

4598 **Effect of *Bdellovibrio bacteriovorus* on clinical pathogens and biofilms**
S. Kahraman, Y. Tekintas (İzmir, Turkey), F. Cilli, M. Hosgor-Limoncu*

4820 **A new ultra-fast specimen preparation method for SEM visualization of bacterial biofilms**
I. Chebotar (Moscow, Russian Federation), A. Subbot, Y. Bocharova, N. Fedorova, I. Novikov*

4881 **Investigation of electric signaling in bacterial biofilms with the Specialised Thin Agar Method (STAM)**
J. Assmann (Berlin, Germany), S. Bürge, C. Schaudinn, B. Walther*

8109 **Study of microbial adhesion to nanostructured and nanocoated orthoprosthetic material through dynamic models**
S. Leonetti (Pisa, Italy), B. Tuvo, B. Campanella, M. Onor, S. Legnaioli, E. Bramanti, A. Baggiani, M. Totaro, P. Parchi, B. Casini*

8387 ***In vitro* model of *Pseudomonas aeruginosa* pulmonary biofilm to evaluate the efficacy of cationic antibiotics**
R. Awad (Poitiers, France), F. Tewes, S. Marchand, W. Couet, M. Nasser*

Session accepted as 1-Hour Oral Session

Novel therapeutics approaches for bacterial infections

1004 **A surface-engineered scaffold implant with direct antibacterial activity against *Staphylococcus aureus***
S. Comini, F. Menotti, B. Coppola, A. Cuffini, P. Palmero, G. Banche, V. Allizond (Turin, Italy)*

1305 **Cold plasma activated liquid reduces bacterial biofilm produced by *Staphylococcus aureus* and *Escherichia coli***
M. Fallon (Dublin, Ireland), S. Kennedy, S. Babu, S. Daniels, H. Humphreys*

6846 ***Acinetobacter baumannii* and *Klebsiella pneumoniae*: intelligent design of phage cocktails against multidrug-resistant pathogens**
M. Jalasvuori (Jyvaskyla, Finland), K. Koskinen, M. Ylänne, R. Penttinen*

8342 **Exploiting CRISPR-*Cas*9 to eradicate ESBL genes and tracing conjugative plasmids within complex microbial communities at single-cell resolution**
R. Penttinen (Turku, Finland), L. Ambrosio Leal Dutra, P. Ruotsalainen, O. Franz, C. Given, K. Nurminen, P. Salmi, M. Tiirola, M. Jalasvuori*

Session accepted as Paper Poster Session

Overcoming infections caused by non-fermenters

1255 **Filamentous bacteriophage (Pf-8) in *Pseudomonas aeruginosa* isolates belonging to the international cystic fibrosis clone (CC274)**
A. Ambroa Abalo (A Coruña, Spain), L. Blasco, C. Lopez Causape, R. Trastoy Pena, L. Fernandez Garcia, I. Bleriot Rial, M. Ponce-Alonso, O. Pacios, M. Lopez, R. Del Campo, R. Canton Moreno, T. Kidd, G. Bou Arevalo, A. Oliver, M. Tomas*

1290 **The *in vitro* effect of azithromycin on *P. aeruginosa* biofilms**
A. Jimenez San Mauro, N. Høiby, O. Ciofu (Copenhagen, Denmark)*

1576 **Ceftolozane/tazobactam for multidrug-resistant *Pseudomonas aeruginosa* in a swine model of severe pneumonia**
A. Motos (Barcelona, Spain), G. Li Bassi, F. Pagliara, L. Fernandez Barat, H. Yang, E. Aguilera Xiol, T. Senussi, F. Idone, C. Travierso, C. Chiurazzi, R. Amaro, M. Yang, J. Bobi, M. Rigol, G. Frigola, R. Cabrera, D. Nicolau, A. Torres*

1679 **First evidence of systemic efficacy of a pathogen-targeted, engineered lysin (GN-370) against carbapenem-resistant *Pseudomonas aeruginosa* in a rabbit pneumonia model**
D. Lehoux (Yonkers, United States), W. Abdelhady, Y. Xiong, K. Sauve, J. Oh, A. Watson, S. Swift, C. Cassino, A. Bayer, R. Schuch*

2250 **Efflux pump inhibitors based on novel cyclic peptides as an approach against ESKAPE pathogens**
J. Moreno Morales (Barcelona, Spain), C. Cosgaya Castro, C. Ballesté, E. Giralt, J. Vila Estape*

2411 **Co-evolutionary adaptations of *Acinetobacter baumannii* and an OXA-23-encoding plasmid under carbapenem pressure**
L. Zhang (Hangzhou, China), X. Hua, Y. Yu*

3520 **Effects of ceragenins to intracellular *Pseudomonas aeruginosa* infections formed in human airway epithelial cells**
Ö. Oyardı (Istanbul, Turkey), C. Bozkurt Guzel, P. Savage*

3704 **Modulation of antibiotic-associated virulence of *Pseudomonas aeruginosa* in cystic fibrosis bacterial biofilms**
M. Hassan, N. Harrington (Coventry, United Kingdom), F. Harrison*

3923 ***In silico* and *in vitro* investigation of a novel putative toxin-antitoxin system in *Acinetobacter baumannii***
S. El-Banna (Cairo, Egypt), R. Samir, R. Aziz, N. Moneib*

4326 **The solitary *parE-type* toxin gene in *Pseudomonas aeruginosa* sequence type 111 clinical isolates collected in a paediatric intensive care unit in Moscow**
Y. Bocharova (Moscow, Russian Federation), T. Savinova, D. Shagin, I. Chebotar*

6082 **Estimation of the prevalence of the plasmid-encoded septicolysin gene in carbapenem-resistant *Acinetobacter baumannii***
N. Rakovitsky (Tel Aviv, Israel), S. Frenk, P. Elmalih, R. Rov, E. Temkin, D. Schwartz, Y. Carmeli, J. Lellouche*

6268 **Comparative *in vitro* activities of eravacycline and various antibiotics against multidrug-resistant clinical strains of *Acinetobacter baumannii* isolated from intensive care units**
M. Ataman (Istanbul, Turkey), E. Mataraci-Kara, B. Ozbek Çelik*

6355 **Comparative metabolomics of *Pseudomonas aeruginosa* in response to polymyxin B**
M. Hussein (Melbourne, Australia), M. Han, B. Tsuji, R. Hancock, T. Velkov, J. Li*

6930 **Carbapenem-resistant *Acinetobacter baumannii* fitness in murine model is associated with 14-day mortality in humans**
A. Nutman (Tel-Aviv, Israel), J. Lellouche, E. Temkin, G. Daikos, A. Skiada, E. Durante Mangoni, Y. Dishon, R. Bitterman, D. Yahav, V. Daitch, M. Bernardo, D. Lossa, L. Friberg, U. Theuretzbacher, L. Leibovici, M. Paul, Y. Carmeli*

7204 **Plasticity in a bacterial global regulator drives the switch to antibiotic resistance and virulence**
A. Correia, E. Manners, B. Evans (Norwich, United Kingdom), J. Malone, J. O'Grady, S. Arminu, M. Usai, S. Mcmillan, G. Kay, C. Hill, P. Sudhakar, E. Meader, K. Schmidt, T. Korcsmaros, A. Desbois, L. Crossman, J. Wain, G. Langridge*

7823 **Fighting a rare cystic fibrosis pathogen: characterisation of *Burkholderia cenocepacia* cell division machinery**
V. Scoffone (Pavia, Italy), G. Trespidi, L. Chiarelli, G. Manina, V. Makarov, G. Riccardi, S. Buroni*

7897 **The growth dynamics of *Pseudomonas aeruginosa* isolated from peritoneal fluid, blood and homogenates of the organs of septic mice**
M. Cherkasova (Moscow, Russian Federation), V. Zhukhovitsky, T. Borovaya*

7967 **Efficacy of an engineered protegrin-1 analogue in a murine model of *Pseudomonas aeuriginosa* sepsis**
M. Dughbaj (Hawthorne, United States), R. Ganesan, S. Beringer, J. Camarero, P. Beringer*

8038 ***In vivo* virulence of different growth states of *Pseudomonas aeruginosa***
F. De Winter (Antwerp, Belgium), R. Ruhal, B. S. Jongers, B. Xavier, C. Lammens, H. Goossens, S. Malhotra-Kumar, S. Kumar-Singh*

9140 **The profile of virulence gene *exoS*, *exoT*, *exoU* and *exoY* from gene encoding effector protein type III secretion system of *Pseudomonas aeruginosa* in clinical isolates in Sanglah Hospital Bali**
I. Saputra (Bali, Indonesia), N. Mertaniasih, N. Fatmawati*

Session accepted as 1-Hour Oral Session

Staphylococcus aureus in-host evolution

1985 **Host adaptative changes of *Staphylococcus aureus* through respiratory colonisation and bloodstream infection**
A. Carrera-Salinas (L'Hospitalet de Llobregat, Spain), A. González Díaz, D. Vázquez-Sánchez, I. Salto, M. Mrakovcic, M. Cubero, M. Domínguez Luzon, S. Niemann, S. Marti*

3670 **Lower respiratory tract infection by *Staphylococcus aureus* in mechanically-ventilated patients: genotypical and phenotypical characterisation**
A. Lacoma (Badalona, Spain), M. Laabei, G. Godoy, B. Muriel-Moreno, J. Moreno, F. Arméstar, C. Prat*

6469 **In-host evolution of methicillin-resistant *Staphylococcus aureus* within individual carriers using core genome multi-locus sequence typing and single-nucleotide polymorphism analysis**
A. Campillay Lagos (Örebro, Sweden), M. Sundqvist, F. Dyrkell, M. Stegger, B. Söderquist, P. Mölling*

Session accepted as 2-Hour Oral Session

Translational studies of streptococci and enterococci

523 **Unravelling the mechanism of virulence of M1 protein of *Streptococcus pyogenes***
E. Torres Sangiao (Santiago de Compostela, Spain), L. Happonen, F. Palm, P. Pyl, O. Shannon, C. García-Riestra, J. Malmström*

1546 **Bronchial abundance of *Streptococcus* as a potential biomarker for lung cancer**
M. Ponce-Alonso (Madrid, Spain), J. Vengoechea, C. Saralegui Díez, A. Rezusta, N. Huertas, J. Sánchez López, R. Del Campo, S. Bello*

1568 **Transcriptome analysis of pneumococci isolated from meningitis patient's cerebrospinal fluid identifies multiple genes important for pathogenesis, including a novel operon of unknown function**
E. Wall (London, United Kingdom), J. Guerra-Assunção, M. Yang, S. Panagiotou, T. Audshasai, R. Aprianto, E. Ramos Sevillano, V. Terra, D. Van De Beek, J. Veening, D. Lalloo, B. Wren, A. Kadioglu, R. Heyderman, J. Brown*

3684 ***Enterococcus faecalis* inhibits *Klebsiella pneumoniae* growth in polymicrobial biofilms**
V. Ballén Torres (Barcelona, Spain), S. Soto*

7108 **Microdiversity of *Enterococcus faecalis* isolates from infective endocarditis**
G. Royer (Créteil, France), L. Roisin, S. Lo, D. Vanessa, H. Jacquier, R. Lepeule, V. Fihman, P. Lim, C. Rodriguez, P. Woerther*

8427 **Identification of new small-RNAs involved in growth and virulence of *Enterococcus faecium***
M. Cacaci (Rome, Italy), A. Budin-Verneuil, R. Torelli, F. Bugli, T. Hain, H. Putzer, M. Sanguinetti, N. Tourasse, A. Hartke, C. Giraud*

8490 **Development of a new murine model for *Enterococcus faecium* intestinal colonisation**
S. Reissier (Rennes, France), V. Bordeau, F. Brice, V. Cattoir, M. Revest*

Session accepted as 2-Hour Oral Session

Understanding and treating biofilms

906 ***Staphylococcus aureus* inhibits opsonophagocytosis and modulates neutrophils extracellular traps formation efficiently during the early stages of biofilm formation**
A. Sultan (Rotterdam, Netherlands), N. Lemmens-Den Toom, A. Verbon, W. Van Wamel*

927 **Co-infection with *Staphylococcus aureus* after primary influenza virus infection results in endothelial damage**
S. Deinhardt-Emmer (Jena, Germany), A. Van Krüchten, E. Schicke, K. Rennert, S. Ludwig, Z. Cseresnyes, M. Figge, A. Mosig, R. Heller, B. Löffler, C. Ehrhardt*

1095 **Methicillin-resistant *Staphylococcus aureus* USA300 persister cells show chaperone upregulation in contrast to planktonic cells and the biofilm phenotype**
J. Vlaeminck (Wilrijk, Belgium), B. Xavier, Q. Lin, S. De Backer, H. De Greve, S. Kumar-Singh, H. Goossens, S. Malhotra-Kumar*

2154 **Sub-inhibitory concentrations of mupirocin stimulate *Staphylococcus aureus* biofilm formation by up-regulating *cidA***
Y. Jin (Hangzhou, Zhejiang Province, China)*

2697 **Genomic adaptation of *Staphylococcus aureus* in a diabetic foot environment**
C. Pouget (Nimes, France), M. Hosny, A. Pantel, B. La Scola, F. Laurent, A. Sotto, C. Dunyach-Remy, J. Lavigne*

4379 **The mouse ear skin model reveals specific innate immune signatures into study of the dynamics of innate immune responses against to *Staphylococcus aureus* biofilms**
A. Abdul Hamid (Clermont-Ferrand, France), A. Cara, A. Diot, J. Josse, E. Billard, F. Laurent, P. Gueirard*

4972 ***Candida albicans* adhesion to central venous catheters: impact of yeast and hyphae morphotypes**
J. Jung (Homburg, Germany), C. Mischo, G. Gunaratnam, C. Spengler, S. Becker, K. Jacobs, M. Bischoff*

6589 **Three-dimensional *in vitro Staphylococcus aureus* abscess communities are not affected by antibiotics or neutrophils**
M. Hofstee (Davos Platz, Switzerland), M. Riool, K. Thompson, M. Stoddart, S. Zaat, F. Moriarty*

7336 **An innovative model to analyze anti-biofilm immune response *in vivo***
L. Sauvat (Clermont-Ferrand, France), A. Abdul Hamid, C. Blavignac, F. Laurent, O. Lesens, P. Gueirard*

8504 **Non-steroidal anti-Inflammatory drug administration impairs antibiotic treatment of orthopaedic device-related infection in a rat model**
F. Moriarty (Davos, Switzerland), G. Richards, K. Thompson*

Session accepted as Mini-oral ePoster Session

What happens when the host and pathogen meet

787 **A pathogen and a non-pathogen spotted fever group *Rickettsia* trigger differential proteome signatures in macrophages**
P. Cardoso Curto (Cantanhede, Portugal), C. Santa, P. Allen, B. Manadas, I. Simoes, J. Martinez*

1757 **Impact of corticosteroids on alveolar macrophage interaction with mucorales**
F. Arrivé (Poitiers, France), K. Brunet, J. Martellosio, I. Lamarche, S. Marchand, B. Rammaert*

3347 **Insight into *Chlamydia trachomatis* persistence**
C. Foschi, M. Bortolotti, C. Zalambani, R. Fato, L. Polito, A. Bolognesi, A. Marangoni (Bologna, Italy)*

3408 **Evaluation of neuro-filament light chain as a biomarker for neuronal damage in experimental pneumococcal meningitis**
N. Le (Bern, Switzerland), D. Grandgirard, J. Kuhle, D. Leppert, S. Leib*

3660 **Estrogen enhances host-pathogen interactions in *ex vivo* and *in vitro* models of the inflammatory phase of age-related impaired healing**
M. El Mohtadi (Manchester, United Kingdom), K. Whitehead, N. Dempsey-Hibbert, J. Ashworth*

5146 **Perinatal hormones favor CC17 Group B *Streptococcus* intestinal translocation through M cells and hypervirulence in neonates**
C. Hays, G. Touak, A. Bouaboud, A. Fouet, J. Guignot, C. Poyart, A. Tazi (Paris, France)*

5185 **Markers of inflammation, neural injury and regeneration in a neonatal mouse model of *Listeria monocytogenes* meningoencephalitis**
J. Seele, M. Ballüer, S. Tauber, S. Bunkowski, K. Schulz, C. Stadelmann, A. Beineke, D. Pägelow, M. Fulde, R. Nau (Göttingen, Germany)*

7974 **Impact of interferon gamma on *Staphylococcus aureus* internalisation within human osteoblasts**
C. Pierre, A. Souche, L. Abad, P. Verhoeven, J. Josse, T. Ferry, F. Laurent, F. Valour (Lyon, France), A. Diot*

31st ECCMID

10–13 APRIL 2021
VIENNA, AUSTRIA

ESCMID

Abstract Programme

10. Immunology & Vaccinology

- Host genetics: infection susceptibility & immunodeficiency
- Clinical epidemiology of infections in immunocompromised hosts
- General vaccinology (incl. policy, social aspects)
- Antiviral vaccines
- Antibacterial vaccines
- Immune response to infection (excl sepsis biomarkers)
- Other

Session accepted as 2-Hour Oral Session

An ever-looming threat: infections in immunocompromised hosts

966 **Ceftazidime-avibactam for the treatment of carbapenemase-producing *Enterobacteriaceae* bacteraemia in oncohaematological patients: calm after the storm**
F. Herrera (Buenos Aires, Argentina), R. Jordan, A. Valledor, I. Roccia Rossi, A. Laborde, A. Carena, S. Lambert, P. Costantini, L. Berruezo, M. Pereyra, A. Nenna, M. Dictar, J. Benso, F. Pasteran, A. Corso, M. Pinoni, L. Barcán, E. Inwinkelried, M. González Ibáñez, L. Tula, M. Luck, N. Baldoni, A. Racioppi, D. Torres*

1521 **Predictors of mortality in solid-organ transplant recipients with bloodstream infections due to carbapenemase-producing *Enterobacterales*: the impact of cytomegalovirus disease and lymphopenia**
E. Perez-Nadales (Cordoba, Spain), B. Gutiérrez-Gutiérrez, A. M.Natera, E. Abdala, M. Reina Magalhães, A. Mularoni, F. Monaco, L. Pierrotti, M. Freire, R. Iyer, S. Mehta Steinke, E. Grazia Calvi, M. Tumbarello, M. Falcone, M. Fernandez Ruiz, J. Costa-Mateo, M. Rana, T. Varejao Strabelli, M. Paul, M. Fariñas, W. Clemente, E. Roilides, P. Muñoz, L. Dewispelaere, M. Loeches Yague, W. Lowman, B. Tan, R. Escudero Sánchez, M. Bodro Marimont, P. Grossi, F. Soldani, F. Gunseren, N. Nestorova, A. Pascual Hernandez, L. Martinez-Martinez, J. Aguado Garcia, J. Rodríguez-Baño, J. De La Torre Cisneros, I. Investigators*

1816 **Burden of surgical site infections after solid organ transplantation in the Swiss transplant cohort study**
P. Schreiber (Zurich, Switzerland), B. Vanessa, K. Boggian, D. Neofytos, C. Van Delden, P. Dutkowski, A. Egli, M. Dickenmann, L. Gürke, S. Hillinger, C. Hirzel, S. Kuster, O. Manuel, M. Matter, O. De Rougemont, B. Schmied, M. Koller, S. Rossi, C. Toso, M. Wilhelm, N. Mueller, S. Cohort Study*

2108 **Pre-emptive therapy utilisation after haematopoetic cell transplantation**
G. Papanicolaou (New York, United States)*

2121 **Bloodstream infection survey in high-risk oncology patients (BISHOP) with fever and neutropenia (FN) in the United States: Gram-negative susceptibility and treatment patterns**
A. Zimmer, E. Stohs, L. Handke, P. Fey, Y. Zhang, C. Arnold, J. Baddley, P. Chandrasekar, Z. El Boghdadly, E. Maziarz, J. Montoya, S. Pergam, K. Rolston, M. Satlin, G. Satyanarayana, S. Shoham, L. Strasfeld, R. Taplitz, J. Young, A. Freifeld (Omaha, United States)*

3161 **Infectious complications in kidney transplant recipients: a prospective cohort study**
A. Scemla (Paris, France), M. Perier, O. Aubert, V. Manda, N. Kamar, S. Girerd, V. Garrigue, C. Kerleau, F. Buron, F. Lanternier, C. Legendre, M. Giral, A. Loupy*

6606 **Burden of viral infections among autologous stem cell transplant patients: a prospective longitudinal study**
G. Destras (Lyon, France), A. Bal, P. Sesques, C. Sarkozy, L. Generaz, G. Oriol, G. Salles, B. Lina, F. Mallet, A. Pachot, G. Billaud, L. Josset, T. Sophie, V. Cheynet, K. Brengel-Pesce, F. Morfin*

7744 **Short versus extended antibiotic treatment with a carbapenem for high-risk febrile neutropenia in haematology patients (SHORT trial): results from a randomised multi-centre non-inferiority trial**
N. De Jonge (Amsterdam, Netherlands), J. Sikkens, J. Janssen, S. Zweegman, A. Beeker, P. Ypma, A. Herbers, W. Vasmel, J. Coenen, W. Ter Haar, B. Lissenberg-Witte, A. De Kreuk, A. Budding, M. Kramer, M. Van Agtmael*

8752 **Infectious complications after chimeric antigen receptor modified T cells in adolescent and young adult relapse/refractory B cell precursor acute lymphoblastic leukaemia: report of the French experience**
F. Rabian (Paris, France), N. Boissel, M. Lafaurie, J. Larghero, I. Madelaine, E. Azoulay, J. Molina, B. Denis*

8938 **Home-based care of low-risk febrile neutropenia in children: an implementation study in a tertiary paediatric hospital**
G. Haeusler (Melbourne, Australia), B. Teh, F. Babl, L. Orme, F. Mechinaud, P. Bryant, B. Phillips, R. De Abreu Lourenco, M. Slavin, K. Thursky*

Session accepted as 1-Hour Oral Session

***Deus ex machina:* can machine learning predict infection risk?**

1664 **Validation of a machine learning model for prediction of mortality among patients with community-acquired pneumonia**
L. Ward (Aalborg, Denmark), M. Mogensen, R. Méndez, P. Gonzalez-Jimenez, C. Cilloniz Campos, A. Ceccato, A. Torres, R. Menendez*

3545 **Can machine learning predict a positive blood culture?**
B. Mcfadden (Perth, Australia), M. Reynolds, T. Inglis*

7478 **A machine learning-based model to predict bloodstream infections**
R. Murri (Rome, Italy), G. De Angelis, C. Masciocchi, B. Posteraro, N. Capocchiano, A. Marchetti, A. Damiani, P. Sergi, G. Scambia, R. Cauda, V. Valentini, M. Fantoni, M. Sanguinetti*

7615 **Artificial intelligence to support antibiotic decision-making processes in haematological patients with febrile neutropaenia**
C. Garcia Vidal (Barcelona, Spain), G. Sanjuan-Gomez, P. Puerta, E. Moreno, M. Chumbita, N. Garcia-Pouton, M. López-Garrido, C. Pitart, C. Cardozo, M. Bodro Marimont, L. Morata, J. Martínez Martínez, M. Rovira, J. Esteve, J. Mensa, A. Soriano*

8115 **Supervised machine learning algorithms to predict the patient outcome during febrile neutropenia**
C. Jakob (Cologne, Germany), M. Schons, M. Stecher, F. Fuchs, A. Walker, O. Cornely, J. Vehreschild*

Session accepted as Paper Poster Session

Epidemiology and prevention of infection in immunocompromised hosts

52 ***Clostridioides difficile* infection in immunocompromised hospitalised patients is associated with a high recurrence rate**
A. Atamna (Petah Tikva, Israel), T. Avni, J. Bishara*

645 **Interplay between inflammation and infection in a single-centre cohort of patients with X-linked agammaglobulinemia**
O. Paccoud (Paris, France), N. Mahlaoui, F. Lanternier, C. Picard, S. Blanche, O. Hermine, O. Lortholary*

2093 **Epidemiology of *Pneumocystis jirovecii* pneumonia in HIV-negative patients from 2005-2014 in the United States**
B. Hollenbeck (Boston, United States), K. Counterman, G. Miley*

2779 **Infectious complications of patients with breast cancer treated with palbociclib: unexpected serious and opportunistic infections**
M. Luck (Buenos Aires, Argentina), P. Costantini, G. Zapata, P. Garcia, A. Sorge, M. Vallejos, V. Lopez, A. Aguilar, J. Serer, M. Savignano, G. Roganovich, L. Albi, M. Bronzi, D. Bucher, V. Caceres*

3808 **TB screening and treatment in an Italian cohort of haematopoietic stem cell transplant recipients**
A. Della Vecchia (Genoa, Italy), C. Di Grazia, A. Dominietto, A. Raiola, E. Angelucci, M. Bassetti, V. Claudio, M. Mikulska*

4076 **Strategy for cytomegalovirus reactivation prevention with ganciclovir and high dose of valacyclovir in allogeneic stem cell transplantation**
M. Lopez (Bogota, Colombia), E. Pedraza, J. Figueroa, E. Mora, M. Gómez, S. Ardila, A. Guarín, O. Peña, C. La Madrid, G. López, L. Villamizar, D. Díaz*

5413 **Antifungal prophylaxis in acute myeloid leukaemia patients receiving chemotherapy is cost-effective in a resource-limited country**
T. Pungprasert (Lampang, Thailand), P. Phikulsod, V. Srinonprasert, D. Dhirachaikulpanich, N. Tantai, S. Maneeon*

5632 **Treating nocardiosis with cotrimoxazole monotherapy in solid organ transplant recipients: real-life data from a multi-centre retrospective study**
C. Pierre-Louis (Saint-Mandé, France), M. Marie, A. Bleibtreu, H. Guillot, S. Van Laecke, H. Brenier, R. Crochette, M. Giovanna, M. Fernandez-Ruiz, J. Dantal, L. Walti, C. Levi, C. Chauvet, J. De Greef, S. Marbus, N. Mueller, M. Ieven, F. Vuotto, O. Lortholary, J. Coussement, D. Lebeaux*

5686 **The effectiveness of antibiotic prophylaxis in the prevention of respiratory tract infections in antibody-deficient patients: a single-centre cohort study**
M. Albur (Bristol, United Kingdom), A. Grammatikos, S. Johnston*

5744 **Prevalence of infections in the risk for infection in immunosuppression outpatient consultation:a retrospective analysis between 2014-2018**
J. Granado (Lisbon, Portugal), A. Miranda, M. Sanches, S. Casanova, J. Domingos, J. Vasconcelos, J. Alves, T. Baptista, S. Peres, K. Mansinho*

6495 **Prospective study of breakthrough invasive fungal infections in haematologic patients in Spain**
E. Moreno (Zaragoza, Spain), P. Puerta, J. Soto-Debrán, C. Martin Gandul, M. Batlle, J. Badiola, A. Fernandez-Cruz, M. Machado, J. Ramos Ramos, L. Gomez, C. Gudiol, I. Ruiz, M. Chumbita, P. Martín-Dávila, L. Yañez, L. Vázquez, N. Garcia-Pouton, J. Fortun Abete, J. García Rodríguez, P. González, F. Marco Reverte, I. Sanchez-Romero, M. Quesada, J. Guinea Ortega, M. Aguilar-Guisado, A. Soriano, A. Alastruey-Izquierdo, C. Garcia Vidal*

8636 **Efficacy of a screening and prophylaxis protocol to prevent infections in patients treated with anti-CD20/CD52 for multiple sclerosis**
A. Buonomo, E. Zappulo, R. Scotto, L. Bruno, B. Pinchera (Naples, Italy), I. Gentile*

9606 **Oral empiric antibiotic treatment given in an ambulatory setting for febrile neutropenic patients with a solid tumour, predicted at low-risk for serious complication**
A. Loizidou (Brussels, Belgium), A. Georgala, J. Klastersky, M. Aoun*

Session accepted as Paper Poster Session

Evaluating host responses to diagnose infection

437 **Dynamic monitoring of sTREM-1 and other biomarkers in biliary tract infection**
J. Jiang (hangzhou, China), D. Yu*

1528 **Comparison of host immune responses *in vivo* versus *ex vivo* lipopolysaccharide stimulation in humans using an immune transcriptomic profiling panel**
D. Tawfik (Lyon, France), J. Lankelma, L. Ganee, E. Cerrato, A. Pachot, W. Wiersinga, J. Textoris*

1655 **Comparison of prognostic capacity of presepsin and procalcitonin in adult septic patients: results from a prospective observational study in two university clinical centres**
A. Aliu Bejta (Prishtine, Kosovo), S. Namani, B. Halili, D. Pllana-Hajdari, B. Baršić, A. Atelj*

1726 **Reactive hyperaemia measured by peripheral arterial tonometry correlates with glycocalyx degradation and the presence of sepsis in the critically ill patient**
L. Malheiro (Porto, Portugal), R. Gaio, M. Vaz-Da-Silva, S. Martins, A. Sarmento, L. Santos*

4008 **Comparison of a cartridge-based host gene expression test to a manual method for use in the diagnosis of sepsis**
W. Sinclair (Salt Lake City, United States), J. Mccleave, P. Sillekens, I. Keuleers, T. Vanhoey, S. Cermelli, B. Lopansri*

4338 **Host biomarkers to differentiate bacteraemias from microbiologically proven viral infection in adults with acute fever episodes attending outpatient clinics in Tanzania**
L. Lhopitallier (Lausanne, Switzerland), M. Richard-Greenblatt, K. Zong, Z. Mbarak, J. Samaka, T. Mlaganile, T. Kazimoto, A. Mamin, B. Genton, L. Kaiser, K. Kain, V. D'Acremont, N. Boillat-Blanco*

4750 **Predictive value of CD4+T helper lymphocytes, associated biomarkers and procalcitonin in the prognostication of polytrauma patients with sepsis**
S. Khurana (Delhi, India), P. Mathur, N. Bhardwaj, S. Kumar, S. Sagar, R. Aggarwal, K. Soni, R. Malhotra*

5096 **The REAnimation Low Immune Status Markers study: phenotypic and functional alterations of innate immune response in critically ill patients**
V. Moucadel (Lyon, France), F. Venet, J. Textoris, S. Blein, M. Rol, B. Canard, P. Cortez, L. Tan, L. Quemeneur, A. Griffiths, E. Peronnet, A. Pachot, G. Monneret, T. Rimmelé*

5206 **Pro-protein convertase subtilisin/kexin type 9 (PCSK9) is elevated in bloodstream infections and correlates with c-reactive protein**
C. Pallotto (Perugia, Italy), V. Scaglione, S. Bastianelli, C. Busti, D. Francisci*

8135 **Proinflammatory biomarkers are not useful as sepsis outcome predictors in patients older than 75**
S. Mitic (Novi Sad, Serbia), S. Adamovic, A. Vukelic, D. Becejac, D. Lendak*

Session accepted as Paper Poster Session

Host responses to infection evaluated *in vitro* and *in vivo*

529 **Regulation of intestinal bacterial translocation by intestinal lamina propria dendritic cells expressing TLR5 after trauma/haemorrhagic shock**
Z. Yun (Hangzhou, China), J. Zhang, C. Zhang*

681 **Generation of protective antibodies against heterologous *Acinetobacter baumanni* isolates**
G. Kamuyu (London, United Kingdom), S. Willcocks, C. Kewcharoenwong, R. Stabler, B. Wren, G. Lertmemongkolchai, J. Brown*

1257 **The role of liposome positive charge on immune response generated in BALB/c mice immunized with *Leishmania* homologue of receptors for Activated C Kinase (LACK) of *Leishmania major***
M. Soosaraei (Sari, Iran)*

1508 **Serum active Granzyme A: a new biomarker that contributes to the pathogenesis of peritoneal sepsis**
M. Garzón (Zaragoza, Spain), J. Sierra Monzón, L. Comas, I. Uranga Murillo, E. Morte Romea, S. Algarate, T. Khaliulina Ushakova, C. Seral, P. Luque Gómez, J. Paño Pardo, E. Gálvez, M. Arias, J. Pardo Jimeno*

1663 **Bacterial DNA promotes tau and beta-amyloid aggregation and is suggested as a novel therapeutic target for Alzheimer's disease**
G. Tetz (New York, United States), S. Pritzkow, M. Pinho, N. Mendez, C. Soto, V. Tetz*

2212 **Efficacy of memory B lymphocytes in experimental model of pneumonia caused by *Pseudomonas aeruginosa***
T. Cebrero Cangueiro (Seville, Spain), G. Labrador Herrera, M. Carretero Ledesma, Y. Smani, J. Pachon-Diaz, M. Pachon-Ibáñez*

2226 **Efficacy of immunoglobulin enriched in IgM, alone and in combination, in experimental model of pneumonia caused by *Pseudomonas aeruginosa***
T. Cebrero Cangueiro (Seville, Spain), G. Labrador Herrera, M. Carretero Ledesma, Y. Smani, J. Pachon-Diaz, M. Pachon-Ibáñez*

2930 **Two-photon microscopy contribution for exploration of innate immunity pulmonary mechanism after influenza virus infection of mice model**
F. Riviere (Bretigny sur Orge, France), C. Vigne, J. Burger, A. Garnier, J. Tournier, E. Billon-Denis*

3919 **Type I interferons mediate antiviral resistance to Zika virus in human macrophages**
A. Hanrath (Newcastle upon Tyne, United Kingdom), C. Hatton, C. Browne, J. Vowles, S. Cowley, W. James, S. Hambleton, C. Duncan*

4842 **Investigation of the pro-autophagic effect of IL-36α and lipopolysaccharide in THP-1 cell line**
Z. Al-Luhaibi (Szeged, Hungary), K. Megyeri, G. Seprényi*

6558 **Monocyte progenitors are effector cells in mycobacterial infections**
A. Loesslein, P. Henneke (Freiburg, Germany)*

7487 **Pharmacokinetics of radiolabeled anti-mousePD-L1 in immune-challenged tumour-bearing mice**
G. Sandker, P. Wierstra, J. Molkenboer-Kuenen, M. Gotthardt, G. Adema, J. Bussink, S. Heskamp, E. Aarntzen (Nijmegen, Netherlands)*

8201 **Cell immunity in maxillofacial actinomycosis diseases**
N. Agayeva (Baku, Azerbaijan), V. Narimanov, E. Agayeva, H. Aliyeva, R. Bayramova*

8555 **Inflammatory response of murine macrophages and alveolar epithelial cells following exposure to *Aspergillus fumigatus* spores**
F. Agostini (Oullins Cedex, France), M. Delles, T. Déméautis, G. Devouassoux, A. Bentaher, J. Menotti*

Session accepted as Paper Poster Session

Human host response and susceptibility to Infection

1697 **NK cell deficiency and cryptococcosis**
M. Martinot (Colmar, France), C. Farnarier, S. Li, C. Piperoglou, C. Démerle, M. Mohseni-Zadeh, C. Mody, F. Vely*

1788 **Characterisation of immune response of patients with rheumatic disorders and latent tuberculosis infection**
E. Petruccioli, V. Vanini, G. Cuzzi, T. Alonzi, L. Petrone, F. Palmieri, G. Ippolito, D. Goletti (Rome, Italy)*

1835 **Tuberculosis impacts immune-metabolic pathways resulting in perturbed cytokine responses**
A. Llibre, V. Rouilly, M. Musvosvi, E. Nemes, C. Posseme, S. Mabwe, B. Charbit, V. Saint-Andre, V. Bondet, P. Bost, H. Mulenga, N. Bilek, M. Albert, T. Scriba, D. Duffy (Paris, France)*

2669 ***Streptococcus pneumoniae*** **intracellular survival in THP-1 macrophages activated with different doses of lipopolysaccharide**
P. Conde, N. Vázquez Burgos (Molins de Rei, Spain), R. López, L. Fernandez Barat, A. Torres*

2688 **Toll like receptors, IFN-lambdas and IFN-stimulated genes expression in cystic fibrosis patients with rhinovirus infection**
F. Frasca (Rome, Italy), C. Bitossi, A. Viscido, G. Oliveto, M. Scordio, M. Trancassini, V. Pietropaolo, F. Midulla, G. Cimino, P. Palange, A. Pierangeli, C. Scagnolari, G. Antonelli*

2921 **Bacteraemia with ESBL-producing** ***Enterobacteriaceae*** **is associated with increased levels of IgG antibodies specific to CTX-M-15 and/or CTX-M-27**
T. Sahlström, O. Ljungquist (Skäret, Sweden), Y. Su, F. Resman, E. Mattsson, J. Tham, K. Riesbeck*

4044 **Th2 response may be deleterious to protect against** ***Staphylococcus aureus*** **bacteraemia**
A. Le Bot (Rennes, France), V. Bordeau, S. Reissier, S. Dion, C. Gonzalez, M. Gregoire, M. Lesouhaitier, S. Chabelskaia, F. Brice, M. Revest*

5514 **Pentameric IgM does not improve clinical outcome in adults with sepsis after major abdominal surgery**
A. Perrella (Naples, Italy), L. Rinaldi, M. Castriconi, M. Mazzone, P. Pafundi, M. Montanaro, P. Saturnino*

5764 ***Clostridioides difficile*** **infection is associated with persistent high level of innate immune response**
A. Oliva (Rome, Italy), M. Zingaropoli, M. De Angelis, F. Mengoni, M. Ciardi, V. Vullo, C. Mastroianni*

6943 **Utility of early kinetics of TTV DNA in stool for the prediction of intestinal graft versus host disease in the allogeneic haematopoietic stem cell transplantation setting**
E. Giménez (Valencia, Spain), A. Eliseo, F. Bueno, C. Ubeda, J. Piñana, J. Hernández-Boluda, J. Montoro, M. Salavert, M. Tormo, R. Hernani, A. Pérez, M. Gomez, C. Solano, D. Navarro*

7383 **Association of IL-27 and STAT3 genetic polymorphism on the susceptibility of tuberculosis in western Chinese Han population**
M. Li (Chengdu, China), L. Jiao, W. Min Jin, H. Bai, Q. Wu, X. Chen, B. Ying*

7525 **Innate immunity measured by leukocyte deformability predicts outcomes in undifferentiated emergency department patients with urinary symptoms**
C. Thomas, M. Musso, D. Hamer, R. Sheybani, T. Caffery, H. Tse, A. Shah, H. O'Neal Jr (Baton Rouge, United States)*

8221 **Controlled human infection with** ***Neisseria lactamica*** **induces B cell responses that are cross-reactive with** ***Neisseria meningitidis***
A. Dale (Southampton, United Kingdom), A. Theodosiou, J. Laver, E. Roche, A. Hill, A. Gorringe, M. Polak, A. Vaughan, R. Read*

Session accepted as Paper Poster Session

Immunisation: new challenges and new solutions

445 **Immunisation and multiple sclerosis: recommendations from the French Multiple Sclerosis Society**
C. Lebrun-Frenay (Nice, France), S. Vukusic*

600 **Impact of a catch-up strategy of Tdap vaccination during hospitalisation on vaccination coverage among people over 65 years of age in Sarthe: the HOSPIVAC study**
S. Blanchi (Le Mans, France), N. Crochette, L. Hery, S. Laforest, J. Toque, J. Vaux*

668 **Analysis of the vaccination coverage in a dispensary in Mayotte, an oversea department and region of France**
C. Pascal (Blavozy, France), O. Lesens*

813 **Physicochemical characterisation of aluminium hydroxide and aluminium phosphate and their potential adjuvant function in combination with squalene emulsion for EV71 vaccine development**
M. Huang (Zhunan, Taiwan)*

930 **Factors influencing vaccination coverage among children age 12–23 months in Afghanistan**
M. Mohammad Yousuf (Kabul, Afghanistan), A. Aalemi, K. Shahpar*

1330 **Vaccination Perception (VP) and Vaccination Coverage (VC) among healthcare students (HCS), a prospective French study : PERCEVAC Study**
A. Baldolli (Caen, France), A. Fournier, X. Lecoutour, R. Verdon, J. Michon*

2263 **Initiation of an immunisation and catch-up programme in schools in a country with a high vaccine hesitancy: yes we can!**
J. Michon (Caen, France), A. Fournier, F. Appia, S. Villedieu, C. Porterie, A. Leprieur, R. Verdon, A. Baldolli*

2640 **Pertussis among ≤ 3 months old in Finland, 2015-2018: should we refine our adult immunisation schedule or switch to maternal immunisation?**
T. Dub (Helsinki, Finland), M. Gissler, T. Möttönen, J. Sane, H. Nohynek*

4608 **Live probiotic vaccine against influenza virus infection**
T. Gupalova, Y. Desheva, G. Leontieva, E. Kuleshevich, T. Kramskaya, E. Bormotova, A. Tsapieva, A. Suvorov (St. Petersburg, Russian Federation)*

5619 **Research priorities to increase vaccination coverage (EU Joint Action on Vaccination)**
F. Francis-Oliviero (Bordeaux, France), S. Bozoki, M. Kieny, G. Chêne, J. Lelievre*

Session accepted as Paper Poster Session

Infection, haematological malignancy and stem cell transplants

395 **The economic burden of** ***Clostridioides difficile*** **infection in patients with haematological malignancies: a case-control study**
L. Duhalde, L. Lurienne (Paris, France), S. Wingen-Heimann, L. Guillou, R. Buffet, P. Bandinelli*

936 **Risk factors and clinical characteristics of virus Infection after haematopoietic stem cell transplantation**
G. Kalın Ünüvar (Kayseri, Turkey), Z. Ture Yuce, A. Ulu Kilic*

1895 **Dalbavancin as definitive therapy for Gram-positive infections in patients with haematologic malignancies and haematopoietic cell transplant recipients**
C. Howard (Morgantown, United States), A. Cumpston, D. Slain*

4889 **Infections in haematological patients receiving CD19 CAR-T cell immunotherapy: real-life data**
C. Cardozo (Barcelona, Spain), J. Delgado, V. Ortiz-Maldonado, P. Puerta, E. Moreno, M. Chumbita, N. Garcia-Pouton, A. Urbano-Ispizua, J. Esteve, M. Juan, A. Soriano, C. Garcia Vidal*

5088 **Trends in Gram-negative bacteraemia in adult febrile neutropaenic cancer patients in a high-resistance setting during the last decade**
C. Ayaz, E. Bilgin, G. Hazırolan, B. Sancak, M. Akova (Ankara, Turkey)*

5470 **Catheter-related and non-catheter-related bloodstream infections in oncological patients**
M. Blanco, C. Traseira, A. Ramos Martínez, I. Sanchez-Romero, E. Muñez Rubio, A. Callejas, J. Sánchez, M. Méndez, L. Gutiérrez, B. Núñez, M. Provencio, A. Fernandez-Cruz (Madrid, Spain)*

5474 **Infectious complications during anti-CD19 targeted chimeric antigen T cell receptors (CAR-T) immunotherapy in relapsed/refractory aggressive B cell non-Hodgkin lymphomas (NHL): observational retrospective study in one centre**
R. Di Blasi (Paris, France), S. Chevret, J. Paillassa, B. Denis, L. Aguinaga, S. Bernard, H. Moatti, M. Lafaurie, E. Azoulay, M. Darmon, E. Galli, C. Thieblemont*

6970 **Predictive value of a positive *Pneumocystis jirovecii* DNA result in the diagnosis of *Pneumocystis jirovecii* pneumonia in haematological patients**
A. Eliseo (Valencia, Spain), E. Giménez, F. Bueno, J. Piñana, M. Gomez, A. Pérez, A. Balaguer, J. Hernández-Boluda, J. Montoro, M. Salavert, M. Tormo, R. Hernani, R. Borras, J. Sanz, C. Solano, D. Navarro*

7421 **Infections associated with kinase and antiapoptotic *Bcl*-2 inhibitors in a cohort of real-life haematological patients**
E. Moreno (Zaragoza, Spain), P. Puerta, N. Garcia-Pouton, V. Rico Caballero, C. Roig, C. Castillo, C. Helguera, M. Chumbita, C. Cardozo, T. Baumann, E. Giné, J. Delgado, J. Correa, V. Ortiz-Maldonado, A. Soriano, C. Garcia Vidal*

7604 **Incidence and utility of follow-up blood cultures in haematology/oncology patients with Gram-negative bacteraemia**
A. Clemmons (Augusta, United States), D. Chastain, H. Young, M. Hayashi, E. Kennedy, C. Bland*

7710 **Clinical characteristics and mortality-related factors of bloodstream infections in patients with acute leukaemia: a single-centre experience with 152 patients**
G. Mendez, C. Niveyro (Posadas, Argentina), P. Villalba, K. Salvatierra, C. Villalba, H. Bernard*

7863 **The management of *Enterococcus* bloodstream infections in cancer patients: impact of central venous catheters**
H. Awadh, M. Khalil, A. Chaftari (Houston, United States), J. Fares, Y. Jiang, R. Wilson Dib, S. Ali, R. Hachem, I. Raad*

7994 **Potential role of procalcitonin in antimicrobial stewardship programme in febrile neutropenic cancer patients**
P. Chaftari (Houston, United States), A. Chaftari, R. Hachem, S. Yeung, Y. Jiang, A. Malek, V. Mulanovich, I. Raad*

8178 **Application of WISCA (Weighted Incidence Syndromic Combination Antibiogram) to guide empiric therapy in oncological paediatric patients with febrile neutropenia**
E. Barbieri (Padova, Italy), D. Bottigliengo, P. Costenaro, A. Marzollo, M. Petris, M. Pierobon, G. Biddeci, C. Giaquinto, A. Biffi, D. Donà*

8465 **Infectious complications in patients with relapsed/refractory Hodgkin's lymphoma during new agents' therapy**
Y. Rogacheva (Saint Petersburg, Russian Federation), M. Popova, K. Lepik, E. Kondakovae, Y. Zalylov, L. Stelmah, A. Volkova, I. Nikolaev, O. Goloshapov, I. Barkhatov, S. Bondarenko, I. Moiseev, V. Baykov, N. Mikhaylova, N. Klimko, B. Afanasyev*

9053 **Trends in antimicrobial resistance in Gram-negative pathogens among haematological patients: results of multi-centre study**
G. Klyasova (Moscow, Russian Federation), A. Korobova, S. Khrulnova, A. Fedorova Mironova, I. Frolova, K. Tandilova, A. Vetokhina, I. Molchanova, O. Kutsevalova*

9131 **Carbapenemase-producing *Klebsiella pneumoniae* belonging to sequence type 23 is a predictor of poor outcome in haematological patients**
K. Tandilova (Moscow, Russian Federation), G. Klyasova, S. Khrulnova, P. Elena, S. Kravchenko, E. Gribanova, E. Zvonkov, G. Galstyan, V. Savchenko*

9377 **Discontinuation of antimicrobial therapy during fever of unknown origin in adult neutropenic patients according to ECIL-4 criteria: RELAPS, a descriptive cohort study**
R. Paret (Brest, France), A. Lebourgeois, P. Peterlin, T. Gastinne, R. Lavergne, F. Morio, D. Colin, R. Lecomte, S. Legouill, D. Boutoille, B. Gaborit*

9542 **Outcome of infections caused by carbapenemase-producing *Enterobacterales* in patients with haematological disorders**
K. Tandilova (Moscow, Russian Federation), G. Klyasova, S. Khrulnova, P. Elena, S. Kravchenko, E. Gribanova, E. Zvonkov, G. Galstyan, V. Savchenko*

9566 **Cytomegalovirus reactivation in allogeneic stem cell transplant recipients: frequency, time to reactivation and dynamic of viraemia in different types of donors and in repeated episodes**
M. Garnica (Rio de Janeiro, Brazil), S. Dalcolmo, B. Gaio, I. Alves, M. Valetim, A. Maiolino*

Session accepted as Paper Poster Session

Infections after solid organ transplant

429 **Late-onset *Pneumocystis jirovecii* pneumonia in renal transplant recipients**
A. Cruz (Sterling Heights, United States), C. Jarrin Tejada*

1577 **Efficacy of beta-lactam/beta-lactamase inhibitors to treat extended-spectrum beta-lactamase-producing *Enterobacterales* bacteraemia secondary to urinary tract infection in kidney transplant recipients**
E. Perez-Nadales (Cordoba, Spain), L. Pierrotti, M. Fernandez Ruiz, B. Gutiérrez-Gutiérrez, T. Ban Hock, J. Carratalà, I. Oriol Bermúdez, M. Paul, N. Cohen-Sinai, F. Lopez-Medrano, R. San Juan Garrido, M. Montejo Baranda, M. Freire, E. Cordero Matias, M. David, E. Merino De Lucas, S. Mehta Steinke, P. Grossi, Á. Cano Yuste, E. Seminari, M. Valerio Minero, F. Gunseren, M. Rana, A. Mularoni, P. Martín-Dávila, C. Van Delden, M. Demirkaya, Z. Kocak Tufan, M. Loeches Yague, R. Iyer, F. Soldani, B. Eriksson, P. Benoit, M. Rizzi, J. Coussement, W. Clemente, E. Roilides, A. Pascual Hernandez, L. Martinez-Martinez, J. Rodríguez-Baño, J. De La Torre Cisneros, J. Aguado Garcia, I. Investigators*

1883 **Post-transplant lymphoproliferative disorders and association of antiviral prophylaxis in a nationwide cohort study**
L. Walti (Bern, Switzerland), C. Mugglin, D. Sidler, M. Mombelli, O. Manuel, H. Hirsch, N. Mueller, K. Boggian, C. Garzoni, D. Neofytos, C. Hirzel*

1993 **Characterisation of differences in infectious disease events between first liver transplantation and re-transplantation in the STCS**
P. Schreiber (Zurich, Switzerland), K. Kusejko, D. Neofytos, H. Hirsch, P. Meylan, O. Manuel, K. Boggian, C. Hirzel, C. Garzoni, R. Kouyos, N. Mueller, S. Cohort Study*

2187 **Risk factors for developing BK virus associated nephropathy: a single-centre retrospective cohort study of kidney transplant recipients**
C. Lorant (Uppsala, Sweden), G. Westman, A. Bergqvist, B. Von Zur-Mühlen, B. Eriksson*

2509 **Hospital-acquired pneumonia in liver transplant recipients**
V. Khillan (New Delhi, India), G. Pindi, V. Pamecha, P. Kale*

3373 **High-dimensional single cell analysis identifies unexpected distribution of T cell populations in liver transplanted HIV-positive patients**
E. Franceschini (Modena, Italy), S. De Biasi, M. Digaetano, M. Menozzi, L. Gibellini, G. Tarantino, D. Lo Tartaro, E. Bianchini, M. Nasi, M. Codeluppi, G. Guaraldi, F. Di Benedetto, A. Cossarizza, C. Mussini*

3581 **Epidemiology and outcomes of microbiologically documented bacterial foodborne infections in solid organ transplant recipients: a 10-year nationwide cohort**
L. Van Den Bogaart (Lausanne, Switzerland), A. Egli, L. Walti, D. Neofytos, C. Garzoni, K. Boggian, C. Berger, N. Mueller, O. Manuel, M. Mombelli*

3905 **Intra-abdominal candidiasis after pancreatic transplantation: epidemiology, use of antifungal prophylaxis, risk factors and impact on pancreatic graft**
L. Linares, L. Nuzzolo, L. Pacho, P. Ventura, F. Cofan, J. Ferrer, F. Marco Reverte, F. Diekmann, M. Moreno Camacho, M. Bodro Marimont (Barcelona, Spain)*

3968 **Measles seropositivity in renal transplant recipients in the presence of ongoing outbreaks: a single centre analysis**
F. Wagner, D. Sidler, M. Barbani, F. Suter-Riniker, P. Jent, C. Hirzel, L. Walti (Bern, Switzerland)*

5297 **Impact of pretransplant norfloxacin prophylaxis on multidrug-resistant post–liver transplant infections**
C. Pérez-Cameo, I. Oriol Bermúdez, N. Sabe, L. Castells, L. Lladó Garriga, R. Charco, C. Dopazo, V. Vargas Blasco, F. Nuvials, M. Lung, M. Viñado, I. Los-Arcos, J. Gavaldà, O. Len (Barcelona, Spain)*

5409 **Investigating the microbiological growth of donor organ preservation fluid in liver and kidney transplantation**
J. Helliwell, N. Cutmore (Leeds, United Kingdom), N. Young*

5638 **Risk factors for carbapenem-resistant *Enterobacteriaceae* acquisition among kidney transplant recipients**
M. Freire (Sao Paulo, Brazil), L. Carvalho, F. Spadao, F. De Paula, W. Nahas, E. David Neto, L. Pierrotti*

5681 **Usefulness of human cytomegalovirus (HCMV)-specific immunological monitoring in the management of HCMV infection in lung transplant recipients**
S. Uceda Renteria (Milan, Italy), I. Cassaniti, L. Morlacchi, V. Rossetti, R. Carrinola, G. Giacomel, M. Spolti, C. Vigano, L. Tartaglione, A. Orlandi, M. Oggioni, E. Benazzi, A. Paleschi, F. Baldanti, G. Lunghi*

6370 **Protective role for cytomegalovirus-specific neutralising antibodies in kidney transplant recipients treated with T-cell-depleting agents**
M. Fernandez Ruiz (Madrid, Spain), V. Sandonis, T. Ruiz Merlo, P. Parra, F. Lopez-Medrano, R. San Juan Garrido, L. Corbella Vazquez, I. Rodriguez Goncer, A. Andrés, D. Navarro, J. Aguado Garcia, P. Pérez-Romero*

6841 **Infections due to multidrug-resistant bacteria among Swiss solid organ transplant recipients between 2012 and 2017**
P. Kohler (St. Gallen, Switzerland), A. Wolfensberger, S. Stampf, A. Brönnimann, K. Boggian, C. Van Delden, C. Hirzel, N. Khanna, S. Kuster, D. Neofytos, O. Manuel, S. Ragozzino, P. Schreiber, L. Walti, N. Mueller*

7210 **Brucellosis in different types of transplantation**
M. Rabiei, F. Imanzade, I. Alavidarazam (Tehran, Iran), S. Shokouhi*

7891 **Early cytomegalovirus reactivation and bacterial infections affect the mortality of patients after kidney transplant**
I. Spalliera (Rome, Italy), M. Iannetta, N. Cesta, M. De Masi, V. Malagnino, C. Cerva, L. Ferrari, L. Toti, G. Tisone, M. Andreoni, L. Sarmati*

Session accepted as Mini-oral Flash Session

Moving targets: vaccines and the changing epidemiology of measles and pneumococcal disease

1232 **Increase in potentially measles-susceptible young healthcare workers in South Korea**
Y. Kim (Wonju, South Korea), B. Ha, H. Jeong, G. Hwang, Y. Uh, I. Jung, H. Kim*

1840 **Comparison of early effects of *Streptococcus pneumoniae* vaccination policies on nasopharyngeal carriage in a Palestinian population**
M. Ramlawi (Jerusalem, Palestine), K. Azmi, Z. Abdeen*

2283 **Vaccination perception and factors influencing MMR vaccination decisions during a university measles outbreak in a country with a high vaccine hesitancy**
J. Michon (Caen, France), A. Fournier, F. Appia, S. Villedieu, A. Leprieur, C. Porterie, R. Verdon, A. Baldolli*

4730 **Vitamin D3 supplementation with a daily dose of 400 or 1200 IU results in similar antibody concentrations to measles, mumps and rubella in vaccinated 2-year-old Finnish children**
M. Melin (Helsinki, Finland), N. Ekström, M. Kontio, J. Rosendahl, S. Valkama, E. Holmlund-Suila, M. Enlund-Cerullo, H. Hauta-Alus, T. Hytinantti, H. Viljakainen, S. Andersson, O. Helve*

5130 **The proportion of invasive pneumococcal disease and pneumococcal pneumonia in UK adults potentially covered by the 13-valent and the next-generation of higher-valency pneumococcal conjugate vaccines under development**
A. Vyse (Waton Oaks, Tadworth, United Kingdom), J. Campling, C. Czudek, G. Ellsbury, M. Slack*

5390 **Invasive pneumococcal disease among adults in Germany, nine years after PCV13 introduction**
M. Van Der Linden (Aachen, Germany), A. Itzek, S. Perniciaro, M. Imöhl*

6555 ***Streptococcus pneumoniae*: serotype distribution in adults with invasive disease after 8 years of systematic vaccination of children with PCV13**
P. Juiz González (Ferrol, Spain), S. Mendez Lage, N. Somaza Serantes, I. Losada, M. Rodriguez Mayo, G. Barbeito, F. Vasallo Vidal, I. Paz Vidal, F. Garcia Garrote, V. Pulián Moráis, M. Serrano López, J. Alba, P. Alonso Alonso, I. Rodriguez Conde, J. Agulla Budiño*

6757 **Potential coverage of invasive pneumococcal disease by current and next generation of anti-pneumococcal vaccines in children and adults in Spain**
S. De Miguel, M. Domenech, J. Sempere, I. Del Rio, B. López Ruiz, F. González Camacho, J. Yuste (Madrid, Spain)*

6820 **Mapping a nosocomial outbreak of measles, coinciding with a period of sustained transmission in south London in 2018**
J. Vink, L. Snell (London, United Kingdom), K. Bernard, H. Mitchell, R. Thorn Heathcock, W. Newsholme*

9350 **A prolonged measles outbreak in a vaccine refusing community, Austria, 2019**
L. Henszel (Vienna, Austria), D. Schmid, A. Grisold, H. Holzmann*

Session accepted as Mini-oral ePoster Session

Multidrug-resistant infections in patients with haematological malignancy

794 ***Stenotrophomonas maltophilia* bloodstream infections in umbilical cord blood transplant recipients**
M. Kimura (Tokyo, Japan), H. Araoka, S. Ogura, M. Yuasa, D. Kaji, K. Kageyama, Y. Taya, S. Takagi, H. Yamamoto, G. Yamamoto, Y. Asano-Mori, N. Uchida, S. Taniguchi, A. Yoneyama*

965 **Shortened antibiotic treatments for Gram-negative bacteraemia in cancer patients: less is possible**
F. Herrera, D. Torres, A. Carena, M. Jorge, E. Temporiti, F. Nicola, A. Rearte (Buenos Aires, Argentina), S. Zerboni, F. Bues, P. Bonvehi*

1557 **Incidence of bloodstream infection from multidrug-resistant bacteria in haematological patients with rectal colonisation**
M. Peradotto (Turin, Italy), G. Bianco, M. Boattini, A. Bondi, M. Iannaccone, Z. Teresa, R. Cavallo, C. Costa*

2142 **Breakthrough blood culture isolates whilst on broad spectrum antimicrobial therapy for high-risk neutropenic fever: more common and resistant that previously thought**
A. Douglas (Parkville, Australia), S. Tio, K. Thursky, L. Worth, A. Bajel, M. Slavin*

2851 **Optimal treatment duration of *Pseudomonas aeruginosa* infections in allogeneic haematopoietic cell transplant recipients**
F. Olearo (Hamburg, Germany), I. Kronig, N. Mueller, U. Schanz, N. Khanna, J. Passweg, M. Medinger, S. Masouridi Levrat, Y. Chalandon, C. Van Delden, D. Neofytos*

4809 **Intestinal colonisation by multidrug-resistant *Enterobacteriaceae* and infections in patients receiving an allogeneic haematopoietic stem cell transplantation: the ENTHERE-SCT Study (PI16/01415)**
C. González Rico (Santander, Spain), M. Fernández-Martínez, M. Bermudez-Rodriguez, I. Gracia-Ahufinger, I. García-García, G. Maestro, C. Fariñas Alvarez, C. Martín Calvo, J. Aguado Garcia, L. Vázquez, L. Martinez-Martinez, M. Fariñas*

8002 **Haematology/oncology patients might have different risks for MDR according to different types of chemotherapy**
J. Barbosa (São Paulo, Brazil), K. Yaqub Ibrahim, P. Bonazzi, D. Peixoto, R. Ito, E. Abdala, M. Freire*

9123 **Impact of non-use of levofloxacin prophylaxis during neutropaenia on reduction of resistance among Gram-negatives causing bloodstream infection in haematopoietic stem cell transplantation patients: very successful preliminary data**
T. Guimaraes (São Paulo, Brazil), F. Spadao, L. Caroline, M. Nascimento, V. Rocha, S. Figueiredo Costa*

9141 **The probability of infection caused by carbapenemase-producing *Enterobacterales* (CPE) in haematological patients with rectal carriage of CPE**
K. Tandilova (Moscow, Russian Federation), G. Klyasova, S. Khrulnova, P. Elena, S. Kravchenko, E. Gribanova, E. Zvonkov, G. Galstyan, V. Savchenko*

Session accepted as Mini-oral ePoster Session

New ideas in vaccinology

3340 **Identification of anti-TPI H8 antibody-epitope analogues as putative active vaccine against *Staphylococcus aureus***
L. Rummler (Cologne, Germany), S. Mertins, M. Kroenke, A. Klimka*

5418 **Novel lipid A mimetics (BECC438 and BECC470) act as potent adjuvants in bacterial and viral subunit vaccines**
E. Harberts, D. Varisco, A. Jain, C. Middaugh, R. Ernst (Baltimore, United States)*

5425 **Nanoparticles loaded with extracts of *Brucella abortus* vaccine (strain RB51) trigger protective immune responses in murine macrophages and splenocytes**
A. Cubero Ribas, G. March Rosselló, M. Gutiérrez, D. Gobelli, C. Durantez, D. Miguel Angel, M. Simarro, A. Orduna Domingo (Valladolid, Spain)*

5531 **The recombinant NP-HA2 fusion protein as a candidate for designing of universal influenza vaccines**
M. Zeinolabedin, M. Moghadaszadeh (Tabriz, Iran), P. Zeinolabedini*

7091 **Cross-reactivity of antigenic enterococcal proteins against *Staphylococcus aureus* for the development of a vaccine to fight Gram-positive ESKAPE pathogens**
F. Romero-Saavedra (Munich, Germany), D. Laverde, J. Huebner*

Session accepted as 1-Hour Oral Session

The contribution of host genetics to infection risk

3669 **Increased risk of bacteraemia caused by *Staphylococcus aureus* or *Escherichia coli* in patients with C10X polymorphism in the NLRP3 inflammasome gene *CARD8***
G. Rasmussen (Örebro, Sweden), B. Asfaw, G. Jacobsson, H. Enroth, C. Jendle Bengten, A. Brauner, A. Kelly, E. Särndahl, B. Söderquist*

3911 **Genetic score involving polymorphisms of innate immune receptors for predicting cytomegalovirus infection in solid organ transplant recipients: a prospective multi-centre cohort study**
M. Bodro Marimont (Barcelona, Spain), C. Cervera, F. Lozano, L. Linares, J. Llopis, G. Sanclemente, M. Fernandez Ruiz, M. Farinas, S. Cantisan, M. Montejo Baranda, E. Cordero Matias, I. Oriol Bermúdez, M. Marcos, M. Moreno Camacho*

5416 **Susceptibility to Group A *Streptococcus* invasive infections in children: preliminary results of a multi-centre prospective study in France: the STREPTOPEDIA study**
J. Gaschignard (Paris, France), B. Philippe, C. Levy, F. Dubos, J. Toubiana, Y. Gillet, E. Grimprel, S. Bonacorsi, B. Boisson, J. Bustamante, C. Picard, A. Faye*

8675 **High-frequency of Specific Polysaccharide Antibody Deficiency (SPAD) in adults with unexplained recurrent and/or severe bacterial infections: the SPIDAC French Study**
S. Stabler (Lille, France), C. Lamblin, S. Gaillard, N. Just, M. Mihailescu, N. Viget, T. Sy N Diaye, E. Dzeing, G. Brunin, P. Weyrich, A. Prevotat, F. Vuotto, A. Leurs, E. Hachulla, S. Sanges, L. Terriou, D. Launay, B. Lopez, M. Bahaud, F. Batteux, M. Labalette, G. Lefèvre*

9287 **Integrating genome-wide association study with bulk and single-cell RNA sequencing reveals a role for *LY86* in the anti-*Candida* host response**
V. Kumar (Groningen, Netherlands), D. De Vries, V. Matzaraki, O. Bakker, H. Brugge, H. Westra, M. Netea, L. Franke, M. Van Der Wijst*

Session accepted as 1-Hour Oral Session

Think about it! CNS infections in immunocompromised hosts

1581 **The difficulties of differentiating central nervous system infection from disease relapse in a cohort of adult patients with haematological malignancy: 10 years' experience from a central London hospital**
E. Lim, R. Gnanadurai, M. Escobedo-Cousin, L. Bell (London, United Kingdom), N. Mccann, J. Ellis, D. Ming, K. Cwynarski, R. Miller, E. Wall, R. Heyderman, H. Hyare*

1907 **Epidemiology, clinical characteristics and outcomes of central nervous system infections in solid organ transplant recipients: a nationwide cohort study**
L. Van Den Bogaart (Lausanne, Switzerland), D. Neofytos, L. Walti, N. Mueller, N. Khanna, K. Boggian, K. Hadaya, C. Garzoni, M. Mombelli, O. Manuel*

4686 **Maraviroc in PML-IRIS associated with immunotherapies: a case series**
R. Bernard-Valnet (Lausanne, Switzerland), X. Moisset, N. Maubeuge, J. Ouallet, M. Roumier, C. Lebrun Frenay, P. Labauge, P. Clavelou, J. Neau, R. Du Pasquier, R. Liblau, D. Brassat, G. Martin-Blondel*

5097 **Human polyomaviruses in the cerebrospinal fluid of neurological patients**
S. Delbue (Milan, Italy), D. Franciotta, M. Dolci, S. Lucia, R. Ticozzi, S. D'Alessandro, G. Campisciano, M. Comar, P. Ferrante, M. Ciotti*

7797 **Infectious complications in patients with multiple sclerosis treated with monoclonal antibodies (anti-CD20 and anti-CD52) and autologous stem cell transplantation**
R. Ungaro (Milan, Italy), A. Signori, M. Inglese, A. Laroni, G. Novi, G. Boffa, C. Lapucci, M. Ghigliotti, G. Mancardi, A. Uccelli, V. Claudio, M. Bassetti, M. Mikulska*

Session accepted as 2-Hour Oral Session

Vaccination: new tools, new populations at risk

2200 **Long-term immune response to yellow fever vaccination in HIV-infected and non-infected adults: ANRS EP46 study**
C. Durier (Villejuif, France), S. Mercier-Delarue, N. Colin De Verdiere, V. Meiffredy, S. Matheron, A. Samri, M. Resch, L. Marchand, B. Autran, O. Launay, F. Simon*

2243 **Exploration of gonococcal MtrE-based antigens as prophylactic and therapeutic vaccines**
S. Wang (Hangzhou, China), S. Van Der Veen*

3832 **Comparison of vaccine opinion of parents in 5 key European countries: learnings from Vaccinoscopie Europe**
J. Stahl (Grenoble, France), R. Cohen, J. Gaudelus, B. Leboucher, D. Subtil, P. Pujol, V. Picquet, H. Lepetit, L. Longfier, A. Martinot*

5326 **Booster dose of trivalent inactivated influenza vaccine is superior to double- and standard-dose regimens in kidney transplant recipients: a randomised controlled parallel pilot study**
F. Odongo, P. Braga, R. Palacios, J. Miraglia, A. Sartori, K. Yaqub Ibrahim, M. Lopes, H. Caiaffa Filho, M. Timenetsky, F. Agena, L. Fonseca De Azevedo, E. David-Neto, A. Precioso, L. Pierrotti (São Paulo, Brazil)*

5580 **Increased burden of invasive pneumococcal disease caused by non-vaccine serotypes in individuals with underlying diseases: a population-based case-control study**
P. Naucler (Stockholm, Sweden), E. Petropoulos, I. Galanis, E. Morfeldt, A. Örtqvist, B. Henriques-Normark*

6729 **Migration and outbreaks of vaccine-preventable disease in Europe: a systematic analysis (1990-2019)**
A. Deal (London, United Kingdom), M. Ramsay, M. Edelstein, S. Mounier-Jack, I. Campos-Matos, K. Rustage, S. Hayward, A. Majeed, F. Knights, J. Carter, J. Friedland, S. Hargreaves*

7618 **18 years of surveillance of nasopharyngeal pneumococcal carriage before, during, and after PCV7 then PCV13 implementation in children with acute otitis media**
R. Cohen (Créteil, France), C. Levy, N. Ouldali, S. Béchet, J. Gaudelus, I. Hau, F. Angoulvant, B. Philippe, S. Bonacorsi, E. Varon*

7632 **Does selective mandatory vaccination affect vaccine coverage of recommended vaccinations?**
G. Rezza (Rome, Italy), P. D'Ancona, S. Iannazzo*

8691 **Human transcriptomic response to vaccination with recombinant VSV expressing Ebola virus glycoprotein**
F. Santoro (Siena, Italy), A. Donato, S. Sorgi, A. Gerlini, A. Huttner, C. Siegrist, D. Medaglini, G. Pozzi*

9248 **Evidence for diminishing returns in supplementary immunisation activities: a spatio-temporal analysis of oral polio vaccination**
M. Auzenbergs, K. O'Reilly (London, United Kingdom)*

Session accepted as Paper Poster Session

Vaccines against bacterial diseases

358 **Pneumococcal vaccination introduced between the chemotherapy cycles decreases the incidence of pneumonias in patients with multiple myeloma**
I. Stoma (Minsk, Belarus), I. Karpov, I. Iskrov, I. Lendina, A. Uss*

679 **Potential benefit of the new pneumococcal conjugate vaccines in Navarra, Spain**
M. Portillo (Pamplona, Spain), I. Arregui, M. Adelantado Lacasa, J. Castilla, M. Guevara Eslava, J. Torroba Alvarez, A. Navascués Ortega, C. Ezpeleta Baquedano*

2381 **Cost-effectiveness analysis of pneumococcal vaccines in older adults in Argentina**
N. Giglio (Buenos Aires, Argentina), V. Castellano, P. Mizrahi, P. Micone*

2944 **Clinical effectiveness of 13-valent and 23-valent pneumococcal vaccination among middle-aged and older adults with immunocompromising conditions**
A. Vila-Córcoles (Tarragona, Spain), O. Ochoa-Gondar, E. Satue, C. De Diego, A. Vila-Rovira, C. Rodriguez*

3251 **Tetanus prophylaxis in wound management of patients with rheumatoid arthritis**
A. Vollaard (Amsterdam, Netherlands), A. Bos, M. Gonçalves, M. Andersson, I. Furtado, L. Santos, O. Manuel*

3562 **Surface plasmon resonance as a new tool to measure vaccine response to 13-pneumococcal conjugated vaccine**
M. Garrido Jareño (Valencia, Spain), L. Orti Pérez, M. Meyer García, J. Mollar Maseres, M. Giménez Martí, C. Lloret Sos, A. Gil Brusola, J. López-Hontangas, J. Beltrán Garrido, J. Peman Garcia, A. Pineda Lucena*

3700 **Clinical development of a meningococcal group A, C, W, and Y tetanus toxoid conjugate vaccine**
L. Serra, P. Balmer, J. Perez, P. Peyrani, J. Findlow (Surrey, United Kingdom), S. Mather, M. Marsden, C. Webber*

4511 **Assessment the immunogenicity of UpaH autotransporter of uropathogenic *Escherichia coli* isolates admixed with vitamin D as a novel vaccine candidate against urinary tract infection**
M. Asadi Karam (Tehran, Iran), M. Habibi, S. Azimi, S. Bouzari*

4564 **Bioinformatic studies and investigation of the immunogenicity of a vaccine candidate composed of ExoS and PcrV of *Pseudomonas aeruginosa* against urinary tract infections in an animal model**
M. Habibi (Tehran, Iran), H. Alaie, S. Bouzari, M. Asadi Karam*

4851 **Serotype and susceptibility of invasive pneumococcal disease in adult population**
L. Vinuela, C. García, G. Santillana, P. Bardon, R. Martinez, E. Clavijo, M. García López (Málaga, Spain)*

5457 **Evaluation of the efficacy of vaccination programmes in HIV-positive patients against vaccine-preventable diseases**
A. Uyan, M. Isikgöz Tasbakan, T. Yamazhan, D. Gökengin, A. Zeytinoglu, H. Pullukcu (Izmir, Turkey)*

6616 **Designing and structure evaluation of uropathogenic *Escherichia coli* multi-epitope subunit vaccine**
M. Rezaei (Tehran, Iran), M. Habibi, M. Asadi Karam, P. Ehsani, N. Moazzezy, S. Bouzari*

8617 **IgM antibody to pneumococcal serotype 3 polysaccharide activates the classical pathway**
S. Pelton, R. Lapidot (Boston, United States), M. Lee*

Session accepted as Paper Poster Session

Vaccines against viral disease

970 **Measles: clinical manifestations and complications during an outbreak in Bulgaria in 2019**
P. Velikov (Sofia, Bulgaria), N. Kyuchukova, T. Chervenyakova*

1848 **Investigation and control of measles outbreak in Balkh province, Afghanistan, Dec 2016- 2017**
A. Shirpoor (Mazar-i-Sharif, Afghanistan)*

1977 **Variable anti-Hepatitis B surface titres in vaccinated birth-cohorts: a cross-sectional population based study in northwestern Romania**
A. Istrate, A. Radulescu (Cluj-Napoca, Romania)*

3114 **French general practitioner attitude regarding human papilloma virus vaccine in females and males: positive perceptions but missed opportunities**
M. Degoue, O. Epaulard (Grenoble, France)*

3619 **The results of laboratory monitoring of post-vaccination measles immunity**
A. Ereshchenko, O. Gusyakova, G. Frida, A. Kozlov (Samara, Russian Federation)*

3639 **Toward an improvement of the measles vaccine platform by rationalizing the muscle immune response**
E. Billon-Denis (Brétigny-sur-Orge, France), A. Garnier, L. Cheutin, C. Vigne, T. Cédric, J. Burger, F. Tangy, J. Tournier*

3735 **Measles issue in Georgia**
E. Vashakidze (Tbilisi, Georgia), T. Megrelishvili, I. Mikadze, E. Pachkoria, N. Kipiani, N. Tavlelashvili, M. Kvitashvili*

3914 **Correlation between rubella IgM positivity and detection of cytomegalovirus/parvovirus B19 primary infection in pregnant women accessing the Tuscany Reference Centre for Infectious Diseases in Pregnancy**
S. Giachè (Florence, Italy), L. Zammarchi, B. Borchi, G. Millotti, A. Bartoloni, M. Trotta*

4516 **Validation of a measles virus detection assay for early clinical management**
S. Haim-Boukobza (Saint Ouen L'Aumone, France), E. Hedbaut, V. Dubois, N. Day, J. Poveda*

4801 **Prolonged viral shedding in bronchial aspirate fluids in a patient with measles-related severe pneumonia**
L. Bordi, M. Antonini, C. Castilletti, E. Nicastri, F. Colavita, A. D'Abramo (Rome, Italy), L. Scorzolini, M. Maritti, M. Capobianchi, E. Lalle*

5203 **Factors associated with non-vaccination against human papilloma virus among girls aged 14-15 years in France: a pooled cross-sectional analysis**
F. Dib (Paris, France), P. Mayaud, L. Longfier, P. Chauvin, O. Launay*

7159 **Rapid reduction in rotavirus gastroenteritis in children aged 0-59 months following the introduction of universal rotavirus vaccination in Palestine**
M. Hindiyeh (Bethlehem, Palestine), W. Rennert, R. Khalawi, A. Issa, A. Ramlawi, H. Marzouqa*

7482 **French health students' knowledge about human papilloma virus infections and vaccine: it is time to fill the gaps**
S. Bruel, Z. Rakoto, N. Agrinier, M. Gignon, N. Ndiaye, C. Lasset, N. Thilly, G. Amandin (Saint Etienne, France)*

9039 **Evaluation of hepatitis B vaccine efficacy and factors affecting its response in patients receiving anti-tumour necrosis factors**
G. Okay (İstanbul, Turkey), E. Biberci Keskin, Y. Akkoyunlu*

9407 **How partnership network and HPV type interaction shape the distribution of HPV infection before and after vaccine introduction**
M. Bonneault (Paris, France), C. Poletto, M. Flauder, M. Pons-Salort, D. Guillemot, E. Delarocque-Astagneau, A. Thiébaut, L. Opatowski*

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Abstract Programme

11. Other

- Education and career
- Publishing, ethics, other academic and professional affairs
- Other

Session accepted as Open Forum

Gaming infectious diseases

8183 **Pragmatic ranking of antibiotics based on spectrum and ecologic impact for educational purposes: results from a Delphi survey for Dawaa**
L. Binh Luong Nguyen (Paris, France), C. Cazanave, V. Dubee, C. D'Humieres, S. Jauréguiberry, S. Kerneis, A. Lefort, R. Lepeule, B. Pilmis, S. Abbara*

9703 **BacteriaGame, a serious game to revise knowledge in medical Bacteriology**
N. Pineros, E. Carbonnelle, V. Berry, M. Lescat (Paris, France)*

Abstract Programme

12. Late breakers

- New drugs
- Clinical trials
- Outbreaks and public health emergencies
- Other

Session accepted as Paper Poster Session

ECCMID 2020 Latebreakers

9700 **The penicillin allergy delabelling program: A prospective multicentre interventional study**
K. Chua, S. Vogrin, S. Bury, A. Douglas, N. Holmes, E. Phillips, J. Trubiano (Victoria, Australia)*

9701 **Paediatric meningoencephalitis due to entero- and human parechoviruses in Cork, Ireland - epidemiology and neurodevelopmental follow-up by parental report**
C. Stephens, R. Barry (Cork, Ireland), L. Gibson, U. Morley, C. De Gascun, S. Felsenstein*

9738 **Diabetic status and the risk of tuberculosis: a nationwide population-based study**
Y. Jung Eun (Seoul, South Korea)*

9739 **Siderophores of environmental *Pseudomonas* for application against human opportunistic pathogens**
V. Vollenweider (Zurich, Switzerland), K. Rehm, L. Bigler, R. Kümmerli*

9752 **Phage cocktails in the treatment of bacteriophage insensitive mutants**
P. Manohar (Haining, China), R. Nachimuthu, S. Leptihn*

9757 **Decreased sensitivity of rapid influenza diagnostic test among vaccinated adults in influenza season 2018-19**
R. Auvinen (Espoo, Finland), N. Ikonen, R. Loginov, A. Haveri, S. Kurkela, H. Nohynek, R. Syrjänen, J. Ollgren, E. Ruokokoski, K. Skogberg*

9779 **Impact of the introduction of EUCAST's concept of the "Area of Technical Uncertainty"**
E. Van Honacker (Ghent, Belgium), S. Vandendriessche, L. Coorevits, B. Verhasselt, J. Boelens*

9810 **Antibiotic resistance prediction by analysis of whole genome sequence data using ARESdb**
I. Ferreira (Wien, Austria), S. Beisken, L. Lueftinger, T. Weinmaier, M. Klein, J. Bacher, R. Patel, A. Von Haeseler, A. Posch*

9814 **Vancomycin loading doses in the emergency department: a Bayesian approach**
K. Raja (Belleville, United States), A. Debnath, C. Bezzubik, B. Chen, M. Attalla, R. Patel, S. Kang, M. Patel, M. Philips*

9817 **Increased enterococcal abundance and low microbial diversity are early predictive markers of a microbiota primed for development of *Clostridioides difficile* infection**
M. Berkell (Antwerpen, Belgium), M. Mysara, B. Xavier, C. Van Werkhoven, P. Monsieurs, C. Lammens, A. Ducher, M. Vehreschild, H. Goossens, J. De Gunzburg, M. Bonten, S. Malhotra-Kumar*

9827 **Phenotypic and genotypic characterisation of BLNAR and BLPACR strains of *Haemophilus influenzae*: A rare finding of presence of ESBLs and highly resistant *ftsI* mutations in Australian isolates**
S. Naqvi (Nsw, Australia), H. Varadhan, R. Givney*

9828 **Intact EfrEF operons seem essential for chlorohexidine tolerance among *Enterococcus faecalis* from different hosts and genetic backgrounds**
A. Pereira (Porto, Portugal), B. Duarte, P. Antunes, L. Vieira Peixe, A. Freitas, C. Novais*

9831 **Colistin resistance detection: an easy test for routine laboratories**
D. Guneser (Istanbul, Turkey), K. Özgüler, T. Bozan, A. Karahasan*

9834 **Declining antibiotic use in Infants and falling asthma Incidence in children: New findings from population and prospective cohort studies suggest a causal link mediated through the gut bacterial community**
D. Patrick (Vancouver, Canada), H. Sbihi, D. Dai, A. Al Mamun, D. Rasali, C. Rose, F. Marra, R. Boutin, C. Petersen, L. Stiemsa, G. Winsor, A. Kozyrskyj, M. Azad, A. Becker, P. Mandhane, T. Moraes, M. Sears, P. Subbarao, B. Finlay, S. Turvey*

9844 **The approach to HCV treatment in patients with haematologic malignancies: an ESGVH-ESGICH cross-sectional survey**
L. Nicolini (Genova, Italy), A. Lombardi, M. Bassetti, M. Mikulska*

9866 **Surprisingly low levels of measles immunity in persons with HIV: a seroprevalence survey in a United States HIV clinic**
L. Rearigh (Omaha, United States), S. Bares, S. Swindells, H. Sayles, J. O'neill, M. Kubat*

9869 **A hospital outbreak of linezolid-resistant and vancomycin-resistant ST80 *Enterococcoccus faecium* harbouring an *optrA*-encoding conjugative plasmid investigated using whole-genome sequencing**
S. Egan (Dublin, Ireland), S. Corcoran, H. Mcdermott, M. Fitzpatrick, A. Hoyne, O. Mccormack, B. O'Connell, G. Brennan, D. Coleman*

9879 **Safety, tolerability and clinical outcomes of RSV infection challenge in older adult volunteers**
P. Dayananda (London, United Kingdom), S. Ascough, Z. Gardener, E. Bergstrom, S. Ung, M. Kalyan, V. Avadhan, S. Kar, S. Paterson, M. Begg, E. Hessel, P. Openshaw, C. Chiu*

9885 **Different impact of modification of voriconazole therapy following therapeutic drug monitoring (TDM) on the prevention of hepatotoxicity and visual symptoms: Japanese multicenter study**
T. Ueda, Y. Takesue (Nishinomiya, Japan), Y. Hamada, K. Nakajima, K. Fukunaga, T. Miyazaki, N. Nakada-Motokawa, M. Nagao, H. Kawamura, A. Shigemi, F. Ebihara, K. Ikegame, T. Kimura, Y. Miyazaki*

9896 **Validation of an isothermal amplification platform for microbial identification and antimicrobial resistance detection in blood: a prospective study**
H. Maheshwarappa (Secunderabad, India), P. Guru, S. Majumder, V. Mangale, R. Mundre, N. Lawrence, A. Sigamani, S. Adak*

9897 **Therapeutic drug monitoring of antibiotics in intensive care patients treated with extracorporeal membrane oxygenation (ECMO): an observational single-center study**
D. Kühn (Homburg, Germany), C. Metz, F. Seiler, H. Wehrfritz, M. Alqudrah, A. Becker, R. Bals, M. Hoffmann, U. Hübner, J. Geisel, P. Lepper, S. Becker*

9898 **Prospective validation in children with adenovirus detectionof a TRAIL/IP-10/CRP host-protein assay for guiding antibiotic treatment decisions**
L. Etshtein, A. Argentiero, C. Papan, T. Gottlieb, E. Barash, N. Mastboim, L. Shani, E. Simon, E. Moscoviz, T. Ilan-Ber, R. Navon, A. Cohen, M. Paz (Tirat Carmel, Israel), O. Boico, E. Bamberger, K. Oved, E. Eden, E. Farinelli, I. Testa, M. Pasticci, D. Mezzetti, K. Perruccio, M. Porwoll, U. Hakim, A. Simon, J. Liese, M. Knuf, M. Stein, R. Yacobov, S. Schneider, S. Esposito, T. Tenenbaum*

9899 **Effect of CMV replication on relapse and survival in pediatric AML**
J. Kühl, S. Voigt (Berlin, Germany)*

9907 ***In vivo* efficacy of NP339 against Invasive Pulmonary Aspergillosis (IPA)**
D. Smith (Bridge of Don, United Kingdom), L. Katvars, D. O'Neil*

9911 **Global distribution of the known mobile colistin resistance- *mcr* genes across different microbiomes**
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9985 **Safety and immunogenicity of a replication deficient simian adenoviral vectored Zika vaccine: preliminary results of a phase I, first-in-human, dose escalation trial**
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T. Clark (Southampton, United Kingdom), K. Beard, N. Brendish, S. Poole, C. Chan, N. Cortes, A. Malachira, S. Mills, S. Ewings*

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J. Sojo-Dorado, I. López-Hernández, I. Borreguero, I. Morales, Z. Palacios Baena, A. Hernandez Torres, E. García Vázquez, E. Merino De Lucas, C. Pigrau, E. Bereciartua Bastarrica, V. Pintado, L. Boix-Palop, Á. Cano Yuste, L. Sorlí, N. Borrell, C. Gil-Anguita, E. Shaw, A. Jóver-Sainz, J. Molina, R. Martínez Álvarez, D. Carlos, J. Calvo-Montes, J. Sequeira, M. Cárdenas, M. Alonso Socas, V. Pomar, L. Valiente De Santis, V. Merino Bohórquez, C. Rosso, A. Pascual Hernandez, J. Rodríguez-Baño (Sevilla, Spain)*

9930 **Seven versus 14 days of antibiotic treatment for patients with male urinary tract infection (PROSTASHORT) : a randomized study**
M. Lafaurie (Paris, France), L. Escaut, L. Bernard, C. Gatey, A. Froissart, A. Bourgarit, V. Meyssonnier, A. Chabrol, S. Chevret, J. Molina, A. Lefort*

9975 **Outcomes of the novel β-lactam/β-lactamase inhibitor combination of cefepime-enmetazobactam versus piperacillin-tazobactam in adult patients with complicated urinary tract infections – the ALLIUM phase 3 trial**
K. Kaye (Ann Arbor, United States), A. Belley, O. Lahlou, P. Barth, P. Motta, S. Kashyap, P. Knechtle, P. Velicitat*

9977 **An optimised dosing regimen vs. a standard dosing regimen of vancomycin for the treatment of late onset sepsis due to Gram-positive microorganisms in infants less than 90 days: the NeoVanc trial**
L. Hill (London, United Kingdom), M. Clements, M. Turner, I. Lutsar, E. Jacqz-Aigrain, P. Heath, E. Roilides, S. Walker, M. Sharland*

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Abstracts

Abstract 1

The impact of microbiome DNA enrichment methods on host DNA depletion efficiency and bacterial community structure of infected tissue samples

Fatemah Sadeghpour Heravi*[1], Martha Zakrzewski[2], Karen Vickery[1], Honghua Hu[1]

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Background: Shotgun metagenomic sequencing is a genome-wide sequencing approach to explore bacterial communities directly from their habitat or infected sites. However, extracting high-quality bacterial DNA with minimum host DNA contamination from infected tissue samples suitable for metagenomics studies is very challenging. Although metagenomics has shown great promise in environmental samples, it is particularly difficult in infected tissue samples with a great amount of host DNA contamination. The co-extraction of host DNA with bacterial DNA can mask the microbial signals in the sequencing process.

Materials/methods: In this study, we evaluated the impact of different microbiome DNA enrichment methods (NEBNext Microbiome DNA Enrichment kit, Molzym Ultra-Deep Microbiome Prep, QIAamp DNA Microbiome kit, and HostZERO microbial DNA kit) on host DNA depletion efficiency and bacterial composition of infected tissue samples (diabetic foot infection) using quantitative real-time PCR and 16S ribosomal RNA sequencing methods. The host DNA depletion ratio and the microbial profile of diabetic foot infections were compared before and after applying the selected microbiome enrichment kits.

Results: Molzym extracted the lowest amount of bacterial load with a high level of host DNA contamination. In contrast, HostZERO and QIAamp methods recovered the highest amount of bacterial genomes with a minimum amount of host DNA contamination, attesting to the efficacy of these two methods in shotgun metagenomic sequencing studies. Microbial composition was also highly similar between the original and enriched samples processed by NEBNext, resembling most of the predicted taxa in the control sample. Also, ten of the sixteen genera predicted in the control sample were recovered by all the enrichment methods of which the NEBNext method recovered all of the genera and Molzym recovered the lowest number of bacterial genera.

Conclusions: Our findings can provide a useful guideline for scientists in selecting DNA enrichment methods, particularly those who wish to deplete a high amount of host DNA contamination and preserve a high amount of bacterial DNA load from infected tissue samples for shotgun metagenomic sequencing.

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Abstract 7

Bacteraemia with anaerobic bacteria and association with colorectal cancer

Ulrik S. Justesen*[1], Stig Lønberg Nielsen[2], Thøger Gorm Jensen[1], Ram B. Dessau[3;4], Jens Kjølseth Møller[5], John E. Coia[6], Steen Lomborg Andersen[7], Court Pedersen[2], Kim Oren Gradel[8]

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Background: Studies have reported an association between Bovis group streptococci, *Clostridium septicum* and colorectal cancer (CRC). Recently associations between different *Bacteroides* spp., *Fusobacterium nucleatum* and CRC have also been reported. We wanted to investigate this further in a large scale study.

Materials/methods: We performed a population-based cohort study including data on blood cultures from 2007 to 2016 covering a population of more than 2 million people. We combined blood culture data with the national register for colorectal cancer (Danish Colorectal Cancer Group Database) and identified incident CRC after bacteraemia. The risk of incident CRC until 2018 was investigated for *Bacteroides* spp., *Clostridium* spp. and *Fusobacterium* spp. and compared with Bovis group streptococci, *Escherichia coli*, *Staphylococcus aureus* and negative blood culture controls matched 1:5 by age and sex.

Results: We included 45760 bacteraemia episodes, of which 492 (1.1%) were diagnosed with CRC after the bacteraemia; 241 (0.5%) within 1 year. The risk of CRC for selected bacteria is shown in Table 1 (results for *E. coli* and *S. aureus* are not shown but were similar to negative blood cultures). Most anaerobic species were associated with a considerable increased risk of CRC (up to 40 times) compared with negative blood cultures.

Conclusions: In this large scale cohort study, it was found that in patients with bacteraemia caused by selected anaerobic bacteria the risk of incident CRC was increased up to 40 times compared with patients with bacteraemia caused by non-anaerobic bacteria or negative blood cultures. Bacteraemia with certain anaerobic bacteria could potentially result in a recommendation of further evaluation for CRC in selected patients.

Table 1. No. bacteraemia episodes followed by CRC/total no. episodes (%)

Bacteria	Without a time limitation	Within 1 year
Bacteroides spp. (excluding *B. pyogenes*)	25/1085 (2.3)	23/1085 (2.1)
- *B. fragilis*	11/583 (1.9)	11/583 (1.9)
- *B. ovatus*	2/30 (6.7)	2/30 (6.7)
Clostridium spp.	22/457 (4.8)	20/457 (4.4)
- *C. perfringens*	3/167 (1.8)	3/167 (1.8)
- *C. septicum*	12/53 (22.6)	11/53 (20.8)
Fusobacterium spp. (excluding *F. necrophorum*)	6/100 (6.0)	3/100 (3.0)
Bovis group streptococci	6/117 (5.1)	5/117 (4.3)
Negative blood cultures	2475/231629 (1.1)	1035/231629 (0.5)

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Abstract 16

Crimean-Congo haemorrhagic fever in an emergency department in Spain

Lia Monsalve-Arteaga*[1], Moncef Belhassen García[1;2], Juan-Luis Munoz-Bellido[1;2], Montserrat Alonso Sardón[1], Anabel Negredo[3], Maria Paz Sanchez-Seco[3], Fernando De Ory Manchón[3], Nuria Leralta[3], Isabel Bas García[3], Jesús Sánchez Serrano[2], Jorge García Criado[2], Antonio Muro Alvarez[1], Amparo López Bernús[2]

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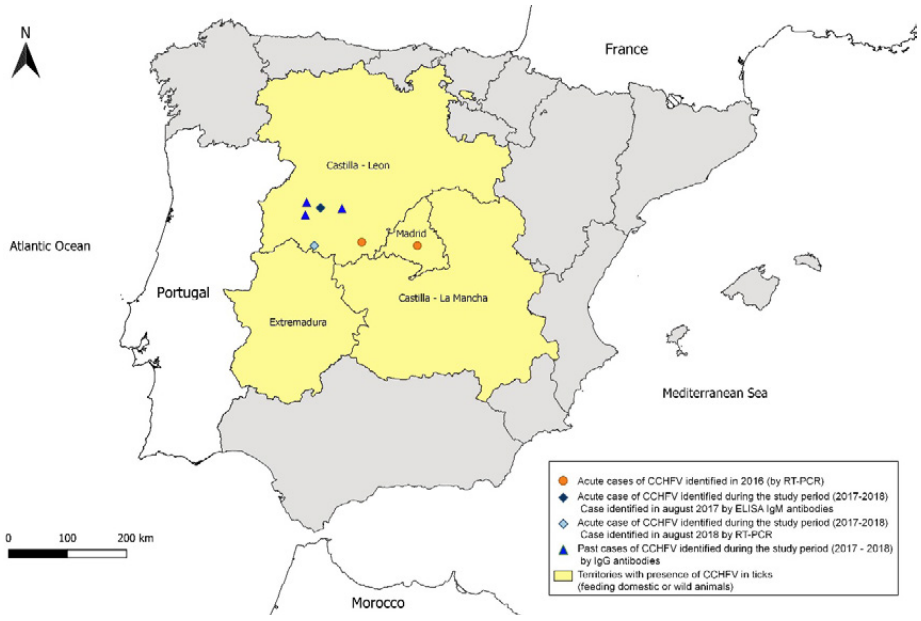
Background: Crimean Congo haemorrhagic fever (CCHF) is a widespread tick-borne viral disease caused by the homonymous virus (CCHFV), a *Nairovirus* of the *Nairoviridae* family. It has been implicated in severe viral haemorrhagic fever outbreaks. During the summer of 2016, the first two cases of this disease were reported in Spain. Nowadays, this disease is difficult to get eradicated because of its enzootic life cycle. The aim of this study was to determine the presence of CCHF among patients coming for a febrile illness to Complejo Asistencial Universitario de Salamanca (CAUSA), Salamanca, western Spain, during the spring-summer periods in 2017 and 2018.

Materials/methods: We evaluated prospectively patients older than 18 years, who came to the Emergency Department of CAUSA presenting fever as the only or main symptom. We determined specific IgM and IgG antibodies against CCHFV by the VectoCrimea ELISA kit-test (Vector-Best, Russia), an in-house ELISA and two immunofluorescence assays (Euroimmun, Germany) against two different glycoproteins (nucleoprotein and glycoprotein), and an in-house nested RT-PCR. Details were collected from the medical records.

Results: 133 patients were selected for the study. Mean age (±SD) was 67.63 years (±18.8). 81 patients (60.9 %) were male. Most patients were diagnosed as genitourinary or respiratory syndromes. The 3rd most frequent diagnosis was acute undifferentiated febrile illness. Three patients had anti-CCHFV IgG antibodies, suggesting a past infection. Two patients were found to have anti-CCHFV IgM antibodies, and one of them was also positive by RT-PCR. Both patients lived in the province of Salamanca (western Spain). One patient was involved in animal husbandry. None of these two cases where associated to a nosocomial outbreak.

Conclusions: This study suggests that CCHF is an identifiable cause of febrile illness in Spain, and therefore should by suspected when a patient comes to the emergency department with fever and hepatic impairment, and/or haemorrhagic phenomena, especially in spring and summer seasons, and if they have risk activities. All of this, in order to establish support treatment and isolation measures as soon as possible, thus reducing the risk of mortality and nosocomial outbreaks.

Figure 1: Acute and past infections by CCHFV identified in Spain



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Abstract 19

Genetic characterisation of co-circulating community *Staphylococcus aureus* and *Streptococcus pyogenes* causing skin and soft tissue infections in Gambia

Alexander Keeley*[1], Saikou Y Bah[1;2], Edwin Armitage[2], Elina Senghore[2], Jarra Manneh[2], Saffiatou Darboe[2], Abdul Karim Sesay[2], Bruno Pichon[3], Ulf Schaefer[3], Claire Turner[1], Thushan I De Silva[1;2]

[1]*The University of Sheffield, The Florey Institute, Sheffield, United Kingdom*, [2]*Medical Research Unit The Gambia at the London School of Hygiene and Tropical Medicine, Faraja, Gambia*, [3]*Public Health England, National Infection Service, London, United Kingdom*

Background: *Staphylococcus aureus* and *Streptococcus pyogenes* are major global pathogens. Infection ranges from asymptomatic carriage to fatal invasive infection. Understanding the transmission dynamics and genetic diversity within low- and middle-income countries (LMIC) with a high burden of disease is required for effective vaccine development and public health interventions. We aimed to characterize the genetic diversity of *S. aureus* and *S. pyogenes* causing skin and soft tissue infection (SSTI) in children in The Gambia using whole genome sequencing.

Materials/methods: A point prevalence study of pyoderma was conducted over 4 months in randomly-selected census-derived geographical clusters of Sukuta, a peri-urban area in The Gambia. Swabs from pyoderma lesions were cultured for *S. aureus* and *S. pyogenes*. A single colony of each bacteria was sub-cultured, DNA extracted and sequenced using an Illumina MiSeq platform. Multi-locus sequence typing (mlst, MOST), de novo assembly (SPAdes), gene annotation (prokka), *emm* typing (CDC-typing-tool), core genome determination (roary) and maximum likelihood phylogenetic tree construction (RAxML) were used to analyse sequence data.

Results: Of 1441 children from nine geographical clusters, 251 (17.4%) had pyoderma. Of these, *S. aureus* was isolated from 202 children (80.5%) and *S. pyogenes* from 129 (51.4%). Co-infection was seen in 104 children (41.4%), which is comparable to the limited data from LMICs. Thus far sequence data from 93 *S. aureus* isolates and 105 *S. pyogenes* isolates were suitable for analysis. The predominant *S. aureus* MLST clonal complexes (CC) were CC15 (29%), CC152 (20.4%), CC1 (14%) and CC5 (12.9%), collectively representing 76.3% of all sequenced isolates. *S. pyogenes* showed no *emm*-type predominance, with no single *emm*-type representing more than 5.7% of sequenced isolates and 44 distinct *emm* types. Within the three geographical clusters with the largest number of pyoderma cases, a single CC type was responsible for 25.5 – 35.7% of *S. aureus* infections, compared to 8.7 – 12.0% caused by any single *S. pyogenes emm*-type.

Conclusions: Our study provides the first whole genome sequence analysis of co-circulating community *S. aureus* and *S. pyogenes* causing SSTI from The Gambia. Further detailed interrogation of the larger dataset is ongoing, including evidence for transmission using combined epidemiological and genetic data.

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Abstract 24

High-dose ceftaroline fosamil recommendations for paediatric patients with *Staphylococcus aureus* complicated skin and soft-tissue infections using an extrapolation approach

Phylinda Chan*[1], Margaret Lynn Mcfadyen[1], Andrea Quaye[2], Heidi Leister-Tebbe[3;4], Vicky Hendrick[1], Jennifer Hammond[3], Susan Raber[5]

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Abstract third-party references: Study sponsored by Pfizer.

Background: For adults and adolescents (aged 12 to <18 years with body weight ≥33 kg), the standard ceftaroline fosamil dose is 600 mg by 5–60 min intravenous (IV) infusion every 12 h (q12h) for complicated skin and soft-tissue infections (cSSTIs) caused by *Staphylococcus aureus* with ceftaroline minimum inhibitory concentration (MIC) ≤1 mg/L, whereas a "high dose" of 600 mg by 2-h IV infusion q8h is approved in Europe for MICs of 2 or 4 mg/L, based on population pharmacokinetic (PopPK) analyses and Phase III clinical trial data (NCT01499277). We conducted further PopPK analyses to support high-dose recommendations for paediatric patients (aged 2 months to <18 years) with cSSTI caused by *S. aureus* with suspected high MIC (2 or 4 mg/L).

Materials/methods: A PopPK model for ceftaroline fosamil and ceftaroline based on adult (n=944) and paediatric (n=304) data was used to simulate steady-state ceftaroline exposures and perform probability of target attainment (PTA) simulations for various paediatric high-dose regimens and renal function categories. PTA was calculated as the percentage of simulated patients achieving free ceftaroline plasma concentrations above the MIC per dosing interval (%*f*T>MIC) of 27%, 31% and 35% (*S. aureus* PK/pharmacodynamic targets for stasis, 1-$\log_{10}$ and 2-$\log_{10}$ kill, respectively). Exposures and PTA were matched to adults with normal renal function (body surface area-normalised creatinine clearance ≥80 mL/min/1.73 m^2) receiving ceftaroline fosamil 600 mg by 2-h IV infusion q8h. Safety/tolerability data were extrapolated from paediatric trials of higher ceftaroline fosamil doses.

Results: For the proposed ceftaroline fosamil high-dose regimens (Table), across paediatric age groups and renal function categories, simulated ceftaroline exposures were similar to adults with normal renal function, with PTA >99% for MIC of 2 mg/L, and PTA similar to or higher than that in adults with normal renal function (>80%) for MIC of 4 mg/L.

Conclusions: These analyses support the extrapolation of efficacy based on PTA from adult to paediatric patients (aged 2 months to <18 years) with cSSTI caused by *S. aureus* with ceftaroline MICs of 2 or 4 mg/L at the proposed ceftaroline fosamil high-dose regimens for paediatric patients.

Table. Steady-state exposures and PTA based on simulations for paediatric patients (aged 2 months to <18 years) with normal renal function or renal impairment, at the proposed high-dose regimens of ceftaroline fosamil for treatment of cSSTI with MIC >1 mg/L

Age group	Recommended high-dose (2-h IV infusion)	$C_{max,ss}$ (mg/L)†	$AUC_{24,ss}$ (mg/L*h)†	$C_{max,ss}$ Ratio to adults	$AUC_{24,ss}$ Ratio to adults	35% *f*T>MIC of 2 mg/L	35% *f*T>MIC of 4 mg/L
Reference: Normal renal function (nCrCL ≥80 mL/min/1.73 m²)							
Adults	600 mg q8h	18.4 (10.4, 32.2)	155 (85.7, 285)	N/A	N/A	99.7	82.7
Normal renal function (nCrCL ≥80 mL/min/1.73 m²)							
12 to <18 years	12 mg/kg (max 600 mg) q8h	21.7 (12.6, 35.9)	173 (99.1, 209)	1.18	1.12	99.8	90.2
6 to <12 years		23.5 (14.5, 37.5)	178 (106, 302)	1.28	1.15	99.8	91.8
2 to <6 years		21.4 (13.2, 33.9)	153 (90.9, 258)	1.16	0.987	99.5	81.8
12 to <24 months	10 mg/kg q8h	19.2 (11.9, 30.4)	146 (86.9, 247)	1.04	0.940	99.7	80.8
2 to <12 months		20.3 (12.6, 32.0)	168 (98.9, 284)	1.11	1.08	99.9	90.8
Mild renal impairment (nCrCL ≥50 to <80 mL/min/1.73 m²)							
12 to <18 years	12 mg/kg (max 600 mg) q8h	23.2 (13.5, 38.6)	193 (111, 334)	1.23	1.22	100	94.6
6 to <12 years		24.9 (15.3, 39.7)	197 (116, 333)	1.33	1.25	100	95.3
2 to <6 years		22.7 (14.1, 36.1)	170 (101, 286)	1.22	1.08	99.8	89.7
12 to <24 months	10 mg/kg q8h	21.8 (13.3, 35.2)	183 (104, 322)	1.16	1.16	99.9	93.0
2 to <12 months		23.2 (14.1, 37.3)	210 (119, 370)	1.23	1.32	100	97.0
Moderate renal impairment (nCrCL ≥30 to <50 mL/min/1.73 m²)							
12 to <18 years	10 mg/kg (max 400 mg) q8h	18.2 (10.4, 31.6)	168 (94.2, 299)	0.974	1.06	100	88.7
6 to <12 years		23.1 (14.1, 37.0)	201 (119, 338)	1.23	1.28	100	96.8
2 to <6 years		21.7 (13.4, 34.4)	178 (106, 301)	1.16	1.13	100	93.2
Severe renal impairment (nCrCL ≥15 to <30 mL/min/1.73 m²)							
12 to <18 years	8 mg/kg (max 300 mg) q8h	17.0 (9.58, 30.0)	178 (98.7, 326)	0.907	1.13	100	91.2
6 to <12 years		22.3 (13.5, 36.1)	222 (130, 379)	1.19	1.41	100	98.7
2 to <6 years		21.2 (13.1, 33.9)	200 (119, 343)	1.13	1.27	100	97.2

†Median (5^{th}, 95^{th}) based on summary of 100 trials and corresponds to median (90% prediction interval).
$AUC_{24,ss}$, area under the plasma concentration–time curve over 24 h at steady state; $C_{max,ss}$, maximum concentration at steady state; cSSTI, complicated skin and soft-tissue infection; %*f*T>MIC, percent of time that free plasma concentrations are above minimum inhibitory concentration; MIC, minimum inhibitory concentration; nCrCL, body surface area-normalised creatinine clearance; PTA, probability of target attainment; q8h, every 8 h.

Study sponsored by Pfizer.

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Abstract 32

Metatranscriptomic analysis reveals active bacterial communities in diabetic foot infections

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Background: DNA sequencing approaches have identified the complexity of bacterial communities present in diabetic foot infections. Despite the extended view of diabetic foot ulcers (DFUs) and diabetic foot infections (DFIs) microbiota, little is known about which active bacteria, bacterial pathways, and resistance genes are pertinent to infection, and if any differences in function are associated with increased infection severity.

Materials/methods: In this study, we applied RNA sequencing (metatranscriptomics) of DFI tissue samples to analyze the bacterial taxonomic composition, function, and antibiotic resistance of the active DFI microbiota at mild, moderate and severe stages of infection. Total RNA was extracted from infected tissue samples and rRNA was depleted. Putative bacterial mRNA was sequenced using the Illumina TruSeq protocol. Human RNA was filtered and quality control and trimming were performed on the sequencing reads. Bacterial mRNAs were mapped to bacterial genomes using Kraken, KEGG and CARD databases to identify the taxonomic composition, functional pathways, and antibiotic resistance profile of active DFI microbiota.

Results: Taxonomic profiling of bacterial transcript indicated that the main features in DFI consisted of fourteen bacterial phyla. Bacterial transcripts assigned to genera *Spiroplasma*, *Vibrio*, and *Mycoplasma* were significantly different between different infection severity (Anova, $p<0.05$). Mild and severe stages were dominated by the species *Staphylococcus aureus* and *Porphyromonas asaccharolytica,* respectively. The functional activity profile of the DFI microbiota was comprised of 132 metabolic pathways of which ribosome and thiamin being among the most highly expressed pathways. Moreover, a total of 131 antibiotic resistance genes, primarily involved in the expression of multidrug efflux pumps/exporters, and resistance to beta-lactam, macrolide, and tetracycline antibiotics were identified in the active DFI microbiota.

Conclusions: Taxonomic profiling, functional characterization and antibiotic resistance identification of the transcriptionally active microbial community analyzed in this study may help to provide an understanding of the role of key microorganisms in DFI and their association with disease severity. Such information may be clinically useful allowing replacement of DFI empirical therapy with targeted treatment.

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Abstract 35

Evaluation of EUCAST rapid antimicrobial susceptibility testing (RAST) directly from blood culture bottles

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Background: Rapid antimicrobial susceptibility testing (RAST) method for direct disk diffusion from positive blood cultures (BCs) with shortened incubation time was released by EUCAST in late 2018. An evaluation was performed for Gram-negative BC isolates at a 24-hour laboratory in a tertiary hospital.

Materials/methods: BCs positive with Gram-negative-bacilli between 23/4/2019 and 21/6/2019, and forty-one spiked isolates were included. RAST was performed using six disks (ceftazidime, piperacillin-tazobactam, meropenem, ciprofloxacin, gentamicin, and amikacin) and compared against the routine method, Vitek 2 (bioMérieux). An audit of Vitek turnaround-time was also performed.

Results: Sixty-eight *Escherichia coli* (EC), forty-seven *Klebsiella pneumoniae* (KP), and thirty-three *Pseudomonas aeruginosa* were included. Categorical agreement (CA), very major errors (VME), and major errors (ME) were determined among interpretable results. The highest error rates were MEs in piperacillin-tazobactam for EC at four hours (7/11, 63.6%), and PA at 6 hours (1/1, 100%). Combined results of all isolates are presented in the table. Median turnaround-time to availability of Vitek results was 19.58 hours for EC (IQR: 17.38 – 21.38 hours), 19.43 hours for KP (IQR: 17.72 – 20.67 hours), and 23.3 hours for PA (IQR: 21.32 – 24.35 hours).

Conclusions: Introduction of RAST could significantly shorten turnaround-time of susceptibility testing. With the exception of piperacillin-tazobactam, the absolute number of errors for the majority of drug-bug combinations was low. A larger-scale evaluation is required to confirm these findings.

Drug	4-hour-reading			6-hour-reading			8-hour-reading		
	CA	VME	ME	CA	VME	ME	CA	VME	ME
Ceftazidime	71/73 (97.3%)	0/30 (0%)	2/43 (4.7%)	105/108 (97.2%)	0/41 (0%)	0/64 (0%)	126/131 (96.2%)	0/51 (0%)	2/77 (2.6%)
Piperacillin-tazobactam	37/45 (83.2%)	0/21 (0%)	8/24 (33.3%)	73/76 (96.1%)	0/33 (0%)	3/43 (7.0%)	98/102 (96.1%)	0/42 (0%)	4/60 (6.7%)
Meropenem	92/99 (92.9%)	0/9 (0%)	1/84 (1.2%)	114/122 (93.4%)	0/13 (0%)	2/103 (1.9%)	129/138 (93.5%)	0/18 (0%)	0/111 (0%)
Ciprofloxacin	84/85 (98.8%)	1/49 (2.0%)	0/36 (0%)	109/111 (98.2%)	1/58 (1.7%)	1/53 (1.9%)	125/129 (96.9%)	0/65 (0%)	2/62 (3.2%)
Gentamicin	85/86 (98.8%)	0/17 (0%)	1/69 (1.4%)	117/119 (98.3%)	0/21 (0%)	0/97 (0%)	133/135 (98.5%)	0/28 (0%)	0/105 (0%)
Amikacin	56/60 (93.3%)	0/5 (0%)	0/51 (0%)	77/80 (96.3%)	0/5 (0%)	0/72 (0%)	70/73 (95.9%)	0/6 (0%)	0/64, (0%)

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Abstract 40

Mass-Up: free software for the analysis of mass spectra biomarkers

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Background: In Clinical Microbiology, MALDI-TOF analysis of proteins is mainly used to obtain mass spectra for bacterial identification. Furthermore, discriminatory mass peaks (biomarkers) have been searched to identify different strain-specific traits such as antimicrobial resistance or virulence determinants. "Mass-up" is an open-source software that can be used in the analysis of MALDI-TOF-obtained spectra that allows the quick and easy identification of specific mass-peaks.

Materials/methods: This study was performed in the Microbiology Department of Donostia University Hospital (Basque Country, Spain). Mass-up software was used to find biomarkers to differentiate between *Shigella spp.* and *Escherichia coli* studying the MALDI-TOF mass spectra of 40 clinical isolates (4 *S. boydii*, 1 *S. dysenteriae*, 10 *S. flexneri,* 11 *S. sonnei*, 14 *E. coli)* and 6 reference strains (*S. boydii* CECT583, *S. dysenteriae* CECT584, *S. flexneri* CECT4804, *S. sonnei* CECT457, *S. sonnei* CECT4887 and *E. coli* ATCC25922). Mass-up software was also used to try to discriminate between *S. aureus* and MRSA (methicillin-resistant *S. aureus*) by analysing the mass spectra of 32 MRSA and 9 *S. aureus* clinical isolates based on described biomarkers (reviewed in Østergaard C. et al. Int J Med Microbiol. 2015;305:838.) To identify specific biomarkers, bacterial mass spectra were analysed using the Mass-up software (http://www.sing-group.org/mass-up/) developed by the University of Vigo (Galicia, Spain). This software allows in ten easy steps to perform different analysis such as quality control, discriminatory peaks discovery (biomarkers), principal component analysis, hierarchical clustering, biclustering and classification analysis on the aligned peak list.

Results: No species-specific peaks were observed in the mass spectra of *E. coli* and *Shigella* isolates: their differentiation was not possible. In addition, probably due to variation in the methodologies, previously reported biomarkers to differentiate between *S. aureus* and MRSA only partially matched with our findings. Some of the 44 MRSA biomarkers analyzed were found in both *S. aureus* and MRSA isolates, enabling the differentiation of 28/41 (68.3%) of the strains.

Conclusions: Mass-up is an easy-to-use, quick, free and reliable tool for the analysis of MALDI-TOF-obtained mass spectra. Using Mass-up no biomarkers could be found to differentiate between *E. coli* and *Shigella* species or between *S. aureus* and MRSA.

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Abstract 45

In vitro activity of manogepix (APX001A) and comparators against 1294 fungal isolates collected worldwide during the SENTRY surveillance programme (2018)

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Abstract third-party references: This study was performed by JMI Laboratories and supported by Amplyx Pharmaceuticals, which included funding for services related to preparing this abstract.

Background: Existing antifungal agents are active against many common opportunistic fungal pathogens; however, breakthrough fungal infections occur and often involve less frequently encountered yeast and mould isolates. These rarer isolates tend to exhibit diminished susceptibility to current agents. Manogepix (APX001A) is a novel inhibitor of the fungal Gwt1 enzyme (required for acylation of inositol during glycosylphosphatidylinositol anchor biosynthesis. The prodrug fosmanogepix, is being evaluated in Phase 2 clinical trials for invasive candidiasis/candidemia, *Candida auris* infections, invasive aspergillosis, and *Cryptococcus* meningitis. Manogepix is active against *Candida* (except *C. krusei*), *Aspergillus*, and difficult -to-treat moulds including *Fusarium* and *Scedosporium* species. In this study, we evaluated the *in vitro* activity of manogepix (MGX), anidulafungin (ANF), micafungin (MCF), fluconazole (FLU), and others against 1,294 clinical fungal isolates collected worldwide during 2018.

Materials/methods: Fungal isolates were collected from 69 medical centers in 24 countries in North America (46.3%), Europe (36.5%), Asia-Pacific (11.3%), and Latin America (5.9%). Among the isolates tested, 75.0% were *Candida*, 4.2% were non-*Candida* yeasts, including 33 *Cryptococcus neoformans* var. *grubii* (2.6%), 19.0% were *Aspergillus*., and 1.9% were other moulds. All isolates were tested by CLSI reference broth microdilution.

Results: MGX ($MIC_{50/90}$, 0.008/0.03 mg/L) was the most potent antifungal agent tested against *Candida* isolates (Table); ANF, MCF, and FLU MIC_{90} values were 64-, 32-, and 128-fold higher, respectively. MGX ($MIC_{50/90}$, 0.25/0.5 mg/L) was ≥8-fold more active than ANF, MCF, and FLU against *C. neoformans* var. *grubii*. Similarly, MGX ($MIC_{50/90}$, 0.06/1 mg/L) was ≥4-fold more active than ANF, MCF, and FLU against other yeast. Against *Aspergillus*, MGX ($MIC_{50/90}$, 0.008/0.015 mg/L) was comparable in activity to ANF and MCF. MGX (MIC_{90}, 0.03 mg/L) was ≥128-fold more active than ANF and MCF against *Scedosporium* isolates.

Conclusions: MGX demonstrated potent antifungal activity against *Candida*, *Aspergillus*., *C. neoformans*, and less common non-*Aspergillus* moulds including *Scedosporium*. Notable activity was seen against *C. auris,* echinocandin-resistant *Candida*, azole-resistant *Aspergillus*, and *Scedosporium* isolates. Further clinical development of fosmanogepix in difficult-to-treat resistant fungal infections is warranted.

	MIC$_{50/90}$ (mg/L)			
Organism (no. tested)	**Manogepix**	**ANF**	**MCF**	**FLU**
Candida spp. (970)	0.008/0.03	0.06/2	0.03/1	0.5/4
C. albicans (238)	0.004/0.008	0.015/0.03	0.015/0.03	0.12/0.25
C. auris (5)	0.03/-	0.25/-	0.25/-	>128/-
C. dubliniensis (42)	0.004/0.004	0.03/0.06	0.03/0.03	0.12/0.25
C. glabrata (266)	0.03/0.06	0.06/0.12	0.015/0.03	2/16
C. krusei (11)	>8/>8	0.03/0.06	0.12/0.12	32/32
C. lusitaniae (34)	0.03/0.06	0.25/0.5	0.12/0.25	0.25/1
C. parapsilosis (174)	0.008/0.015	2/2	1/2	0.5/4
C. tropicalis (127)	0.008/0.015	0.015/0.06	0.03/0.06	0.25/1
Cryptococcus neoformans var. *grubii* (33)	0.25/0.5	>4/>4	>4/>4	2/8
Other yeast[a]	0.06/1	4/>4	2/>4	8/32
Aspergillus spp. (246)[b]	0.008/0.015	0.008/0.015	0.008/0.015	- / -
Scedosporium spp. (11)[c]	0.03/0.03	4/4	0.5/>4	- / -

[a] *Aureobasidium pullulans* (1), *Cryptococcus gattii* (2), *C. laurentii* (1), *C. neoformans var. neoformans* (3), *Geotrichum clavatum* (3), *Pichia norvegensis* (4), *Rhodotorula minuta* (1), *R. mucilaginosa* (2), *Saccharomyces cerevisiae* (1), *Trichosporon asahii* (1), *T. loubieri* (1), *unspeciated Pichia* (1)

[b] *Aspergillus flavus species complex* (34), *A. fumigatus* (168), *A. lentulus* (1), *A. niger* (21), *A. niger species complex* (7), *A. nomius* (1), *A. parasiticus* (1), *A. tamarii* (1), *A. terreus* (5), *A. terreus species complex* (5), *A. versicolor* (2)

[c] *Scedosporium apiospermum/Scedosporium boydii* (8), *S. aurantiacum* (2), *S. boydii* (1)

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Abstract 46

Post-viral fatigue in dengue infection

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Background: Dengue is the most significant mosquito borne viral infection in the world in terms of morbidity. Post-viral fatigue (PVF) is observed after a dengue infection in both adults and children, but not studied extensively in the adult population.

Materials/methods: A prospective study was carried out to assess the incidence of fatigue in hospitalized dengue patients after 2 months of their hospital discharge. Non-pediatric (>12 years of age) and non-pregnant patients with an acute febrile illness (≤ 3 days) admitted to National Hospital of Sri Lanka from January 2018 to April 2019 were included this study. Dengue fever was confirmed with NS1 antigen testing or RT-qPCR. PVF was measured by contacting the patients, using the fatigue questionnaire developed by Dittner et al in 2004. The score of 4 or above consider as the cut off for fatigue. Demographic characteristics and clinical data of the patients were also collected.

Results: A total of 104 patients were recruited to the study (mean age – 34 years, SD ± 14.9, males – 61%): 69 dengue patients and 35 non-dengue patients. Out of 69 dengue patients, 27 (26%) were diagnosed with dengue hemorrhagic fever and 15 (14%) with severe dengue. PVF was present in 16 patients (13 dengue patients and 3 without dengue). There was no difference of development of fatigue between dengue and non-dengue patients ($p<0.05$).

Among dengue patients, symptoms of vomiting and bleeding, decreased hemoglobin level and decreased hematocrit within the first three days of fever showed a significant association with PVF ($p<0.05$). But after correction for multiple comparisons by Bonferroni correction, none of the variables showed a significant association with PVF. Severity of dengue and presence and absence of plasma leakage ($p<0.05$) had no association with PVF. Among non-dengue patients, only increased aspartate aminotransferase level showed a significant association with PVF ($p<0.05$) but it was not significant when corrected for multiple comparisons.

Conclusions: Severely symptomatic disease in early dengue fever may be associated with PVF but none of the predictors were significantly associated with PVF in this study after corrections for multiple comparisons. Financial assistance from, University of Colombo is gratefully acknowledged.

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Abstract 48

The phylogenetic landscape and nosocomial spread of the multidrug-resistant opportunist *Stenotrophomonas maltophilia*

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Background: Recent studies portend a rising global spread and adaptation of human- or healthcare-associated pathogens, thereby challenging the prevailing concepts of disease acquisition and transmission of these pathogens in the hospital setting. Global genome-based collections are missing for the emerging pathogen *Stenotrophomonas maltophilia*, listed by the World Health Organization as one of the leading drug-resistant nosocomial pathogens worldwide.

Materials/methods: Here, using a novel whole genome multilocus sequence typing scheme, we analyzed an international collection of 1,305 isolates of the emerging, multidrug-resistant, opportunistic pathogen *Stenotrophomonas maltophilia* from 22 countries to infer population structure, clonality, and transmission dynamics at a global level.

Results: We show that the *S. maltophilia* complex is divided into 23 monophyletic lineages, most of which harboured strains of all degrees of human virulence. Lineage Sm6 comprised the highest rate of human-associated strains, linked to key virulence and resistance genes. Transmission analysis identified a number of potential outbreak events of genetically closely related strains isolated within days or weeks in the same hospitals.

Conclusions: This first, large scale sequencing study at global scale for *S. maltophilia* provides evidence for the global prevalence of particular circulating lineages with hospital-linked clusters collected within short time interval suggesting transmission. This emphasizes the need to instate or re-enforce hygiene and infection control practices to minimize in hospital spread of these pathogens.

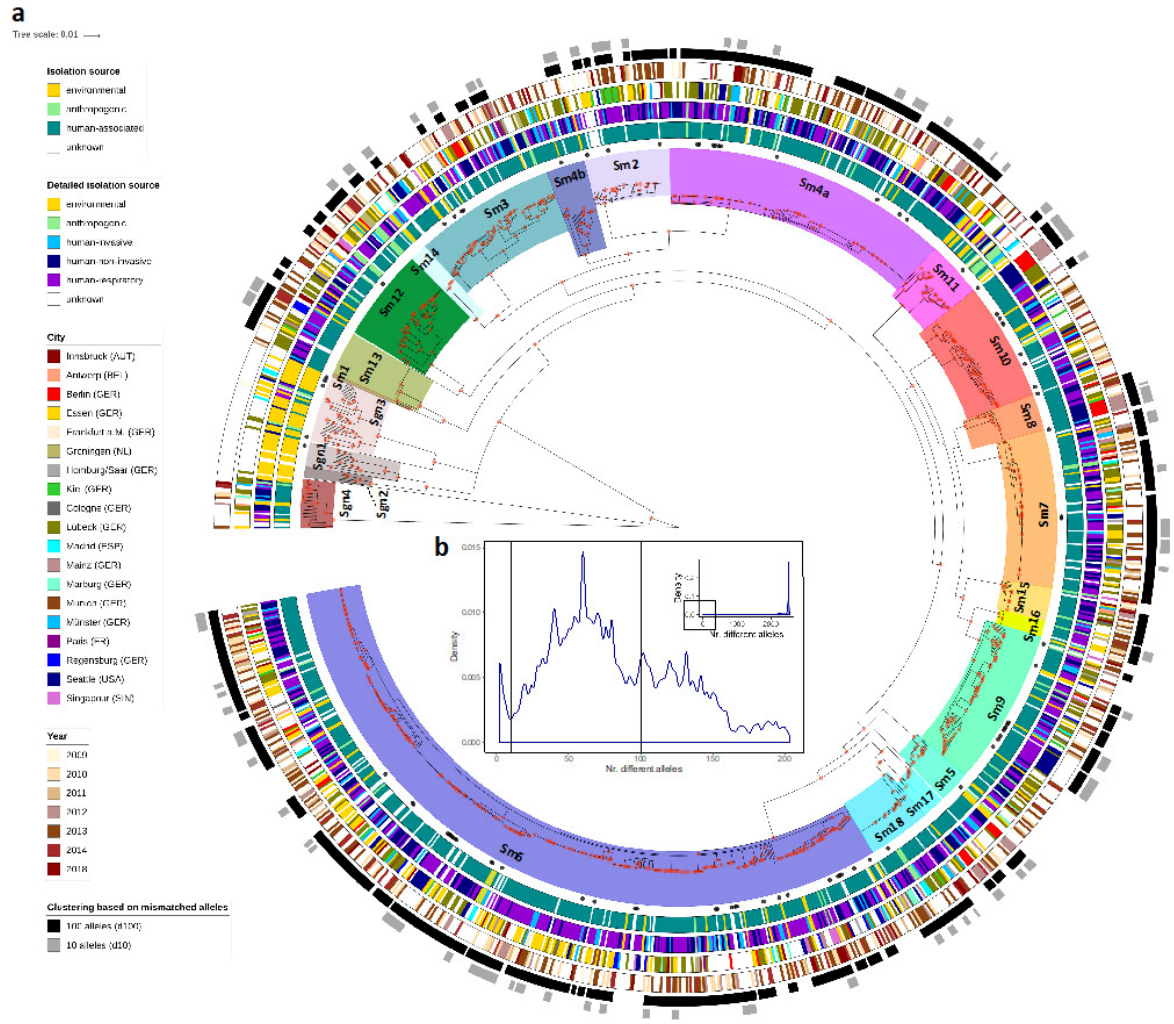

Figure: Spatiotemporal cluster analysis of 1,305 *S. maltophilia* complex strains. a, The coloured ranges across the outer nodes and branches indicate the 23 lineages. The black dots indicate the location of the genome datasets used for whole genome Multilocus sequencing tying scheme generation. The rings, from inside towards outside denote: i) the isolation source of the strains classified as either environmental, anthropogenic, human, or unknown; ii) the detailed isolation source of strains similar to the first ring with the human strains subclassified into human-invasive, human-non-invasive, and human-respiratory; iii) the city of isolation; iv) the year of isolation (where available), with light colours representing earlier years and darker brown colours more recent isolation dates. The outer rings in black-to-grey indicate the single linkage-derived clusters based on the number of allelic differences between any two strains for 100 (d100 clusters) and 10 (d10 clusters) allelic mismatches. Red dots on the nodes indicate support values of 100%. **b,** Distribution of the number of wgMLST allelic differences between pairs of strains among the 1,305 *S. maltophilia* strains.

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Abstract 52

Clostridioides difficile infection in immunocompromised hospitalised patients is associated with a high recurrence rate

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Abstract third-party references: Rabin medical center, Beilinson hospital

Background: *Clostridioides difficile* infection (CDI) may pose a serious threat to immunocompromised patients (IMC). Herein, we evaluated the clinical outcomes of IMC patients with CDI.

Materials/methods: All consecutive hospitalized patients between January 1, 2013 and December 31, 2018 with laboratory confirmed CDI, were included in the study. Subjects were divided into two groups: IMC patients and controls. Primary outcome was the recurrence rate of CDI (rCDI) at 30/90 days after the first CDI episode. Secondary outcomes included 30/90 day all-cause mortality, length of hospital stay (LOS) and readmission rates. A multivariate analysis adjusted other risk factors for recurrence. An analysis of IMC patient subgroups (based on type of IMC conditions) was also performed. Results are reported as odds ratios (OR) with a 95% confidence interval (95% CI).

Results: A total of 573 patients were included, amongst them 149 IMC patients (36 solid organ transplants, 38 undergoing chemotherapy, 62 haematological conditions, 13 receiving high dose prednisone) and 424 controls. IMC patients were younger, independent and exhibited less significant comorbidities. On multivariable analysis, the rate of rCDI was significantly higher in IMC patients (OR 2.7, 95% CI 1.6-5). rCDI was also associated with vancomycin therapy, haemodialysis and previous hospitalizations. Mortality, LOS, CDI complications and rehospitalization rates were similar in both.

Conclusions: IMC patients with CDI have an increased risk of 90 days rCDI. Vancomycin treatment for CDI endangers recurrence in IMC patients. Further research should explore other therapies for IMC patients with CDI with alternative agents such as Fidaxomicin and Bezlotoxumab.

Table. Univariate and Multivariate Model for Risk Factors of rCDI at 90 Days

Variable	Univariate OR (95% CI)	Multivariate OR (95% CI)	p value
Immunocompromising condition	2.7 (1.6-4.7)	2.19 (1.2-4.4)	0.02
Younger age	0.9 (0.97-1.01)	1.001 (0.982-1.02)	0.9
Past abdominal surgery	1.9 (1.1-3.5)	1.3(0.7-2.4)	0.5
Antibiotic exposure during the last 3 months	3.6 (1.9-6.5)	1.9 (0.9-3.9)	0.06
Previous hospitalization during 3 months	4.5 (2.2-9.4)	2.51 (1.1-5.9)	0.04
Vancomycin treatment for CDI	2.2 (1.3-3.9)	1.9 (1.03-3.4)	0.04
Hemodialysis	3.8 (1.4-10.1)	3.2 (1.1-9.4)	0.03

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Abstract 57

Combined antibiotic stewardship and infection control measures to contain an outbreak of linezolid-resistant *Staphylococcus epidermidis* in an interdisciplinary intensive care unit

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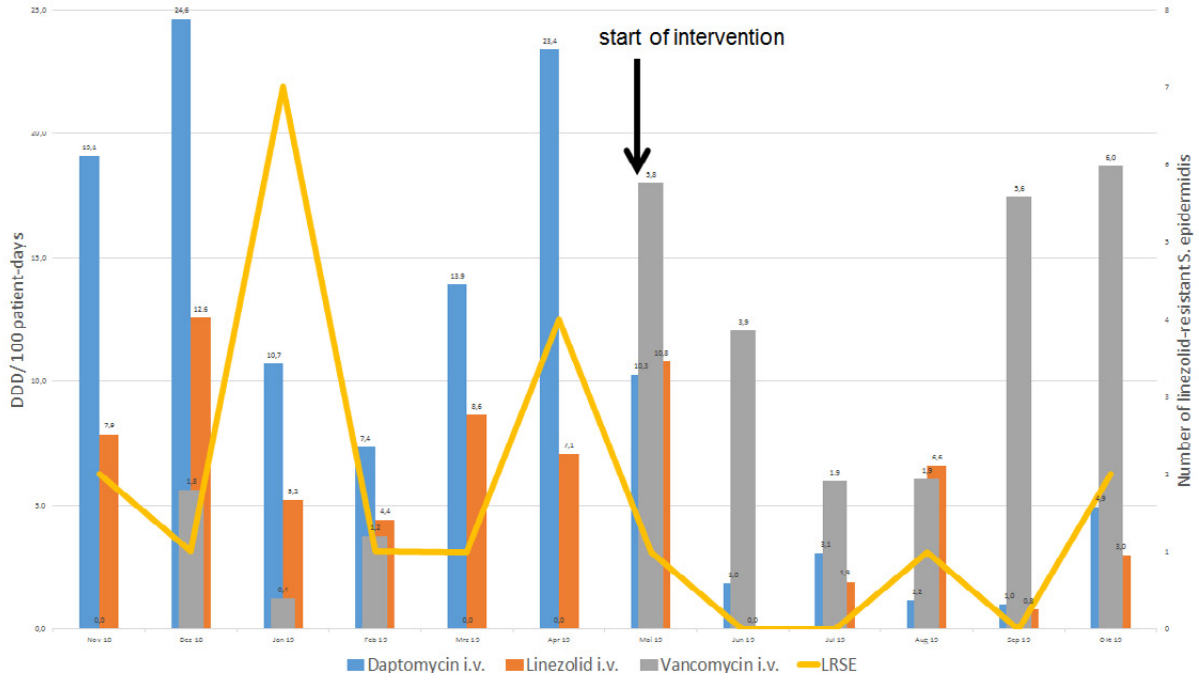
Background: *Staphylococcus epidermidis* constitutes a major part of the human skin flora, but can cause healthcare-associated infections, especially in immunocompromised patients. The imprudent use of linezolid has been linked to the emergence of linezolid-resistant *S. epidermidis* (LRSE). We report an outbreak in an interdisciplinary intensive care unit (ICU) and the effects of combined antibiotic stewardship and infection control measures.

Materials/methods: Microbiological and infection surveillance data were reviewed to identify all LRSE between November 2018 and October 2019 detected in clinical or screening samples. Quantitative data on the use of antibiotics with Gram-positive coverage were obtained in defined daily doses (DDD) per 100 patient-days (PD). An antibiotic stewardship intervention was started in May 2019, focusing on linezolid restriction and promoting vancomycin, wherever needed. In addition, a catheter-care bundle as an infection control measure was initiated. We compared data from the pre-intervention period (November 2018 through April 2019) to the post-intervention period (June 2019 through October 2019).

Results: Infection control measures were implemented immediately upon outbreak recognition. In the pre-intervention period, LRSE were isolated from 16 patients, 6 of which were blood culture isolates. The average consumption of linezolid and daptomycin decreased from 7.6 DDD/100 PD and 16.5 DDD/100 PD per month in the pre-intervention period to 2.5 DDD/100 PD and 2.4 DDD/100 PD per month in the post-intervention period, respectively. Conversely, vancomycin consumption increased from 0.6 DDD/100 PD per month to 3.9 DDD/100 PD per month. In the post-intervention period, three LRSE isolates were detected in clinical or screening samples, while the total number of all *S. epidermidis* isolates from blood cultures dropped from 74 (of 840 ordered blood cultures; 8.8%) in the pre-intervention period to 27 (of 617 ordered blood cultures; 4.4%) in the post-intervention period.

Conclusions: Complementing infection control measures by targeted antibiotic stewardship proved to be beneficial in the efforts to contain this LRSE outbreak in an interdisciplinary ICU. Next-generation sequencing results will help to clarify the genetic relatedness of the isolates (results pending). Follow-up measures and a high level of alertness are critical in order to sustain this favorable outcome.



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Abstract 64

Tuberculosis among migrant people in Sicily: a real-life report

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Abstract third-party references: on behalf of I.Ta.C.A. (Immigrant Take Care Advocacy) team, Palermo

Background: From 2014 to 2017, the number of migrants who came to Italy via the Mediterranean route has reached an unprecedented level. The majority of refugees and migrants were rescued in the Central Mediterranean and disembarked in the Sicily region. Tuberculosis represent a social disease and migration, as a social determinant of health, increases tuberculosis-related morbidity and mortality. In May 2014 the World Health Assembly passes a resolution in which calls on governments to adapt and implement the "end tuberculosis strategy". Early diagnosis, particularly in high-risk group, such as migrants, is the first step to achieve the aim. This study aims to estimate the frequency of both tuberculosis and latent tuberculosis infection among migrant population, from 2011 to 2017, afferent to the permanence centers of different Sicilians cities.

Materials/methods: Migratory phenomenon shown different scenario and socio-political context among years. Consequently, methodology used for taking charge, diagnostic procedure and the data collection have not always been homogeneous, highlighting possible sample bias, often justified by the critical nature of the migratory phenomenon and the need to ensure early correct diagnosis and treatment. In the most cases observed, the screening was done by Mantoux or quantiferon test and was carried out 4-6 weeks after arrival and, in any case, within 2 months of landing. In all migrant with the screening test positive it was performed x-ray chest and smear examination.

Case definition: Latent tuberculosis infection case: defined by positivity of Mantoux or quantiferon test with x-ray chest and smear examination negative.

Active tuberculosis case: radiological and/or clinical and/or sputum positivity in a patient with a Mantoux/quantiferon positivity.

Results: From 2011 to 2017 we evaluate a total of 6.020 migrants, all African. 4.711 males, 1.309 females with an age range from 16 to 29 years. tuberculosis infection was diagnosed in 1.304 people (21,6%); active tuberculosis disease was diagnosed in 185 (3,1%) people, 50 of these (0,8%) were bk-positive on the smear.

Conclusions: Despite the particular vulnerability of this cohort, the frequency of a smear positive tuberculosis infection was less than 1%, data already seen in other Italian experiences.

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Abstract 65

Impact of referral bias on prognostic assessment in infective endocarditis: insights from a population-based cohort

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Background: Most prognostic studies on infective endocarditis (IE) are derived from samples of patients managed in tertiary hospitals, mixing patients admitted directly and referred secondarily to tertiary hospitals, which may introduce referral bias. We aimed to assess this bias.

Materials/methods: We analysed data from a population-based cohort study conducted in France in 2008. A total of 497 patients with Duke-Li definite IE were included. Patients had been admitted directly to a tertiary hospital (group T), or admitted to a non-tertiary hospital and referred secondarily to a tertiary hospital (group NTT) or not (group NT). We compared patients' characteristics, 1-month, 3-month and 1-year survival rates between groups. Using Cox models, we identified prognostic factors first in the whole sample, and then in the pooled (NTT+T) group.

Results: Compared to group T patients (N=291), group NTT patients (N=144) were more often males (81.3% vs 72.5%, p=0.046), injection drug users (9.7% vs 4.5%, p=0.033), had higher proportions of echocardiographic abnormalities (97.2% vs 91.1%, p=0.017) and of indications for valve surgery (78.5% vs 64.3%, p=0.003). Compared to group NT patients (N=62), group NTT patients were more often males (81.3% vs 67.7%, p=0.034) and presented more often with indications for valve surgery (78.5% vs 19.4%, p<0.001). One-year survival was higher in (NTT+T) patients than in NT patients (73.0% vs 56.1%, p=0.01). The same prognostic factors were identified across groups, although the magnitude of their effect (HR estimates) differed.

Conclusions: When derived from samples mixing IE patients admitted directly and secondarily referred to tertiary hospitals, validity of patients' characteristics description and survival estimates is threatened by referral bias. Studies based on these heterogeneous samples also result in biased estimation of HRs.

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Abstract 76

Architecture fundamentally influences opportunity costs during an outbreak in a neonatology unit: real-life data and simulation of room designs

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Background: Limiting the spread of nosocomial pathogens and stopping outbreaks at an early stage are fundamentally relevant aims of infection control especially in neonates. Timely isolation of infected from exposed and non-infected babies is a cornerstone in termination of outbreaks. However, rising costs challenge hospitals without the opportunity to reimburse lost revenues. The aim of this investigation was to define the best room design during an outbreak from the cost perspective

Materials/methods: An outbreak of *Serratia marcescens* in a neonatal ICU and a neonatology ward including six patients and 34 contacts was assessed. Opportunity costs based on the G-DRG system were calculated for real-life scenario (ICU: two 2-bed, one 3-bed, two 4-bed, one 5-bed room; neonatology: two 3-bed, two 4-bed, one 7-bed room) and compared to simulation A (ICU: two 1-bed, four 2-bed, two 3-bed, one 4-bed room; neonatology: two 1-bed, four 2-bed, one 3-bed, two 4-bed rooms) and simulation B (four 1-bed, others 2-bed rooms; neonatology: five 1-bed, others 2-bed rooms), respectively.

Results: Patients were enrolled during 05-07/2018. In the real life setting a total of 128 (N1(ICU)=29 and N2(neonatology ward)= 99) bed-days could not be served, thereof 97 due to isolation of colonized or infected patients and 31 due to isolation of contacts. This resulted in opportunity costs of 130.379€.

In simulation A the number of contacts was reduced by 41% to 20, the number of bed-days not served due to isolation was reduced by 23% to 99, and finally the costs were reduced by 23% to 100.839€, respectively.

In simulation B the number of contact patients was reduced by 76% to 8, the number of bed-days not occupied for isolation was reduced by 42% to 74, and finally the costs were reduced by 42% to 75.375€, respectively.

Conclusions: Room design has a relevant impact on patients at risk for infection. Moreover, room design with rooms caring for less patients saves costs during an outbreak. These findings should be a) verified for transferability and generalizability, b) assessed for potential shortcomings and c) taken into account for planning and constructing new wards or hospitals.

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Abstract 81

A regional survey on the level of implementation of key infection prevention and control structures in acute-care hospitals in Crete, Greece

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Background: Data on assessment of Infection Prevention and Control (IPC) programmes in Greek hospitals are scarce. We conducted a situational survey on the level of implementation of the WHO guidelines on core components of IPC programmes aiming to identify local strengths and gaps that can inform planning and promote the use of standardized IPC assessment tools.

Materials/methods: The survey took place on August 2019 including all of 7 hospitals in one health region in Greece. The WHO IPC Assessment Framework (IPCAF) was completed through discussions between an external assessor and Infection Control Committee members. ICPAF is a facility-level diagnostic tool to identify areas for improvement based on 81 IPC indicators grouped into 8 sections reflecting the WHO IPC core components. An associated scoring system (maximum score, 800), classifies the level of IPC promotion and practice as inadequate (score, 0-200), basic (201-400), intermediate (401-600), or advanced (601-800).

Results: Surveyed hospitals had 2,166 beds and admitted 183,129 patients in 2018 (6.6% and 7.3% of the country's total, respectively). The overall mean IPCAF score for all hospitals was 465 out of 800 (range 340-618), corresponding to an intermediate level of IPC. Only 1 (14%) hospital achieved an advanced IPC level, whereas 3 (43%) hospitals attained an intermediate level and 3 (43%) hospitals had a basic level. More profound variability was found between the respective core components of IPC. A high mean score of 90 out of 100 (range, 85-95) was obtained in relation to built environment, materials and equipment for IPC. Basic or intermediate scores were obtained regarding the implementation of IPC programmes (mean, 72; range, 58-95), guidelines (mean, 63; range, 43-88) and surveillance activities (mean, 47; range 25-83). Particularly low scores were revealed for education and training (mean, 47; range, 250-85), multimodal strategies (mean, 39; range, 10-85), monitoring/audit and feedback (mean, 47; range, 15-68), and workload and staffing (mean, 46; range, 35-55).

Conclusions: Surveyed hospitals in Greece are, on average, at an intermediate level of IPC implementation. This IPCAF-based survey helped us recognise areas for improvement in IPC and motivated regional hospitals to develop long-term improvement plans.

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Abstract 97

Vimentin may inhibit dengue virus invasion of HBMEC cells

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Background: Dengue virus (DENV), belongs to the genus flavivirus, caused dengue fever prevalent in tropical and subtropical regions whose epidemic has intensified in recent years. Vimentin, one of the cytoskeletal components involved in the infection of DENV, was observed to reorder significantly during infection. However, the mechanism of infection is still poorly understood.

Materials/methods: A vimentin knockout human brain microvascular endothelial cells (HBMEC) cell model was first exploited to clarify the role of vimentin when DENV2 invasion the cells, and we further built a knockout SV129 suckling mouse model for DENV2 infection. Finally, the dynamic changes of vimentin in vitro and the changes of disease course in vivo were combined to demonstrate the relationship between vimentin and dengue infection.

Results: Phosphorylation and soluble percentage of vimentin were observed to change dynamically during DENV2 infection of HBMEC, suggesting that DENV2 infection regulates these dynamic changes. During this process, the phosphorylation reaction of vimentin has a certain consistency with the dynamic change of the percentage of soluble, and the two may be related. Compared with the control group, the DENV2 viral load detected in vimentin knockout HBMEC cells was significantly increased. Interestingly, 4-5 days after the suckling mice injected DENV2, SV129 (vim-knockout) had higher viral loads in serum and brain tissue, and this result is consistent with the cell experiments. Compared with SV129, SV129(vim- knockout) suckling mice not only have disordered cerebral cortical nerve cells, but also disappeared in the molecular layer, outer cone layer, outer granular layer, inner cone layer, inner granular layer, and a large number of necrotic apoptosis, which confirmed that vim-knockout mice were more susceptible to DENV2 infection and caused severe brain damage based on animal models.

Conclusions: DENV2 infection can cause cell vimentin to rearrange, and both dynamic changes are highly correlated during the infection process. Presence of vimentin may inhibit viral infection to reduce disease or affect disease course. This helps to identify a possible host-targeted antiviral strategy to combat DENV infection, or avoids potential resistance of direct-acting antivirals.

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Abstract 101

A new nano-sized formulation of amphotericin B-loaded chitosan with remarkable improved antileishmanial effects for the treatment of *Leishmania major*

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Background: This study aims to improve the *leishmania major's* pathological effects through increasing the dose of loaded amphotericin B (Amp) into nanochitosan.

Materials/methods: Nanochitosan was synthesized and loaded with Amp using phase separation method. To perform this, a novel solvent was designed. The therapeutic effects of the synthesized nanodrug were evaluated in vitro and in vivo environments using pathological studies.

Results: A nanodrug was synthesized with the high drug loading efficiency (90%) and cellular uptake (98.6%) which released Amp in a slow drug release manner. To evaluate the toxicity effects of the nanodrug, MTT assay and balb/c mice peritoneal macrophages were used. The results showed that Amp-chitosan (AK) caused a significant decrease in the toxicity effects of Amp by 100%. Also, the efficacy of the nanodrug to inhibit the promastigotes and amastigotes of the parasite (*leishmania major*) was evaluated and the results showed that the nanodrug inhibited the parasite by 85%.

To evaluate the potency of the nanodrug in vivo environment, a novel solvent was prepared which could dissolve Amp-nanochtiosan10 mg/kg (AK10 mg/kg). Then, the toxicity effects of the formulation (AK10 mg/kg) were evaluated using measurement the kidney and liver related enzymes and pathological studies. The results showed that the nanodrug had no toxicity effects. Next, the potency of AK in the treatment of *leishmania major*-infected balb/c mice was evaluated. For this purpose, the lesion size was measured using a caliper and the results showed that the nanodrug was completely effective to reduce the lesion size and improve the wound healing. These results were confirmed by pathological studies. The potency of the nanodrug to inhibit the parasite burden was also evaluated using limited dilution assay (LDA) and popliteal lymph node and the results showed that AK10 mg/kg was effective to inhibit the parasite by 83% ($p<0.001$).

Conclusions: Increasing the therapeutic dose of AK to 10 mg/kg was found critical in the treatment process and caused *l. major's* pathological effects to be successfully treated in vitro and in vivo environments.

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Abstract 105

Comparison of molecular rapid diagnostic testing panels for Gram-negative bacteraemia using Desirability Of Outcome Ranking Management of Antimicrobial Therapy (DOOR-MAT)

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Background: Rapid diagnostic tests (RDTs) are becoming increasingly employed to assist in the management of gram-negative bacteremia. Given the diversity of pathogenic organisms and resistance mechanisms, clinical data regarding optimal management using RDT is lacking. Moreover the choice of optimal RDT platform remains elusive, as comparisons are limited to sensitivity and specificity in small samples. This study compared a key clinical outcome, potential antimicrobial decisions, based on results of different commonly used RDT platforms, using a novel methodology termed Desirability of Outcome Ranking Management of Antimicrobial Therapy (DOOR-MAT).

Materials/methods: Retrospective observational study at University of Maryland Medical Center from 08/2018 – 11/2019 of adult patients with gram-negative bacteremia comparing Verigene® Blood Culture (VBC) to BioFire® FilmArray® Blood Culture Identification (BCID) and BCID 2 research use only (RUO) panels for clinical blood cultures. Verigene was part of standard of care, BCID and BCID 2 were run on discarded frozen samples. The RDT results and local susceptibility data were applied by an Infectious Diseases-trained pharmacists to make decisions regarding potential antimicrobial selection. DOOR-MAT, a partial credit scoring system, was used to compare antimicrobial decisions as a function of final phenotypic susceptibly patterns as determined by VITEK® 2 automated susceptibility testing (Figure 1). DOOR-MAT scores were compared between panels using Kruskal-Wallis with $p < 0.05$ statisticaly significant.

Figure 1: Condensed Example DOOR-MAT Scoring E. Coli and Kleb spp.

Antibiotic	Phenotypic Resistance Profile						
Cefazolin	S	R	R	R	R	R	R
Ceftriaxone	S	S	S	R	R	R	R
Piperacillin-tazobactam	S	S	S	R	R	R	R
Ertapenem	S	S	S	S	S	S	R
Meropenem	S	S	S	S	S	S	R
Ceftazidime-Avibactam Meropenem-Vabrobactam	S	S	S	S	S	S	S

Optimal	Score = 100
Slight Overtreatment	Score = 50
Moderate Overtreatment	Score = 25
Under treatment	Score = 0

Results: A total of 103 patients with positive clinical cultures for gram-negative bacteria were included. The average DOOR-MAT score for VBC was 85.8 (SD 25.7) and median score was 100 (IQR 62.5, 100). BCID resulted in an average score of 60.8 (SD 33.4) and median 50 (IQR 50,100). BCID 2 (RUO) demonstrated an average score of 89.7 (SD 24.7) and median score 100 (IQR 100, 100). Overall, BioFire® FilmArray® BCID 2 (RUO) produced the highest scores for optimal therapy/ There was a significant difference in DOOR-MAT scores ($p < 0.0001$) between tested panels.

Conclusions: The BioFire® FilmArray® BCID 2 (RUO) performed best among the three panels tested. Use of a partial credit scoring system such as the DOOR-MAT allows for comparisons between RDT systems beyond sensitivity and specificity allowing for enhanced clinical interpretation.

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Abstract 107

Risk factors for non-ventilator-associated hospital-acquired pneumonia in patients outside the intensive care unit

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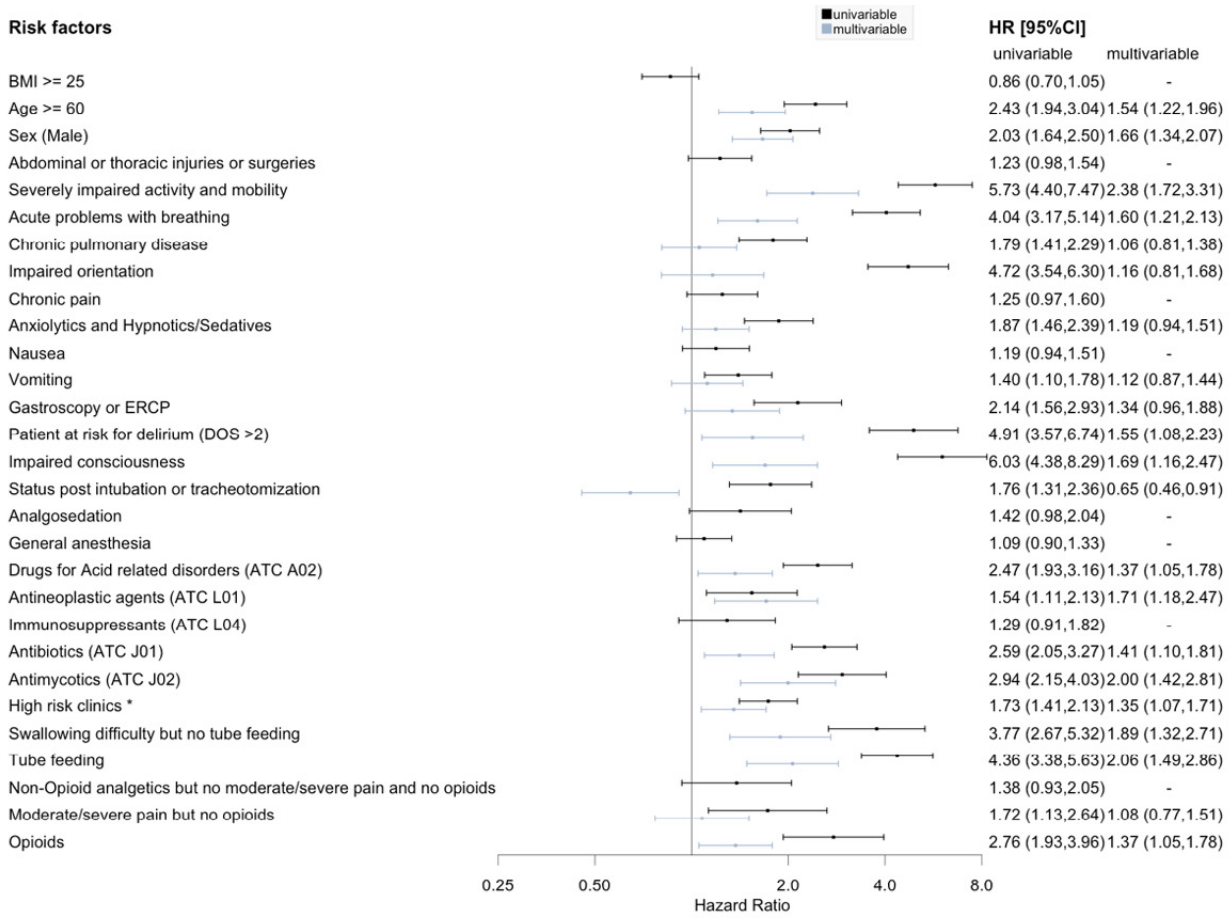
Background: Hospital-acquired pneumonia in non-ventilated patients (nvHAP) belong to the most common healthcare-associated infections. As understanding of risk factors for nvHAP is key for targeting prevention measures to patients at highest risk, this study aimed to investigate risk factors for nvHAP in patients outside the intensive care unit (ICU).

Materials/methods: We included patients ≥18 years of age who were discharged during the years 2017 and 2018 from the University Hospital Zurich, Switzerland. A total of 29 potential risk factors - both constant and time-varying - were extracted from electronic medical records, including demographic data, signs and symptoms (many assessed by daily nursing assessments), procedures, medication, and devices. Hazard ratios for nvHAP were derived from univariable and multivariable Cox proportional hazards models. Patient days on ICUs were excluded from analyses.

Results: We included 69'559 patients of whom 396 (0.57%) had nvHAP. Median age was 57 years (Interquartile range (IQR): 39-72) and 34'558 (49.7%) patients were male. Independent risk factors for nvHAP were: age ≥60 years (hazard ratio (HR): 1.54, 95% confidence interval (CI): 1.22-1.96), male sex (HR: 1.66, CI: 1.34-2.07), affiliation to high risk clinic (HR: 1.35, CI: 1.07-1.71), impaired activity and mobility (HR: 2.38, CI: 1.72-3.31), acute problems with breathing (HR: 1.60, CI: 1.21-2.13), being "at risk for delirium" (HR: 1.55, CI: 1.08-2.23), impaired consciousness (HR: 1.69, CI: 1.16-2.47), drugs for acid related disorders (HR: 1.37, CI: 1.05-1.78), antineoplastic agents (HR: 1.71, CI: 1.18-2.47), antibiotics (HR: 1.41, CI: 1.10-1.81), antimycotics (HR: 2.00, CI: 1.42-2.81), opioids (HR: 1.37, CI: 1.05-1.78), swallowing difficulty without tube feeding (HR: 1.89, CI: 1.32-2.71), and tube feeding (HR: 2.06, CI: 1.49-2.86).

Conclusions: We identified several modifiable and non-modifiable risk factors for nvHAP. The modifiable risk factors like impaired activity and mobility, might be conditions potentially targetable by specific prevention measures. Non-modifiable risk factors like male gender, older age or swallowing difficulties will allow to identify high-risk patients and focus nvHAP prevention efforts on these patients.

Figure 1 – Forest plot of hazard ratios for potential risk factors for nvHAP



Abbreviations: ATC, anatomical therapeutic chemical classification; BMI, body mass index; CI, confidence interval; DOS, delirium observation scale; ERCP, endoscopic retrograde cholangiopancreatography; HR, hazard ratio; ICU, intensive care unit; nvHAP
* High risk clinics: Internal medicine and all subspecialties, clinics performing major surgical procedures on chest, abdomen, or extremities.

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Abstract 118

Olorofim for a case of severe disseminated Lomentospora prolificans infection

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Abstract third-party references: F2G, Ltd.

Background: Though rare, invasive *Lomentospora prolificans* infection causes significant morbidity and mortality particularly in immunocompromised patients. Mortality rate is least 65%, and near 100% if infection becomes disseminated. We describe a case of disseminated *Lomentospora prolificans* infection in an immunosuppressed patient who failed to respond to conventional therapy, and was commenced on Olorofim under clinical trial (NCT03583164).

Case report: A 56-year-old lady developed disseminated *Lomentospora prolificans* infection following HyperCVAD cycle-1b for T-cell acute lymphoblastic leukemia (T-ALL), including fungaemia, endophthalmitis, lumbar spine (L4/5 vertebrae) and presumed pulmonary involvement [avid pulmonary nodule on Positron Emission Tomography (PET)]. Voriconazole and terbinafine were immediately started. She was unable to achieve therapeutic voriconazole levels despite measures to augment levels, and had worsening PET uptake in the lumbar spine. *Lomentospora prolificans* was again isolated from lumbar vertebral biopsy after 3 months of combination regime. Failure of medical therapy prompted surgical debulking and spine stabilisation surgery.

Patient then developed new PET uptake at aortic root and aortic valve five months after spinal surgery. Serial echocardiography showed progressive moderate to severe aortic regurgitation. Eleven months into management of the infection, Olorofim was started at loading dose 180mg followed by 60mg twice daily (BD), and later increased to 90mg BD as guided by drug levels. Serial PET scan over six months demonstrated improvement in uptake at aortic root and lumbar spine, despite needing radiotherapy and Pralatrexate to control relapsed T-ALL (Figure 1). As of November 2019 patient has been on Olorofim for a year without adverse effects. Regular therapeutic drug monitoring confirmed stable drug levels. She is well, active and has gained weight since on Olorofim. Her vision is stable and reports of no further back pain.

Conclusions: *Lomentospora prolificans* is routinely intrinsically resistant to all antifungals, hence poses a therapeutic challenge. An open-label single-arm phase IIb study of F901318 is currently underway. Olorofim monotherapy has successfully controlled a case of osteomyelitis due to this pathogen, demonstrating its potential use in treatment of resistant invasive mould infections in patients lacking suitable alternative treatment options.

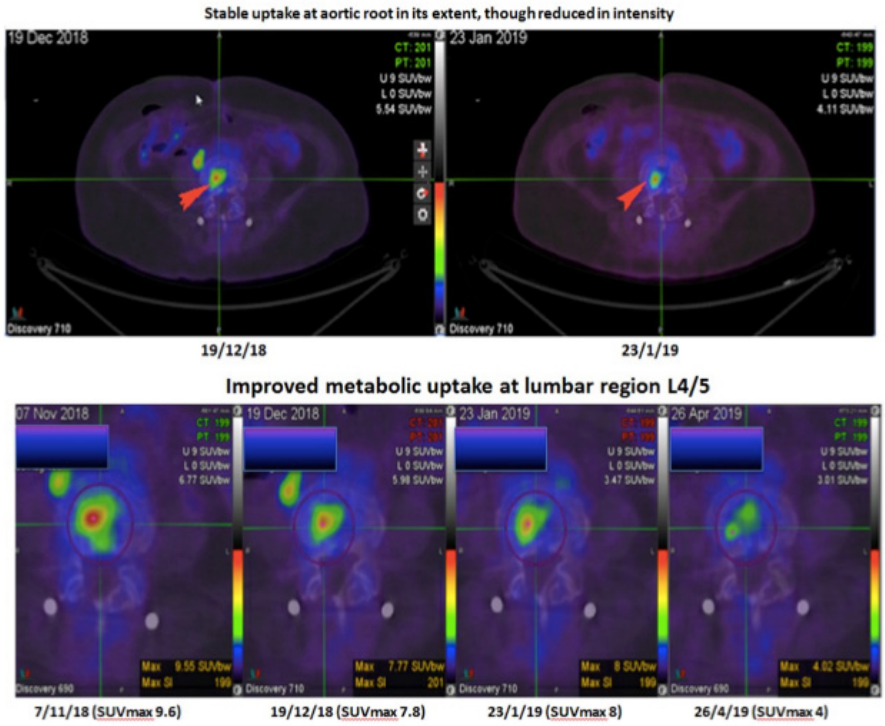

Figure 1. Serial PET showing improvement in metabolic uptake at aortic root and lumbar spine.

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Abstract 119

Dynamic *in vitro* pharmacodynamics evaluation of piperacillin/tazobactam-tobramycin combination therapy against *Escherichia coli* and *Klebsiella pneumoniae* clinical isolates

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Background: Piperacillin/tazobactam monotherapy has been associated with increased mortality for treating patients with ceftriaxone-resistant *Escherichia coli or Klebsiella pneumoniae* bloodstream infection; however this leads to a reliance on carbapenem therapy. Consequently, rationally optimized antibiotic combination therapy could be a promising carbapenem-sparing approach to maximize bacterial killing and suppress the emergence of resistance. A piperacillin/tazobactam-tobramycin combination was tested against less-susceptible extended-spectrum beta-lactamase (ESBL) producing *E. coli* and *K. pneumoniae* clinical isolates using the dynamic hollow-fiber infection model (HFIM).

Materials/methods: Piperacillin/tazobactam and tobramycin pharmacokinetics observed in critically-ill patients were simulated in the HFIM over 168h (initial inoculum ff10^7 CFU/ml). We evaluated piperacillin/tazobactam (4/0.5g every 6h, given as 0.5h and 3h infusions, and 16/2g continuous infusion) alone and in combination with tobramycin (7mg/kg daily) regimens against CTX-M-55 producing *E. coli* 50 (EC50) and SHV-106 producing *K. pneumoniae* 68 (KP68) clinical isolates (MIC 8mg/L). The total and less-susceptible bacterial populations were quantified using cation-adjusted Mueller-Hinton agar with and without antibiotic at a concentration fourfold the baseline MIC respectively.

Results: For all dosing regimens of piperacillin/tazobactam monotherapy against EC50 and KP68, there was an initial 4 $\log_{10}$ bacterial kill over 8h [Figure 1]. However, regrowth of a less-susceptible subpopulation exceeded the initial inoculum within 24h for all dosing regimens tested. The MIC of resistant subpopulations exceeded 256mg/L after 72h. Tobramycin monotherapies, displayed rapid initial killing (≥6 $\log_{10}$ at 8h) followed by extensive regrowth within 24h. A combination of piperacillin/tazobactam and tobramycin against EC50 and KP68 achieved synergistic killing (≥6 log10 at 8h) and prevented regrowth throughout the 7-day HFIM course.

Conclusions: This study shows that piperacillin/tazobactam monotherapy (C_{min}/MIC >5) was insufficient to achieve sustained bacterial killing and suppress resistant subpopulation against EC50 and KP68. Piperacillin/tazobactam-tobramycin combination therapy provided rapid bacterial killing and suppressed the emergence of resistance over 7-days. These results support the re-evaluation of the potential clinical utility of combination therapy against less-susceptible ESBL producing isolates as a carbapenem-sparing approach.

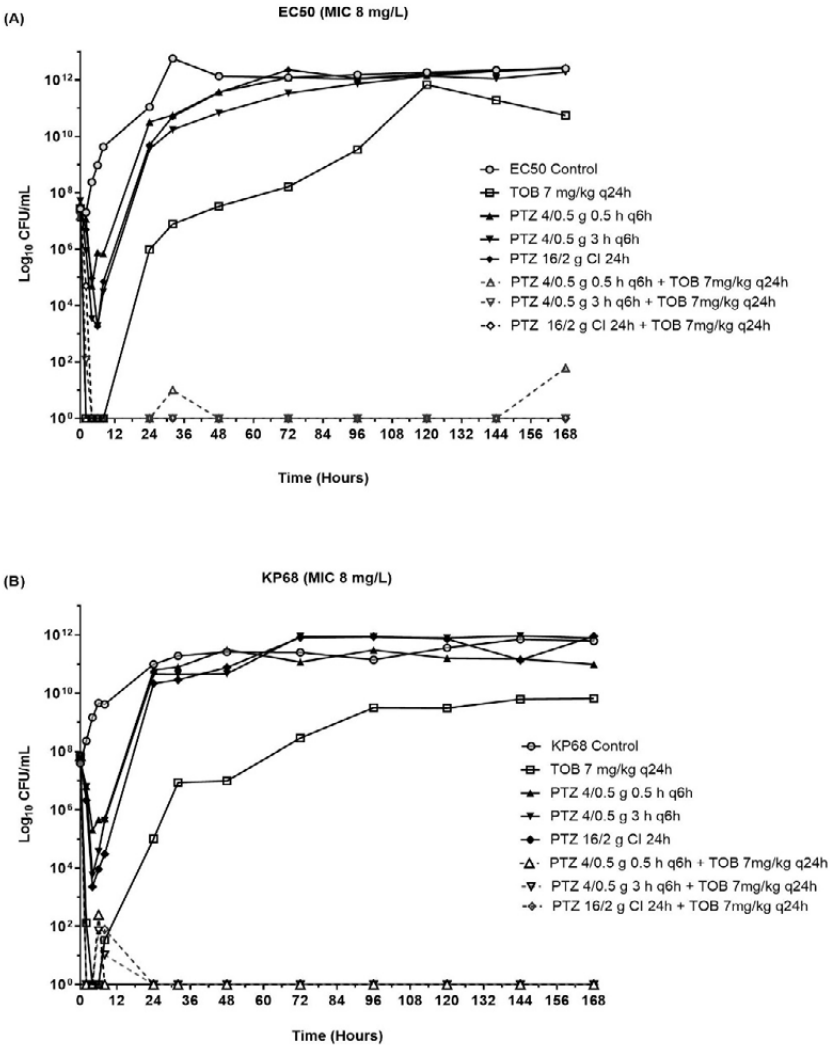

Figure 1: Effect of each dosing regimen on the total bacterial population using simulated human exposures of piperacillin and tobramycin against ESB-producing EC50 and KP68 (q6h, every 6 h; q24h, every 24 h)

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Abstract 136

Microscopic agglutination test in determining leptospirosis seroprevalence in Western Province, Sri Lanka

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Background: Leptospirosis is a globally distributed zoonosis common in tropical regions, including Sri Lanka. Microscopic agglutination test (MAT) is considered to be the gold standard in leptospirosis diagnosis, which uses panels of live leptospires representing the circulating serovars from the area. MAT provides epidemiological data on infecting serovars. In this study, we analyzed MAT results of confirmed cases of leptospirosis in Western province, Sri Lanka to determine commonly infecting serovars.

Materials/methods: This was a prospective hospital based study carried out during 2017 in 2 selected hospitals in Western province of Sri Lanka. Clinically suspected leptospirosis patients were recruited according to Communicable Disease Epidemiology Profile Sri Lanka, WHO. Leptospirosis was confirmed by either single MAT titre ≥1:320 or by positive polymerase chain reaction (PCR). MAT was carried out at the Medical Research Institute, Sri Lanka which is the national reference laboratory for leptospirosis and consists of a panel of 15 *Leptospira* serovars.

Results: Out of 172 clinically suspected patients, 42.44% were confirmed leptospirosis patients by either MAT (50.68%) or PCR (67.12%). Of the 37 MAT positive patients, 29 (78.37%) were positive for *L. interrogans* serovar bakeri, strain LT79 in Tarassovi. Two patients were positive for *L. interrogans* serovar poi, Strain Poi in Javanica, while one patient each was positive for *L. interrogans* serovar cynopteri, strain 3522C in Cynopteri and *L. interrogans* serovar bangkinang, starin Bangkinang 1 in autumnalis respectively. Four patient sera was found to be positive for two serovars (*L. interrogans* serovar bakeri, strain LT79 in Tarassovi with one of the following serovars: serovar rathnapura, strain wimalasena in Grippotyphosa, serovar bangkinang, strain Bankinang 1 in Autumnalis, serovar pyrogenes, strain Salinem in pyrogenes and serovar australis, strain Ballico in Australis) each having similar MAT titres, while 9 were positive for two serovars with a MAT titre ≥1:320 including serovars namely serovar australis, serovar bataviae, serovar bakeri, serovar icterohaemorrhagiae, serovar canicola, serovar bangkinang, serovar hebdomadis, serovar poi and serovar pyrogenes.

Conclusions: *L. interrogans* serovar bakeri, strain LT79 in Tarassovi was the predominant serovar identified in this study among patients of leptospirosis in the Western province, Sri Lanka.

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Abstract 146

Sexually-transmitted infections in soldiers: a cross-sectional assessment and a review of literature

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Background: Sexually transmitted infections (STI) show a wide prevalence range in military forces, ranging up-to more than 40 per cent in cross-sectional studies. Scarce information is available on STI in soldiers from Europe. Therefore, we have performed a retrospective assessment on prevalence and determinants of occurrence of STI in German paratroopers and navy soldiers by anonymously analyzing medical records from the medical departments of two German barracks.

Materials/methods: Medical records from 80 paratroopers and 80 navy soldiers were screened for records of STI as well as documented medical history associated with the likely mode of transmission next to information on risk factors as well as diagnostic and therapeutic management.

Results: Proportions of suspected STI were 17.5% and 20%, proportions of diagnosed STI 13.9% and 11.3% for predominantly male paratroopers and navy soldiers, respectively. On average, acquisition of STI occurred in the second half of the third decade of the patients' life. The proportion of infected officers was higher in the population of the navy soldiers, while more infected privates were among the paratroopers. Living as singles or unmarried but with a primary partnership was the most frequently observed lifestyle. Only one case of STI acquisition on deployment was documented for the navy soldiers and no such incident for the paratroopers, although nearly half of the assessed patients in both groups had deployment experience. In a relevant minority of about 20%, partner therapy was neglected and especially for the navy soldiers, considerable delay between onset of clinical symptoms and medical assessments was registered. While pharmacological therapy was always performed and adherence with national guidelines was acceptable with more than 80%, adherence with diagnostic therapy control was poor with proportions round about 50%, while clinically apparent recurrences were occasionally observed.

Conclusions: Although clinical hints for STI were frequently observed, clinical management was usually restricted to syndrome-based antibiotic treatment without detailed diagnostic workup. Altogether, occurrence of STI was comparable with reports from other armed forces, stressing an ongoing need for preventive medical approaches.

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Abstract 150

Assessment of trimethoprim-sulfamethoxazole susceptibility testing methods for fastidious Haemophilus spp.

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Background: Several discrepancies were found in clinical routine regarding trimethoprim-sulfamethoxazole (SXT) susceptibility determination depending on antimicrobial susceptibility (AST) method used and growth media. We aimed to compare the determinants of SXT resistance with established susceptibility values for fastidious *Haemophilus* spp., in order to provide recommendations for optimal SXT measurement.

Materials/methods: We collected 50 strains each of *Haemophilus influenzae* and *Haemophilus parainfluenzae* at Bellvitge University Hospital. SXT susceptibility was tested by microdilution, E-test, and disc diffusion using both Mueller-Hinton Fastidious (MH-F) and *Haemophilus* Test Medium (HTM) following EUCAST and CLSI criteria respectively. Mutations in *folA*, *folP* and additional determinants of resistance were identified in whole-genome sequenced isolates.

Results: Strains presented generally higher rates of SXT resistance when grown on HTM than on MH-F, independent of the methodology used (average MIC 2.6-fold higher in *H. influenzae* and 1.2-fold higher in *H. parainfluenzae*). The main resistance-related mechanisms were as follows: I95L and F154S/V in FolA; 3 and 15 base pair insertions and substitutions in *folP*; acquisition of *sul* genes; and FolA overproduction potentially linked to mutations in -35 and -10 promoter motifs. Of note, 2 of 19 *H. influenzae* strains (10.5%) and 9 of 33 *H. parainfluenzae* strains (27.3%) with mutations and assigned as resistant by microdilution were inaccurately considered susceptible by disc diffusion. This misinterpretation was resolved by raising the clinical resistance breakpoint of the EUCAST guidelines to ≤30 mm.

Conclusions: Given the routine use of disc diffusion, a significant number of strains could potentially be miscategorised as susceptible to SXT despite having resistance-related mechanisms. A simple modification to the current clinical resistance breakpoint given by the EUCAST guideline for MH-F ensures correct interpretation and correlation with the gold-standard method of microdilution.

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Abstract 151

A meta-analysis of the burden of non-typhoidal *Salmonella* in humans in the Middle East and North Africa

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Background: To enhance efforts related to controlling foodborne pathogens in the Middle East and North Africa (MENA), we quantified the overall regional and country-specific NTS prevalence in different human populations and identified the most common serotypes.

Materials/methods: Published literature of NTS prevalence was systematically reviewed and reported following PRISMA guidelines. Pooled NTS prevalence measures were estimated using a random-effects model.

Results: We identified 46 research reports that reported 84 NTS prevalence measures in 15 countries in MENA. The pooled NTS prevalence in MENA was estimated at 6.6% (95% confidence interval (CI): 5.4–7.9%). The highest pooled prevalence measures were in Morocco (17.9%, 95% CI: 5.7–34.8%), Tunisia (10.2%, 95% CI: 4.3–18.0%), and Sudan (9.2%, 95% CI: 6.5–12.2%) while the lowest were in Jordan (1.1%, 95% CI: 0.1–3.0%), Oman (1.2%, 95% CI: 1.2–1.3%), and Palestine (1.2%, 95% CI: 0.4–2.1%). NTS pooled prevalence in gastrointestinal asymptomatic and food handlers population groups was 11.4%, and 3.8%, respectively. *S. Enteritidis* (29.8%) and Typhimurium (23.6%) were the most common.

Conclusions: NYT is a common foodborne pathogen in MENA countries, particularly in North African countries. Findings inform the scientific community, the public, and the decision makers with NTS prevalence and gaps in evidence in MENA to support control and prevention strategies.

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Abstract 152

Whole genome sequencing of *Pseudomonas aeruginosa* isolates from across the United Kingdom: population structure and molecular predictors of resistance

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Background: *Pseudomonas aeruginosa* (PSA) infections are difficult to treat due to virulence and antibiotic resistance. We present a large whole genome sequencing (WGS) study of PSA from non-cystic fibrosis (CF) patients to examine the epidemiology, virulence and resistance to anti-pseudomonal antibiotics, including ceftolozane/tazobactam (C/T).

Materials/methods: 1,123 consecutive, clinically relevant, non-CF PSA isolates from 14 participating centres from Jan/15-Apr/2018 were studied. In vitro activity of C/T and nine other antibiotics were evaluated using EUCAST disc diffusion testing, a subset of 159 isolates (C/T diameter ≤26mm) tested by broth microdilution (BMD) with 7 antibiotics. Data were collected on the infection site, specimen and ward type.

304 isolates were chosen for WGS on Illumina HiSeq platform. Isolates were chosen based on C/T BMD (MIC ≥4 µg/mL) plus control isolates based on site and resistance pattern (1:8 ratio). Assembled sequences were annotated then the contigs screened using abricate: on CARD for resistance, VFDB for virulence factors. Reference alignment was performed to identify known resistance mutations. In addition, Multi-Locus Sequence Types (MLST) were generated from assemblies.

Results: 26/1,123 (2.3%) isolates were resistant to C/T and 10 had an MIC ≥ 4 µg/mL. MLST were identified in 281/304 (92%) isolates with 106 distinct MLSTs.14 MLST comprised 50% of isolates. Dendrogram and analysis of virulence genes showed two PSA populations, one containing the exoS type III secretion systems, and the other exoU.

BMD of 159 isolates found sensitivity to colistin (93%), C/T (84%), ceftazidime (66%), piperacillin/tazobactam (61%) and imipenem (71%). Beta-lactamase sequences were found in 10/26 (38%) C/T resistant isolates, however no resistance mechanism was found for 16/26 (62%). Similarly, beta-lactamases were found in 10/46 (22%) of carbapenem resistant isolates. Carbapenemases detected were IMP, VIM, NDM, but also unusual carbapenemases including OXA-119, OXA386 DIM1 and L1 (only reported in Stenotrophomonas).

Conclusions: Clinically significant PSA in non-CF patients has a diverse population across the UK with a division into 2 groups based on type III secretion systems**.** The majority of resistance in PSA to beta-lactams is not due to carbapenemases. Several unusual or unique carbapenemases to PSA were identified. C/T was the most effective beta-lactam against PSA.

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Abstract 154

Population pharmacokinetic/pharmacodynamic assessment of a clinical imipenem/cilastatin and relebactam dose in patients with hospital-acquired bacterial pneumonia and ventilator-associated bacterial pneumonia

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Abstract third-party references: This work was supported by Merck Sharp & Dohme Corp., a subsidiary of Merck & Co., Inc., Kenilworth, New Jersey, USA (MSD)

Background: Imipenem/cilastatin and relebactam (IMI/REL)—a fixed-dose combination of imipenem, a carbapenem antibacterial agent, cilastatin, a renal dehydropeptidase, and relebactam, a β-lactamase inhibitor—was compared with piperacillin/tazobactam for the treatment of patients with HABP/VABP in a phase 3 clinical trial. We developed population pharmacokinetic models, integrating data from this trial with prior phase 1–3 data, to evaluate the effects of covariates on imipenem and relebactam exposure and analyze the probability of target attainment (PTA) among patients with HABP/VABP.

Materials/methods: A previous population pharmacokinetic model was updated with data from the phase 3 trial (NCT02493764) to include patients who were exposed to a ≥1.25-g IMI/REL dose (500 mg imipenem, 500 mg cilastatin, and 250 mg relebactam) and had ≥1 measurable postdose concentration. The updated population pharmacokinetic model, comprising data from 1197 participants among 12 completed phase 1–3 trials, was used to assess the effect of clinical covariates on imipenem and relebactam pharmacokinetic parameters. Joint PTA analyses were performed to assess achievement of pharmacokinetic/pharmacodynamic targets.

Results: A 2-compartmental model with first-order elimination best described both the imipenem and relebactam plasma concentration–time profiles. Significant covariates for both imipenem and relebactam included body weight on clearance (CL) and central volume of distribution (V_1), creatinine clearance (CrCL) on CL, pneumonia on CL and V_1, and ventilation status on V_1 (but not on CL). Among patients with normal renal function (90 mL/min≤ CrCL <150 mL/min), area under the concentration–time curve (AUC) and maximum plasma concentration (C_{max}) were higher in patients with HABP/VABP compared with healthy participants, while AUC, C_{max}, and CL were comparable across ventilated and nonventilated patients with pneumonia (Table). Among patients with HABP/VABP, joint PTA was >98% regardless of renal clearance or ventilation status.

Conclusions: Inclusion of data from patients with HABP/VABP into the imipenem and relebactam population pharmacokinetic models demonstrated that pharmacokinetic exposures are higher in patients with HABP/VABP compared with healthy participants. The joint PTA was sufficient to justify the 1.25-g IMI/REL dose administered every 6 hours in this patient population. No dose adjustments are required for patients with HABP/VABP based on ventilation status.

Table. Summary of steady-state pharmacokinetic exposures in healthy participants and patients with pneumonia with normal renal function (90 mL/min≤CrCL<150 mL/min)

Drug	Population	Pharmacokinetic Parameters[a]		
		AUC_{0-24h} (μM·h)	C_{max} (μM)	CL (L/h)
Imipenem	Healthy participants	483.3 (60.4)	114.0 (66.3)	13.8 (60.4)
	Patients with pneumonia	812.2 (59.4)	159.1 (62.3)	8.2 (59.4)
	Ventilated patients with pneumonia	808.0 (58.8)	151.5 (62.7)	8.3 (58.8)
	Nonventilated patients with pneumonia	816.3 (59.9)	167.0 (61.4)	8.2 (59.9)
Relebactam	Healthy participants	348.4 (49.6)	62.4 (44.1)	8.2 (49.6)
	Patients with pneumonia	655.2 (47.9)	87.6 (43.8)	4.4 (47.9)
	Ventilated patients with pneumonia	663.4 (47.0)	81.6 (42.1)	4.3 (47.0)
	Nonventilated patients with pneumonia	647.2 (48.8)	94.2 (44.0)	4.4 (48.8)

AUC_{0-24h}, area under the concentration–time curve from 0 to 24 hours; CL, clearance; C_{max}, maximum plasma concentration; CrCL, creatinine clearance.

[a]Shown as geometric mean parameter estimates with percent geometric coefficient of variation values in parentheses.

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Abstract 159

Plasma levels of hepcidin, a potential biomarker during septic shock

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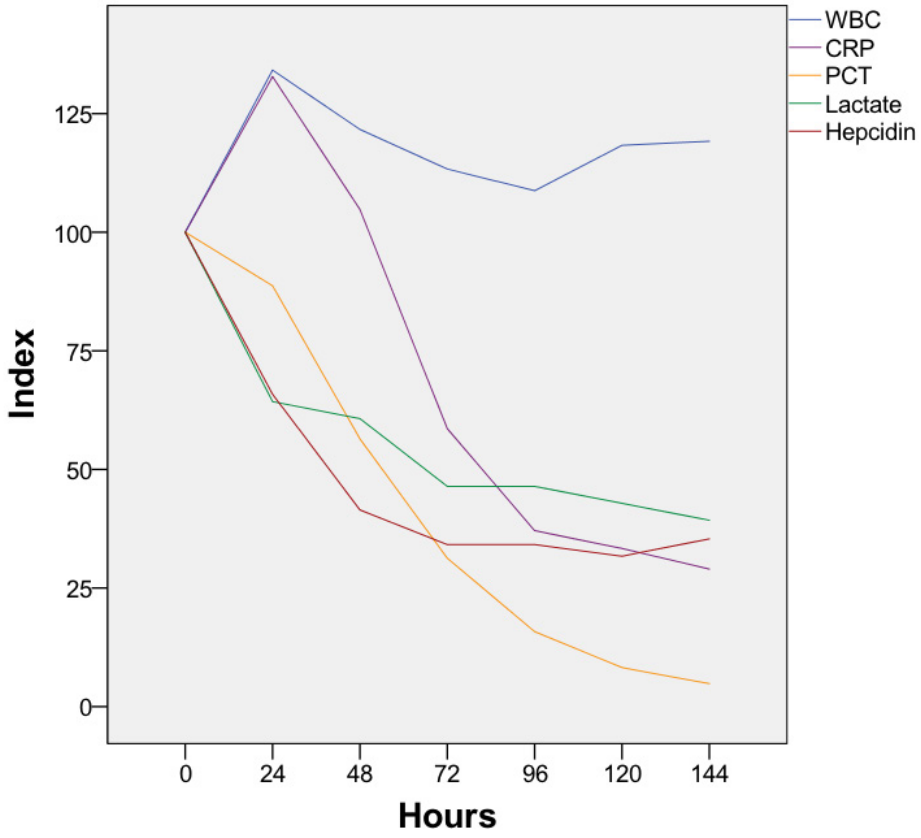
Background: Septic shock is a severe infectious condition with high mortality despite intensive care treatment. In conditions of acute systemic inflammation *e.g.* sepsis, iron metabolism, in which hepcidin plays a key role, is disturbed. The objective for this observational prospective study was to explore whether hepcidin has a potential as a biomarker for septic shock complementary to conventional biomarkers, *i.e.* procalcitonin (PCT), C-reactive protein (CRP) and white blood count (WBC).

Materials/methods: Patients with septic shock (n=81) or non-infectious conditions (n=44) who fulfilled the pre-set clinical and ethical inclusion criteria were included within an hour of admittance to the Intensive Care Unit (ICU) at Helsingborg hospital, Sweden. Patients were included at random, blood samples taken every day for 7 consecutive days. Adequate microbiological tests and cultures were obtained before or at inclusion. Sequential Organ Failure Assessment (SOFA)-score as well as plasma levels of hepcidin, WBC, CRP, PCT, and lactate, were determined directly after inclusion and then every morning for seven consecutive days. Alterations of hepcidin and conventional biomarkers in the group with septic shock are presented descriptively.

Results: Hepcidin was significantly elevated in patients with septic shock (median 41 nmol/L; reference interval 1-12 nmol/L, p-value<0.001), compared to non-septic patients (median 14.5 nmol/L, p-value<0.001). Maximal plasma levels of hepcidin were seen on Day 1 in the group with septic shock, whereafter levels declined steadily with a time course similar to lactate. PCT, CRP, lactate, and WBC demonstrated a dynamic pattern as expected from previously published results, whereas WBC and lactate were not significantly elevated. The linear graph presented shows the dynamics of the biomarkers in the group with septic shock (n=81). The median inclusion value of each biomarker was indexed to 100% and the daily change from the arrival value was calculated.

Conclusions: Hepcidin was shown to be a rapidly changing biomarker in septic shock, the initial high values were significantly higher in patients with septic shock compared to non-septic patients. Hepcidin decreased rapidly within the first 48 hours upon recovery of the patients, superior to PCT, CRP, lactate and WBC.



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Abstract 174

Primary care re-consultation after hospitalisation for community-acquired pneumonia in England: a large population-based cohort study

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Abstract third-party references: This study was supported by the National Institute for Health Research (NIHR) Nottingham Biomedical Research Centre (BRC).

Background: There is paucity of information on the burden of disease during recovery from community acquired pneumonia (CAP). This study aims to describe primary care re-consultations within 30 days after hospitalisation for CAP.

Materials/methods: Adults aged ≥18 with the first ICD-10 code for CAP (J12- J18) recorded in Hospital Episode Statistics (HES) between July 2002 and June 2017 were included. Patients were followed-up for 30 days from hospital discharge. Re-consultation was defined as recording of any medical Read codes (excluding admin-related codes) in a primary care database of anonymised medical records from general practitioners (Clinical Practice Research Datalink) after the discharge date. Re-consultation was counted as a single episode if there were multiple Read codes recorded in a day per patient.

Results: There were 93,687 patients with CAP. Excluding patients who died (n=5,456; 5.8%) or were readmitted within 30 days of hospital discharge (n=13,729; 15.1%), 38.7% (n=29,037) re-consulted primary care at 30 days for any reason. The highest rate of re-consultation was within 7 days (26 per 100 person-days).

Multivariate analysis found the strongest predictor for re-consultation was higher number of primary care consultations in the previous 2 years. Patients were less likely to re-consult if they were females, aged ≥65 years, from more deprived areas (Carstairs index=3) and if they had a Charlson comorbidity index score of between one and four.

Of those who re-consulted, 43.2% (n=12,546) re-consulted primary care twice or more. A large proportion of patients re-consulted for a respiratory disorder (37.5%, n=10,880) whilst a lower proportion re-consulted for a cardiac disorder (7.1%, n= 2066). At re-consultation, 30.8% (n=8,951) received a further course of antibiotics; most (76.9%, n=6,884) received a single course of antibiotic. Penicillins (41.9%, n=5290) and macrolides (21.9%, n=2762) were the commonest antibiotics prescribed.

Conclusions: A high burden of re-consultation is placed on primary care following hospital admission for CAP. Approximately 40% re-consult primary care more than once following CAP. Of those who re-consult, 30% are prescribed a further course of antibiotics.

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Abstract 179

A rapid direct from specimen MALDI-TOF MS diagnostic for bacterial and fungal pathogens

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Background: Pathogen identification from single colonies by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) analysis of high abundance proteins is now well established in large hospitals in the EU and US. We present updates to BACLIB, a MALDI-TOF MS method previously shown to utilize mass spectra of readily extracted bacterial lipids as chemical barcodes for identification and speciation (Leung et al. Sci Repo 2017). Unlike protein-based methods, direct from specimen identification is possible and we now show that the same extraction protocol allows fungi to be identified.

Materials/methods: Microbial lipids were extracted directly on a MALDI plate. Mass spectra were acquired in negative ion mode on a Bruker Microflex using the matrix norharmane. A mass spectral library was developed with over 2000 primary clinical and laboratory isolates, including Gram-negative and -positive bacteria, acid-fast bacteria including Mycobacterium *tuberculosis*, filamentous fungi, and over 15 Candida species. For unknown identification, mass spectra were submitted to a secure web service machine-learning software platform called Postal Service (unpublished) that reported speciation and resistance profiles by comparison to the library.

Results: Time required for a single analysis (from colony selection to identification) by BACLIB is approximately 60 minutes. Postal Service independently identified over 150 bacterial and fungal species (and where appropriate subspecies) with confidence scores similar to protein-based results reported for the Bruker Biotyper and bioMérieux VITEK MS platforms. BACLIB was also able to identify pathogens directly from blood bottles, but also urine, BALs and wound effluent, without culture on solid medium and determine antimicrobial peptide resistance (i.e. colistin) as well as identification from polymicrobial mixtures (Fondrie et al. Sci Repo 2018).

Conclusions: Previously, BACLIB has been shown to be a novel diagnostic approach for identifying Gram-negative and -positive bacteria from single colonies and mixtures, but here we report its use for identification of budding yeast and filamentous fungi. BACLIB can stand alone or strengthen the overall diagnostic power of microbial speciation using current protein-based diagnostics in clinical microbiology laboratories. Postal Service allows BACLIB to work via an internet-based approach that is capable of independently reporting speciation and where appropriate, antimicrobial peptide resistance patterns.

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Abstract 193

Antimicrobial susceptibility of *Streptococcus pneumoniae* strains, isolated from children carriers after PCV10 in Bulgaria

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Background: Bulgaria introduced PCV10 in 2010 in the National Immunization Calendar. Prior the vaccine invasive *S. pneumoniae* isolates were analyzed and the dominant resistant serotypes were 19F, 6B, and 19A. In the current study we aim to detect the serotype distribution and patterns of resistance in vaccinated healthy children.

Materials/methods: Vaccinated healthy children n=834, aged 1 to 6 years were sampled in the period 2017-2019 by a nasopharyngeal swab. Specimens were cultured on Columbia CNA Agar with 5% Sheep Blood and optochin disk, 37° C for 24 hours, in an aerobic atmosphere enriched with CO2. Identification of *S. pneumoniae* was done by the presence of alpha-hemolysis and inhibition by optochin. Typing of cultures was made by DNA based methods - conventional PCR and the Operon S.PneumoStrip kit. Antibiotic susceptibility testing was done with the disc-diffusion method for oxacillin (MIC Benzylpenicillin and Ampicillin), tetracycline, erythromycin, clindamycin, vancomycin, teicoplanin, linezolid, norfloxacin, trimethoprim-sulfamethoxazole (TMP-SMX). Interpreted by the EUCAST Clinical Breakpoint Tables v. 9.0.

Results: The total number of isolated strains was 174 (21% culture positive samples). Each sample was typed and predominantly there were the non-vaccine serotypes – 6C (27%), 24 B/F (12,5%), 3 (11%), 11A/D (10%) and 23A (7,5%) from all cultures respectively. The antimicrobial susceptibility of *S. pneumoniae* cultures to different agents during the study period was: 100% to vancomycin, teicoplanin and linezolid, 96.5% to norfloxacin, 93% to sulfamethoxazole / trimethoprim, 85.6% to oxacillin (at screening), 58% to tetracycline, 50% to clindamycin and 48.9% to erythromycin. Multidrug resistant (MDR) strains that were not sensitive to at least three antimicrobial classes were 44% of the isolated strains. Erythromycin-resistant pneumococci in the study were 51.2% of all cultures, most of them co-resistant to clindamycin.

Conclusions: The high macrolide resistance detected in carriage corresponds to the data from invasive *S. pneumoniae* isolates in the ECDC report and can serve as a tool for measuring resistance patterns in the country. There were less serotypes expressing β-lactam non susceptibility in low levels mainly serotypes 19A, 24 B/F, 35B that are non-vaccine clones.

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Abstract 195

Implementation and one-year results of antimicrobial stewardship programme in a tertiary reference hospital in San Jose, Costa Rica

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Background: Antimicrobial Stewardship Programs (ASP) are relatively new in Latin America when compared to other regions, in most cases as individual projects, in response to rising rates of resistance and adverse effects associated with inappropiate antimicrobial utilization, and not in answer to official national policies. This study evaluated the impact of a multidisciplinary, rounding-based APS strategy on antimicrobial utilization (AU), prescribing practices and health-care associated infection (HAI) rates

Materials/methods: This is a one-year review of implementation of ASP in early 2018 in a tertiary-reference hospital in San Jose, Costa Rica. Multidisciplinary ASP committee was established with representation from infectious diseases, clinical pharmacy, infection control, nursing, microbiology and epidemiology. The hospital implemented targeted stewardship efforts in Orthopaedics and Traumatology, with initial focus on advanced education, daily audit and feedback for targeted antibiotics. We created a checklist of CDC Core Elements for committee review. The primary objective of this initiative was to evaluate changes in AU and to determine HAI rates within the program over time. Subgroup analysis evaluated annual antimicrobial cost. Descriptive statistics were performed on all continuous and categorical data as appropriate

Results: Baseline overall AU analysis was based on 2017 and the intervention period included 2018. Baseline overall AU in 2017 was 425 DDD/100PD. We observed a decline in overall AU in 2018 (257 DDD/100PD). Targeted analysis revealed decline from 2017 to 2018 in carbapenems (32 vs 15 DDD/100PD), colistin (9 vs 3 DDD/100PD) and cefotaxime (26 vs 15 DDD/100PD), as well in ampicillin and cephalotin (66 vs 9 DDD/100PD, and 25 vs 8 DDD/100PD, respectively). Overall decline was also noted in rates of HAI and *Clostridium difficile* infections (CDI). Decline in overall antimicrobial cost was noted from 2017-2018 ($166340.6 vs $128418.3)

Conclusions: We present implementation of an effective health system wide multidisciplinary ASP. With ASP efforts over one year, we were able to show decline and positive correlation in overall as well as targeted AU and HAI rates. We also noticed a decline in antimicrobial cost in this timeframe

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Abstract 203

Diffusion of KPC-carbapenemases among urinary tract isolates of *Klebsiella pneumoniae* in Croatia

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Background: Recently, emergence of carbapenem-resistance was observed among *Klebsiella pneumoniae* causing urinary tract infections in Croatia. Isolates confirmed to harbour KPC carbapenemases were further characterized on molecular level.

Materials/methods: The antimicrobial susceptibility to a wide range of antibiotics was determined by broth microdilution method. The transferability of meropenem resistance was determined by conjugation (broth mating method) employing *E. coli* A15R$^-$ strain resistant to sodium azide. Genes encoding broad and extended-spectrum β-lactamases, plasmid-mediated AmpC β-lactamases, group A and B carbapenemases, and carbapenem hydrolyzing oxacillinases (bla_{OXA-48}), respectively, were determined by PCR. Plasmids were characterized by PCR based replicon typing (PBRT).

Results: In total 23 KPC positive urinary isolates were analysed. Twenty isolates were collected in the University Hospital Centre Split and three in the nursing homes located in Zagreb County. The isolates were uniformly resistant to all tested antibiotics (including ceftaroline and ceftolozane/tazobactam) with the exception of variable susceptibility to gentamicin and uniform susceptibility to sulphamethoxazole/trimethoprim and ceftazidim/avibactam. Only one strain was resistant to colistin with MIC value of 4 mg/L. Sixteen isolates transferred meropenem resistance to *E. coli* recipient strain by conjugation with the frequency ranging from $7.8x10^{-8}$ to $4.2x10^{-2}$. Other resistance markers to gentamicin, ciprofloxacin, chloramphenicol and tetracycline were not cotransferred alongside with meropenem resistance. PCR was positive for bla_{KPC} and bla_{SHV} genes in all isolates whereas eleven isolates tested positive also for bla_{TEM} genes. Sequencing revealed *bla*SHV-1 and *bla*TEM-1 genes. PBRT revealed the presence of FIIs plasmid in the three ESBL positive isolates from the nursing homes.

Conclusions: The study showed dissemination of KPC producing *K. pneumoniae* in urinary tract isolates in Croatia. Sulphamethoxazole/trimethoprim, ceftazidime/avibactam and colistin remain so far as the only therapeutic options although the colistin resistance already arised. Two different clones of KPC positive *K. pneumoniae* were observed: one with additional ESBL detected in the nursing homes and the other without ESBL identified in the University Hospital. At the national level the spread of carbapenemase-producing isolates began with OXA-48 producing strains, but KPC isolates recently emerged in southeast geographic region of Croatia posing a new epidemiological and therapeutical challenge.

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Abstract 208

Antileishmanial effects of amphotericin B-chitosan, amphotericin B-dendrimer, betulinic acid-chitosan and betulinic acid-dendrimer in the treatment of *Leishmania major*: real-time PCR assay plus

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Abstract third-party references: Part of PhD student thesis in Pasteur institute of Iran

Background: Amphotericin B (A) and Betulinic acid (B) are antileishmanial agents with low water solubility and high toxicity.

Materials/methods: To increase the solubility and reduce the toxicity, they were loaded into chitosan nanoparticles (K) with the size of 102 nm and Anionic Linear Globular Dendrimer (D) with the size of 90 nm for the first time and used as the nanoformulationsfor the treatment of *leishmania major*.

Results: The drug loading efficiency of 90% for Amphotericin B-chitosan (AK), 93% for Betulinic acid-chitosan (BK), 84% for Amphotericin B-dendrimer (AD) and 96% for Betulinic acid-Dendrimer (BD) was obtained. The characterization results confirmed that A and B were loaded into nanoparticles physically. The drug solubility rate was increased by 478 folds in AD and 790 folds in BD and by using a novel solvent, these values were increased by 80 folds for AK and 300 folds for BK. Also, the results of drug release studies showed that the all nanodrugs showed the slow drug release pattern with cellular uptake of 98.6%for AK10 µg/ml, 98% for BK20 µg/ml, 64% for AD50 µg/ml and 94.6% for BD40 µg/ml. Moreover, the nanocarriers reduced the toxicity effects of A and B by 100% in vivo and in vitro environments. AK10mg/kg and BK20 mg/kg caused a reduction in the parasite burden by 83% ($P<0.001$), while AD50 mg/kg and BD40 mg/kg reduced toxicity effects to a lesser extent. Overall, all of the synthesized nanodrugs were found to be completely effective in the improvement of the pathological effects caused by *leishmania major* by 100% in infected footpad.

Conclusions: The results of this study showed that AK and BK were effective to a large extent in the treatment of *leishmania major* infectious ($P<0.001$), suggesting that AK and BK can be considered as suitable alternatives of choices drugs.

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Abstract 216

Evaluation of newly formatted *Aspergillus* lateral flow assay for IgG antibody detection in chronic pulmonary aspergillosis

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Background: Detecting Aspergillus-specific IgG is critical to diagnosing chronic pulmonary aspergillosis (CPA). Existing assays are often costly and require sophisticated equipment, making them unsuitable for use in low- and middle-income countries where tuberculosis prevalence is high. It is necessary to diagnosis CPA in early stage to distinguish it from tuberculosis with similar presenting conditions. Genobio Parmaceutical Co., Ltd. has recently commercialized a lateral flow assay based on immunochromatographic technology that detects Aspergillus IgG antibody in 10 minutes without any instruments.

Materials/methods: 137 CPA patient serum and control patient serum collected from the China-Japan Friendship Hospital (Beijing, China) were evaluated. Samples were applied to the FungiXpert® Aspergillus IgG Detection K-Set (Lateral Flow Assay) for IgG antibody detection and results were read qualitatively. Outcomes were compared with Aspergillus IgG titers in CPA patients, measured by Platelia™ Aspergillus IgG. Gradient dilutions were performed on samples that both assays were positive, then detect the samples repeatedly by FungiXpert® kit and results were semi-quantitatively.

Results: For proven CPA patients versus controls, sensitivity and specificity for the FungiXpert® Aspergillus IgG were 97.87% and 99.0%, respectively. And, the routinely-used Platelia™ Aspergillus IgG exhibited 95.74% sensitivity for the same cohort (cut off of 10 AU/mL). For the 45 samples that both assays were positive, the semi-quantitative results of FungiXpert® were similar to the titers of Platelia™ for each sample.

Conclusions: The FungiXpert® Aspergillus IgG lateral flow assay exhibits excellent sensitivity and specificity for serological diagnosis of CPA. Due to the short run time, simplicity, and limited resources needed, the Aspergillus IgG lateral flow assay is a suitable diagnostic tool for CPA in resource-constrained settings.

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Abstract 218

Binding interference between Bartonella adhesin A and fibronectin as a novel therapeutic concept to treat bacterial infections

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Background: *Bartonella henselae* is a facultative intracellular bacterium, responsible for various human diseases like cat scratch disease and vascular proliferations (bacillary angiomatosis). *Bartonella* adhesin A (BadA), a trimeric autotransporter adhesin, is a major pathogenicity factor of *B. henselae* mediating bacterial adherence to endothelial cells and extracellular matrix (ECM) proteins. The identification of specific binding sites between BadA and ECM proteins might give insights about the use of BadA-specific antibodies or peptides interfering with fibronectin binding ("anti-ligands") to treat bacterial infections by a new class of antibiotics. The project aims the detailed analysis of fibronectin and BadA binding as the basis of the interaction between BadA and ECM proteins in host-cell adhesion processes, and the design of adhesion-inhibiting peptides for later anti-ligand application.

Materials/methods: *B. henselae* strains (wildtype and BadA deficient) were exposed to fibronectin and human endothelial cells to study binding interactions using *in vitro* infection models. A broad screening of fibronectin binding sites was performed using standardized *in vitro* binding assays. The relation between fibronectin and BadA was analyzed using mass spectrometry. As further steps, fibronectin will be genetically modified (e.g. deletion/modification of the identified binding domains). Finally, after definition of the BadA-fibronectin binding sites, synthetic molecules will be generated for the inhibition of bacterial adhesion.

Results: We expect the definition of the fibronectin domains involved in the bacterial adhesion process to use this information in the generation of artificial peptides for bacterial adherence inhibition to host cells (anti-ligands). To this purpose binding experiments using fibronectin fragments were performed showing binding with a 70 kDa fragment located at the N-terminal of the fibronectin molecule. To further analyze this interaction, crosslinking and mass spectrometry analysis using the complete fibronectin molecule and proteolytic fragments were performed to describe the sequence of amino acids involve in this interaction.

Conclusions: The project aims the detailed analysis of fibronectin and BadA binding as the basis of the interaction between BadA and ECM proteins in host-cell adhesion processes, and the design of adhesion-inhibiting peptides for later anti-ligand application.

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Abstract 221

Identification of novel pathogenicity factors in Bartonella bacilliformis

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Background: Carrion´s disease is a vector-borne biphasic illness restricted to the South American Andes. The causative agent of this neglected disease is *Bartonella bacilliformis*. The pathogen infects human erythrocytes causing a serious, acute hemolytic anemia called "Oroya fever" with mortality rates as high as 80% in untreated patients. In a second chronic phase the infection of endothelial cells results in the formation of blood-filled nodular hemangiomas in the skin ("verruga peruana"). Underlying molecular mechanisms of host infection are still widely unknown. Trimeric autotransporter adhesins (TAAs) play an essential role in bacterial pathogenicity, and are encoded in all *Bartonella* spp. *Bartonella bacilliformis* adhesin A (BbadA), has been identified in the genome of *B. bacilliformis*.

Materials/methods: Molecular genetic strategies using bacterial mutants (e.g., transposon mutagenesis library, promoter library) and recombinant protein expression strategies (e.g., heterologous expression library) are used to identify immunodominant proteins and pathogenicity factors of *B. bacilliformis*. The genomes of *B. bacilliformis* (strains KC583 and KC584) are sequenced using PacBio technology. Deletion mutants of BbadA and flagellin are generated using homologue recombination techniques. We want to predict possible immunodominant outer membrane proteins by using reverse vaccinology. A genomic deletion of *bbadA* and subsequent infection experiments with erythrocytes and endothelia cells will be performed to characterize the role of BbadA in the infection process.

Results: A genomic DNA expression library containing random genomic *B. bacilliformis* DNA inserts was established in *E. coli* BL21 (DE3). The development of a high throughput screening for immunodominant proteins is still ongoing. Electron microscopy clearly reveals the presence of BbadA on the surface of *B. bacilliformis*. Furthermore, the deletion of *bbadA* leads to a reduction in cell adhesion to endothelial cells. Western blot analysis with recombinant BbadA or flagellin reveals immunodominance using rabbit- anti *B. bacilliformis* serum.

Conclusions: The object of this work is the identification and characterization of immunodominant proteins of *B. bacilliformis* and the genetic and functional characterization of BbdA and flagellin. Furthermore, potential target proteins will be analyzed for diagnostic and therapeutic usability and to establish a basis for the development of a vaccine.

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Abstract 223

Evaluation of diagnostic method with sonication and culturing of orthopaedic implant-associated infection at Karolinska University Hospital, Sweden

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Background: Despite known low sensitivity, culture of prosthesis tissue specimens in Fastidious Anaerobe Broth (FAB) is a routine procedure in many laboratories. For increasing the chance to detect more positive specimens in order to improve the diagnosis of prosthesis infections caused by the bacteria that are apt to form biofilms, our laboratory in Stockholm since November 2018 has introduced a new method with sonication fluid inoculated into blood culture from prosthesis material in combination with culturing of periprosthetic tissue specimens in FAB. The aim of this retrospective study is to compare the results obtained after sonication and culturing of the prosthesis/implant with tissue-culture.

Materials/methods: The materials used in this study is the prosthesis/implant and infected tissues taken from the patients with suspected orthopedic implant-associated infection during November 2018 until October 2019. Data are obtained from the results recorded in the laboratory analysis system. In this study we considered include only patients with delivery of material both from prosthesis/ implant and infected tissues. The prosthesis has been sonicated and the fluid of sonication were inoculated into a blood culture bottle. All tissues have also been cultured into a FAB according to routine procedures

Results: A total of 88 patients' sample were analyzed with both sonication and FAB Culture at Karolinska laboratory/Huddinge during study period. Of these samples 47 showed growth and 41 samples showed no growth with sonication method which showed a total of 83% agreement with FAB culture method. The disagreement was found in 15 samples. Of these samples 12 were positive with just sonication and 3 samples were just positive in FAB with growing of *Cutibacterium acnes*.

Conclusions: Overall this study shows that after introduction of sonication in routine diagnostic method, we have increased the possibility to detect 25% more bacteria, but sonication is still not optimal method for detection of low growth bacteria. At this moment it is necessary to combined both methods for detection of low growth bacteria such as *Cutibacterium Acnes.*

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Abstract 227

Genome-wide analysis of resistance-related transposable elements in multidrug-resistant *Haemophilus parainfluenzae* clinical isolates

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Background: *Haemophilus parainfluenzae* is emerging as an opportunistic multidrug-resistant (MDR) pathogen. Since data about the acquisition of resistance are scarce, we aimed to determine the contribution of mobile transposable elements (Tn) to enhance antimicrobial resistance in clinical *H. parainfluenzae* isolates.

Materials/methods: All the available MDR *H. parainfluenzae* strains (n=57) collected at Hospital Universitari de Bellvitge between 2013 and 2017 were characterized by Next-Generation Sequencing (Illumina MiSeq). *In-silico* screening of mutations targeting genes was performed with Geneious R9, using the closed genomes of *H. parainfluenzae* T3T1 and *H. influenzae* Rd KW20 as references. The acquired resistance mechanisms were screened using Abricate v0.8.0 for ResFinder databases. The antimicrobial susceptibility was tested by microdilution following EUCAST guides.

Results: Tn-family elements were identified in 47 of the 57 MDR *H. parainfluenzae* strains. Overall, 38.6% (22/57) of the strains carried two or more Tn-elements conferring them resistance to at least three antimicrobial families; eleven of them (19%) had the three transposable elements detected. Tn-elements distribution was as follows: Tn*10* which harboured efflux-related genes associated with tetracycline resistance (*tetBCDR*) was carried by 66.7% (38/57) of the strains, of which 15 also contained a *catA2* related to chloramphenicol resistance. Additionally, a Tn*3* that included a bla_{TEM-1} involved in ampicillin resistance was found in 54.4% (31/57) of the strains. Finally, 21.1% (12/57) of the strains presented a Tn*6026*-like, similar to that identified in *Enterobacteriaceae* and linked to aminoglycoside and co-trimoxazole resistance. Among this group, 8 strains harboured the *strB-strA-sul2* cluster and aph(3')-Ia; 2 strains lacked the *sul2* gene; 1 strain had an additional ant(2")-Ia; and 1 strain harboured aac(3)-IIa instead of aph(3')-Ia, also conferring aminoglycoside resistance. These Tn structures were identified forming part of an integrative conjugative element (ICE) derived from *H. influenzae* (ICEHin1056) and *H. parainfluenzae* (ICEHpaT3T1), that also included genes involved in replication, secretion (type IV system), and integration. Concomitantly, 31.6% (18/57) of the strains acquired the MEGA-element linked to tetracycline (*tetM*) and azithromycin (*mefA* and *msrD*) resistance.

Conclusions: The acquisition of transferable elements is common among *H. parainfluenzae* and responsible for the multidrug resistance, becoming a reservoir and contributing to the spread of antimicrobial resistance.

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Abstract 228

Gut microbiome interferes with host tryptophan metabolism pathway and regulates basal anxiety-like behaviour

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Background: Host-microbiome interactions has emerged as promising research field to understand complexity of this symbiotic relationship. Microbiome–gut–brain axis is bidirectional communication system involved in regulation of host brain development and functions. Gut microbiome communicates with brain *via* neural, endocrine and immune pathways. Germ free mice have decrease basal anxiety levels due to alterations in their brain ultrastructure. The aim of this study was to explore the microbiome related changes in host basal anxiety levels with mechanistic insights in conventional laboratory mice.

Materials/methods: Gut dysbiosis mice model was developed using combination of non – absorbable antibiotics and anxiety level was evaluated using EPM. Neurochemical changes in brain were analyzed with HPLC. 16S rRNA sequencing of fecal content was performed to study gut microbial profiles, data was processed using standard bioinformatics tools, taxonomic and statistical analysis was performed on MEGAN and STAMP. Transcription levels of specific genes were analyzed using RT-qPCR.

Results: Behavioral analysis showed anxiolytic – like behavior in dysbiosis group. The hippocampus of antibiotic treated mice showed significant decrease in levels of tryptophan, serotonin and 5-HIAA. Beta diversity analysis showed taxonomic shift of microbial communities among groups. At genus level control group microbiome was dominated by *Muribaculum, Clostridium* and *Bacteroides*, while dysbiosis group showed dominance of *Klebsiella, Escherichia* and *Enterobacter*. Gene expression studies showed down regulation of serotonin transporter in mice hippocampus.

Conclusions: Our data suggest that taxonomic shift in gut microbiome can modulate host anxiety levels *via* interfering with its tryptophan metabolism pathway, as low levels of tryptophan in brain attributes to the reduce synthesis of serotonin which regulate basal anxiety – like behavior. This study highlights gut microbiome as drug and drug target due to inter-indiviadual differences in gut microbial profiles and will further lead to advancement in personalized medicine by inclusion of individual's microbiome profile.

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Abstract 229

Misuse of tampons and menstrual toxic shock syndrome in France: a community-based case-control study

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Background: Menstrual tampons are widely used in western countries. Here we assessed whether tampon misuse was associated with increased risk of menstrual toxic shock syndrome (MTSS).

Materials/methods: We conducted a community-based, nationwide, case-control study in France, including women with MTSS diagnoses reported to the French National Staphylococcal Center of Lyon between 2011–2017. Controls were women with no MTSS history. Using a standardized questionnaire, we collected information regarding tampon use during a 6-month period. Associations between tampon misuse and MTSS were assessed using logistic regression models stratified by residential area.

Results: We analyzed data from 181 subjects (age≤30 years; 55 cases and 126 controls). Compared to controls, cases more frequently reported maximum tampon wear of >6 hours (62% vs. 41%, P<0.05), overnight tampon use (77% vs. 54%, P<0.05), and not having read and followed tampon instructions (65% vs. 42%, P<0.05). In univariate analysis, MTSS risk was two-fold higher with tampon use for >6 consecutive hours [odds ratio (OR)=2.3, 95% CI: 1.2–4.6, P<0.05), and three-fold higher with tampon use during sleep for >8 hours (OR=3.2, 95% CI: 1.4–7.7). In multivariate logistic regression analysis, maximum tampon use for >6 hours (OR=2.3; 95% CI: 1.04–3.98), and not reading and following the tampon instructions (OR=2.25; 95% CI: 1.15–4.39) were independent MTSS predictors.

Conclusions: MTSS risk can be reduced by using sanitary napkins overnight, using tampons for <6 consecutive hours, and receiving education about tampon use and its relation with MTSS. These findings have major public heath implications for women's health.

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Abstract 235

Effects of previous antibiotic exposure on the clinical course of pneumonia in the elderly: a single-centre prospective observational study

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Background: The aim of this study was to investigate the effects of previous antibiotic exposure on the outcomes of pneumonia in the elderly population.

Materials/methods: In this prospective observational study, the patients with pneumonia were stratified into two groups as younger (18 to 64 years) and older (≥65 years). A "poor prognosis" was assessed as the development of septic shock associated with infection and/or the need for intensive care and/or death within 30 days. Poor prognostic indicators for each group were determined and compared.

Results: There were 184 pneumonia episodes in 155 patients. The median age of the cases was 72 (range, 18-104) of whom 127 (69%) were ≥65 years old and 110 (59.8%) were male. Mental status changes were significantly more frequent in the elderly group (p=0.04). *Pseudomonas species* (n=11, 29.7%) was the most common agent, followed by *Streptococcus pneumoniae* (n=6, 16,2%), *Haemophilus influenzae* (n=5, 13.5%), *Acinetobacter species* (n=4, 10.8%) and *Staphylococcus aureus* (n=4, 10.8%). The rates of carbapenem resistance were high; 45.4% in *Pseudomonas spp.* and 50% in *Acinetobacter spp.* And 25% of *Staphylococcus aureus* strains were methicillin resistant. Multivariate regression analysis determined three variables that could be potential independent risk factors for poor prognosis in the elderly: dyspnea at the onset (OR:5.85, CI:5.18-6.52, p=0.01), previous antibiotic use within the last 3 months (OR:2.97, CI:2.51-3.43, p=0.02), and acute renal failure (OR:2.51, CI:2.06-2.96, p=0.04). A receiver operating characteristic analysis showed that the area under the curves of procalcitonin and C-reactive protein (CRP) as indicators of poor prognosis in the elderly were 0.846 (p<0.001) and 0.650 (p=0.008) respectively (Figure 1). In addition, mental status changes (p<0.001), the CURB-65 score (p<0.001), and the pneumonia severity index (PSI) (p<0.001) were associated with poor prognosis.

Conclusions: Previous antibiotic exposure, serum procalcitonin and CRP levels along with the PSI and the CURB-65 scores should minutely be evaluated in terms of need for hospitalization and intensive care. Furthermore, local epidemiology and resistance profiles should be taken into consideration for appropriate antimicrobial therapy.

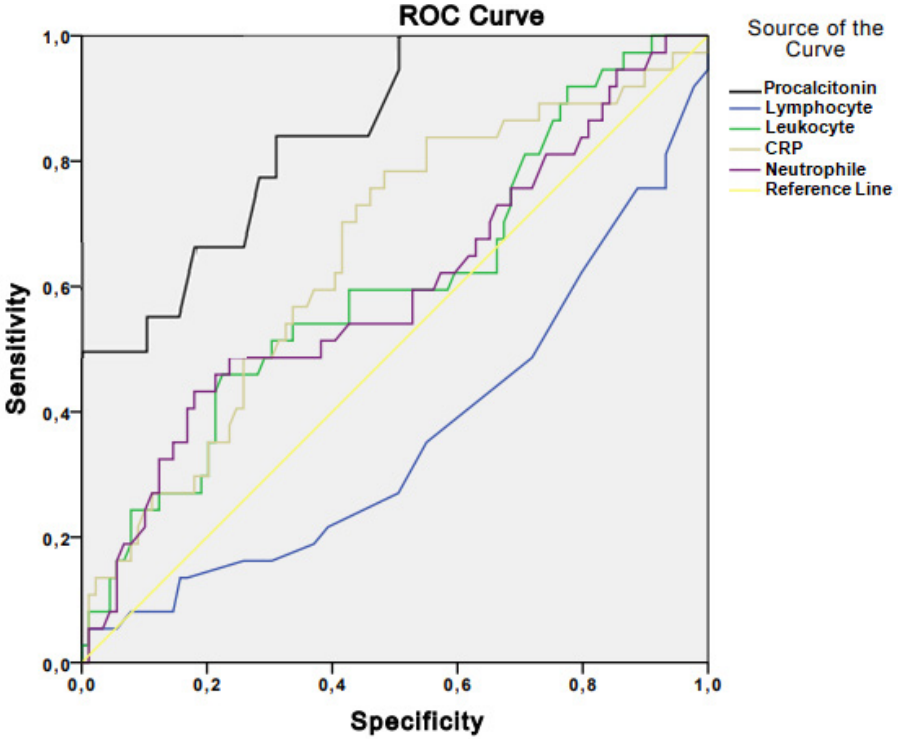

Figure 1. Receiver operating characteristic curves of serum parameters for prediction of poor prognosis of elderly with pneumonia

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Abstract 244

Hospital-acquired influenza characteristics and its correlation with the population-based surveillance in a tertiary care centre in Istanbul

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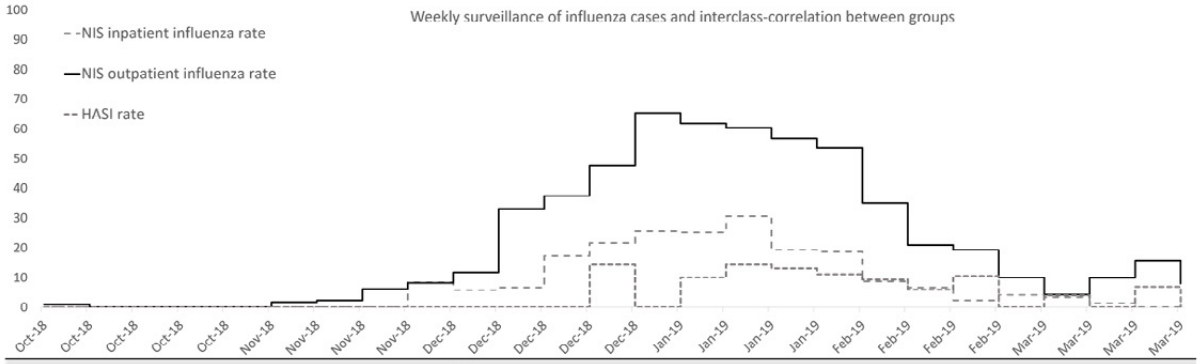
Background: Influenza virus related respiratory infections causes major mortality and morbidity. Hospital acquired seasonal influenza (HA-SI) is reported up to 55% of inpatient influenza cases in Geneva University Hospital. Also, the proportion of HA-SI is correlated with the population-based influenza surveillance in some studies. We investigated the incidence of HA-SI and correlation with national influenza surveillance (NIS) data in a tertiary care center in Istanbul, Turkey.

Materials/methods: This is a retrospective study which includes seasonal influenza cases between October 2018 and March 2019. (The Sofia Influenza A+B Fluorescent Immunoassay, Quidel, USA) and/or Influenza A/B RT-PCR test (The Film Array Respiratory Panel, Biomérieux, France or Xpert Flu, Cepheid, USA). Cases were defined as HA-SI when symptoms onset and/or positive influenza PCR ≥ 72 hours after hospital admission, without previous respiratory symptoms or with negative influenza screening. The correlation between HA-SI and NIS data was analyzed using interclass-correlation test.

Results: During the study period 4423 patients tested for influenza and 786 (17.8%) of them were found positive. Out of 786 patients 119 were inpatients (15.1%) Of these 119 patients 29 (24.6%) were defined as HA-SI. Influenza-A represents the 88.2% of all inpatients with influenza and 89.7% of HA-SI. Majority of HA-SI cases occurred in medical wards (65.5%) and intensive care units (17.2%). The incidence density of HA-SI was 16.1 per 10.000 patient-admissions for the given period. Weekly rate of HA-SI cases and weekly NIS data for of sentinel inpatient influenza rate were significantly correlated. Whereas the NIS data for outpatients showed no correlation with HA-SI rates (Figure-1). The influenza vaccination coverage of health-care-workers was 10% for 2018-2019.

Conclusions: This study shows that during the 2018-2019 influenza season nearly 25% of the inpatient influenza cases acquired from the hospital. The data show the potential room for improvement in our medical center. Education about infection-prevention and control measures for influenza and achieving high vaccination coverage for health-care-workers and patients must be a priority. Also, the population-based surveillance can estimate the burden of HA-SI in our medical center which can be used to guide the institutional policies for influenza management in our medical center.



	HASI rate		
	Interclass-correlation-coefficient	p	95% CI
NIS inpatient influenza rate	0.696	0.002	0.192-0.760
NIS outpatient influenza rate	0.471	0.059	-0.181-0.763

NIS: National Influenza Surveillance, HASI: Hospital acquired seasonal influenza

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Abstract 245

Carbapenem antimicrobial stewardship programme

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Background: The prevalence of carbapenem resistance throughout the world is increasing and carbapenems are considered critically important antimicrobials by the WHO. The aim of study is to evaluate clinical and antibiotic resistance impact of carbapenems Antibiotic Stewardship Programs (ASP).

Materials/methods: Descriptive study between January-2012/December-2018, pre-post-intervention. A carbapenems ASP was initiated in January 2015, in patients who started treatment with carbapenems (meropenem/ertapenem). An infectious diseases physician performed treatment recommendations to prescribers. Prospective information was collected to evaluate adequacy of carbapenems prescription to local guidelines and to compare results between cases with accepted or rejected intervention. Cases with carbapenems prescription during the last 4 months of 2014 were retrospectively reviewed, this sample of the pre-intervention period was used to compare with patients who started treatment with carbapenems during the intervention period. Appropriate treatment with carbapenems was considered when it was prescribed in patients with: 1. Severe sepsis; 2. history of ESBLs colonization; or 3. hospital-acquired infection in which a broad-spectrum antibiotic treatment was considered necessary. Analysis was performed to verify variables associated with any significant change in clinical evolution, carbapenems consumption, hospital-acquired multidrug-resistant (MDR) bloodstream infections (BSIs) and 30-day all-cause crude death in MDR-BSIs.

Results: Adequacy of carbapenems prescription improved progressively over time, after ASP implementation (p <0.001). Interventions on prescription were performed in 416 (34.5%) patients without carbapenems justified treatment (meropenem 389/ertapenem 27), in 339 (81.5%) intervention was accepted and in 77 was not. Intervention acceptance was associated with shorter duration of treatment (11.3±10.2 vs 13.4±8.6) and inpatient days (18.4±16.8 vs 27.3±23.6, p=0.002), without differences in clinical evolution. During the 2015-2018 period meropenem consumption in DDD/100 patients-day decreased compared with 2012-2014 [Rate ratio 0.61; 95%CI: 0.58-0.64, p<0.001), and ertapenem consumption increased somewhat (Rate ratio 1.07; 95%CI: 0.94-1.22). Hospital-acquired MDR-BSIs rate and 30-day all-cause crude death in MDR-BSIs deceased (0.66; 95%CI: 0.44-1.00, p=006) and (RR 0.60; 95%CI: 0.28-1.34, p=0.29), respectively, coinciding in time with ASP start-up.

Conclusions: The decrease and better use of carbapenems achieved was associated with shorter duration of treatment and of inpatient days, without differences in clinical evolution, and with a decrease of hospital-acquired multidrug-resistant bloodstream infections rate.

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Abstract 246

Delineation of the direct impact of *Candida auris* ERG11 mutations on clinical triazole resistance

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Background: *Candida auris* has emerged as a healthcare-associated multi-drug resistant pathogen of great clinical concern. When isolated, approximately 90% of all clinical *C. auris* isolates are highly resistant to fluconazole, the most widely utilized antifungal, with modal MIC ≥256mg/L. While the majority of fluconazole-resistant clinical isolates are found to possess one of three different mutations in *ERG11*, the gene encoding the target of the triazoles, it remains unknown whether these mutations alone explain the high level of fluconazole resistance present among clinical *C. auris* isolates.

Materials/methods: To assess the direct contribution of all three clinically relevant *C. auris ERG11* mutations, *ERG11* alleles encoding the amino acid substitutions VF125AL, Y132F, and K143R, as well as a wildtype control were introduced into the fluconazole susceptible clinical isolate AR0387 using CRISPR-Cas9 mediated transformation system. Introduction of *ERG11* mutations were confirmed using Sanger sequencing. Additionally, the K143R encoding mutation present in the highly fluconazole-resistant clinical isolate AR0390, was corrected to the *ERG11* wildtype sequence. In vitro antifungal susceptibility testing was then performed using CLSI broth microdilution methodology.

Results: Introduction of each of the three mutant *ERG11* alleles into the AR0387 fluconazole-susceptible background was observed to increase fluconazole MIC by 8 to 16-fold, while fluconazole MIC were unchanged upon introduction of the wildtype control allele. The MIC for the other clinically available triazoles were more minimally impacted by any of the three *ERG11* mutations, with the most prominent change observed in voriconazole MIC (2 to 4-fold change). In the AR0390 fluconazole-resistant clinical isolate background, correction of the K143R encoding mutation to the wildtype sequence led to a corresponding 8-fold decrease in fluconazole MIC, and 4-fold decrease in voriconazole MIC, while the MIC of other triazole antifungals was unchanged.

Conclusions: Taken together, the findings of this study demonstrate mutations in *C. auris ERG11* significantly contribute to the fluconazole resistance, but alone cannot explain the substantially elevated MIC observed among clinical isolates of *C. auris*. Further research is needed to identify additional mechanisms contributing to fluconazole resistance in clinical isolates of *C. auris*.

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Abstract 248

Stay in the emergency department increases the risk of colonisation by carbapenem-resistant *Enterobacteriaceae* in the intensive care unit

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Background: Carbapenem-resistant *Enterobacteriaceae* (CRE) colonization on admission to the intensive care unit (ICU) is common and the impact that hospitalization in the emergency department (ED) has on colonization is unknown. CRE-colonization on admission to ED was described in approximately 7% of patients of our hospital and one third of patients arrive in the ICU from ED. This study aimed to evaluate the impact of previous hospitalization in the ED on CRE-colonization at ICU admission.

Materials/methods: Hospital das Clinicas (HC) is a 2,200-bed public tertiary-care hospital in São Paulo, the largest hospital complex in Latin America. The ED is a very busy unit, with more than 69 thousand emergency consultations performed per year. In order to monitor and control colonization by CRE, all patients admitted to ICUs are routinely submitted to CRE surveillance cultures on admission to the unit. This is a retrospective case-control study that covered the period from September 2015 to July 2017, with 103 cases and 201 controls, analyzing ED hospitalization and other risk factors for colonization by CRE on ICU admission. Cases were patients colonized by CRE on admission to ICU and controls were patients admitted to ICU not colonized by CRE on admission.

Results: We found ED stay longer than 2 days (OR: 2.60; 95%CI: 1.35-4.99; p: 0.004), transfer from another institution (OR: 2.61; 95%CI: 1.43-4.74; p: 0.002), use of carbapenem on ICU admission (OR: 4.56; 95%CI: 1.92-10.83; p: 0.001), dialysis (OR: 2.94; 95%CI: 1.05-8.24; p: 0.04), and upper digestive endoscopy (OR: 4.15; 95%CI: 1.14-15.07; p: 0.031) as risk factors for CRE colonization on ICU admission.

Conclusions: This is the first study to demonstrate that prolonged ED stay (> 2 days) is a risk factor for CRE colonization on admission to the ICU. Other risk factors were transfer from another hospital, use of carbapenem, dialysis, and upper digestive endoscopy. The implications of these findings should lead to interventions in the ED if we are to control CRE in other hospital units.

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Abstract 256

Evaluation of a novel method for detection of carbapenem hydrolysis with an automated software (Clover BioSoft) by MALDI-TOF MS

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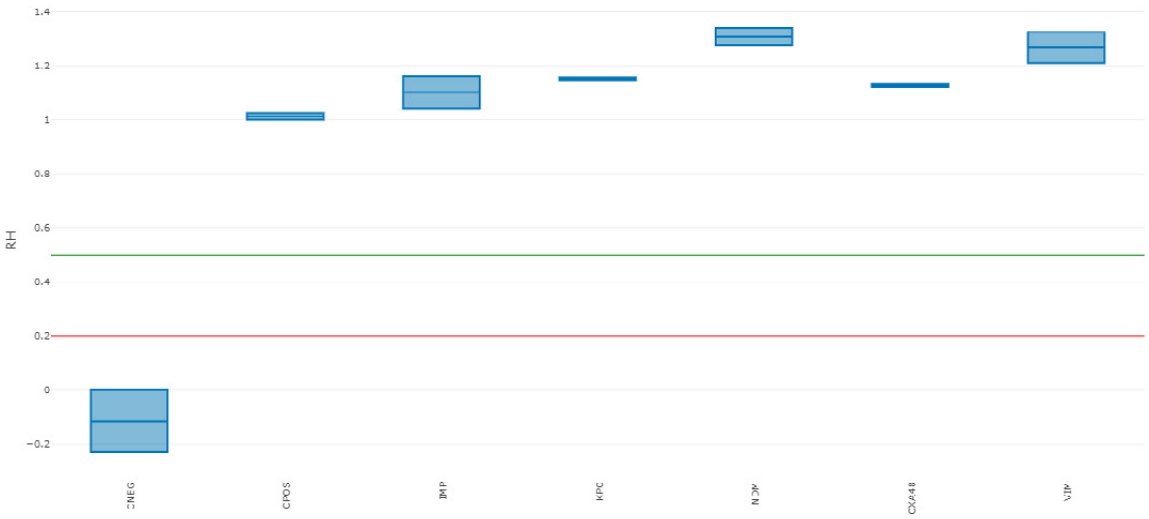
Background: Rapid detection of Carbapenemase-producing Enterobacterales (CPE) is one of the main goals of microbiology laboratories. One of the recommended methodologies by the EUCAST guidelines is using MALDI-TOF MS for measuring the hydrolysis of carbapenems. However, all assays evaluated are single center studies and no multicenter evaluation has ever been made to standardize the methodology as recommended. Here, we expose our first objectives of a further multicenter study, that is the development of a universal and in-house protocol for measuring carbapenem hydrolysis by MALDI-TOF MS and the development of an automated software (Clover BioSoft) for spectra interpretation.

Materials/methods: A total of 81 Enterobacterales fully characterized, 50 CPE and 31 isolates with different resistance mechanisms (not carbapenemases) or no resistance mechanisms at all, were submitted to a standard operating procedure, using imipenem as carbapenem and 30 min of incubation. The developed software (Clover BioSoft) allows the semi-quantification of the hydrolysis of imipenem. For the calculation of the ratio of hydrolysis (RH), two different analyses were applied. The first one (a) took into account the intensity and the second one (b) the area of imipenem mass peaks (Image 1). The procedure was performed in parallel with the only commercially available method, the MBT STAR®-Carba IVD Kit in the MBT STAR®-BL IVD Module (Bruker Daltonik) following manufacturer's instructions (c).

Results: According to the sensitivity analysis (ROC curve) the AUC was 0.994 (a), 0.990 (b) and 0.977 (c), proving our in-house method with the developed software (a) as best method. The optimum cut-of for the RH was ≥ 0.5 for positivity with a 94% sensitivity and 100% specificity. The negative cut-of is stablished for a RH ≤ 0.2 with 100% sensitivity and 90% specificity.

Conclusions: The optimized methodology proved useful for detection of CPE in less than 1 hour with a novel and online software (Clover BioSoft). The next phases of the study will include an international and multicenter validation of the technology for CPE detection in both MALDI biotyper (Bruker Daltonik) and VITEK MS (BioMérieux) systems.

Image 1. Boxplot diagram for imipenem hydrolysis with the main carbapenemases included in the study.



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Abstract 260

The role of food and environment in the transmission of *Clostridioides difficile*

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Background: *Clostridium difficile* is the most common cause of healthcare-related diarrhea in high-income countries. However, with increased reports of (i) community-associated *C. difficile* infection (CA-CDI), (ii) the findings of clinically-important *C. difficile* in animals, food and the environment, and (iii) whole-genome sequencing (WGS) showing that the majority of hospital-associated CDI cases are genetically distinct from one another, the traditional notion that CDI is primarily a hospital infection transmitted between symptomatic patients is currently being challenged. Yet, little is known about the possible role of community reservoirs in the transmission of CDI.

Materials/methods: Food and environmental samples were collected in Western Australia (WA). Enrichment culture, toxin profiling, PCR ribotyping and antimicrobial resistance (AMR) susceptibility testing were performed. WGS and core genome single nucleotide variant (cgSNV) analysis were carried out on a selection of *C. difficile* ribotypes (RTs) that frequently cause CDI in humans and animals.

Results: A high prevalence of *C. difficile* was found in retail vegetables (30.0%), compost (27.2%) and public lawn (58.5%) in WA. A diversity of strains was isolated including RTs associated with CDI in humans and animals [RTs 014/020 (28.3%) and 056 (3.0%)]. Food and environmental *C. difficile* displayed AMR patterns comparable to already published data of human and animal isolates with multidrug resistance only detected in compost isolates. Two clusters of human and food/compost RT 056 strains with ≤2 SNV suggest a very recent shared ancestry, consistent with recent transmission.

Conclusions: Currently, there are ample published genomic data that demonstrate CDI has a zoonotic and/or anthroponotic transmission, with little to no evidence of an epidemiological link between humans and animals. Food and the environment are likely acting as a conduit between the two hosts, in part due to the practice of recycling human and animal waste for agricultural use and decades of antimicrobial use/misuse in production animals that has amplified *C. difficile* in animals and promoted AMR. Community acquisition of *C. difficile* from reservoirs is undoubtedly contributing to CA-CDI and asymptomatic colonization. To address this CDI issue, a One Health approach is needed.

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Abstract 262

Epidemiological and clinical characteristics of patients with *Campylobacter* bloodstream infection: a retrospective case-control study

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Background: *Campylobacter* is a frequent cause of sporadic enterocolitis, but is considered a rare cause of bloodstream infection.

Materials/methods: We performed a single center retrospective case-control study comparing patients with C*ampylobacter* bloodstream infection (C-BSI) (cases) to nonbacteremic patients with positive *Campylobacter* stool culture (controls) from 2007 through 2016. Case and control patients were matched by age and sex at a ratio of 1:2. Demographic characteristics, clinical features and microbiology data were extracted from patient medical records. Death within 30 days of culture, hospital stay duration, need for intensive care and recurrent hospitalization were compared between groups.

Results: We identified 42 patients with C-BSI and matched them with 83 nonbacteremic patients with positive *Campylobacter* stool culture. The rate of C-BSI increased sharply in 2014, with 38 cases (90%) identified from 2014 to 2016. Case patients were more likely than controls to be infected with *C. jejuni* (85% vs. 59%, P=0.008). Cases and controls did not differ in age, sex and comorbidities (median Charlson score 5 in both groups). Cases were more likely to present with fever (78% vs 53%, P=0.006) and functional deterioration (19% vs 4%, P=0.008), whereas control patients were more likely to have abdominal pain (54% vs 28%, P=0.008) and diarrhea (94% vs 57%, P<0.001). More patients with C-BSI were treated with PPI at baseline (55% vs 34%, P=0.056) and had a report of recent antibiotic exposure (33% vs 11%, P=0.002).

C-BSI was associated with higher 30-day mortality (19% vs. 2.4%, P=0.002), more frequent need for intensive care (11.9% vs. 1.2%, P=0.008) and doubling of the median hospital duration (6 days vs. 3 days, P<0.001). Rates of recurrent hospitalization were similar. Neutropenia and hematological malignancy were associated with higher mortality rate.

Conclusions: C-BSI is identified more frequently in recent years, possibly as a result of improved sensitivity of blood culture systems. Compared with nonbacteremic patients with positive stool culture, patients with C-BSI had significantly higher rates of death and other adverse outcomes. Previous antibiotic exposure, PPI use and infection with *C. jejuni* were identified as risk factors for C-BSI.

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Abstract 267

Acute cholangitis secondary to choledocholithiasis in older population: subtle presentation and severe illness

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Background: Acute cholangitis continues to be a serious and possibly life-threatening diagnosis despite the advances and widespread availability of abdominal imaging and endoscopic intervention.

The classic Charcot's triad lacks sensitivity and is reported to be positive in only 30% of acute cholangitis cases. Older population, defined in different studies by age >65 to >80 years old, are higher risk group with sparse literature regarding differences in clinical presentation and outcome.

Materials/methods: Retrospective chart review of 383 cases with acute cholangitis secondary to biliary stones managed between January 2012 and December 2017.

We reviewed clinical presentation, diagnostic criteria, disease severity, microbiology and 30 day outcome of acute cholangitis in patients aged >75 years.

Results: Our sample included 183 patients aged >75 years, 107 (58%) males, median age was 85 years (IQR 80-89) and 11/183 (6%) were immuno-suppressed.

The clinical presentation was with abdominal pain in 160 (87.4%), subjective fever in only 102 (55.7%), jaundice in 62 (33.8%) and altered mentation in 39 (21.3%). At time of presentation, LFTs of >1.5 upper normal limit was found in 171 (94%), abnormal WBC count (>10 or <4) was found in 150 (82.8%), total bilirubin of >= 2 mg/dL was in 145 (80%) and abnormal abdominal imaging was found in 167 (92%).

Severity of cholangitis following 2018 Tokyo guidelines was grade III in 46%, grade II in 45% and grade I in 9%.

Blood cultures were positive in 79/155 (51%). This was with gram-negative organisms in 63/79 (80%), gram-positive organisms in 7/79 (9%) and polymicrobial in 9 (11%).

Biliary drainage was pursued in 178 (97.2%). This was with ERCP in 170 (95%) cases. Overall mortality was 11/183 (6%).

Conclusions: Compared to younger population, acute cholangitis in patients >75 years is characterized by high-grade disease but with a more subtle clinical presentation. This group was found to have higher incidence of altered mentation but absence of fever in almost half of the cases. Laboratory blood testing and radiological imaging were abnormal in more than 80% of the cases.

Our findings suggest need for a high index of suspicion to pursue appropriate treatment and timely source control.

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Abstract 272

Adjunction of daptomycin for the treatment of bacterial meningitis: *in vitro* study

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Background: Due to intrinsic virulence factors, *Streptococcus pneumoniae* is responsible for the highest morbimortality associated with bacterial meningitis worldwide. Despite a global reliance on the use of beta-lactam antibiotics, several studies suggest a significant risk of worsening cerebral lesions owing to the release of pro-inflammatory toxins during bacterial cell lysis. As non-bacteriolytic antibiotic may help containing an excessive inflammatory host response, the adjunction of daptomycin is currently under clinical evaluation in a multicenter phase II study to improve the prognosis and survival of pneumococcal meningitis (AddaMAP, NCT03480191). However, its impact on the activity of standard treatment for other bacterial meningitis remains unknown. The present project aims at evaluating *in vitro* the antimicrobial activity of daptomycin-based associations against the most frequent species associated with bacterial meningitis.

Materials/methods: National Reference Centers were contacted for an epidemiological selection of the most relevant strains regarding five bacterial species : *Streptococcus pneumoniae*, *Neisseria meningitidis*, *Listeria monocytogenes*, *Haemophilus influenzae* and *Streptococcus pyogenes*. The antimicrobial activity of amoxicillin, cefotaxime, and rifampicin - either alone or in association with daptomycin - was explored through the determination of minimal inhibitory concentration (MIC), fractional inhibitory concentration index (FICI) and Time-Kill Kinetics Assay (TKA) using broth microdilution method.

Results: All species taken together, the adjunction of daptomycin had no deleterious impact on the antimicrobial activity of amoxicillin, cefotaxime and rifampicin *in vitro*. Regarding Gram-positive bacteria, FICI values confirmed a significant improvement of growth inhibition due to the adjunction of daptomycin, up to a synergistic effect with FICI largely below 0.5 for *Streptococcus pyogenes*. In addition, TKA analysis showed increased bactericidal activity with daptomycin, as demonstrated by the reduction of integrated AUC/24h by a factor varying from 1.5 to 3, depending on the species and antibiotic (Figure). Finally, lipopeptide-based associations did not modify the activity of beta-lactam antibiotics or rifampicin against Gram-negative bacteria, notably *Neisseria meningitidis*.

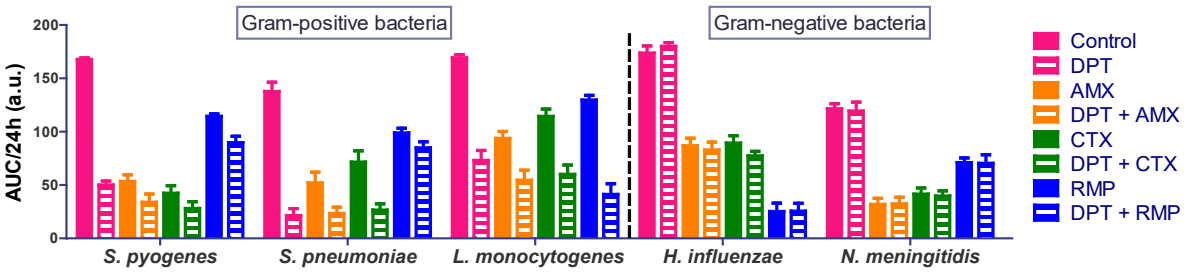

Figure. TKA of DPT-based associations against the main species responsible for bacterial meningitis

Conclusions: These results bring comforting evidence towards the potential of daptomycin adjunction in the treatment of bacterial meningitis. Such additional *in vitro* data constitute critical supplementary information supporting the ongoing AddaMAP clinical trial.

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Abstract 275

Assessment of the quality of data supporting the efficacy of new antibiotics for multidrug-resistant bacteria

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Background: Infections caused by multidrug resistant (MDR) bacteria are major public health threat. We aimed to assess the data supporting US Food and Drug (FDA) approval of new agents aimed to treat MDR bacterial infections, and the data provided by post-marketing studies.

Materials/methods: We identified all drugs with in-vitro activity against MDR bacteria initially approved by the FDA between January 2010 and December 2018. Characteristics of trials supporting approval and regulatory pathways were collected from Drugs@FDA. Characteristics of post-marketing studies were extracted from drug labels and ClinicalTrials.gov entries effective on June 1, 2019.

Results: Initial approval of 11 newly approved antibiotics with anti-MDR activity was supported by 20 trials, all with non-inferiority design. All initially approved indications were for common infections, mostly acute bacterial skin and skin-structure infections, regardless of causative microorganism. The proportion of MDR bacteria in most trials was low (<10% for Gram-negative infections, <1% for Gram-positive pneumonia). Most trials (90%) excluded immunocompromised and critically ill patients. Of 16 additional post-marketing phase III trials identified through ClinicalTrials.gov, only 2 exclusively included infections caused by MDR bacteria, comprising 116 patients. No drug was granted accelerated approval, which would mandate post-marketing efficacy studies.

Conclusions: The approval of new drugs presumed to have clinical activity versus MDR bacteria is supported by trials evaluating infections caused by non-MDR organisms, using non-inferiority design and excluding the patients most likely to require these agents. Subsequent post-marketing efficacy data against these organisms are scarce. Healthcare professionals and regulators should demand more robust data to support clinical decision making.

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Abstract 287

Screening of *Chlamydia trachomatis* and *Neisseria gonorrhoeae* in female sex workers: pooled versus single site testing

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Background: As the majority of women infected with *Chlamydia trachomatis* (CT) and *Neisseria gonorrhoeae* (NG) are asymptomatic, targeted screening of patients in specified risk groups is indicated in order to reduce transmission and (long-term) complications. Testing of extra-genital is warranted for optimal detection and treatment of those infected. As this comes with a substantial cost, analysis of a pooled sample from vaginal and extra-genital sites could be beneficial. In this study, we evaluated the feasibility of CT/NG testing in pooled versus single site samples in a large cohort of female sex workers.

Materials/methods: We sampled 501 women with the Abbott multi-ColleCTSpecimen Collection Kit in the pharynx (taken by the physician), vagina and rectum (either self-collected or by the physician). For each woman, all three samples were vortexed and 400 µL of transport medium was pooled into an empty tube. The pooled sample was tested for CTand NG alongside each single-site sample using the Abbott RealTime CT/NG assay on the m2000sp/rt system.

Results: Overall, 5.1% of sex workers were positive for CT; 2.0% were positive for NG and 1.4% were co-infected, resulting in an overall prevalence of 6.5% for CT and 3.5% for NG. From the 42 women positive on at least one single-site sample, only 5 had a negative result on the pooled sample resulting in a sensitivity of 94% for CT and 82% for NG. The false negative pooled samples were from women with a single-site NG (n=3) or CT (n=2) infection with low bacterial load. Inadequate self-sampling was ruled out as a possible cause of false negativity, as the number of samples from infected women collected by the physician was comparable to the number of self-collected samples. Testing extra-genital samples led to a significantly higher detection rate, as 40% of the CT and 60% of the NG infections would have been missed if only vaginal samples were tested.

Conclusions: Pooling samples is a cost-effective strategy for the detection of CT and NG in females, with minimal decrease in sensitivity. By reducing costs, more extra-genital samples can be tested, resulting in higher detection rates

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Abstract 288

Patient transfers as a risk factor for *Clostridioides difficile* infection: a case-control study

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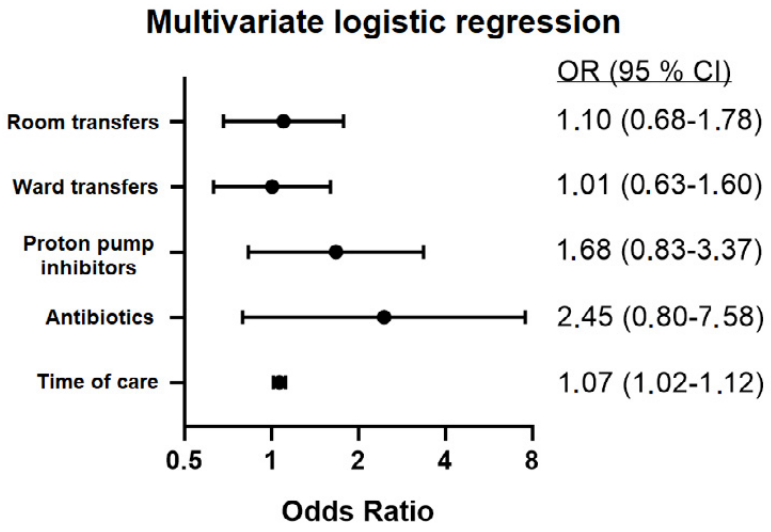
Background: *Clostridioides difficile* (previously: *Clostridium difficile)* is a spore-forming bacterium; the spores are highly resilient and can survive for long periods in the hospital environment despite cleaning and disinfection efforts. Most *Clostridioides difficile* infections (CDI) are hospital-acquired. Colonization of spores or vegetative bacteria in the large intestine is necessary for infection to occur, and the risk of infection is modulated by the state of the intestinal microbiome and the host´s immune status. Patient transfers within and between wards are commonplace in modern healthcare, exposing patients to more areas of the hospital environment where spores may exist. We hypothesised that frequent transfers between wards and/or rooms within a ward is a risk factor for developing CDI.

Materials/methods: A case-control study of all hospital-acquired CDI cases at Södra Älvsborg Hospital, Borås, Sweden, during two years: 2012 and 2015 (n=65). A random selection of patients tested negative for CDI served as control group (n=101). Odds ratios were calculated by univariate logistic regression followed by multivariate logistic regression for variables where there was a statistically significant difference in the univariate analysis. These covariates were room transfers, transfers or ward, use of proton pump inhibitors, and use of antibiotics.

Results: The number of patient transfers both between and within wards was significantly higher in the case group in univariate analysis, however, there was no significant difference between groups when data were adjusted for other known risk factors. In the multivariate analysis, time of care was the only statistically significant variable (OR per additional day of care: 1.07, 95 % confidence interval: 1.02-1.07).

Conclusions: The study could not demonstrate patient transfers as an independent risk factor for CDI, but underlines the importance of time of care as a risk factor for CDI.



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Abstract 292

Risk of invasive pneumococcal infection in patients with asplenia/hyposplenism: a nationwide population-based study compared to the general population

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Abstract third-party references: This study was supported by Basic Science Research Program through the National Research Foundation of Korea (NRF) funded by the Ministry of Education (2019032869)

Background: Asplenia is a well-known risk factor of invasive pneumococcal infection (IPI), but nationwide cohort studies have not been conducted on how the risk increases in patients with asplenia compared to the general population.

Materials/methods: All cases of newly-diagnosed asplenia that were claimed to the National Health Insurance Service in South Korea from January 2009 to December 2018 were included. Information were extracted from Health Insurance Review and Assessment Service database. Asplenia patients were defined as those who were diagnosed with congenital asplenia/hyposplenism or underwent splenectomy. To compare the incidence of IPI between these patients and the general population, we used the case definition and the 2017 data of National Infectious Disease Surveillance System at Korean Center for Disease Control.

Results: Over a period of 10 years, a total of 21,376 cases were identified; 20,524 cases (96.0%) underwent splenectomy and 852 cases (4.0%) had diagnosis of congenital asplenia/hyposplenism. Fifty-seven patients had an IPI, and one was accompanied by *H. influenza* infection. Six deaths (10.5%) were reported within 2 weeks of antimicrobial treatment. The incidence of IPI was 38.4 per 100,000 person-year, and the cumulative incidence of IPI was 0.1%, 0.4%, and 0.6% at 1-year, 5-year, and 8-year, respectively. The 8-year cumulative incidence rate of infection in the group aged under 5 years old was 14.2%, which was significantly higher than that in other age groups (0.5%, $p<0.0001$ by log-rank test). The relative risk of IPI in asplenia group was 37.6 times higher than that in the general population. In particular, the standardized incidence ratios (SIRs) in the age groups of 5 to 19, 20-39, and under 5 were 349.0, 342.2, and 225.8, respectively.

Conclusions: To our knowledge, this is the largest population-based study to show a significant increase of IPI in asplenia patients compared to the general population. Our findings reinforce that asplenia patients, especially those aged under 5 years, are at a very high risk for IPI.

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Abstract 293

Sexually-transmitted infections detection using real-time PCR Allplex in the east coast of Spain

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Background: Worldwide sexually transmitted infections (STIs) stand as a major global health concern, and more than a million of STIs are acquired per day. Common bacterial agents causing STIs are: *Chlamydia trachomatis*, *Neisseria gonorrhoeae*, *Mycoplasma genitalium*, and *Trichomonas vaginalis*. The aim of this study has been to establish the prevalence of STIs in the area of Consorcio Hospital General de Valencia, Spain during a two-year period of time.

Materials/methods: A total of 4541 clinical specimens from different anatomical sites (urine and endocervical, pharyngeal and anal swabs) according to the reported type of sexual practices (vaginal, oral and/or anal intercourse) of 3894 participants were included in the study. Testing was performed using the multiplex RT-PCR Allplex™ STI Essential Assay (Seegene, Seoul, Korea). This assay can simultaneously detect 7 STI pathogens (*C. trachomatis*, *N. gonorrhoeae*, *T. vaginalis*, *M. genitalium*, *M. hominis*, *U. urealyticum* and *U. parvum.*

Results: Global sexually-transmitted infection rates in our area are around 40%. In the table below there is the distribution of the different infections and the number of cases for each infection. *Chlamydia trachomatis* and *Neisseria gonorrhoeae* co-infections were detected in four cases, whereas co-infections of different species of Mycoplasma and Ureaplasma were found in more than 20% of the cases.

Sexually-transmitted microorganism	**Number of cases (%)**
Chlamydia trachomatis	326 (8%)
Mycoplasma genitalium	104 (3%)
Mycoplasma hominis	494 (14%)
Ureaplasma parvum	1013 (29%)
Ureaplasma urealyticum	498 (14%)
Neisseria gonorrhoeae	188 (5%)

Conclusions: Untreated STDs can lead to serious long-term health consequences, especially for adolescent girls and young women. Testing STI with multiplex PCR allows a more accurate diagnosis and covers the main agents causing these type of infections that could not be diagnosed otherwise. This is of major importance, as nowadays we are attending to a notorious increase in the rate of sexual infections that need to be detected and treated.

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Abstract 295

Characterisation of airborne fungi present in two hospitals in Kabale District, Uganda

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Background: Fungi are an increasing public health problem worldwide because they have a great impact on human health and on different areas of our activities. Fungi infection are a serious threat to quality of human life. Hospital environments contain different types of microorganisms such as airborne fungi which causes fungal diseases. In the present study, the total count and diversity of airborne filamentous and yeasts fungi were investigated in indoor air of selected wards of two major hospitals in Uganda. The study also examined the proportion in fungal infection cases most commonly reported in the two hospitals.

Materials/methods: Samples of indoor air from Outpatient ward, Maternity, Pediatrics and Emergency wards were collected by open plate technique on Potato dextrose agar media once a week. Samples were collected in triplicates. The cultures were then examined and evaluated according to macroscopic and microscopic examination criteria for genotypic identifications. The obtained results were analyzed by SAS and Plotly software.

Results: a total of 22 different fungi species were isolated from the two hospitals with *Aspergillus flavus* (17.9%) followed by *Aspergillus fumigatus* (12.3%), *yeast* (9.6%), *penicillium citrinum* (8.5%), as the most abundant and frequently surveyed fungal species in the two hospital while *Trichoderma*, *Nigrospora* and *P. marneffei* had the least values of spore count in all locations. All the wards showed high rates of contamination by various fungi. However, the analysis of the data showed that indoor air of OPD department (28.4%) had the highest number of fungi colonies in Kabale hospital while maternity ward (31.1%) had the highest for Rugarama hospital with the highest fungal pollution. Females also had more asthma cases for Kabale hospital with patient's ages 6-59 years visiting the hospital for either asthma or fungi infection cases while for Rugarama hospital, fungi infection cases was more prevalent. Rainfall and relative humidity were positively correlated with high fungi load in the atmosphere of the two hospitals.

Conclusions: Data on the abundance/prevalence of fungi spores in hospital environment of sub-Saharan Africa is limited. Therefore, it is important to evaluate and strengthen the infection prevention practice of the hospital.

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Abstract 301

Whole genome analysis of vancomycin-resistant *Enterococcus faecium* causing nosocomial outbreaks suggests the occurrence of few endemic clonal lineages in Bavaria, Germany

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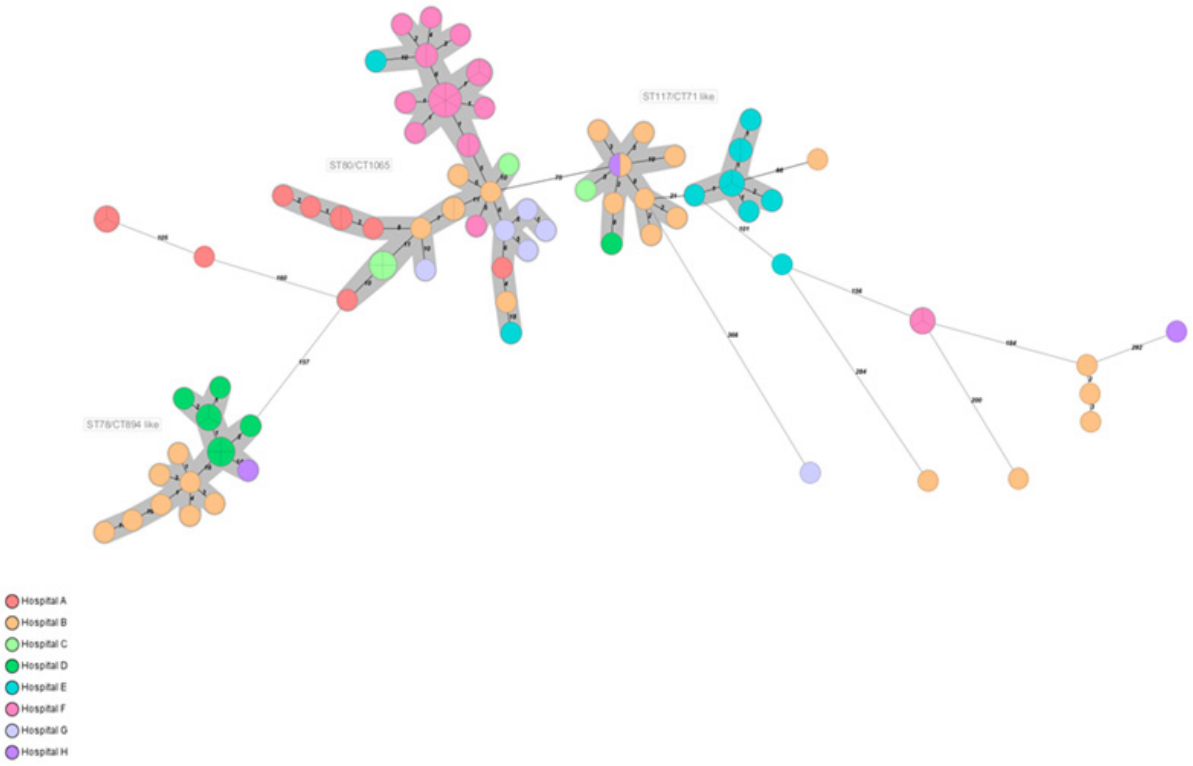
Background: Among clinical isolates of vancomycin-resistant *Enterococcus faecium* (VREfm), sequence type (ST) 117 and ST80 are highly prevalent in German hospitals and represent a frequent cause of nosocomial outbreaks. In this study, we investigated the genetic diversity of clinical isolates of VREfm recovered from different nosocomial outbreaks in Bavaria, Germany, by whole-genome sequencing (WGS).

Materials/methods: Between January 2018 and April 2019, 100 non-replicate clinical isolates of VREfm originating from nosocomial outbreaks at eight different hospitals in Bavaria were investigated for genetic diversity by WGS using the Illumina MiSeq platform (Illumina Inc., San Diego, USA) and laboratory procedures according to the manufacturer´s instructions. Afterwards, complex types (CTs) were identified by a gene-by-gene approach based on 1423 genes (core genome multilocus sequence typing, cgMLST) using SeqSphere+ software version 6.0.2 (Ridom GmbH, Muenster, Germany). Furthermore, a single-nucleotide polymorphisms (SNP)-analysis was conducted for all VREfm strains using BioNumerics 7.6 software (Applied Maths, Sint-Martens-Latem, Belgium).

Results: Most of the isolates of this study (84%) belonged to three major clonal groups: ST80/CT1065like vanB (n = 45; 6 hospitals), ST117/CT71like vanB (n = 20; 5 hospitals) and ST78/CT894like vanA (n = 19; 3 hospitals) (Figure 1). Isolates of the predominant lineage ST80/CT1065like vanB occurred in 6 different Bavarian hospitals and showed by SNP analysis a maximum difference of 34 SNPs.

Conclusions: Whole-genome analysis of VREfm causing nosocomial outbreaks suggests the occurrence of few endemic clonal lineages (ST80/CT1065like vanB, ST117/CT71like vanB and ST78/CT894like vanA) in Bavarian hospital settings.

Figure 1: Minimum-spanning-tree of all vancomycin-resistant Enterococcus faecium (VREfm) isolates of this study based on core genome multilocus sequence typing (cgMLST).



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Abstract 303

Management of tuberculosis: are the practices homogeneous in Europe?

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Abstract third-party references: On behalf of the ESGMYC Group

Background: Tuberculosis remains a global burden. This study aims to evaluate and to compare practices regarding the diagnosis, isolation and treatment of tuberculosis (TB) in Europe.

Materials/methods: A survey was conducted from November 2018 to April 2019 within the ESCMID study group for mycobacterial infections (ESGMYC). The practices observed were compared to the main international guidelines.

Results: Among 136 ESGMYC members, 58 responded to the questionnaire representing 14 countries. The participants are working in an infectious diseases (67%, n=43) or clinical microbiology (30%, n=19) department. In their practice, two (20.7%) or three sputum samples (79.3%) were collected for the diagnosis of pulmonary TB. If a patient was unable to provide a sputum sample, the alternatives were induced sputum (n = 37 / 67.2%), bronchoscopy (34 / 58.6%), and gastric aspiration (15 / 25.9%). Nucleic acid amplification tests were performed by 41 (64%) respondents whatever the smear result and by 47 (73%) in case of smear-positive specimens, to detect mutations conferring resistance to rifampicin by 84% (n= 52), to isoniazid by 29% (n=18), and to other drugs by 7% (n=4) of 62 respondents. NAAT and adenosine deaminase measurement were used for extrapulmonary TB diagnosis in 83.6% and 40.4% of cases, respectively. For isolation duration, 21 respondents (42.9%) are keeping isolation until smear negativity. An initial treatment without ethambutol was offered by 14% (n=9) of respondents. Corticosteroid therapy, cerebrospinal fluid opening pressure testing, and repeated lumbar puncture were carried out for central nervous system TB by 79.6%, 51.9% and 46.3% of the respondents, respectively. For patients with HIV-TB coinfection, the preferred antiretroviral therapy included dolutegravir 50mg BID (56.8%). For HIV-positive patients with latent TB, all respondents offered preventive treatment.

Comparing with the recommendations of the main guidelines, the practices are not totally consistent.

Conclusions: This study shows heterogeneous practices within Europe, particularly for diagnosis and isolation, although the role of rapid molecular testing seems to be important in most centers. Recent international recommendations are not followed. Better dissemination of these recommendations in collaboration with ESCMID and the promotion of studies validating good TB management practices in the European context are necessary.

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Abstract 306

Genomic analysis and exploration of putative drug resistance loci in malaria parasites

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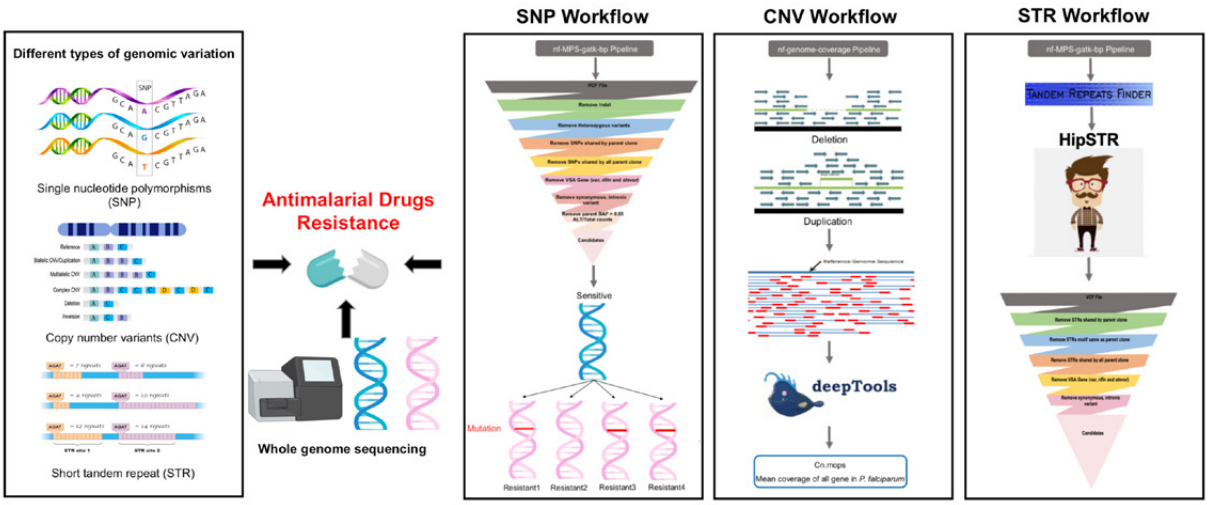
Abstract third-party references: The University of Melbourne, Walter and Eliza Hall Institute of Medical Research

Background: *Plasmodium falciparum* (Pf), the major parasite causing malaria, accounts for over 90% of malaria deaths, and demonstrates considerable resistance to current antimalarial drugs. Whole-genome sequencing can be employed to identify regions that are under high drug selective pressure, notably by looking at the single nucleotide polymorphism (SNPs), copy number variants (CNVs), and short tandem repeats (STRs). Here, we re-analysed data from a published study in which Cowell *et al.* set out to identify drug resistance inducing variants, which were either SNPs, CNVs or STRs.

Materials/methods: The druggable-genome dataset was downloaded from the NCBI Sequence Read Archive which contains 237 *P.falciparum* strains, resistant to 31 diverse compounds derived from 3 background strains: 3D7 (168), 7G8 (5) and Dd2 (64). As there is a considerable difference between the genome of 3 background strains, reads were aligned to corresponding reference genome, compared to only single reference genome (3D7) in Cowell *et al*. We used our in-house pipelines to re-analyse the SNPs and CNVs, and HipSTR to analyse STRs, which were not analysed in Cowell *et al*. Variants were then compared between isogenic parent and offspring compound-resistant clones to explore mutations possibly associated with drug resistance.

Results: Our results showed that alignment to the appropriate reference genome greatly reduces the number of variants, allowing causative variants to be better identified. We identified 305 putative drug resistance genes from 3D7 samples, 146 genes from Dd2 samples, and 7 genes from 7G8 samples. Among them, 68 genes were observed in multiple, independent clones, 4 of which were known drug resistance loci (*pfcytb*, *pfcrt*, *pfmdr* and *pfmrp*). Additionally, 17 genes were identified associated with multi-drug resistance. Compared with Cowell *et al*., we have 20 putative drug resistance genes that are identical between their and our analysis, 6 genes identified only by them, and 45 genes unique to our analysis.

Conclusions: This study presents a comprehensive analysis of the different types of genomic variations to identify mutations possibly associated with drug resistance. This information can be used for the investigation of drug resistance mechanisms and help in designing combination drug therapies to overcome emerging drug-resistance.



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Abstract 314

Fully automatic (1-3)-β-D-glucan test for the invasive fungal detection

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Background: Invasive fungal disease threats millions of human's life every year, people are exploring the diagnosis solutions currently. Fungus (1-3)-β-D-Glucan (BG) test is a widely recommended and used technology for the detection of pan-fungal infections. However, BG test has high requirements for the personnel operation and requires very careful operation because (1-3)-β-D-Glucan is a substance that also exists in the environment. Era Biology's FungiXpert Fully Automatic Kinetic Tube Reader (IGL-200) was introduced to make BG test automated. This technique would allow elimination of contamination origin from human operation and reduce the operational error.

Materials/methods: The aim of this study was to evaluate the performance of fully automatic BG test. The evaluation test was performed at Ruijin Hospital, Shanghai Jiao Tong University School of Medicine, a total 140 serum samples were involved and collected on site. Samples were tested by both manually (performed on kinetic tube reader MB-80X) and automatically (performed on Fully Automatic kinetic tube reader IGL-200) immediately after collection. The reagent used in this program is Goldstream® Fungus (1-3)-β-D-Glucan Test (Chromogenic Method). The final detection results were compared with clinical evidences and diagnostic from hospital.

Results: Compared with results performed on MB-80X and fully automatic IGL-200, the total coincidence rate of IGL-200 results was 97.85% (137/140). Among the 3 inconsistent samples, one is the special hemolysis sample; one sample showed weak positive on IGL-200 and in indeterminate with manual operation. Another inconsistent sample was clinically proved to be negative but show positive on MB-80X with unknown cause, which was suspected to be the result of man-made contamination. For the experiment on IGL-200, there is no complicated procedures but only need place the reagents and samples on the rack, much easier for laboratory.

Conclusions: The BG test on Fully Automatic Kinetic Tube Reader IGL-200 has a high agreement rate and low contamination rate compared with manual operation. IGL-200 permits a quick result and convenient operation, benefits clinical laboratory with its high efficient and intelligent. BG test automated with IGL-200 is a significant diagnostic method.

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Abstract 318

Renal function and albumin are drivers for exposure of flucloxacillin in critically ill patients

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Background: Our objective was to describe population pharmacokinetics (PPK) of flucloxacillin in critically ill patients and to identify covariates that can explain variability in PK behavior, in order to optimize flucloxacillin dosing regimens.

Materials/methods: First, we developed a PPK model and estimated between patient variability (BPV) through non-linear mixed effect analysis, using total and unbound concentrations obtained from adult critically ill patients treated with intermittent flucloxacillin for (suspected) infections. Second, we identified covariates that could explain BPV. Third, the impact of the identified covariates on flucloxacillin exposure and probability of PK/PD target attainment (PTA, 100% fT>MIC, ECOFF *S. aureus* cloxacillin 0.50mg/L) was evaluated by Monte Carlo simulations and externally validated in two critically ill patient cohorts.

Results: Thirty-five patients yielded 79 total and 104 unbound flucloxacillin plasma concentrations. In a two-compartment model with non-linear protein binding, BPV of the maximum binding capacity decreased from 42.2% to 30.4% upon inclusion of serum albumin concentrations (ALB). BPV of unbound clearance decreased from 88.1% to 71.6% upon inclusion of estimated glomerular filtration rate (eGFR, CKD-EPI). The model with ALB and eGFR performed statistically significantly better than the model without covariates in the external patient cohorts: median absolute percentage error (MAPE) of population predicted concentrations decreased from 55.3 to 39.6% (p=0.004) for total and from 59.2 to 51.7% (p=0.01) for unbound flucloxacillin in the Nijmegen dataset, and from 70.3 to 33.4% (p=0.0005) for unbound flucloxacillin in the Brisbane dataset. The PTA was 91% for patients with eGFR 33ml/min and 1g q6h, 87% for patients with eGFR 96ml/min and 2g q4h and 71% for patients with eGFR 153ml/min and 2g q4h.

Conclusions: For patients with high creatinine clearance infected with moderately susceptible pathogens, therapeutic drug monitoring is advised as a risk for underexposure exists even with the currently used highest dosing regimens. When total flucloxacillin concentrations are measured and converted using protein binding values from the literature, there is a risk of underestimating unbound concentrations, especially in patients with hypoalbuminemia.

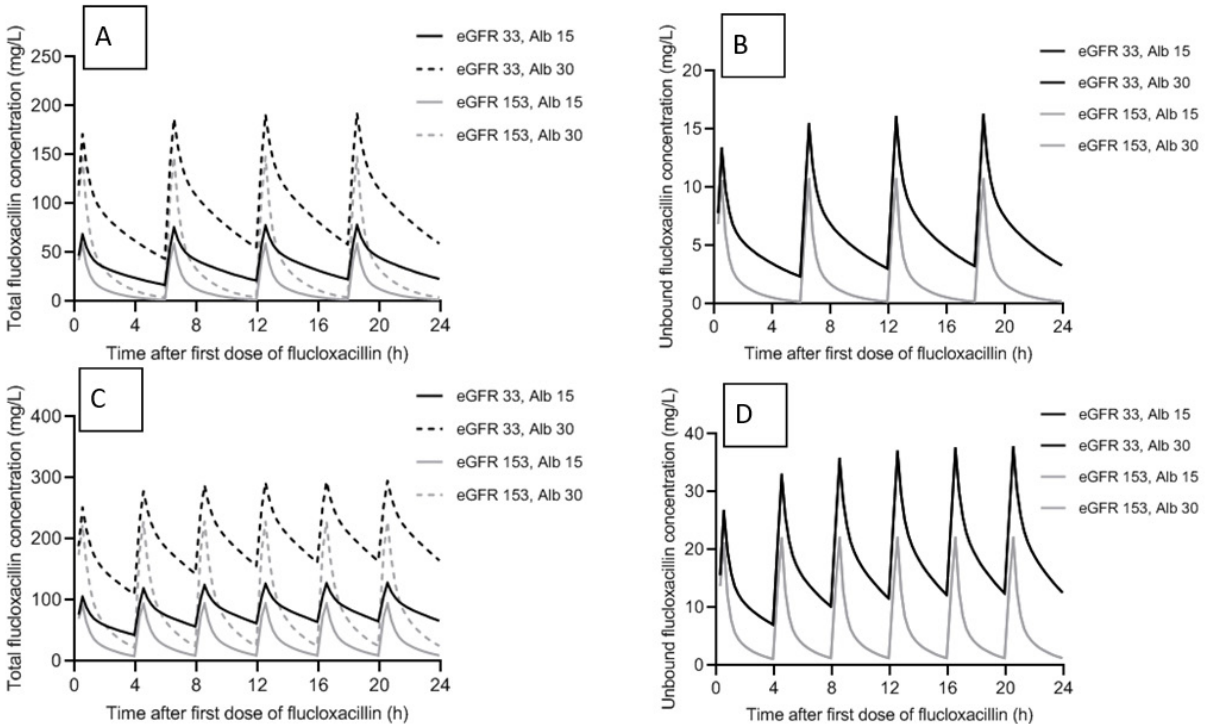

Figure 1. Simulated flucloxacillin concentration-time profiles: (A) total and (B) unbound concentrations after 1g q6h; (C) total and (D) unbound concentrations after 2g q4h.

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Abstract 329

Rapid semi-quantitative format PCR for the detection of *Pneumocystis jirovecii* replacing the direct examination

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Background: *Pneumocystis jirovecii* (PCJ) is an opportunistic pathogen causing infection inimmunocompromised patients. Conventional diagnostic is done on respiratory samples by microscopy. However PCR exhibits a higher sensitivity and allows accurate quantification. At the CHUV we developed a quantitative RT-PCR on our molecular platform and the PCJ DNA copy number was correlated with clinical significance (P#2194, ECCMID 13-16 APRIL 2019 AMSTERDAM, NETHERLANDS). However our platform has a TAT of 4 hours and is opened 5/7 days a week. We, thus decided to transfer this home-brew PCR on the rapid BD MAX™ system (BD Diagnostics) providing results in 90 minutes, 7/7days a week. We now aimed to extrapolate PCJ quantity from the obtained BD MAX™ system Ct in order to give to clinicians a clinical significant result.

Materials/methods: A prospective study on 247 patient respiratory samples was performed to compare both PCR systems: Quantification (Ct=copy number/ml) home-brew PCR on the platform and semi-quantification (Ct) on the BD MAX™ system.

Results: On 247 samples, 8 were not taken into account in our analysis due to technical problems on one or another platform. On the 239 remaining samples, 18 were not concordant due to very low quantities (high Ct value) of DNA, not corresponding to clinical significant amount of PCJ. On the 49 positive on both platforms, a good correlation (R^2 = 0.93) of the Ct values between the two systems was observed with an average of 0.68 +/- 1.3 Ct difference (BD MAX™ system Ct - molecular platform Ct).

Conclusions: These results allow us to extrapolate PCJ DNA copy number for a given Ct value obtained with the rapid BD MAX™ system allowing the clinicians to interpret a positive result according to the clinical situation. Due to these results, direct examination was stopped for PCJ and replaced by the rapid PCR system 7/7 days a week.

1- Perret et al., Ability of Pneumocystis jirovecii quantitative PCR to discriminate pneumocystosis from colonisation. 29th ECCMID 13-16 APRIL 2019 AMSTERDAM, NETHERLANDS, Poster #2194.

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Abstract 331

Systemic antifungal therapy (AFT) with isavuconazonium sulfate (ISAVUSULF) or other AFT in adults with invasive mucormycosis (IM) or invasive aspergillosis (IA) caused by a non-fumigatus species (IA-nf): A multi-centre, non-interventional registry study

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Background: ISAVUSULF is the prodrug of isavuconazole, a broad-spectrum mould-active triazole antifungal used for the treatment of IM and IA in adults. This real-life registry examined all-cause mortality (ACM) in adults treated with ISAVUSULF or other systemic AFT for IM or IA-nf.

Materials/methods: Multicentre, noninterventional registry of adult patients with proven/probable IM or IA-nf according to European Organisation for Research and Treatment of Cancer/Mycoses Study Group criteria who received systemic AFT. There were no exclusions based on liver/renal dysfunction. Cumulative data from 33 US centres for participants treated from January 2016 through November 2018 were analysed. Patients were stratified into primary ISAVUSULF, salvage ISAVUSULF for refractory infection/intolerance to another AFT or as oral step-down/maintenance, or other AFT groups (see table for group definitions). ACM was assessed at days 42 and 84 post-AFT initiation. Investigators assessed adverse drug reactions (ADRs) suspected to be related to ISAVUSULF. ADRs for other AFT were only reported during use of ISAVUSULF for non-treatment reasons (prophylaxis or empirical therapy for <4 days) (n=7).

Results: 204 patients were enrolled (104 ISAVUSULF and 100 other AFTs). Seventy-four (71.2%) received ISAVUSULF as primary AFT (24 ISAVUSULF-monotherapy and 50 ISAVUSULF-combination therapy) and 30 (28.8%) as ISAVUSULF-salvage treatment (11 monotherapy and 19 combination therapy). Baseline characteristics were similar in both ISAVUSULF and other AFT groups (Table). Most IA-nf infections affected the lungs±other organs while most IM infections were extrapulmonary (Table). Primary ISAVUSULF, salvage ISAVUSULF and other AFT day 42 ACM rates were 14.8%, 0% and 17.8%, respectively, for IA-nf and 33.3%, 20.0% and 41.3% for IM, respectively (Table). Fourteen ISAVUSULF-treated patients experienced ADRs (primary ISAVUSULF: 7/74 [9.5%]; salvage ISAVUSULF: 7/30 [23.3%]; and other AFT 0/7 [0%]). ADRs leading to ISAVUSULF discontinuation were experienced by 4/74 (5.4%) patients in the primary ISAVUSULF and 3/30 (10%) in the salvage ISAVUSULF groups. Only 3 patients developed serious ADRs: 1/74 (1.4%) and 2/30 (6.7%) in the primary and salvage-ISAVUSULF groups, respectively. No fatal ADRs were reported.

Conclusions: ISAVUSULF, either as monotherapy or combination therapy, is well tolerated, and ACM results are consistent with previous reported results in adult patients with IA-nf or IM.

Table. Baseline characteristics, type of IA-nf or IM (single or mixed), site of infection and ACM

Parameter	Primary ISAVUSULF* (N=74)	Salvage ISAVUSULF† (N=30)	Other AFT‡ (N=100)
Baseline characteristics			
Mean (SD) age, years	55.2 (14.7)	57.2 (14.6)	56.5 (15.6)
Male, n/N (%)	44/74 (59.5)	19/30 (63.3)	53/100 (53.0)
eGFR <60 mL/min/1.73m^2, n/N (%)	31/74 (41.9)	10/30 (33.3)	32/100 (32.0)
Allogeneic BMT recipient, n/N (%)	14/74 (18.9)	4/30 (13.3)	14/100 (14.0)
Other malignancy, n/N (%)	13/74 (17.6)	4/30 (13.3)	15/100 (15.0)
Neutropenia, n/N (%)	31/74 (41.9)	8/30 (26.7)	34/100 (34.0)
Hematologic malignancy, n/N (%)	35/74 (47.3)	11/30 (36.7)	39/100 (39.0)
Use of corticosteroids, n/N (%)	48/74 (64.9)	18/30 (60.0)	60/100 (60.0)
T-cell immunosupression, n/N (%)	37/74 (50.0)	10/30 (33.3)	44/100 (44.0)
Pathogen causing IFD, n/N (%)			
Single IA-nf	27/74 (36.5)	8/30 (26.7)	45/100 (45.0)
Single IM	26/74 (48.6)	18/30 (60.0)	34/100 (34.0)
Mixed IA-nf	0	2/30 (6.7)	5/100 (5.0)
Mixed IM	6/74 (8.1)	2/30 (6.7)	12/100 (12.0)
Site of single IA-nf infection, n/N (%)			
Pulmonary	14/74 (18.9)	3/30 (10.0)	22/100 (22.0)
Disseminated	7/74 (9.5)	2/30 (6.7)	8/100 (8.0)
Extrapulmonary	6/74 (8.1)	3/30 (10.0)	15/100 (15.0)
Site of single IM infection, n/N (%)			
Pulmonary	9/74 (12.2)	3/30 (10.0)	3/100 (3.0)
Disseminated	5/74 (6.8)	1/30 (3.3)	10/100 (10.0)
Extrapulmonary	21/74 (28.4)	12/30 (40.0)	21/100 (21.0)
Unknown	1/74 (1.4)	2/30 (6.7)	0
Serious ADR, no. per group/group total, (%)§	1/74 (1.4)	2/30 (6.7)	0
Day 42¶# ACM, no. deaths/group total, (%)			
IA-nf	4/27 (14.8)	0/8 (0)	8/45 (17.8)
IM	14/42 (33.3)	4/20 (20.0)	19/46 (41.3)
Day 84¶# ACM, no. deaths/group total, (%)			
IA-nf	8/27 (29.6)	1/8 (12.5)	13/45 (28.9)
IM	17/42 (40.5)	5/20 (25.0)	23/46 (50.0)
ACM with unknown pathogen, n/N (%)			
Day 42¶#	0	0	1/1 (100)
Day 84¶#	0	0	1/1 (100)

ACM, all-cause mortality; ADR, adverse drug reactions; AFT, antifungal therapy; BMT, bone marrow transplant; eGFR; estimated glomerular filtration rate; IA, invasive aspergillosis; IA-nf, invasive aspergillosis caused by a non-*fumigatus* species; IFD, invasive fungal disease; IM, invasive mucormycosis; ISAVUSULF, isavuconazonium sulfate. Data are number with characteristic or event/total number (%) unless otherwise stated *Non- ISAVUSULF systemic AFT as primary therapy and received at least one dose of ISAVUSULF against IM or IA-nf after primary AFT due to intolerance, refractory or oral step-down/maintenance. †ISAVUSULF as primary therapy against IM or IA-nf. ‡Patients received non- ISAVUSULF systemic AFT as primary therapy and received no ISAVUSULF against IM or IA-nf after primary AFT due to intolerance, refractory or oral step-down/maintenance. Patients who received ISAVUSULF as prophylaxis or empirical therapy for <4 days were included in this group. §Noncardiac chest pain and liver-enzyme elevation with primary ISAVUSULF; leukopenia and hypoesthesia/paresthesia with salvage ISAVUSULF. ¶For the ISAVUSULF and other AFT groups, days are relative to the first dosing day of ISAVUSULF or the primary AFT. Day 84 mortality rates are cumulative. #Patients who died or whose survival status was unknown were classified as dead.

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Abstract 334

Prevalence of the suggestion of the influenza vaccine to pregnant women among gynaecologists and obstetricians

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Background: Influenza is a systemic infectious disease and pregnancy is a factor that increases the mortality of the disease. Therefore, it is recommended that all pregnant women receive an influenza vaccine. However, rates of influenza vaccination in pregnant women are low. The aim of this study is to estimate the prevalence of Gynecologists and Obstetricians (GOs) recommending the influenza vaccine to their pregnant patients.

Materials/methods: This study was designed as a cross-sectional survey. The population of the study was calculated to be 364 people based on a 95% confidence interval and a 5% margin of error. The data were collected through a questionnaire consisting of 17 questions, distributed through a Facebook group.

Results: Of the physicians participating in the study, 43.5% reported that they recommended the influenza vaccine to pregnant women and 62.8% reported that 50% or more of the pregnant women to whom they recommended the vaccine, rejected the vaccine. According to a Multivariate Logistic Regression analysis, three factors increased the rate of physicians not recommending vaccination: their age, not having had an influenza vaccination themselves, and not knowing that the cost of the vaccine would be reimbursed. The mean age of the 384 GOs participating in the study was 39.7 ± 10.2 years.

Conclusions: Vaccinating pregnant women is necessary because of increased influenza mortality during pregnancy. Even though GOs are not vaccination practitioners in routine pregnancy follow-up, they can contribute to vaccination rates by recommending vaccination. Physicians' application of scientific knowledge and transfer of this knowledge to their patients will contribute to increased adult immunization rates.

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Abstract 335

Risk factors for mortality in patients with pulmonary mucormycosis

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Background: Pulmonary mucormycosis (PM) results in serious burden in terms of morbidity and mortality in immunocompromised patients. However, there are limited studies with small number of patients on prognostic factors in patients with PM.

Materials/methods: Adult patients who were diagnosed with proven and probable PM according to the modified definitions of the EORTC/MSG criteria were enrolled at a tertiary hospital, Seoul, South Korea, between 1992 and 2014 (retrospectively) and 2015 and 2019 (prospectively). Proven PM was defined as positive fungal culture results for mucormycosis from lung biopsy specimens and/or histologic evidence of tissue invasion of hyphae with positive mucormycosis immunohistochemistry test result. Probable PM was defined as the presence of host and clinical factors together with mycological evidence of mucormycosis agents in non-sterile culture. Risk factors for 90-day mortality of PM were analyzed.

Results: A total of 52 patients including 34 (65%) patients with proven PM and 18 (35%) with probable PM were enrolled. The 90-day mortality rate was 46% (24/52). Neutropenia, thrombocytopenia, use of voriconazole at clinical suspicion, positivity of non-sterile culture, use of steroid, and treatment without surgery were more common in fatal patients than non-fatal patients. Voriconazole use at clinical suspicion for invasive mold pneumonia (adjusted OR 7.78, $P = 0.004$) and prolonged neutropenia (adjusted OR 5.45, $P = 0.02$) were independent risk factors for mortality. Voriconazole use at clinical suspicion was related with positive galactomannan (GM) assay (adjusted OR 6.48, $P = 0.01$) and history of invasive pulmonary aspergillosis (adjusted OR, 7.35, $P = 0.04$).

Conclusions: About half of patients with PM died within 90-day of diagnosis, and these fatal outcomes were common in patients with prolonged neutropenia and empirical voriconazole use. Cautious use of voriconazole is needed even in patients with positive GM results and prior history of invasive pulmonary aspergillosis in whom PM cannot be ruled out in differential diagnosis.

TABLE. Risk factors for mortality in patients with pulmonary mucormycosis.

Risk factor	Univariate analysis		Multivariate analysis	
	OR (95% CI)	*P* value	aOR (95% CI)	*P* value
Age	1.02 (0.98 – 1.07)	0.41		
Neutropenia more than 10 days	6.00 (1.59 – 22.62)	0.01	5.45 (1.27 – 23.33)	0.02
Steroid use (any dose)	3.24 (1.02 – 10.28)	0.046		
Voriconazole use at clinical	8.40 (2.21 – 31.88)	0.002	7.78 (1.89 – 31.94)	0.004
Surgery with antifungal therapy	0.16 (0.32 – 0.84)	0.03		

OR, odds ratio; aOR, adjusted odds ratio

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Abstract 343

Expediting antibiotic therapy management of critically ill patients with pneumonia by the detection of the main carbapenemase and ESBL-encoding genes directly from bronchoalveolar lavage

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Background: Among critically ill patients with pneumonia, the growing treat of antimicrobial resistance hampers the empirical treatment choice and relies heavily on rapid microbiological results. The detection of carbapenemase and extended-spectrum β-lactamase (ESBL) producers *Enterobacterales* (EB) has become a major issue among ICU patients, due to their clinical impact. Our aim was to determine whether molecular assays would expedite the detection of genes encoding carbapenemases and ESBL directly from bronchoalveolar lavage (BAL) and antibiotic therapy management in critically ill patients with pneumonia.

Materials/methods: The CRE and ESBL ELITe MGB® kits are two real-time PCR assays for the detection in less than 3h of the most prevalent carbapenemase and ESBL encoding genes in EB, respectively. From December 2018 to June 2019 all BALs of critically ill patients submitted for standard of care bacterial culture were prospectively collected. The CRE and ESBL ELITe MGB® assays were performed directly on 197 BALs sampled from 120 critically ill patients. Molecular results were compared to routine culture-based microbiological diagnostics results. A retrospective analysis of the therapeutic antimicrobial management was performed to evaluate the potential contribution of molecular assays to early optimization of empirical antibiotic therapy.

Results: Carbapenemase and ESBL encoding genes were detected in 20 (10.2%) and 12 (6.1%) BALs sampled from 15 and 11 patients, respectively. Positive (PPV) and negative (NPV) predictive values of the CRE ELITe MGB® kit were 85% [IC 95%: 64.9-94.6] and 100%, respectively. PPV and NPV of the ESBL ELITe MGB® kit were 75% [IC 95%: 49.4-90.2] and 100%, respectively. Retrospective analysis of medical records revealed that more than 50% of critically ill patients with pneumonia caused by carbapenemase- and/or ESBL-producing EB were initially treated with inadequate therapy. Overall, approximately 50% of patients could have been treated with appropriate therapy at least 24 h earlier if molecular data had been used.

Conclusions: Validity assessment of molecular assays detecting the main antibiotic resistance genes directly from BAL showed a high accuracy when compared to culture-based results. Molecular assays detecting the main carbapenemase and ESBL encoding genes provide an interesting tool for expediting appropriate antibiotic therapy in critically ill patients with pneumonia.

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Abstract 350

Significance of candidaemia causing neonatal sepsis and efficacy of caspofungin therapy

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Background: Invasive candidiasis in extremely premature infants is the second most common cause of infectious disease-related death. The incidence of hematogenous infections due to Candida specially non-albicans species among immunocompromised neonates has increased significantly in recent decade The emerging fungal pathogens comprising the Candida haemulonii complex are notable for their antifungal resistance with higher mortality and morbidity. Caspofungin is effective, safe and well-tolerated as an alternative therapy for persistent and progressive candidiasis in those neonates who are resistant, unresponsive to or intolerant of conventional antifungals.

Materials/methods: We here report our experience of caspofungin therapy in four cases of neonatal fungemia caused by C haemulonii. All these neonates were pre term, low birth weight with multiple invasive devices and had history of bacterial sepsis for which were on broad spectrum antibiotics. All the isolates were recovered in BACTEC Peds plus/F culture vials. Species identification was done in VITEK 2 yeast ID system. Confirmation of the species was done by PCR based molecular methods and MALDI-ToF mass spectrometry-based assay. Caspofungin therapy started with serial blood culture. Caspofungin therapy was continued two weeks after last negative culture.

Results: In all the 4 cases clinical and microbiological cure were possible. The dosage of caspofungin was 2 mg/kg/day, and the mean treatment duration was 14 days and the mean duration of antifungal therapy was 21 days. 2 out of the 4 patients had multifocal multidrug resistant (MDR) colonization and had history of azole exposure. 2 of the patients had adverse events are fever and rash. Increase of hepatic transaminases and hypokalemia was found in 1 patient.

Conclusions: The resistance of C. haemulonii represents a therapeutic challenge in the treatment of invasive candidiasis in immunocompromised neonatal patients. Caspofungin therapy is well tolerated , safe and effective in these resistant fungal infections. Caspofungin is FDA-approved for adults and children >3 months of age. These promising results suggest a potential role for caspofungin as an additional first-line treatment of systemic resistant candidiasis in immunocompromised neonates. This drug should be further investigated in this special patient population group.

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Abstract 358

Pneumococcal vaccination introduced between the chemotherapy cycles decreases the incidence of pneumonias in patients with multiple myeloma

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Background: Invasive pneumococcal infections (IPI) are life-threatening, but vaccine preventable complications in a range of immunosuppressed patients. Among the high-risk groups susceptible to IPI are patients with hematological malignancies receiving target treatment, novel agents and monoclonal antibodies. Novel agents to treat multiple myeloma (bortezomib, lenalidomide, ixazomib) are reported to be associated with high risk of pneumonias. The aim of the study was to assess the clinical efficacy of a 3-dose regimen of vaccination by 13-valent conjugate pneumococcal vaccine introduced in between the chemotherapy cycles with novel agents.

Materials/methods: Adult patients with multiple myeloma were included in this study, based at tertiary hematology and transplantation center in 2017-2019. Vaccination of adult multiple myeloma patients by 13-valent pneumococcal conjugate vaccine (PCV13) was performed during the intervals between the chemotherapy cycles with novel agents (bortezomib, lenalidomide, ixazomib). A vaccination regimen was based on 3 doses of pneumococcal vaccine with a minimum of 1 month interval. There were totally 18 adult patients who were vaccinated by PCV13 along with 18 patients of a control group matched by age, sex, main diagnosis and treatment regimens. Incidence of clinically and radiologically confirmed pneumonias during one-year observation period was taken as a primary outcome. The study has been registered with ClinicalTrials.gov Identifier: NCT03619252. Logistic regression was performed to assess the independent effect of PCV13 vaccination on the risk of pneumonias.

Results: No adverse effects of vaccination were registered, while a statistically significant independent effect of 3-dose regimen of PCV13 vaccination on the incidence of clinically-radiologically confirmed pneumonias was observed (OR 0.14; 95% CI 0.02-0.93; p=0.041). Number needed to treat (NNT) for PCV13 vaccination in multiple myeloma patients receiving novel agents was 3.0 (95% CI 1.61-22.10; p = 0.0571).

Conclusions: Despite the expected decrease in response to vaccination during the chemotherapy with novel agents, we have shown the clinical effectiveness of PCV13 vaccination schedule based on 3 doses given with a minimum 1 month interval between the chemotherapy cycles. Further implication of pneumococcal conjugate vaccines in adult immunocompromised patients may serve as a basis for decrease in frequency of pneumonias.

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Abstract 359

Resolving within-host, full length, dengue virus variants without haplotype reconstruction using Oxford Nanopore Technology

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Background: Despite the advances in sequencing technologies and the small size of RNA viral genomes, identifying full-length within-host viral variants has been a challenge. Previously we developed a protocol for full-length dengue virus sequencing (single molecule) using Oxford nanopore technology (ONT). Now, we introduce a new bioinformatic pipeline to resolve full-length within host dengue variants from ONT sequences

Materials/methods: This pipeline takes an alignment of ONT reads as the input, selects reads with a user-defined length and a starting codon, cleans them of indels and mismatches using a reference sequence and the quality scores at each base position. A hierarchical clustering algorithm is used to identify phylogenetically close read clusters to create a consensus per cluster (a within host variant). The final output of the pipeline is a list of within host variants and their relative abundance as a percentage. The accuracy of the pipeline was tested using *in silico* clonal mixtures of the hepatitis C virus.

Results: Forty clinical dengue samples were sequenced with ONT after multiplexing with either PCR based barcodes or ligated barcodes. Of these, only 19 samples had more than 100 reads (range 105 – 17,672) greater than 10kb after the initial cleaning steps of the algorithm (arbitrary lower limit to proceed to full pipeline). The number of within host variants detected ranged from 2-27 per sample with 2-3 dominant variants and the rest being minor variants. The number of minor variants identified depends on the total read count used (figure 1). More variants can be detected with increasing the input DNA, avoiding multiplexing or multiplexing with ligation barcoding.

Conclusions: This pipeline, combined with our method for pan-serotypic dengue full length genome amplification, offers the capacity to resolve within host viral variants without haplotype reconstruction for the first time for dengue virus (and for any RNA virus with a single open reading frame). This creates a new front in understanding within host viral evolution, closely related human to human transmission events and virological determinants of virulence in dengue.

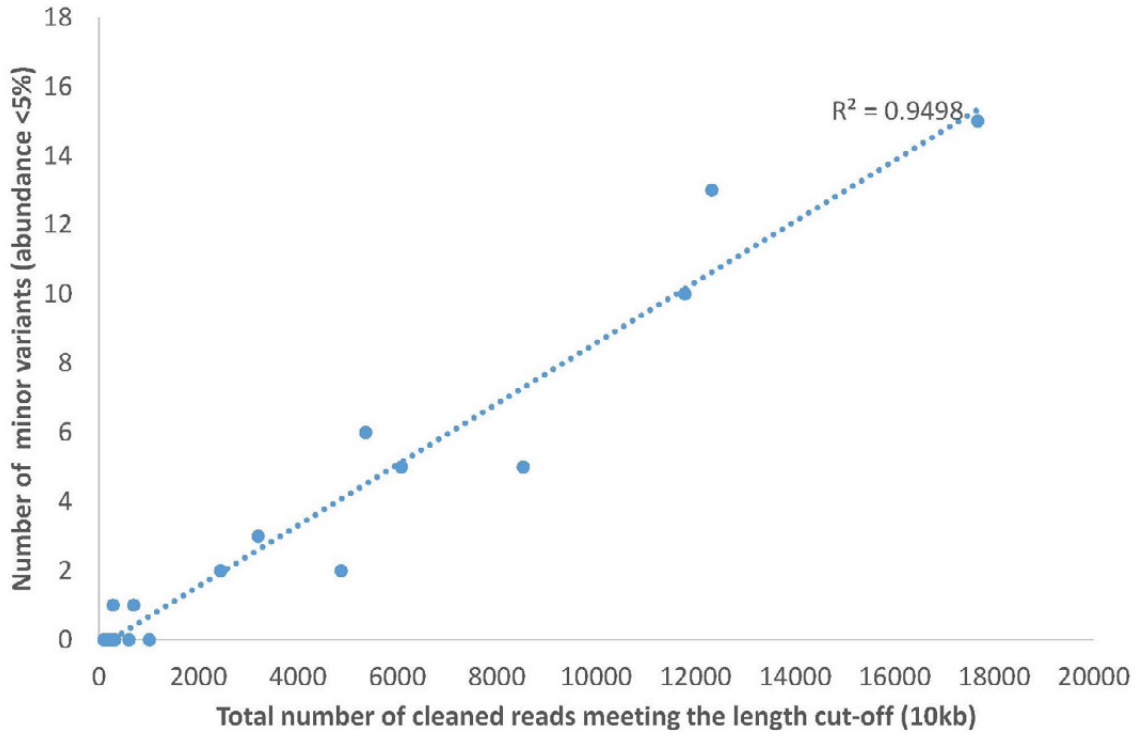

Figure 1. Detected minor variants (<5% abundance) increases linearly with the input number of reads.

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Abstract 369

Molecular characterisation of *Staphylococcus aureus* clinical strains from endotracheal tubes of patients with intensive care unit-acquired pneumonia

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Background: *Staphylococcus aureus* is among the most frequently isolated microorganism responsible for intensive care unit (ICU)-acquired pneumonia of which 29% are resistant to methicillin (MRSA). Our aim was to determine the antimicrobial susceptibility, the associated molecular mechanisms of resistance and the epidemiology relatedness of *S. aureus* strains from the endotracheal tubes (ETT) of intubated critically ill patients with *S.aureus* ICU-acquired pneumonia.

Materials/methods: Clinical *S. aureus* (17 MRSA and 3 methicillin susceptible *S. aureus*) were collected from ETTs after extubation during a prospective observational study carried out in four European tertiary hospitals. Antimicrobial susceptibility test, using the Kirby-Bauer method was performed to vancomycin, linezolid, ciprofloxacin, clindamycin, erythromycin, chloramphenicol, fusidic acid, gentamicin, quinupristin-dalfopristin, rifampicin, Sulfamethoxazole/trimethoprim, and tetracycline. Interpretation of results was carried out according to the European Committee on Antimicrobial Susceptibility Testing (EUCAST). Molecular characterization of each resistance mechanism was screened by PCR, electrophoresis and sequencing. Molecular epidemiology was analyzed by Multi locus sequence typing. Phylogenetic analysis was carried out using comparative eBURST V3 software (http://www.phyloviz.net/goeburst)

Results: *S. aureus* isolates were resistant to ciprofloxacin (85%), erythromycin (65%), gentamicin (35%), tetracycline (30%), clindamycin (20%), and fusidic acid (5%). Three strains showed hetero-resistant subpopulations to linezolid. The most frequent mutations in ciprofloxacin resistant *S. aureus* strains were S84L in the *gyrA* gene, V511A in the *gyrB* gene, S144P in the *grlA* gene, and K401R/E in the *grlB* gene. Strains resistant to erythromycin carried the *ermC*, *ermA,* and *msrA* genes; the same *ermC* and *ermA* genes were detected in strains resistant to clindamycin. The *aac(6')-aph(2")* gene was related to gentamicin resistance, whereas resistance to tetracycline was related to *tetK* (efflux pump). The *fusB* gene was detected in the strain resistant to fusidic acid. The most frequent sequence types were ST22, ST8, and ST217. These were distributed in four clonal complexes (CC5, CC22, CC45, and CC59).

Conclusions: High levels of resistance to second-line antimicrobials threatens the treatment of ICU-acquired pneumonia due to methicillin-resistant *S. aureus*, with decreased susceptibility to linezolid and vancomycin. The wide genotypic diversity found, even within the same ICU, reinforces the crucial role of ICU prevention bundles in cross-transmission.

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Abstract 371

Impact of biocide residues on *Escherichia coli* antimicrobial susceptibility

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Background: There is no standardised approach to predict the residues of biocides remaining on surfaces as a result of the use of disinfectants, nor is there a standardised way to predict the potential risk that these levels might pose to antimicrobial resistance. Although of practical relevance, bacterial selection and adaption to biocide surface residues has not been fully investigated to date. This study explores links between exposure effects of chlorhexidine at concentrations found on surfaces post-application and changes in phenotypes and the metabolome in *E. coli*.

Materials/methods: Chlorhexidine (CHX) surface concentration post-treatment was determined by High-Performance Liquid Chromatography. A modified standard efficacy carrier test was used against five genotypically distinct *E. coli* exposed to *in-situ* concentrations of CHX. Minimal inhibitory concentrations (MIC), antibiotic susceptibility profiles, efflux activity, and conjugative plasmid transfer were assessed and compared before and after exposure to CHX. Changes in susceptibility after CHX exposure were investigated for stability. The effect of CHX exposure on the broader phenotype was assessed using the OmniLog microarray (BioLog, US)

Results: CHX surface concentration post-application was on average 0.006 mg/mL after 0-7 days. CHX susceptible bacteria survived exposure to this residual concentration and were shown to adapt through metabolic alterations, such as those responsible for cell wall biosynthesis, along with transient insusceptibility to CHX, imipenem and cefoxitin, and stable resistance to amoxicillin/clavulanic acid, ampicillin, cefpoxidime and cefotaxime. Results show that a transiently adapted population may be selected amongst less tolerant sub-populations. CHX however did not increase transfer of ampicillin resistance at a residual concentration and prevented conjugative transfer at a concentration of 0.002 mg/mL.

Conclusions: CHX has the potential to promote the emergence of resistance and cross-resistance at concentrations found on surfaces after disinfection. Findings in this study warrant further investigation into residual concentrations of biocides found in the environment, their effects on common pathogens and potential markers for the risk of resistance development as a result of exposure.

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Abstract 379

Staphylococcus aureus bloodstream infection: can the practice of the VIRSTA score replace the infectious disease consultation in case management?

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Background: *Staphylococcus aureus* bacteremia (SAB) causes life-threatening complications such as infective endocarditis (IE). Although de SAB management is well codified, its mortality remains high. The VIRSTA score was developed to guide physicians in the management of SAB, improve outcomes and risk stratification of IE. In this framework, the role of the infectious disease specialist has yet to be specified. Our primary objective was to assess whether an early infectious disease specialist consultation (IDC) could improve the management and outcomes of SAB. Our secondary objectives were to evaluate the adequacy of clinical practices to the VIRSTA score by ID and non-ID management.

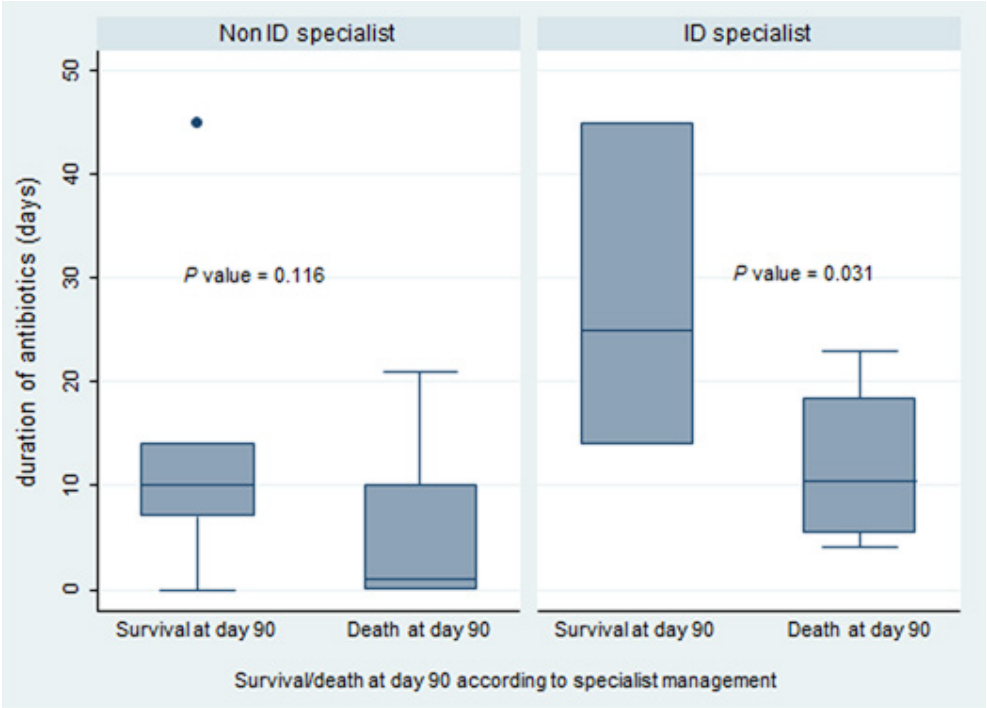
Materials/methods: We performed a retrospective cohort study, in a 800-bed teaching hospital, in Reunion Island, over a one-year period in adult patients with SAB (≥1 positive blood culture with SA). Clinical practice was deemed adequate to VIRSTA score when no transesophageal echography (TEE) but only one transthoracic echography (TTE) was performed for scores ≤2 and when either one TEE or two TTE were performed for scores ≥3.

Results: Fifty-two SAB were included of which 73.1% were of nosocomial origin, and 90.4% were methicillin sensitive. ID specialists were solicited for 28 (53.9%) patients, in an average time of 3.3±6.6 days. ID specialists tended to be more often solicited when blood cultures remained positive beyond 48 hours (*P*=0.054). A TTE (OR 91.00, 95%CI: 13.89-595.97) and a control TTE (*P*=0.005) were more likely when an ID specialist managed the infection.

Antibiotic treatment was more appropriate when the patients benefited from an IDC (OR 25.00, 95%CI: 5.50-113.46). Clearance of bacteremia was more likely achieved after ID management (OR 4.28, 95%CI: 1.13-16.27).

Patients who benefited an IDC had a decision more likely conform to VIRSTA score (OR 4.60, 95%CI: 1.31-16.14). An IDC was associated with protection against the risk of death within three months (OR 0.26, 95%CI: 0.06-0.98).

Conclusions: Our study supports a central role of the ID specialist in the management of patients with SAB, this being associated with better outcomes and respectful of up-to-date guidelines. The VIRSTA score, when applied early could help the diagnostic strategy of SAB before the IDC.



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Abstract 383

Neural networks for prediction of minimum inhibitory concentration

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Background: Antibiotic resistance is listed by the World Health Organization as one of the biggest threats to global health and causes about 33 000 deaths, in the EU/ESS region only, each year. Lately, several machine learning methods have been purposed for autonomous resistant profiling of bacteria and this work aims to use neural networks for prediction of minimum inhibitory concentration (MIC).

Materials/methods: We have developed a neural network based machine learning model for prediction of minimum inhibitory concentration (MIC) from k-mers extracted from whole-genome sequencing. To handle the curse of dimensionality associated with k-mers we perform dimensionality reduction through principal component analysis. The dataset used consists of 4964 Salmonella samples with MICs measured, for up to 15 antibiotics, for each sample. All MICs were measured on a 2-fold dilution. The evaluation of the model was done using a 5-fold cross validation.

Results: For prediction of exact MIC the accuracy of our model varied from 0.61 for streptomycin to 0.93 for tetracycline with an average for all antibiotics of 0.78. When translating the MICs to labels, S/I/R, our model had an average accuracy of 0.97. Further, the model was compared to already existing machine learning model trained on the same dataset. Our model outperformed the already existing machine learning model when it comes to predicting exact MIC for 13 of the 15 antibiotics considered. Greatest improvement were for the antibiotics ampillicin, amoxicillin-clavulanic acid and tetracycline.

Conclusions: We conclude that our neural network outperforms the other machine learning model and yields a great improvement when it comes to accuracy. This is somewhat expected since neural networks tends to be the superior model in other areas such as image processing and natural language processing. The results also illustrates the complexity of predicting exact MIC. Comparing the exact accuracy to the accuracy for S/I/R of the model, which on average was 0. 97, we observe a vast improvement which shows that prediction of S/I/R is a more feasible and simpler problem compared to prediction of exact MICs.

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Abstract 387

A k-mer-based approach for MLST and cgMLST analysis of nanopore sequenced *Staphylococcus aureus*

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Abstract third-party references: 1928 Diagnostics

Background: Genotypic typing, such as MLST or cgMLST, is an important tool for infection control and is typically used today in combination with NGS data. However, one disadvantage of using NGS is the slow sample-to-result turnaround time, which can amount to several days. With the advent of Nanopore sequencing, it is possible to rapidly generate sequencing data at the expense of higher error rates, which could speed up the analysis and potentially revolutionize the field of clinical infection control.

Materials/methods: Eight double-sequenced bacterial samples (Illumina + Nanopore, *Staphylococcus aureus*, EMBL-EBI project PRJDB8599) were analyzed with MLST and cgMLST. The goal was to evaluate the ability to predict sequence types (STs) and cluster samples based on cgMLST profiles using only Nanopore data. Here, the Illumina data was used as a reference to verify the results. The raw Nanopore reads were analyzed in a custom, kmer-based bioinformatic pipeline and the Illumina reads were analyzed in the 1928D platform (https://1928diagnostics.com/). One of the samples was discarded due to a contamination and the remaining seven samples were included in the full analysis.

Results: The results from the MLST analysis showed that five samples had the same ST prediction between the two platforms. The remaining two samples were classified as novel STs by the 1928D platform, which was consistent with the Nanopore analysis, as these samples did not have any ST hit with full kmer-coverage. As for the cgMLST analysis, different kmer-sizes were used and the similarity to the Illumina result was calculated. A smaller kmer size decreased the allele prediction accuracy and the opposite was true for larger kmer sizes. The distances between samples were, however, different when comparing Illumina to Nanopore regardless of the kmer-size. This was mainly due to novel cgMLST alleles, which could be accurately detected in Illumina data only.

Conclusions: These results show a proof of concept that a kmer-based approach for MLST and cgMLST analysis of Nanopore sequenced *Staphylococcus aureus* is possible. However, a lot of effort needs to be directed towards improving the data quality in order to generate results accurate enough for the clinical setting.

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Abstract 395

The economic burden of *Clostridioides difficile* infection in patients with haematological malignancies: a case-control study

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Background: The burden of *Clostridioides (Clostridium) difficile* infection (CDI) is profound and patients with hematological malignancies are at high risk for developing the infection. Very few studies have assessed the economic burden of CDI in this specific population, whereby primarily hospital costs were analyzed. This study aims at describing all direct healthcare costs attributable to CDI (in-hospital and out-of-hospital) in patients suffering from hematological malignancies.

Materials/methods: A retrospective analysis was conducted based on databases of Truven Health Analytics®, part of the IBM Watson HealthTM business. Comprehensive data of hospital stays and services, out-of-hospital services and drug prescriptions of patients newly diagnosed with hematological cancer (acute myeloid leukemia [AML], acute lymphoblastic leukemia, Hodgkin's lymphoma and non-Hodgkin lymphoma [NHL]) between 01/2014 – 12/2017 were analyzed. Patients with CDI after cancer diagnosis (CDI+ or cases) were matched to patients without CDI (CDI- or controls). Matched cases and controls were compared to identify the CDI-attributable costs and changes in care in the 90 days following the CDI onset (study period).

Results: 622 CDI+ patients were matched with 11,111 controls. NHL and AML were the predominant underlying diseases in the CDI+ group accounting for 41.7% and 30.9% of cases, respectively. Overall, CDI increased costs of care by an average of US$57,159 per patient, an increase of 41.9%, mainly driven by in-hospital costs. Costs data are presented in Table 1.

Conclusions: Findings confirm that CDI treatment results in substantial costs in patients with hematological malignancies, highlighting the need for better treatment and prevention options for this specific patient population.

Table 1: Healthcare costs per patient

Healthcare costs, (over study period, 2017 US$)		CDI+	CDI-	Difference	p-value
In-hospital	Mean (95% CI)	151,208 (136,679 - 165,738)	98,552 (95,896 - 101,207)	52,657 (37,887 - 67,427)	$p=6.10^{-12}$
Out-of-hospital services	Mean (95% CI)	37,612 (34,083 - 41,141)	34,850 (33,691 - 36,010)	2,762 (-952 - 6,476)	p=0.15
Out-of-hospital drugs	Mean (95% CI)	4,704 (4,003 – 5,404)	2,963 (2,802 - 3,125)	1,740 (1,021 - 2,460)	$p=3.10^{-6}$
TOTAL	Mean (95% CI)	193,524 (178,527 - 208,521)	136,365 (133,390 - 139,340)	57,159 (41,870 - 72,448)	$p=6.10^{-12}$
	Median	146,745	89,117		
	Min -Max	0 – 2,004,094	0 - 1,706,303		

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Abstract 411

The first report of concurrent infections by two dengue serotypes among tribal population in central India

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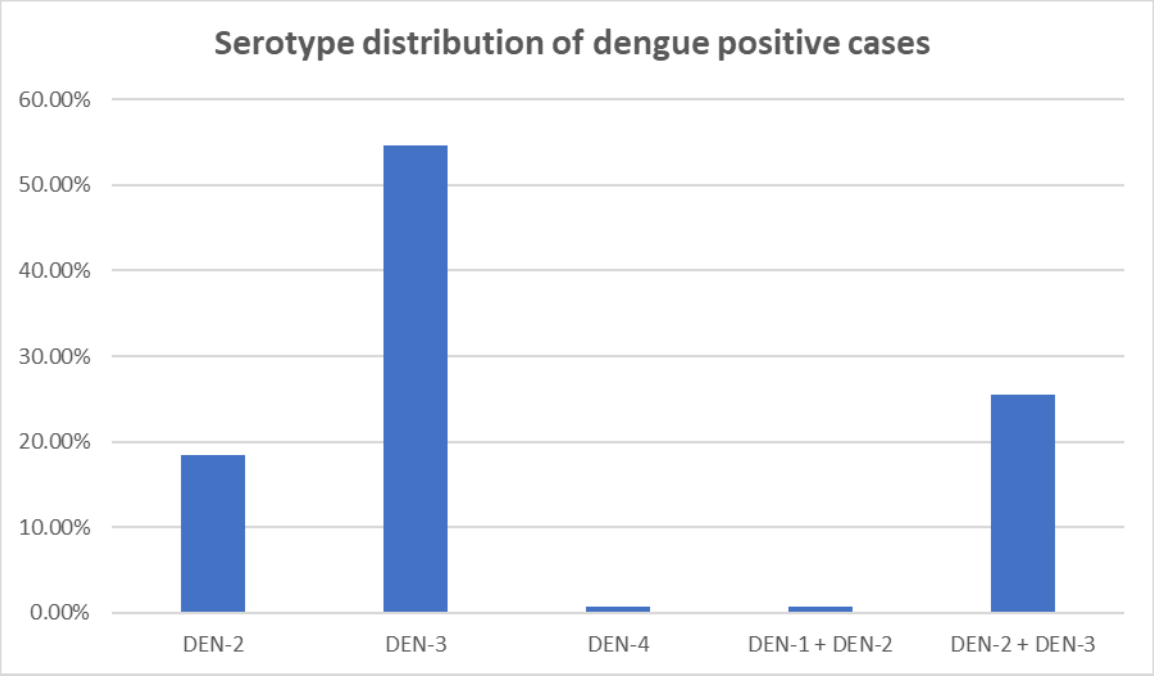
Background: Dengue is spreading to newer areas in the world, including India. Concurrent infection by multiple serotypes are documented in certain areas in India, but not in tribal areas. We investigated an outbreak occurred in a tribal area in central India, during months of August to September 2015. We report markedly high percentage of concurrent infections by 2 dengue serotypes first time among tribal population in India.

Materials/methods: Acute phase sera samples were collected from 746 patients and tested for NS1 ELISA and MAC-ELISA. NS1 positive samples were subjected to serotyping by real time RT- PCR.

Results: - of 746 samples tested, 167 (49.4%) were positive for NS1 ELISA while 171(50.6%) were for MAC-ELISA. Positive NS1 samples were tested for serotyping, all 4 serotypes were found to be circulating in the outbreak, with predomination of DEN-3 serotype. Moreover, concurrent infections by 2 serotypes were observed in 26.2% of cases.

Conclusions: Dengue outbreak in tribal villages of Sukma district in central India experienced all 4 serotypes and concurrent infections, where health authorities never perceived dengue as a major health concern. Thus this outbreak emphasizes on continuous active surveillance to monitor spread of dengue virus, especially in hard to reach areas, so that effective vector control programme could be implemented at the earliest to prevent outbreaks.



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Abstract 414

A descriptive study of tuberculosis hospital admissions in Ireland

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Background: Ireland is a low incidence tuberculosis country with 6.6 cases per 100,000 population in 2018. The last reform of TB services in Ireland was in 2003. It was recommended that most TB management should be delivered on an outpatient basis in general hospitals with a small number of beds allocated in 3 hospitals for inpatient management. This resulted in 3 hospitals (Cork University Hospital, University College Hospital Galway, St. James's Hospital, Dublin) being designated as TB centres. Evaluating resource utilisation by patients admitted to hospital with TB may provide insight into how TB service organization could be improved.

Materials/methods: The Hospital In-Patient Enquiry (HIPE) system is a computerized health information system designed to capture hospital activity data. It is the principal source of demographic and clinical data on inpatient discharges from public hospitals in Ireland. The National Quality Assurance and Improvement System (NQAIS) Clinical is an online interactive application that analyses hospitals' own HIPE data. The NQAIS Clinical was searched for all TB discharges between 01/01/2015-31/12/18. An estimate of the projected cost of respiratory TB admissions was calculated using the Healthcare Pricing Office Admitted Patient Price List 2019.

Results: 1185 discharges with TB as the principal diagnosis were identified. 802/1185 (68%) of admissions were emergencies and 383/1185 (32%) were elective. Most emergency admissions, 735/802 (92%), were discharged after an overnight stay of at least one night while the remainder 67/802 (8%) were same day discharges. In total, 16,005 bed-days were used by patients with a principal diagnosis of TB, an average of 4,001 bed-days per annum. This equates to an average of 12.8 bed-days per notified case of TB. The ten longest emergency admissions made up only 10/802 (1.2%) of admissions but 1,935/14,072.5 (13.8%) of emergency bed-days used. We estimate that between 67% (834/1248) and 74% (928/1248) of TB cases notified were admitted to hospital. We estimate that between 78% (653/839) and 87% (729/839) of respiratory TB cases notified were admitted to hospital. The projected cost of respiratory TB admissions for 2019 is €1,813,346-2,413,137.

Conclusions: There is a significant burden on the acute hospital inpatient service due to TB.

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Abstract 418

The INHALE trial: designing a prescribing algorithm to aid antibiotic choices for the FilmArray Pneumonia Panel Plus

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Background: The NIHR-funded INHALE Programme aims to improve antimicrobial stewardship through molecular diagnostics for HAP/VAP in ICUs. Its first phase selected the BioFire FilmArray Pneumonia Panel as the best-performing relevant test, and this is now deployed at point of care (POC) in 12 UK ICUs, with patients randomized to FilmArray-guided or Standard antimicrobials. The test seeks 34 organism and gene targets, providing results in 1.5h. The results' complexity, combined with rapid round-the-clock availability, prompted us to design an antimicrobial prescribing algorithm to support clinicians at the point of decision. To our knowledge, this is the first instance of prescribing advice being directly linked to a rapid PCR test.

Materials/methods: We designed the algorithm based on (i) organism and resistance gene targets detected alone or in combination, (ii) national resistance surveillance data and (iii) patient's allergy status. Narrow spectrum agents were preferred, and good antimicrobial stewardship encouraged. Site microbiologists, ICU pharmacists, and ICU clinicians were consulted and local adaptation allowed.

Results: Where single organisms are found the algorithm favours, e.g. temocillin *vs*. Enterobacterales, flucloxacillin vs. MSSA and co-amoxiclav vs. *Haemophilus influenzae*; discontinuation is advised if no organism is found and the patient lacks convincing evidence of infection; broader spectrum agents are favoured for combinations of organisms. Among 10 adult sites, 4 adopted the algorithm essentially unaltered and 2 with minor variation only. Common concerns were: unwillingness to adopt: (i) temocillin for Enterobacterales; (ii) ceftazidime vs. *Pseudomonas*; or (iii) cephalosporins for patients with mild β-lactam allergy. There was considerable debate apropos infection control implications of ICU-based (rather than laboratory-based) detection of carbapenemase producers. Substantial variation was needed at 2 paediatric ICUs, principally because temocillin lacks a paediatric licence.

Conclusions: Prescribing algorithms such as this will ensure that potential benefits of rapid syndromic tests are realised at POC. Whilst it was not possible to impose a single algorithm at all hospitals, core elements and principles were retained. An early audit of RCT results indicates that most test-arm treatments are being guided by the algorithm, as sought. The sites' willingness to adopt this approach illustrates the potential for a major shift to molecular-guided chemotherapy.

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Abstract 419

Is it cost effective to use a 2% chlorhexidine gluconate wipes bath to reduce primary bloodstream infection? A quasi-experimental study experience

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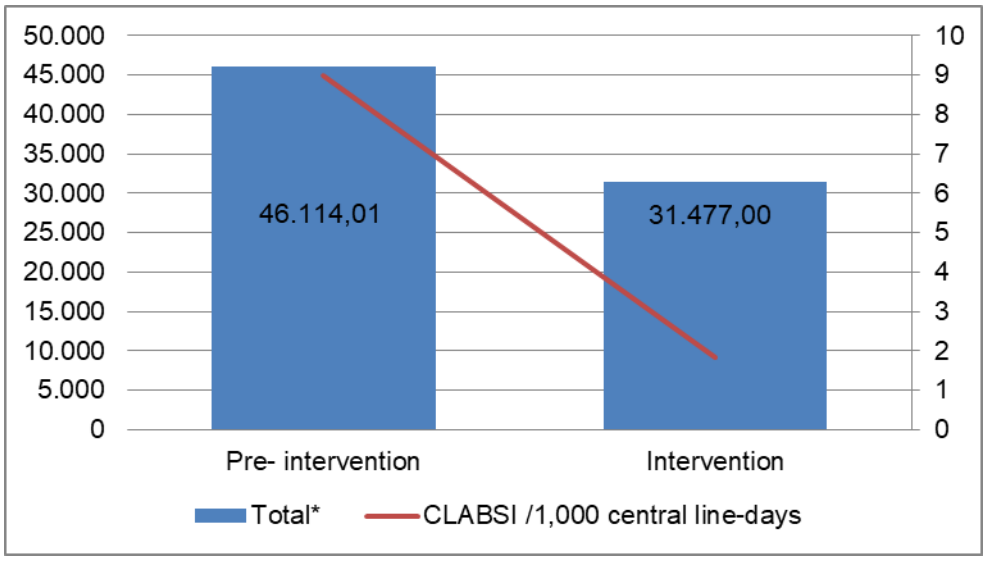
Background: Bathing with 2% chlorhexidine (CHG) wipes is an important measure regarding infection prevention in critically ill patients. At our ICU, central line-associated bloodstream infections rates (CLABSI) was higher than expected (9.05/1,000 central line-days) and as an additional measure were introduced a daily bathing with 2% CHG wipes. The aim of the study were to evaluate the impact of introducing the CHG wipes bath in CLABSI prevention and determine if such measure is cost-effective.

Materials/methods: Quasi-experimental study with pre-intervention period from July 2017 to May 2018, and intervention, June 2018 to April 2019. Were evaluated the CLABSI rate, the costs with guided antimicrobials for proven CLABSI, and CHG wipes. Antimicrobials (ATM) given empirically at the suspicion of the CLABSI were not evaluated.

Results: Were observed a reduction in CLABSI rates in the intervention period (9.05 to 1.35/1,000 central line-days; *P*= 0,01), mainly due to Kp-KPC BSI (P= 0,05) decrease and a substantial cost reduction with guided antimicrobials (US$ 45,278.93 to US$ 1,799.82 in intervention period). The average monthly consumption of CHG wipes in the ICU were 190 towels/month, with unit value of US$ 14.20, generating a monthly cost of US$ 2,698.00. The total costs (guided ATM plus CHG wipes) are shown on TABLE 1.

Conclusions: The introduction of daily bath with 2% CHG wipes at our ICU was effective in CLABSI reduction, being a good cost-effective measure, saving 30% of total costs.

TABLE 1 - Pre-intervention & Intervention period, Costs (US$) x CLABSI rates



*total costs = CHG wipes plus guided ATM

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Abstract 425

Persistence of high-risk clones of carbapenem-resistant *Klebsiella pneumoniae* in a tertiary hospital in Valencia, Spain

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Background: High-risk clones of *Klebsiella pneumoniae* have contributed to the spread of mobile genetic elements among *Enterobacteriaceae*.The aim of this study is to characterize carbapenem-resistant *K.pneumoniae* strains and to determine clonal relationship among them.

Materials/methods: Bacterial identification was performed by mass spectrometry,whereas antimicrobial susceptibility testing was obtained using the MicroScan Walkaway system(Beckman Coulter). Carbapenem-resistant strains were selected. Phenotypic methods for the detection of carbapenemase production included beta-carbatest(Biorad) and disk-synergy test(Rosco Diagnostica). Isothermal amplification with Eazyplex Superbug system(Amplex) was performed to genotypically determine carbapenemase genes.Clonal studies with pulse-field gel electrophoresis included all the strains that shared similar features. Strains belonging to predominant clones were sequenced using next-generation sequencing(NGS).Data from NGS provided information regarding sequence-type, plasmid-typing and resistance genes.

Results: 130 strains were submitted to NGS.Data regarding clones, resistance genes, STs and plasmid replicons is shown in the table below:

Nº of Strains	Years	CLones	MLST	Carbapenemase	CTX-M	DHA-1	SHV	Others	Replicons
22	2016-2017	A	ST101	OXA-48 NDM-1 OXA-48+NDM-1	CTX-M-(1,3,5)	DHA-1	SHV-11	ArmA mphA TetR Qnr Dfr	IncL/M IncQ IncFIB IncFII IncR
37	2015-2016-2017-2018	B1	ST307	OXA-48	CTX-M-15	-	SHV-28 SHV-106	TetR Qnr Dfr	IncL/M IncFI
22	2015-2016-2017-2018	B2	ST307	OXA-48	CTX-M-15	-	SHV-28 SHV-106	TetR Qnr Dfr	IncL/M IncN IncFI
22	2015-2016-2017-2018	C1	ST11	OXA-48	CTX-M-(1,3,5)	DHA-1	SHV-11	ArmA mphA TetR Qnr Dfr	IncL/M IncQ IncFIB IncFII IncR
27	2015-2016-2017-2018	C2	ST11	OXA-48	CTX-M-(1,3,5)	DHA-1	SHV-11	ArmA mphA TetR Qnr Dfr	IncL/M IncQ IncFIB IncFII IncR

Conclusions: During four years, five different clones of *K.pneumoniae*, belonging to three different sequence-types have been circulating in the same hospital. Interestingly, there are differences between the carbapenemase genes detected in 2015 and those detected in 2018, even in the same sequence-type, suggesting that the same clone acts as a recipient and as a donor for resistance determinants, depending on the environmental situation they are found in each time. Non beta-lactam antibiotics are also enormously affected by resistance to carbapenems, as resistance genes to different antimicrobials are usually found in the same plasmid.

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Abstract 428

Doramapimod treatment inhibits granuloma formation and improves antibiotic activity in *Mycobacterium tuberculosis*-infected mice

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Background: *Mycobacterium tuberculosis* (*Mtb*), the causative agent of tuberculosis (TB), is the major killer among infectious agents which led to 1.5 million deaths in 2018. Treatment of TB requires combinations of antibiotics for several months, a strategy which becomes increasingly complicated in times of rising numbers of multi-drug resistant *Mtb*-isolates. Adjunctive host directed therapy (HDT) might improve and accelerate treatment by modifying host pathways targeted by *Mtb.* We have recently shown that genetic or chemical inhibition of p38 mitogen-activated protein kinase (MAPK) results in abrogation of *Mtb*-induced host cell death and decreased release of inflammatory alarmins such as High-Mobility-Group-Protein B1 (HMGB1) *ex vivo.*

Materials/methods: To evaluate the potential of p38 MAPK inhibition as an adjuvant treatment for TB and to determine the risk for exacerbation of the disease during monotherapy, we analyzed the outcome of experimental TB under p38 MAPK inhibition and antibiotic treatment during acute and chronic infection of C57BL/6 mice.

Results: We show that treatment of *Mtb*-infected C57BL/6 mice with doramapimod, a p38 MAP-kinase inhibitor, results in reduced inflammation, granuloma formation and lung pathology. Moreover, doramapimod, together with a standard antibiotic treatment significantly reduced lung and spleen mycobacterial loads compared to antibiotic treatment alone.

Conclusions: Our data suggest the opportunity to repurpose p38 MAPK inhibitors for adjunct host directed therapies. We also provide first data on safety of p38 MAPK inhibition which is of relevance for future application of these substances in inflammatory diseases and concomitant TB.

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Abstract 429

Late-onset *Pneumocystis jirovecii* pneumonia in renal transplant recipients

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Background: The risk of *Pneumocystis jirovecii* pneumonia (PJP) in solid organ transplant patients is 5-15%, with highest risk at 6-12 months post-transplantation. There has been an increase in the number of cases seen much later post-transplant. We describe 7 patients presenting with PJP over 6 months post renal transplant during the period March 2018 thru April 2019. All these patients had their renal transplant and follow-up care at our institution.

Materials/methods: Renal transplant recipients (RTR) presenting with PJP in 2018 and 2019 were retrospectively studied. Definitive diagnosis of PJP was defined as positive PJP stain from BAL. Patients with positive PJP PCR, elevated serum (1→3) β-D-glucan (BDG), elevated serum LDH were also included as possible diagnosis of PJP. Period from renal transplant to development of PJP, clinical presentation and severity of disease, immunosuppression and level of immunosuppressant, presence of rejection, treatment and clinical outcomes were included.

Results: All but 1 patient developed PJP at least two years after their kidney transplant. None of the patients was receiving PJP prophylaxis at the time of diagnosis. Mean period between transplant and infection was 4024 days. Five patients presented with atypical pneumonia and 2 had hypoxic respiratory failure. Four patients had definitive diagnosis of PJP and 3 had possible diagnosis of PJP. Five patients were cured and 2 patients died despite treatment and modification of immunosuppression; these patients also had the highest levels of LDH.

Figure 1: PJP infections in kidney transplant recipients

Age	44	50	70	56	62	45	52
Sex	Male	Female	Female	Male	Female	Male	Male
Comorbidities	Polycystic kidney disease	HTN, DM, Gout, ESRD	DM, HTN, CAD, OSA	HTN	HTN, DM	HTN, ESRD, OSA, atrial fibrillation	HTN
Year of transplant	1996	2001	2003	2008	2012	2015	2018
Type of transplant	DDRT	DDRT	DDRT	DDRT	DDRT	DDRT	DDRT
Maintenance regimen	data not available	MMF 180 BID prednisone 5mg OD Tacrolimus 2mg BID	MMF 1,000mg 4Cap BID prednisone 20mg OD Tacrolimus 7mg BID	MMF 500mg BID, prednisone 5mg OD	MMF 750 mg BID prednisone 5mg OD tacrolimus 1.5mg BID	MMF 360 mg TID prednisone 10mg Tacrolimus 6mg BID	MMF 360 mg TID prednisone 5 mg OD, Tacrolimus 8mg BID
Tacrolimus level (5-15ng/mL)	data not available	26.3	8.6	<2.0	15.6	22.7	9.1
Rejection (Y/N)	Y	N	Y	allograft dysfunction	Chronic Active Ab-mediated rejection	delayed graft function	N
Date of rejection(s)	Apr 2004	N/A	March 2017	August 2017	February 2019	6/1/2018	N/A
Treatment of rejection	data not available	N/A	IVIG after Pheresis	Tacrolimus level decreased then discontinued, hemodialysis, plan for repeat transplant	Tacrolimus increased, intermittent hemodialysis, plan for repeat transplant	Tacrolmius increased	N/A
Period between transplant and development of PJP infection (days)	8011	6936	5414	4582	2137	853	235
Clinical presentation	Atypical pneumonia	Atypical pneumonia	Atypical pneumonia	Atypical pneumonia	Atypical pneumonia	Hypoxic respiratory failure	Hypoxic resp failure
PaO2	58.5	71.6	43.2	78	47.1	66.1	82.4
A-a gradient	95.6	103.8	650.1	600.9	14530.00%	610.1	33.8
Need for adjustment of steroids due to severity of PJP (Y/N)	Y (Hydrocortisone 100 TID)	Y (Hydrocortisone 40 BID)	Y (Hydrocortisone 25mg IV q8)	Y (Prednisone 40 BID)	Y (Prednisone 40 BID)	Y (Prednisone 40 BID)	Y (Prednisone 40 BID)
Tests	PJP BAL stain indeterminate elevated β-D-glucan PCR not done elevated LDH	PJP BAL stain negative elevated β-D-glucan positive PCR BAL elevated LDH	PJP BAL stain negative elevated β-D-glucan PCR BAL positive normal LDH	PJP stain positive BAL elevated β-D-glucan PCR not done elevated LDH	PJP BAL stain positive elevated β-D-glucan PCR not done elevated LDH	PJP BAL stain positive elevated β-D-glucan PCR BAL positive elevated LDH	PJP BAL stain positive elevated β-D-glucan PCR BAL positive elevated LDH
LDH (normal value: 140-271 Units/Liter)	320 (05/08/18)	372 (4/21/19)	207 (6/11/18)	363 (01/21/18)	307 (5/31/18)	415 (3/24/18)	759 (4/17/19)
Treatment	TMP-SMX	Atovaquone, Primaquine/Clindamycin	TMP-SMX	TMP-SMX, Prednisone tapered	TMP-SMX x 8 days Primaquine 30mg/day Clindamycin 450mg TID x 13 days	TMP-SMX (3/25-4/15), Avicaz, Micafungin	TMP-SMX(3/9-3/10) Clindamycin and primaquine (3/10-3/17) due to AKI and hyperkalemia switched back to IV TMP-SMX from 3/17-4/24.
Duration of Treatment	21 days	42 days	21 days	21days	21 days	21 days	44 days
Modification of immunosuppression	MMF stopped during PJP treatment, prednisone stopped	Tacrolimus 2mg q12 and prednisone 5mg daily	continue prednisone 30mg Increased tacrolimus 4mg BID	only prednisone taper continued	prednisone 5mg MMF decreased to 500mg BID Increased Tacrolimus to 2/1 BID	MMF and tacrolimus held, p rednisone continued	MMF 360 mg BID, tacrolimus dose decreased
Date Admitted	May 2018	Apr 2018	Jun 2018	May 2018	Jun 2018	Mar 2018	Mar 2019
Subsequent Prophylaxis	none	TMP-SMX 1DS OD	TMP-SMX 1DS OD x 6mos	none	none	N/A	N/A
Outcome	resolved	resolved	resolved	resolved	resolved	deceased	deceased

Conclusions: *P. jirovecii* should be considered as a cause of atypical pneumonia and/or hypoxic respiratory failure, in RTR receiving immunosuppression who are no longer on PJP prophylaxis. Nosocomial outbreaks of PJP infection should be considered in RTR who present with PJP late into their transplant.

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Abstract 430

Multidrug resistant Gram-negative infections among critically ill patients: analysis of baseline characteristics and factors associated with mortality

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Background: Bacterial infections are a frequent cause of hospitalization and a leading cause of death particularly with the emergence of antibiotics resistance. The emergence of Carbapenem resistance among gram negative bacteria (GNB) is one of the evolving alerts as its use is considered the last resort of treatment. Therefore, this urged studying the risk factors for development of multi-drug resistant (MDR) GNB, identify the clinical outcomes and factors associated with mortality especially among critically ill patients who are expected to have the worst outcomes.

Materials/methods: This is a retrospective observational study of critically ill patients who had an infection with Carbapenem-resistant Enterobacteriaceae (CRE), or MDR *Pseudomonas aeruginosa*, or MDR *Acinetobacter spp.* between May 2016-Nov 2018. Baseline demographics, co-morbidities and clinical outcomes were collected, and were evaluated for association with 28 days mortality. Approval of the research was obtained from the Institutional Review Board (IRB) before commencement of the study.

Results: A total of 255 patients with MDR Gram-negative cultures were screened, 77 patients met the inclusion criteria. *Pseudomonas aeruginosa* was the most common index organism (53% of patients), followed by *Acinetobacter spp*. and CRE, respectively. 28 days mortality was (59.7%). Non survivors were significantly older (mean age 64 vs 44 years, P= 0.0001), had significantly worse disease severity scores on ICU admission, higher incidence of chronic kidney disease (CKD) (43% vs 16%, P= 0.010), and required more continuous renal replacement therapy (CRRT) (54% vs 13% P= 0.0001), longer hospital length of stay prior to infection (median 34 vs 13 days, P= 0.018), required longer inotropic and vasopressors support (median 19 vs 8 days, P = 0.0001). In multivariate logistic regression the following factors were significantly associated with mortality; requirement of inotropic support post infection [OR 10.01 (95% CI 1.55-64.77); P= 0.015], age [OR 1.05 (95% CI 1.0-1.1); P=0.01], and APACHE IV score on ICU admission [OR 1.03 (95% CI 1.0- 1.06); P= 0.04].

Conclusions: MDR Gram-negative infection is associated with significant in-hospital mortality among critically ill patients. Old age, high APACHE IV score, and higher hemodynamic support are associated with higher mortality.

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Abstract 433

Risk factors of environmental dissemination of different multidrug-resistant organisms

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Background: Substantial scientific evidence has accumulated that contamination of environmental surfaces in hospitals plays an important role in the transmission of Multi-Drug-Resistant-Organisms (MDRO). In this work, we propose to assess the overall risk of environmental dissemination of different MDRO, by evaluating the contamination of the environment, taking into consideration the individual risk factors together with the microbiological aspect of resistance.

Materials/methods: We conducted a prospective cohort study form May 2018 to May 2019. We included 91 patients admitted to Avicenne Hospital, older than 18, carriers of MDRO (BLSE-PE, CPE, VRE); known at admission or detected in the first 48 hours. Rectal and environmental sampling were realized. For each patient, we did a quantification of MDRO in stool, a qualitative evaluation of presence of MDRO in 4 different environmental sites and collected data including demographic characteristics, ward and duration of hospitalization, antibiotic administration, Charlson's score of comorbidities, Katz's score of dependence, nursing procedures, urinary/fecal incontinency, MDRO species and mechanisms of resistance.

Results: Fifty-three (58%) patients were admitted in a medical ward, 11 (12%) in surgery and 27 (30%) in ICU. MDRO were *Escherichia coli* (52%), *Klebsiella pneumoniae* (36%), *Enterobacter cloacae* (4%) and *Enterococcus faecium* (8%). Resistance mechanisms of detected MDRO were ESBL (41%), OXA48 (51%) and VanA (8%). Contamination of at least one environmental site was observed for only 14 (15%) patients: 36% (n=5) ESBL-PE, 36% (n=5) CPE and 28% (n=4) VRE. We didn't find any statistically significant difference in age, sex, wards of admission, duration of hospitalization, Charlson's score, Katz's score, antibiotic consumption, recent stay abroad and interestingly relative abundance of MDRO in stool, between the group of patients having contaminated their environment (15%) and those who have not (85%). However, only VRE, among the other MDRO, appeared to colonize significantly more the patients who contaminated their environment (p=0.009).

Conclusions: Our preliminary study shows that only VRE colonized/infected patients seemed to be associated with a higher risk of spreading in the environment. Although this result needs to be confirmed on a larger scale, it raises questions about our national policies for contact isolation.

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Abstract 437

Dynamic monitoring of sTREM-1 and other biomarkers in biliary tract infection

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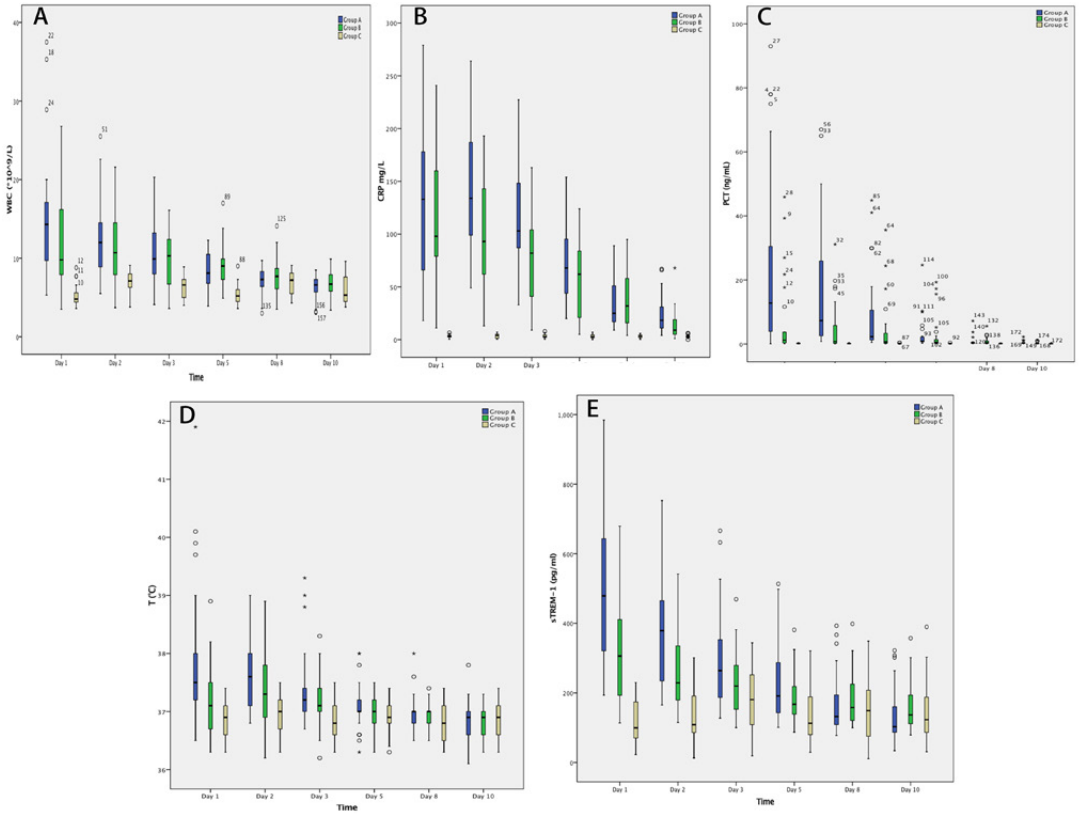
Background: Sepsis is a common complication of biliary tract infection (BTI), which is associated with high mortality. We explored the significance of white blood cell (WBC), C-reactive protein (CRP), procalcitonin (PCT), soluble triggering receptor expressed on myeloid cells 1 (sTREM-1) and temperature (T) alone or combined together in early identification of BTI with or without sepsis and the monitor of treatment effect.

Materials/methods: 65 cases with BTI and 76 control cases were divided into three groups: Group A (BTI patients with sepsis), Group B (BTI patients without sepsis) and Group C (individuals without BTI or other infection). We dynamically measured the levels of WBC, CRP, PCT, sTREM-1 and temperature of all study subjects. Comparisons between groups were made using Non-parametric test. Receiver operating characteristic (ROC) curves were established to evaluate the diagnostic value for discriminating among three groups above. The cutoff values, area under curves (AUC) with corresponding 95% confidence intervals (CI), and sensitivity/specificity at optimal cut-off were calculated. Spearman rank correlation analysis was used to explore correlations between sTREM-1 and WBC in three groups.

Results: CRP had the highest AUC to identify BTI and sepsis from healthy controls (AUC = 1; sensitivity 100%; specificity 100%). Among various single indexes, PCT performed best (AUC = 0.785; sensitivity 75.8%; specificity 72.2%) to distinguish sepsis in patients with BTI. While combined multi-biomarkers didn't perform better. From day 1 to day 5 of hospitalization, the levels of sTREM-1 in Group A were highest ($P<0.05$); on day 8, sTREM-1 levels in Group A and B declined back to normal. Both in Group A and B, sTREM-1 levels declined fast between day 1 and day 2 ($P<0.05$). The results of dynamic monitoring of WBC, CRP, PCR, T and sTREM-1 in three groups were shown in Figure 1.

Conclusions: CRP is the best biomarker to suggest infection.PCT alone is well used for diagnosing BTI with sepsis, meanwhile sTREM-1 and temperature should be taken into account. sTREM-1 has great value to monitor patients' response to antimicrobial therapy and biliary drainage. The correlation between WBC and sTREM-1 was not very strong when diagnosing sepsis and observing curative effect.



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Abstract 442

Antimicrobial resistance and pathogenicity of Corynebacterium striatum clinical isolates collected from three tertiary hospitals in China

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Background: In recent years, more and more reports regarding multi-drug resistance and potential pathogenicity of *Corynebacterium striatum* were published, which may pose a knotty issue for clinicians. The pathogenicity potential of *C.striatum* strains isolated from different origins need to be further investigated.

Materials/methods: *C. striatum* clinical strains were isolated and identified with VITEK-2 ANC card, MALDI-TOF microTyper and 16S rRNA sequencing technique. Broth microdilution method was used to detect the antibiotic susceptibility profiles of 420 *C. striatum* clinical isolates, and PFGE method was used to discriminate different clones. Furthermore, in vitro adherence assay and mouse toxicity assay were performed to assess the pathogenicity of the strains with different genotypes.

Results: 420 *C. striatum* isolates were all sensitive to vancomycin, linezolid and daptomycin. Based on antibiotic resistance results, 420 strains were classified into 19 resistance patterns, when R1, R2 and R3 patterns accounted for 45.2%(190/420), 20.2%(85/420) and 22.4%(94/420), which were all multi-drug resistant patterns. PFGE typing results showed that 107 *C. striatum* strains were classified into 52 types(T01-T52), when 4 epidemic clones(T36, T28, T32, T14) accounted for 14.02%(15/107), 11.21%(12/107) , 5.61%(6/107) and 3.73%(4/107), respectively. All of these 4 clones belonged to resistance patterns R1, R2 and R3. Among 27 *C. striatum* strains, 92.6%(25/27) strains showed moderate to strong in vitro adherence abilities, while only 7.4%(2/27) strains showed weak adherence ability on polystyrene surfaces.. Furthermore, mouse lethality of different strains differed greatly, when non-dominant clone(Strain NMGYC339, T24) showed the strongest mouse lethality(90.0%).

Conclusions: The majority of the *C. striatum* clinical isolates tested in this study were multi-drug resistant, except vancomycin, linezolid and daptomycin. Most of the *C. striatum* strains showed moderate to strong adherence abilities and varied greatly among different hospitals. The *C. striatum* strains belonging to specific genotyes showed significant lethality in vivo, and the potential pathogenicity of *C. striatum* should be paid more attention to.

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Abstract 443

Prevalence and antimicrobial susceptibility of Ureaplasma species and Mycoplasma hominis in female patients in Korea: increasing trend of pristinamycin-resistant isolates

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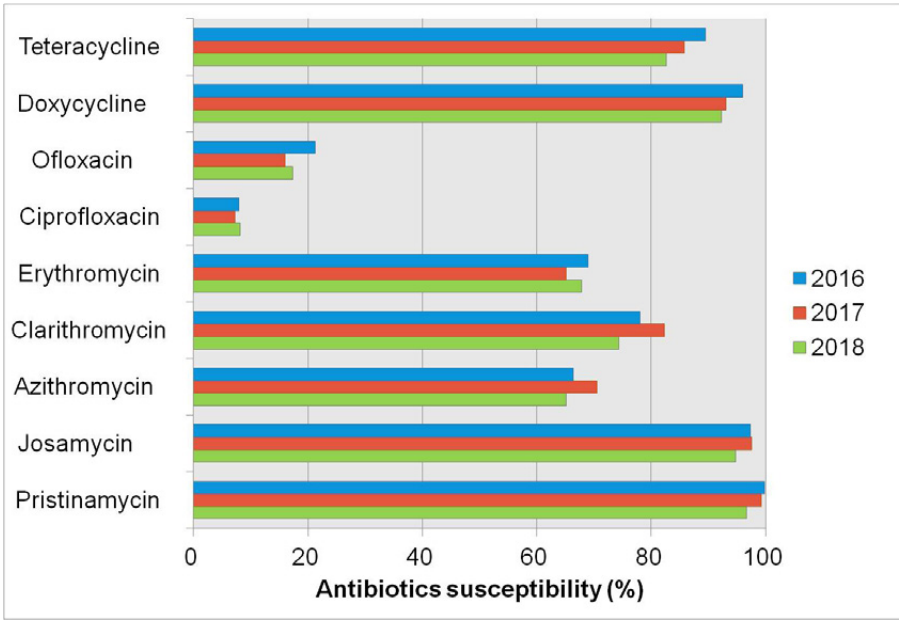
Background: *Ureaplasma* species and *Mycoplasma hominis*, commonly found in the lower urogenital tract, have been associated with various urogenital infections. Tetracycline and macrolide antibiotics are available for the treatment of urogenital tract infections caused by genital mycoplasmas. However, an increase in the prevalence of antibiotic-resistant mycoplasmas has been reported worldwide. Therefore, this study aimed to estimate the prevalence and antimicrobial susceptibility trend of genital mycoplasmas in female patients and to evaluate risk factors for acquisition of pristinamycin-resistant mycoplasma.

Materials/methods: Endocervical swabs from 4,035 specimens obtained from March 2016 to December 2018 were analyzed using Mycoplasma IST2 Kits. Since pristinamycin and josamycin are not available in Korea, we performed an age- and date-matched case-control study to evaluate the risk factors for acquisition of pristinamycin-resistant isolates.

Results: A total of 1,589 (37.4%) cases of genital mycoplasmas were identified, which included 1,243 (78.2%), 49 (3.1%), and 279 (18.7%) cases of *Ureaplasma* species, *Mycoplasma hominis*, and both respectively. The antibiotics susceptibility rate decreased over the years for priastinamycin (99.8%, 99.3% and 96.7% for 2016, 2017, and 2018, respectively, p<0.001), josamycin (97.4%, 97.6%, and 94.8%, p<0.001), tetracycline (89.5%, 85.8%, and 82.7%, p=0.008) and doxycycline (96.0%, 93.1%, and 92.3%, p=0.061). In the multivariate analysis, coinfection with *Candida* species was an independent risk factor for the acquisition of pristinamycin-resistant isolates (Odds ratio 6.35, 95% confidence interval, 1.36 to 29.76, p=0.019).

Conclusions: The antibiotic-resistant genital mycoplasmas have been gradually increasing every year. Nationwide surveillance, proper antibiotics stewardship, and culture-based treatment strategy are needed to control this upcoming threat.



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Abstract 445

Immunisation and multiple sclerosis: recommendations from the French Multiple Sclerosis Society

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Abstract third-party references: on behalf SFSEP and France4MS

Background: Vaccines have been suspected in the past to trigger Multiple Sclerosis (MS) or MS exacerbations. Other concerns arose more recently, with the extension of the immunoactive treatment arsenal, about an increased risk of infections or a decreased effectiveness of immunization in immunosuppressed patients. The objective of this work is to establish recommendations on immunization and multiple sclerosis.

Materials/methods: The French Group for Recommendations in Multiple Sclerosis (France4MS) did a systematic review of articles from PubMed and universities databases (January 1975 through June 2018). The RAND/UCLA appropriateness method, which has been developed to synthesize the scientific literature and expert opinions on health care topics, was used for reaching a formal agreement. Twenty-four MS experts worked on the full-text review and a group of 110 multidisciplinary health care specialists validated the final evaluation of summarized evidences.

Results: Neurologists should double check vaccination status as soon as possible after MS diagnosis and before the disease-modifying treatment (DMT) introduction. The French vaccines calendar should be applied to MS patients and they should be advised to receive seasonal influenza vaccine. If possible, serological status, including A, B, C hepatitis, measles, mumps, pertussis, rubella, small pox, varicella-zoster should be checked before starting a DMT. In case of treatment-induced immunosuppression, MS patients should be informed about infections risks and vaccine standards from the French High council of Health should be applied. Live attenuated vaccines are contra-indicated in MS patients currently or recently treated with immunosuppressive drugs, including corticosteroids; other vaccines can be proposed whatever the treatment, but their effectiveness may be partly reduced with some drugs.

Conclusions: Physicians and patients should be aware of the updated recommendations for immunizations and MS. Practice guidelines will be delivered by the French MS Society (SFSEP) for the medical and patients communities.

On behalf the SFSEP and the FRANCE4MS group

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Abstract 446

Haemophagocytic lymphohistiocytosis in human immunodeficiency virus: a systematic review of literature

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Background: Hemophagocytic lymphohistiocytosis (HLH) is a hyper-immune condition secondary to malignancy, infection or auto-immune conditions. HLH in patients with human immunodeficiency virus infection (HIV) can be either be due to a co-existent malignancy/infection or due to uncontrolled replication of HIV itself. The aim of this systematic review (SR) was to delineate the number of reported cases of HLH in HIV, their possible triggering factors, treatment and outcome.

Materials/methods: Search strategy: We conducted a comprehensive search of English medical literature via the Medline / PubMed database using different synonyms of „HIV" AND „HLH". The review was registered under PROSPERO CRD42018099987. Study selection: The titles and abstracts of 185 articles between January 1986 and April 2018 were screened for inclusion. The reasons for exclusion were- articles not in English (19), absence of either HIV or HLH (48), non-case studies (17), non-availability of full articles (10) and unfulfillment of HLH 2004 diagnostic criteria (50). A total of 41 articles with 52 patients were included in the analysis.

Results: Of the 52 patients, 42 (80.8%) were male. The mean age was 38.2 +/- 14.2 years. The median CD4 count at the time of diagnosis of HIV with HLH was 41/ml (IQR: 8-94/ml). HLH was associated with malignancy in 17 patients [Lymphoma (n=11), Kaposi sarcoma (n=6)] while associated infection was found in 25 patients [Fungal (Histoplasmosis-15, penicilliosis-1, invasive candidiasis-1, invasive aspergillosis-1), Parasitic (leishmaniasis-1, toxoplasmosis-2), Bacterial (bartonellosis-1), Viral (cytomegalovirus-2, Epstein-barr virus-1) and tuberculosis (n=1)]. Presence of either malignancy (p=0.051) or opportunistic infection (p=0.69) was not associated with increased chances of death by uni-variate analysis. A total of 26 patients were treated with steroids while etoposide was used in only four patients. Death was reported in 21 patients. Intake of steroids as a treatment of HLH was associated with more chances of death (p=0.048).

Conclusions: Malignancy and opportunistic infections are important triggers for HLH in HIV. Acute HIV and IRIS by itself can act as a trigger for HLH. Evidence on the use of steroids as a treatment of HLH is not convincing.

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Abstract 453

Value of the CXCL13 ELISA and a CXCL13 lateral flow immunoassay in the diagnosis of Lyme neuroborreliosis

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Background: Diagnosis of Lyme neuroborreliosis (LNB) can be challenging in an early disease stage especially if *Borrelia*-specific intrathecal antibodies are still negative. This study aimed to assess the performance of CXCL13 ELISA and the ReaScan® CXCL13 lateral flow immunoassay (LFA) in the diagnosis of Lyme neuroborreliosis.

Materials/methods: In this dual-center case-control study 90 CSF samples were retrospectively analysed by the Euroimmun CXCL13 ELISA and the ReaScan® CXCL13 LFA. Overall, 34 CSF samples from patients with definite LNB, 10 samples from patients with possible LNB and 46 samples from patients with other predominantly inflammatory CNS diseases (non-LNB control group) were included. Patients with definite or possible LNB were classified according to the EFNS guidelines.

Results: CXCL13 ELISA was significantly elevated in all 34 patients with definite LNB (median 1409 pg/mL) compared to 46 control patients (median 20.7 pg/mL, $p < 0.0001$). In the control group patients with possible LNB were not included. For a cut-off of 78.6 pg/mL a sensitivity of 100% and a specificity of 84.8 % (AUC 0.93) was calculated. The ReaScan® CXCL13 LFA was significantly elevated in 31 patients with definite LNB (median 223.5 arbitrary values) compared to 46 control patients (median 0 arbitrary units, $p<0.0001$). A cut-off of 22.5 arbitrary values (AV) had a sensitivity of 91.2 % and a specificity of 93.5 % (AUC 0.94). Overall, the agreement of the LFA with the ELISA was 90%; 98% for ELISA values <250 pg/mL; 22 % for ELISA values from 250-500 pg/mL and 96 % for ELISA values > 500 pg/mL, respectively. The correlation between the CXCL13 ELISA and the LFA was r = 0.89 and $p<0.0001$.

Conclusions: CXCL13 ELISA and the ReaScan® CXCL13 LFA in CSF are reliable diagnostic tools for the identification of patients with definite LNB.

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Abstract 454

Combined effects of low incubation temperature, minimal growth medium and low hydrodynamics optimise *Acinetobacter baumannii* biofilm formation

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Background: Biofilm formation is an important virulence factor expressed by microorganisms. It shields and protects microbial cells from host immune responses, antibiotics and other anti-infectives. It is hypothesized that microbial cells demonstrate enhanced biofilm formation in nutrient limiting environment. The aim of this study was to investigate if limiting environmental conditions act synergistically to promote biofilm formation in multidrug resistance *Acinetobacter baumannii.*

Materials/methods: Biofilm was cultivated using quantitative microtiter plate method. The combined effects of temperature, medium and shear force were determined by measuring adherence (OD_{570} nm) following incubation at 26 ^{O}C, 30 ^{O}C and 37 ^{O}C for 24 hr. when biofilm was cultivated with minimal nutrient medium (EAOB) and nutrient-rich medium (TSB) without or with agitation at 50 rpm. Antibiotic susceptibility test of selected antimicrobials were tested with Kirby-Bauer disc method. $P < 0.05$ was considered statistically significant for all the tests.

Results: A noticeable variation in adherence was observed among the isolates cultured with both media. Biofilm forming capacity of the isolates range from 0.09 to 0.33. Majority of the isolates had their relative biofilm-forming capacity significantly higher than the positive control, *Acinetobacter baumannii* ATCC 19606. The biofilm biomass during growth in nutrient-rich medium (TSB) without shaking was significantly different ($p < 0.05$) among the three temperatures tested compared with when cultured in EAOB without shaking. A positive correlation was observed between biofilm formation and resistance to imipenem ($r = 0.2889$; $p = 0.05$). There is a statistically significant difference among the median of the three source groups ($p < 0.05$) compared with the median between the source groups.

Conclusions: This observation extended further the view that *A. baumannii* biofilm formation is enhanced when nutrient-poor medium was used at room temperature (26 °C) with or without agitation compared to growth at 37 ^{O}C.

Table:

Table 1. Biofilm formation by *Acinetobacter baumannii* isolates (n= 71) following incubation at 26 ^{O}C, 30 ^{O}C and 31 ^{O}C under dynamic or static conditions in nutrient-rich (TSB) or nutrient-poor (EAOB) media respectively

	Non-Adherent		Weak Adherent		Moderate Adherent		Strong Adherent		Total	
	Num (%)	Average OD ± SD	Num (%)	Average OD ± SD	Num (%)	Average OD ± SD	Num (%)	Average OD ± SD	Num (%)	Average OD ± SD
26°C EAOB dynamic	0	0	8 (11.3)	0.09 ± 0.01	38 (53.5)	0.17 ± 0.02	25 (35.2)	0.25 ± 0.02	71 (100)	0.19±0.02
26°C EAOB static	0	0	1 (1.4)	0.09 ± 0.01	31 (43.7)	0.18 ± 0.02	39 (54.92)	0.25 ± 0.01	71 (100)	0.22 ±0.01
26°C TSB dynamic	0	0	0	0	65 (91.5)	0.25 ± 0.01	6 (8.5)	0.30 ± 0.01	71 (100)	0.26 ±0.01
26°C TSB static	0	0	0	0	48 (67.6)	0.27 ± 0.01	23 (32.4)	0.29 ± 0.01	71 (100)	0.28 ±0.01
30°C EAOB dynamic	0	0	10 (14.1)	0.10 ± 0.01	53 (74.6)	0.19 ± 0.02	8 (11.3)	0.28 ± 0.02	71 (100)	0.18±0.02
30°C EAOB static			3 (4.23)	0.11 ± 0.01	28 (39.4)	0.18 ± 0.02	40 (56.3)	0.25 ± 0.01	71 (100)	0.22 ±0.02
30°C TSB dynamic	0	0	2 (2.8)	0.10 ± 0.02	69 (97.2)	0.25 ± 0.02	0	0	71 (100)	0.24 ±0.02
30°C TSB static	0	0	26 (36.6)	0.22 ± 0.02	45 (63.4)	0.26 ± 0.01	0	0	71 (100)	0.24 ±0.01
37°C EAOB dynamic	3 (4.2)	0.10 ± 0.00	26 (36.6)	0.16 ± 0.01	42 (59.27)	0.25 ± 0.02	0	0	71 (100)	0.21 ±0.01
37°C EAOB static	0	0	11 (15.5)	0.15 ± 0.01	54 (76.1)	0.23 ± 0.01	4 (5.6)	0.30 ± 0.01	71 (100)	0.21 ±0.02
37°C TSB dynamic	2 (2.8)	0.10 ± 0.02	23 (32.4)	0.20 ± 0.01	46 (64.8)	0.26 ± 0.01	0	0	71 (100)	0.23 ±0.02
37 C TSB static	3 (4.2)	0.10 ± 0.01	56 (78.9)	0.21 ± 0.02	12 (16.9)	0.28 ± 0.01	0	0	71 (100)	0.22 ±0.02

Biofilm formation assay data is the mean of three independent experiments carried out in triplicate ± SD after growth in minimal (EAOB) and rich (TSB) media at 26 °C, 30 ° C, and 37 °C under dynamic

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Abstract 456

Insights of colistin resistance and flexible transmission of mcr-1

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Background: Colistin, a cationic antimicrobial peptide, is regarded as one of the last-resorts to treat clinical infections caused by MDR Gram-negatives bacteria. However, colistin resistance has been increasingly emerged recently, primarily mediated by plasmid-mediated colistin resistance gene *mcr-1*, which has drawn attention to *mcr*-like genes and the needs to systemically and accurately monitor colistin resistance.

Materials/methods: Feces were collected from swine, chicken and waterfowl and detected for the *mcr*-positive bacteria. Antimicrobial susceptibility testing and PCR screen were performed to investigate the phenotype and genotype of tigecycline resistance. Conjugation, S1-PFGE, and WGS were used to determine the transferability, location of *mcr* gene, and the further study the bacterial genomic profiles.

Results: We collected 2747, 1217 and 1104 fecal samples from swine, chicken and waterfowl during 2016 to 2018. The results show that 40%, 57.1% and 41.8% of the samples are *mcr-1* positive. A four-year monitoring of colistin resistance in a specific pig farm in Jiangxi, the resistance rate and *mcr-1* positive detection rate displays a downward trend, but the prevalence of *mcr-1* is still high in 2017 (33.78%) and 2018 (23.08%). The *mcr-1*-positive *E. coli* isolates show distinct genetic relatedness, and the *mcr-1* gene can be located on the chromosome and the IncX4, IncI2, IncHI2, IncFII and IncFIB type plasmids. In addition, we observed substantial within-host diversity of *mcr-1*-positive Enterobacteriaceae isolates from different aspects (e.g. species, clone relatedness, plasmid types and genetic context of *mcr-1*). To further clarify the transmission mechanism(s) of rapid and wide spread of *mcr-1* gene, we engineered E. coli strains that carry an intact Tn*6330* transposon or its deletion derivatives, providing direct evidence that *mcr-1* transposition relies on the presence of an intact Tn*6330*.

Conclusions: Extensive heterogeneity and flexibility of *mcr-1* transmission exist in both intra-host and with-in host level. *mcr-1* transposition mediated relies on the presence of an intact Tn*6330*. Considering that gut is a melting pot for active horizontal gene transfer, it will take long for regulations to control colistin resistance, and continuous supervision of colistin usage and colistin resistance genes is necessary.

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Abstract 458

Dissemination of tet(X4)-positive *Escherichia coli* on duck farms in south-east China

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Background: Carbapenems, colistin and tigecycline are critically important antibiotics in clinics and tigecycline is considered the last-resort drug against severe human infections caused by multi-drug resistant bacteria. This is especially true after the global appearance of bla_{NDM} and *mcr* mediating the resistance to carbapenems and colistin respectively. Recently, a mobile tigecycline resistance gene *tet*(X4) has been identified in *Escherichia coli*, *Klebsiella pneumoniae* and *Acinetobacter baumannii* that causes high resistance to tigecycline and other tetracyclines. In this study, the prevalence of *tet*(X4) in *E. coli* isolates from duck farms in Southeast China was identified and characterized.

Materials/methods: Feces, soil, sewage and dust samples were collected from duck and goose farms along with the southeast coast provinces of China. Antimicrobial susceptibility testing and PCR screen were performed to investigate the phenotype and genotype of tigecycline resistance. Conjugation, S1-PFGE, and WGS were used to determine the transferability, location of *tet*(X4) gene, and further study the bacterial genomic profiles.

Results: We collected 1716 samples and 16 isolates (0.9%) were identified carrying the *tet*(X4) gene with tigecycline MICs ≥ 8 mg/L. Sequencing analysis demonstrated these isolates belonged to diverse sequence types, mostly ST3997 from Jiangsu province. Conjugation assay to *E. coli* C600 was succeeded for 11 isolates, and correspondingly IncHI1- and IncX1-plasmids bearing tet(X4) were detected by sequence analysis. *tet*(X4) was found adjacent to an insertion sequence ISCR2 downstream and a *cat*D gene upstream for all isolates. In addition, multiple-drug resistance to meropenem, ceftazidime, ampicillin, ciprofloxacin, trimethoprim/sulfamethoxazole and fosfomycin was profiled in all the *tet*(X4)-positive isolates.

Conclusions: The identification of *tet*(X4) harboring E. coli strains in duck farms and their surroundings enlarges our knowledge of the variety and prevalence of tigecycline resistance. Additionally, the prevalence of *tet*(X4) raises concern for the use of tetracyclines in animal farming and the *tet*(X4) gene should be listed as primary gene for resistance surveillance.

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Abstract 459

Clinical and molecular perspectives of colistin-resistant *Klebsiella* from an oncology centre in a lower-middle income country

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Background: There is limited available data on the clinical and molecular perspectives of colistin resistant *Klebsiella* from Lower Middle Income countries.

Materials/methods: We did a retrospective observational study of a cluster of 20 patients with CoRKp infections in our tertiary care oncology centre, from June to November 2017. Clinical details were collected from the case records. Broth micro dilution was performed to derive colistin MIC. The bacteremic isolates (14) were subjected to Whole Genome Sequencing (WGS) to determine mechanism of colistin resistance.

Results: The study included 20 patients with a median age of 60 years, majority were females (70%) and with a median APACHE score of 18. Most patients (19/20) were immunocompromised, receiving treatment for malignacy. Prior exposure to a polymyxin (B/E) was 50%(10/20), an additional 15% (3/20)patients developing bacteremia while on the drug. Fourteen patients had CoRKp bacteremic and 6 non bacteremic infections(4 pneumonia, one UTI and one intrabdominal). All patients received a polymyxin (B/E) in combination with one or more of the following drugs - tigecycline, fosfomycin, chloramphenicol, minocycline or a carbapenem based on the susceptibility and MIC. The time taken for the development of CoRKp infection was a median of 22 days since hospitalisation. Mortality was 75% (15/20), with a median time of death 7 days since the onset of sepsis. Colistin MIC for the isolates ranged from 32-64µg/ml. Of the 14 bacteremic isolates, 12 belonged to ST231, the other two being ST395 and ST147. The carbapenemases identified were OXA-232 in 11, NDM-1 in one isolate and two isolates did not carry any carbapenemase. Mutations in chromosomal genes such as *eptA* (n=12), *arnB* (n=1) and *arnT* (n=1)) contributed to colistin resistance. *mgrB* was disrupted in one of the isolates by insertion of IS903B. Plasmid mediated colistin resistance due to *mcr* and its variants were absent.

Conclusions: Patients with CoRKp infections have a high mortality rate, despite receiving combination therapy. The commonest carbapenem resistance gene identified was OXA 232. ST231 is the predominant clone among colistin resistant *K. pneumoniae*. *mcr* and its variants were absent in all isolates. Mutations in chromosomal genes contributed to colistin resistance.

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Abstract 460

Prevalence of device use and transmission-based precautions in nineteen large Australian acute care public hospitals: secondary outcomes from a national healthcare-associated infection point prevalence survey

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Background: The use of invasive devices increases the risk of healthcare associated infections (HAI). The recent national Australian HAI point prevalence survey secondary objectives aimed to estimate the prevalence of patients with an indwelling urinary catheter device and vascular access devices; and also identify prevalence of those managed under transmission based precautions (TBP); and those colonised or infected with a multi drug resistant organism (MDRO). Data was also collected on the ratio of infection control professional (ICP) per 100 beds and the proportion of single rooms at each hospital.

Materials/methods: A point prevalence study (PPS) was conducted in large acute care Australian public hospitals. All data were collected by two trained Research Assistants. Surveillance methodology was based on the European Centre for Disease Prevention and Control (ECDC) PPS Protocol. Data was also collected on prevalence of TBPs and MDROs.

Results: A total of 2767 acute adult inpatients were sampled across 19 hospitals. The prevalence of peripheral vascular, central vascular and urinary catheters devices was 55.2% (95%CI: 53.3%-57.1%), 14.8% (95%CI: 13.5%-16.1%) and 20.7% (95%CI: 19.2%-22.3%) respectively. Of the 2767 patients sampled 285 (10.3%, 95%CI: 9.2%-11.5%) were documented as either being infected or colonised with a MDRO, and 781 (11.8%) patients were being managed under the hospital TBP policy. Overall proportion of single rooms was 46% (range 16%-100%) and the mean ICP ratio per 100 beds was 0.9 (range 0.3-1.7).

Conclusions: This is the first national study to describe the prevalence of devices, TBPs and MDROs in Australian healthcare settings. Furthermore, it has identified broad variation in ICP resources (staff and single rooms) across a homogenous sample of 19 Australian hospitals. In an era where device use should be constantly reviewed to minimise risk of HAI, combined with the increasing challenges of managing patients with MDROs, it would appear that some hospitals are clearly better able meet these challenges. This data will serve as a benchmark for future studies.

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Abstract 466

Prevalence of ESBL *Klebsiella pneumoniae* infections in Nigeria: a systematic review

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Background: Surveillance is an important strategy used in the control of antimicrobial resistance. It guides selection of empirical antimicrobial therapy and identifies priority areas for infection prevention and control as well as antimicrobial stewardship interventions. Nigeria has no antimicrobial resistance surveillance system at the moment. This review evaluates the prevalence of Extended Spectrum Beta-Lactamase (ESBL) among clinical *K. pneumoniae* isolates in Nigeria (2007 – 2017).

Materials/methods: This systematic review was conducted in accordance with the Preferred Reporting Items for Systematic Reviews and Meta-Analysis (PRISMA) statements. PubMed, Scopus and Google scholar electronic databases were searched to identify eligible studies. Search terms used include: Extended Spectrum Beta-Lactamse, ESBL, *Klebsiella pneumoniae, enterobacteriaceae*, and Nigeria. **S**tudies that reported prevalence of ESBL *K. pneumoniae* in at least 30 non-duplicate clinical specimens were selected. Studies involving animals and healthy human population were excluded. Study characteristics and prevalence of ESBL *K. pneumoniae* isolates were extracted using a data collection form.

Results: Of the 283 articles screened, only seven met the inclusion criteria including three and four studies conducted in Southern and Northern Nigeria, respectively. All the selected studies used prospective study design. Overall, the selected studies involved a total of 744 *K. pneumoniae* isolates and 237 ESBL phenotypes. Available data indicated that there was an increase in the prevalence of ESBL *K. pneumoniae* in both regions: from 12.7% (2005 – 2007) to 37.5% (2011) in the South-West zone and from 14.8% (2010 – 2011) to 62.9% in (2012 – 2014) in the North-West. The prevalence of ESBL *K. pneumoniae* in the South-South, North-East and North-Central was 43.8%, 33.1% 26.7% respectively. ESBL *K. pneumoniae* was more common in urine and surgical wound specimens.

Conclusions: Prevalence of ESBL *K. pneumoniae* infection in Nigeria was high and has increased during the period under review. Active surveillance of ESBL *K. pneumoniae* infections is recommended. In addition, Infection control and antimicrobial stewardship interventions should be strengthen to reduce the burden of antibiotic resistance.

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Abstract 467

Investigation of positive blood culture bottles with the hemoFISH test: a beacon-based fluorescence in situ hybridisation technique

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Background: Pathogenic isolates that responsible for bacteraemia are need to identified rapidly and accurately. Blood culture is the gold-standard method for detection pathogens in blood, but culture-based methods are time-consuming. Beacon-based fluorescence *in situ* hybridization (bb-FISH) technique is thought to be one of the methods that may fill this gap. Therefore, a bb-FISH test (HemoFISH, Miacom diagnostics, Germany) was evaluated.

Materials/methods: A total of 72 BACTEC Plus Aerobic/F blood culture bottles which were gave positive signal were collected. The isolates growth on subcultures were identified by conventional/automated (Vitek-2, BioMérieux, France) reference methods. Also, appropriate hemoFISH assay (Gram-positive or Gram-negative) was performed from signal-positive blood culture bottles after Gram staining.

Results: From the 72 signal-positive blood culture bottle, 75 different isolate were isolated. A total of 69 (95.8%) specimen had monomicrobial, 3 (4.2%) specimen had polymicrobial growth with two species. Twenty-four (32%) Gram-negative and 51 (68%) Gram-positive strain identified with the reference methods. All of the positive control wells were positive for 72 signal-positive blood culture bottles with the hemoFISH assay. From the 75 of the isolates, 67 (89.3%) were classified within the level of species, genus or family by the specific probes of the assay. From the 8 undetected isolates, 2 (*Alcaligenes faecalis* and *Achromobacter xylosoxidans*) were not identified by the assay due to absence of specific probes to these pathogens. Also, 6 of these isolates (2 *Acinetobacter spp.*, 1 *Klebsiella pneumoniae*, 1 *Pseudomonas aeruginosa*, 1 *Enterococcus spp.* and 1 *Staphylococcus hominis subspecies hominis*) could not classified within the levels despite the presence of probes. Total processing time for one signal-positive blood culture bottle was approximately 45 minutes with the hemoFISH assay. When the classical subculture is applied, minimum time for identification is about 36 hours.

Conclusions: Rapid technologies for the determination of the bacteraemia is important to start appropriate empirical treatment. The hemoFISH assay has shortened the evaluation time of bacteraemia but the ability to identify at species level is limited to some pathogens. Thus, it is recommended to use bb-FISH assays in parallel with reference-methods to ensure appropriate empirical therapy.

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Abstract 470

Molecular differentiation of dengue serotypes in the public health system in Santo André, Brazil

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Abstract third-party references: Supported by Fapesp 2016/14457-0

Background: Dengue virus has four serotypes (DENV1-4). It is an arbovirus belong to the family *Flaviviridae*, whose main vector is the mosquito *Aedes aegypti.* Dengue infection has nonspecific symptoms (high fever, retro-orbital pain, myalgia and rash) and similar to other arbovirus infections, laboratory diagnosis becomes essential. In 2018, 163.236 dengue cases were confirmed in Brazil, and of these 301 cases of severe dengue and 3.386 dengue cases with alarm signals. Until April 2019, 15.953 cases of Dengue were confirmed. Early diagnosis can positively influence the clinical management of these patients and consequently reduce mortality.

Materials/methods: From June 2018 to June 2019, 645 patients were admitted to the public health service of the municipality of Santo André in the state of São Paulo with clinical suspicion of Arboviroses. From each patient 5 mL of peripheral blood were collected. The immunochromatographic test was performed for research of protein NS1, IgG and IgM. Viral RNA was isolated from the patient's serum using the QIAamp Viral RNA kit. Complementary DNA synthesis was performed from 1 µg of viral RNA using the QuantiNova Reverse Transcription kit. RT-qPCR was performed with the aid of specific oligonucleotides for the 4 Dengue serotypes and the endogenous gene RPL13a. Amplification reactions were performed on an ABI 7500 thermocycler.

Results: Of the samples evaluated, 48,9% were female and 51,1% male. In immunochromatographic test 601 (93,1%) were negative, 9 (1,4%) NS1 positive, 3 (0,5%) positive IgM and 32(5%) positive IgG. In RT-qPCR 22/645 (3,41%) dengue 2 was detected and in 12/645 (1,86%) genetic material from the dengue 1 has been detected.

Conclusions: The serological method was able to detect 12 (1,86%) patients in the acute phase while molecular biology testing was able to detect viral RNA in 34 (5,27%) of the samples and even differentiate into dengue 1 and dengue. 2. Therefore, the implementation of molecular diagnosis of the virus in the acute phase of infection in the public health service has shown to be a promising tool in the clinical management of these patients.

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Abstract 473

Antimicrobial activity of ceftazidime-avibactam, ceftolozane-tazobactam and comparators tested against *Pseudomonas aeruginosa* and *Klebsiella pneumoniae* isolates collected from US medical centres in 2016-2018

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Background: Very few agents remain active against *Pseudomonas aeruginosa* (PSA) and *Klebsiella pneumoniae* (KPN) in some geographic regions. We evaluated the *in vitro* activity of ceftazidime-avibactam (CAZ-AVI), ceftolozane-tazobactam (C-T) and many comparator agents against a large collection of contemporary PSA and KPN isolates from United States (US) medical centers.

Materials/methods: A total of 6,210 PSA and 6,041 KPN isolates were consecutively collected from 85 US medical centers (37 states) in 2016-2018. MICs were determined by reference broth microdilution method and susceptibility rates were calculated using EUCAST breakpoints. KPN with elevated MIC for broad-spectrum cephalosporins were submitted to whole genome sequencing analysis to detect resistance genes.

Results: CAZ-AVI (97.1% susceptible [S]) and C-T (97.0%S) were the most active compounds against PSA (Table), and retained activity against meropenem-nonsusceptible (MEM-NS; 88.5-89.0%S) and piperacillin-tazobactam-NS (PIP-TAZ-NS; 86.6-87.0%S) isolates; 40.7% of C-T-NS PSA were CAZ-AVI-S and 44.2% of CAZ-AVI-NS PSA were C-T-S. PSA S rates for MEM, PIP-TAZ and tobramycin were 78.2%, 79.1%, and 93.3%, respectively. The most active agents against KPN were CAZ-AVI (>99.9%S), colistin (98.3%S), amikacin (AMK; 97.6%S), and MEM (97.5%S). C-T was active against 92.3% of KPN and showed limited activity against ESBL- and carbapenemase (CPE)-producers (67.2%S and 0.0%S, respectively). Among KPN, 10.2% were ESBL-producers (excluding CPE co-producers) and 2.7% were CPE-producers. The most common ESBLs were CTX-M-15 (75.9%) and OXA-1/OXA-30 (52.4%); 54.4% produced >1 ESBL, mainly CTX-M-15+OXA-1/OXA-30 (50.2% of ESBL-producers). The most common CPE among KPN were KPC-3 (57.8% of CPE-producers) and KPC-2 (39.8%), and only 1 metallo-beta-lactamase-producing isolate was observed (NDM-1). The most active agents against ESBL-producing KPN were CAZ-AVI (100.0%S), MEM (98.7%S), and colistin (96.2%S), and only CAZ-AVI (99.4%S) and colistin (82.4%S) were active against >45% of CPE-producers.

Conclusions: CAZ-AVI and C-T showed similar coverage (%S) against PSA (97.0-97.1%S), including against isolates resistant to other antipseudomonal agents. In contrast, C-T was less active than CAZ-AVI against KPN in general and exhibited limited activity against ESBL and/or CPE producers.

Organism (no. tested)	MIC50/MIC90 (%S)				
	CAZ-AVI	C-T	PIP-TAZ	MEM	AMK
P. aeruginosa (6,210)	2/4 (97.1)	0.5/2 (97.0)	4/>64 (79.1)	0.5/8 (78.2)	4/16 (88.8)
MEM-NS (1,352)	4/16 (88.5)	1/8 (89.0)	32/>64 (42.3)	8/32 (0.0)	8/32 (75.0)
PIP-TAZ-NS (1,298)	4/16 (86.6)	2/8 (87.0)	>64/>64 (0.0)	8/32 (39.9)	8/32 (75.8)
CAZ-NS (1,025)	4/16 (82.2)	2/16 (83.2)	>64/>64 (6.1)	8/32 (40.0)	8/32 (73.6)
K. pneumoniae (6,041)	0.12/0.25 (>99.9)	0.25/1 (92.3)	4/16 (85.5)	0.03/0.03 (97.5)	1/2 (97.6)
ESBL-producers (614)	0.25/0.5 (100.0)	1/8 (67.2)	8/>64 (53.7)	0.03/0.06 (98.7)	2/8 (93.3)
CPE-producers (161)	1/2 (99.4)	>16/>16 (0.0)	>64/>64 (0.6)	16/>32 (10.6)	16/>32 (42.9)

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Abstract 481

Reducing paediatric blood culture contamination rates: a benefit to arterial catheter-drawn cultures

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Background: Contamination of blood cultures occurs universally, often impeding medical care. Catheter-drawn cultures are considered less reliable compared to cultures obtained by venipuncture in adults. We aimed to reduce pediatric blood culture contamination rates using educational and technical interventions. We also assessed the positive predictive value (PPV) of catheter-drawn cultures in pediatric patients.

Materials/methods: The study was conducted at the Ruth Rappaport Pediatric Hospital, a tertiary medical center in Israel. All blood cultures drawn from patients aged 0-18 years were included. Cultures were drawn by nurses and physicians. For 6 months, we performed specialized training, personal feedbacks, and departmental reports of contamination rates. Blood culture contamination rates during the 6 month intervention period were compared to rates in the preceding year. We analyzed contamination rates according to age, department and drawing method.

Results: Pediatric blood culture contamination rates were reduced from 2.18% in the year prior to intervention to 1.93% during the intervention period (1.93% and 2.18% respectively OR 0.89 (95% CI 0.67 – 1.16). Across all pediatric departments, neonates aged 0-30 days had significantly lower blood culture contamination rates compared to patients aged 12 months or older. Cultures drawn from arterial catheters had lower contamination rates than those drawn from a central venous catheter (2.2% versus 3.7% respectively OR 1.72 95% CI 1.14-2.6, see table).

Conclusions: Reducing pediatric blood culture contamination rates below 2% is challenging. Technical difficulties likely play an important role in contamination, therefore arguing for use of a dedicated phlebotomy team, especially in patients aged >1 month. While drawing from vascular catheters, arterial blood cultures are less likely to be contaminated, suggesting a benefit to blood draw from arterial catheters for cultures obtained in intensive care settings.

Contamination rates according to drawing method

Drawing method (blood source)	Contamination rate %	OR (95% CI)	PPV
Arterial catheter	2.2%	1	84%
Peripheral venous	1.9%	0.86 (0.61 - 1.22)	66%
CVC	3.7%	1.72 (1.14 – 2.6)	38%
PICC	2.3%	1.07 (0.33 – 3.51)	40%

CVC – Central venous catheter, PICC – peripherally inserted central catheter

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Abstract 490

Rough-type and loss of the LPS due to lpx genes deletions are associated with colistin resistance among multidrug-resistant *Escherichia coli* clinical isolates not harbouring mcr genes

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Background: The emergence of multi drug resistant *Escherichia coli* (*E. coli*), is a great challenge in treating nosocomial infections. Colistin is the last line of therapy for such strains, but resistance to colistin is increasingly emerge in the public health systems.

Materials/methods: In this study, we examined 38 clinical isolates of *E. coli*, with decreased susceptibility to colistin. After confirmation of the isolates, antimicrobial susceptibility tests were done to characterized the resistance pattern of these isolates to the different classes of antibiotics, using the disk diffusion test, and then, MIC of colistin was determined by broth micro dilution methods according to CLSI recommendations. The isolates were examined for the presence of mobile colistin resistance (*mcr-1* and *mcr-2*) genes, using the PCR methods. Cloning of *mcr-1* gene was done to prove its role in colistin resistance. LPS was extracted from the isolates to determine the presence or the absence of this bacterial target for colistin. *lpx* genes were analyzed by PCR and sequencing for detecting any mutation.

Results: Among 38 clinical isolates of *E. coli*, with decreased susceptibility to colistin, 52.6% (n=20) were resistant to colistin. The MICs of colistin ranged between 0.5 µg/ml and > 256 µg/ml. among the colistin resistant isolates, 6 isolates were harboring the *mcr-1* gene but not the *mcr-2*. The transformed *E. coli* DHα, showed a 8-foled increase in colistin MIC. The other 14 isolates, were negative for *mcr* genes. Among these, 6 isolates were negative for LPS production in SDS-PAGE analysis and five showed the rough type LPS phenotype, and all were significantly associate with resistance to colistin.

Conclusions: this study, presented evidences that loss of LPS or lipid A-deficiency can lead to colistin resistance among clinical isolates of *E. coli*, according to the loss of the drug target or a less affinity of LPS for colistin.

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Abstract 492

Treatment of influenza and influenza-like illnesses with antiviral having anti-inflammatory efficacy

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Background: Enisamium iodide (EI) (Nobazit) is a Russian drug whose molecule was developed in the Institute of Pharmacology and Toxicology of Ukraine as an anti-inflammatory and antipyretic agent. Later, other properties of EI were found: inhibition of the influenza virus hemagglutinin, increasing the production of interferon-γ, level of Th1, blood antioxidant activity, inhibition TNF-α and other pro-inflammatory cytokines, activation of macrophages and lysozyme activity.

The aim of study was to evaluate the efficacy of antiviral therapy with EI in out-patient patients with influenza and influenza-like illnesses (ILI) without risk factors for severe course of disease.

Materials/methods: 124 patients aged 18-55 years with influenza and ILI within 6-48 hours of symptoms onset were randomized into 2 groups. 1th group (n=66) was treated with EI 500 mg tid 5 days, 2nd group (n=63) received placebo according to the same scheme. In the 1th group the proportion between influenza and other respiratory viruses was 32,2%:67,8%, in the 2th group 31,7%:68,3%, accordingly. Duration of disease and main clinical symptoms , frequency of complications and speed of the virus elimination from the nasopharynx were estimated.

Results: The number of cases with complete recovery within 96 hours was 56 (84,8%±4,2%) in 1st group and 44 (69,8% ±5,8%) in 2nd group (p=0.047). The duration of fever was 68.0±2,8 hours in 1th group and 77.1±2,9 hours in 2nd group (p=0.044), muscle pain - 52.3±2,3 and 60.6±2,6 hours (p=0.041), headache-52.1±2,6 and 65.1±2,5 hours (p=0.032), weakness – 75.5±2,3 and 90.4±2,5 hours (p=0.001), accordingly. On the 4th day of treatment the viruses were isolated in 37.8±5,9% of cases in the 1st group and 57.1±6,2% in 2nd group; p=0.048. Bacterial complications were observed in 3,0±2,1% and 12,6±4,2% accordingly, p=0.048.

Conclusions: The study is demonstrated the effectiveness of EI in the treatment of influenza and ILI in adult outpatient patients. The antiviral and anti-inflammatory effects of the drug, which was administered within 48 hours of the symptoms onset were demonstrated by a more rapid reduction of clinical symptoms, frequency of bacterial complications and reduction in the time of virus elimination. Continuation of EI clinical trials are necessary for more full evaluation of its effectiveness.

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Abstract 494

Tuberculous lymphadenitis: are Asians at greater risk?

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Background: Lymphadenitis are the main localization of extra-pulmonary tuberculosis. Despite the existence of treatment recommendations, clinicians are sometimes faced with diagnostic and treatment difficulties. The objective of this study was to describe characteristics and follow-up of patients with Tuberculous Lymphadenitis (TL).

Materials/methods: Analysis of TL cases diagnosed by PCR (Cepheid MTB/RIF test) and/or by culture in Avicenne Hospital from January 1, 2015 to January 31, 2019. Clinical presentation and evolution were compared by continent of birth.

Results: Seventy-two patients (19%) of the 382 tuberculosis cases diagnosed during the period, were TL. Majority were male (n=58, 81%), median age was 32 years (IQR 26-44). Fifteen percent (n=11) of patients were born in India, 11% (n=8) in Pakistan, 10% (n=7) in Bangladesh and 8% (n=6) in Sri-Lanka. Asians peoples accounted for 44% of TL compared to 22% (68/310) of pulmonary tuberculosis cases (p<0.01). Sub-Saharan African people accounted for 38% of patients. Localization was mainly cervical (54%, n=39), and supra-clavicular (36%, n=26). Lung damage was associated in 31% (n=22) of patients, 7% (n=5) of patients were HIV-infected and none were diabetic. Smears were positive in only 14% (n=10) of cases, while PCR, when performed, was positive in 89% (n=25/28) of cases. Only 8% (n=6) of patients had an isoniazid-resistant strain, all were rifampicin-sensitive. Median duration of treatment was 6 months and 22% (n=16) were treated for 9 months or more. Corticosteroid treatment was associated in 18% of cases (n=13) for a duration of 1 to 3 months. Adenopathy was noted to be persistent on clinical examination at 12 months in 13% (n=6) of the 47 patients reported. Due to poor progress, surgical excision was performed in 3 patients. Clinical presentation and evolution were similar between the different birth continents, except for people born in Asia who had more exclusive lymphadenitis (82% versus 58%, p=0.03).

Conclusions: In our study, TL accounts for nearly 1/5th of tuberculosis cases and affects patients born in Asia in particular. Risk factors or genetic factors that may explain the greater susceptibility of this population have to been studied. The use of corticosteroids and surgery should be better specified.

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Abstract 497

Investigation of hetero-VISA among MRSA isolates in Gaziantep, Turkey

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Background: Heteroresistant vancomycin intermediate *Staphylococcus aureus* (hVISA) is defined as isolates which are susceptible to vancomycin, but with minority populations having MIC>2 µg/ml for vancomycin. hVISA testing is recommended when therapeutic failure is suspected. Since population analysis profile is difficult to perform, Satola et al. proposed a practical method for screening of hVISA using brain heart infusion (BHI) agar containing vancomycin and casein and stated that this test had 90% sensitivity and 95% specificity. This test was also cited by EUCAST guidelines for detection of resistance mechanisms V2.01. Here, we aimed to investigate the prevalence of hVISA among MRSA isolates and compared Satola's test with two other agar screening methods for detection of hVISA.

Materials/methods: One hundred MRSA isolates were collected in our university hospital laboratory between 01.04.2018 and 30.09.2019. For screening of hVISA, we prepared two screening agar plates and one commercial media; BHI agar plates containing 4 µg/ml vancomycin and 16 g/liter casein (Satola's test), BHI agar plates containing 4 µg/ml vancomycin (BHIAV), and commercially obtained vancomycin resistant enterococci (VRE) agar. A standard of 0.5 McFarland from an overnight culture in tripticase soy broth was prepared for each isolate. All three screening plates were inoculated with these bacterial suspensions. Colonies which could grow on plates were counted manually at 24th and 48th hours. MICs of the growing colonies in Satola's test were determined using gradient test for vancomycin to see whether the MICs of VISA colonies would decrease or not.

Results: Among 100 MRSA isolates, 43 (43%) were found as hVISA using Satola's test. BHIAV and VRE agar screening test results were found 70% and 4%, respectively. Finally, at the step of gradient test, MIC values of 20 (47%) hVISA isolates reduced to 2 µg/ml after subculturing for the test.

Conclusions: At the step of gradient test, nearly half of the clones of hVISA isolates remained as VISA (MIC>2) after subculturing. When we compared VRE agar and BHIAV screening test with Satola's method, we concluded that both two tests failed to detect hVISA properly. Finally, we found higher rates of hVISA comparing other studies in Turkey.

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Abstract 503

Dried blood spots tested with the Abbott m2000 sp/rt system perform well to identify patients with active HCV infection in Vietnam

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Background: In recent years, the treatment advances of direct acting antivirals (DAA) have radically changed the management of HCV patients. However, in resource-limited countries, identification of patients with active HCV infection continues to present a challenge in remote settings due to the limited access to laboratories able to measure HCV viral load. Dried blood spots (DBS) transferred to a central laboratory may be able to overcome this challenge.

Materials/methods: A total of 315 HCV-infected patients, who never received anti-HCV treatment, provided each three type of samples: plasma, DBS with calibrated quantities of venous blood and DBS with uncalibrated quantities of capillary blood. Qualitative comparison was conducted in terms if detection of HCV viral load on DBS as opposed to plasma to estimate sensitivity and specificity. Quantitative comparisons were conducted by means of correlation estimation and Bland-Altman analysis.

Results: Of the 250 patients with detected plasma HCV viral load, 245 also had detectable DBS HCV viral load (capillary or venous) leading to a sensitivity of 98.0% (95% confidence interval (CI): 95.4%-99.3%); importantly, all measurements with an HCV viral load >118 IU/mL on plasma were also detected on DBS. When HCV was not detected with plasma, it was also not detected with DBS resulting in 100% specificity (95% CI: 94.5%-100%). Quantitative HCV viral load results were very similar when utilizing plasma or DBS sample types as illustrated by correlations >0.99 and by the Bland-Altman analyses.

Conclusions: DBS sample types performed well to distinguish patients with active HCV infection, and who therefore need treatment, from the other patients. DBS with either uncalibrated capillary blood or calibrated venous blood provided similar results.
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Abstract 505

Potential value of qPCR for the early detection of Mucorales in high-risk patients

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Background: Mucormycosis is a rare but often fatal infection in immunocompromised patients. Early and appropriate treatment is paramount for the outcome of the patients. Diagnosis based on clinical symptoms, histopathology, computerized tomography (ct) can be unreliable. Additionally, culture is often negative despite an infection. In order to evaluate the benefit of qPCR as an early and specific diagnostic marker for *Mucorales* infections we have tested respiratory samples from hematoonco-logical and oncological patients of the University Hospital Essen.

Materials/methods: Overall we have analyzed 120 respiratory samples from 92 patients (64 % male, age 11-78 years, median = 61 years) for the presence of *Mucorales* using an inhouse qPCR (Bialek 2005, Löffler 2016) and culture. The qPCR assay simultaneously detected a 175bp fragment of the 18s rRNA gene and a 107bp fragment of the 28s rRNA gene. Limit of detection (LOD) was established by serial dilutions of *Mucorales* DNA and by serial dilutions of fungal material in a respiratory sample. Aliquots of diluted fungal material were inoculated onto an agar plate for fungal count (fungus forming unit, ffu).

Results: LOD of the qPCR assay was 0.1pg/ µl (18s) and 1pg/ µl (28s) when using diluted DNA, and 2ffu/ ml for both targets when using diluted fungal material. A clinical sample was defined as positive only when both targets were amplified (cycle threshold value below 40). Nine samples (7.5%) of six patients were tested positive for the presence of *Mucorales* DNA by qPCR. Culture was only positive in two samples from two patients (1.7%). Ct scans revealed characteristic signs for mold infections in all six patients. The outcome of all patients was fatal.

Conclusions: Culture based microbiology is of limited value for the early detection of *Mucorales*. Our results generally indicate a good agreement between the qPCR assay and the results of ct scans. The qPCR assay we performed was sensitive and specific enough to detect infected patients. We therefore consider qPCR a potential tool for the early detection for *Mucorales.* Additionally, we recommend regular screening of high-risk patients by qPCR.

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Abstract 507

Evaluation of efficacy of antibacterial prophylaxis in case of paraproctitis

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Background: The treatment of acute paraproctitis is a topical problem in coloproctology. There is little reliable data on the effectiveness of Ceftriaxone / Sulbactam in preventing postoperative complications.The purpose of this study is to evaluate the effectiveness of ceftriaxone / sulbactam in the prevention of postoperative complications, using various schemes of pre- and perioperative prevention.

Materials/methods: In a prospective study conducted in the period from December 2018 to March 2019 were analyzed cases of acute paraproctitis in patients of different age groups. Patients were stratified into 2 groups: patients of the 1st group - with a mild course of paraproctitis, requiring only antibiotic prophylaxis, and the 2nd group - patients with moderate and severe course, who received additional therapy with Ceftriaxone / Sulbactam.

Results: The study involved 95 people. In 25 patients (26.3%) of 95, prolongation of perioperative antibiotic therapy was required.In 88 cases out of 95 (92.6%) bacterial cultures were taken. In 43 bacterial inoculations out of 82 (52.4%) was found monoculture and in 39 cases - association of microorganisms (47.6%).In bacterial inoculations was determined sensitivity to Ceftriaxone. In most cases, seeded pathogens were sensitive to this drug. The causative agents of acute paraproctitis were, as elsewhere in world practice, in most cases typical pathogens:

Were received monocultures of microorganisms:

Escherichia coli. 24 out of 43 (55,8%)
Staphylococcus spp. 9 out of 43 (20,9%)
Streptococcus spp. 4 out of 43 (9,3%)

And association of microorganisms. Escherichia coli with:

Bacteroides spp. 6 out of 39 (15,4%)
Klebsiella spp. 6 out of 39 (15,4%)
Staphylococcus spp. 3 out of 39 (7,7%)
Streptococcus spp. 3 out of 39 (7,7%)
Enterococcus spp. 3 out of 39 (7,7%)

Conclusions: Ceftriaxone/sulbactam shows high clinical efficacy when used as a preparation for pre- and perioperative prophylaxis in patients with acute paraproctitis. The effectiveness of the drug in monotherapy (40% of patients) in the absence of postoperative complications is more than satisfactory with mild to moderate paraproctitis. It is possible to recommend the use of the pre- and perioperative prophylaxis with Ceftriaxone / Sulbactam.

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Abstract 508

Investigation of an *Enterobacter cloacae* OXA-436 carbapenemase outbreak: when everything goes down the drain

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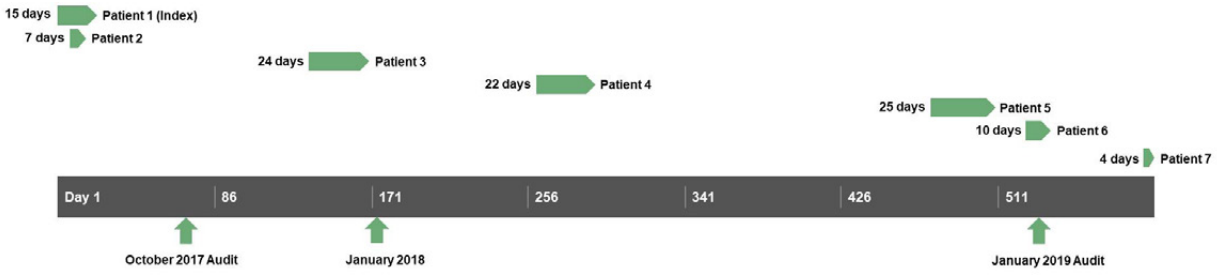
Background: In August 2017, a patient (index) at the Department of Cardiology, Odense University Hospital, Denmark, was diagnosed with *Enterobacter cloacae* ST90 from a wound swab harbouring an OXA-436 (OXA-48 like) carbapenemase gene, located on a conjugative plasmid. This specific combination of sequence type and gene had not been observed in Denmark before (OXA-436 was initially observed in Denmark in September 2013 in *E. asburiae* at a hospital in the Copenhagen area). There was no history of recent travel outside of Denmark. In the following 1½ year, six patients from the same department as the index patient were also diagnosed with the same *E. cloacae* OXA-436 (Figure 1). However, there was no direct epidemiological link between several of the patients apart from the department. Screening (rectal swab) of all patients at the department was performed several times during the outbreak. Staff and procedures were audited by the infection control team, but no source or route of transmission was revealed. Finally, an investigation focusing on the department facilities, including sinks and drains, was performed.

Materials/methods: In February 2019, all drains, sinks and bedpan boilers/instrument washers from the affected department were sampled with eSwab (Copan, Italy) and cultured on selective agars for carbapenemase detection (Chrom ID Carba Smart, bioMerieux, France). Cultured isolates of *Enterobacterales* were submitted for whole genome sequencing and compared to the index patient *E. cloacae* isolate.

Results: Seven drains, 25 sinks and three bedpan boilers/instrument washers were sampled. *E. cloacae* ST90 with the OXA-436 gene were detected from two shower drains in the patient bathrooms.

Conclusions: The shower drains were the most likely source of this outbreak. Staff reported that the shower drains had been partly clogged resulting in regular overflow of water returning from the drains. Drains were unclogged and cleaned, and extra cleaning of the bathrooms was initiated. No further cases have been seen for eight months. Patients and staff should be aware of the potential of transmission of resistant bacteria from shower drains.



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Abstract 509

Trophic cooperation promotes *Pseudomonas aeruginosa* and *Staphylococcus aureus* survival in cystic fibrosis patients

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Background: Lungs of cystic fibrosis (CF) patients are colonized by numerous microorganisms including *Pseudomonas aeruginosa* (PA) and *Staphylococcus aureus* (SA). These bacteria are can co-infect up to 40% of patients according to the age class. Different interaction patterns between PA and SA can be observed throughout infection: PA strains can either inhibit SA growth through well-described mechanisms or coexist with SA. We aim to better understand the coexistence interaction state with SA by characterizing its impacts on PA physiology.

Materials/methods: Twenty-two PA/SA strain pairs in coexistence were isolated from CF patient sputa and cultivated in monocultures or co-culture. PA genic expression was assessed in these conditions by RNAseq (2 strains pairs) and confirmed by RT-qPCR (22 pairs). Deletion mutants of the *aco* system were produced in a clinical PA isolate and cultivated in regular or long-term co-culture with SA, during which acetoin concentration and bacterial survival were monitored. Acetoin dosages were also performed on CF patient sputa.

Results: Transcriptomic analyses show that co-culture with SA significantly affects the expression of numerous genes involved in nutrient metabolism in PA. In presence of SA, 70% of PA strains presented an important overexpression of the *aco* system, involved in acetoin catabolism. Acetoin, produced by clinical SA strains and detected in CF patient sputa, was shown to be responsible for *aco* system induction in PA. Clinical PA strains actually catabolized acetoin produced by SA, especially during coexistence interaction. This catabolism promoted the survival of both pathogens in nutrient-depleted conditions, as acetoin constituted a carbon source for PA and presented a dose-dependence toxicity towards SA.

Conclusions: Our results indicate that coexistence with SA induces the up-regulation of the *aco* system and acetoin catabolism in PA. Due to its beneficial effects on both bacteria, acetoin catabolism could testify to the establishment of trophic cooperation between SA and PA in the CF lung environment, promoting their persistence.

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Abstract 513

Evaluation of prevalence and risk factors of *Helicobacter pylori* infection in an urban population

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Abstract third-party references: Garki Hospital Abuja, Department of Hospital Services, Federal Ministry of Health Abuja

Background: High prevalence rates of *Helicobacter pylori* infection have been reported in developing countries like Nigeria. This infection is known to significantly contribute to the development of gastric cancer and other non-communicable diseases. It is imperative that risk factors associated with this infection are explored to develop evidence-based prevention strategies and improve the health of developing communities.

Materials/methods: A hospital-based cross-sectional study was conducted between May and July 2017 among dyspeptic adults in the GOPD of Garki Hospital Abuja. Two hundred and eighty participants were tested for *Helicobacter pylori* using serum *H. pylori* Immunoglobulin G antibody test kits. Data was collected using pre-tested interviewer-administered questionnaires to assess the risk factors, presenting symptoms and signs and prevalence of *H. pylori*. Epi-info 7.2 was used for data entry and SPSS version 25 for analysis. Logistic regression and odds ratios with 95% confidence intervals were computed to identify risk factors and clinical features associated with *H. pylori* infection.

Results: Out of 280 study participants, 150 (53.6%) tested positive for *H. pylori* infection. Age group 26 – 35 years (OR = 8.40: 95% CI = 1.777 to 39.722), age group 56 – 65 years (OR = 6.78: 95% CI = 1.133 to 40.524), monthly income group $150 to below $200 (OR = 11.81: 95% CI = 1.868 to 74.731) and monthly income group of $300 and above (OR = 7.53; 95% CI = 1.565 to 36.195) were positively associated with *H. pylori* infection. Family history of dyspepsia or peptic ulcer disease (OR = 0.32: 95% CI = 0.128 to 0.784), regular consumption of fruits and vegetables (OR = 0.11: 95% CI = 0.046 – 0.281) and regular hand-washing with soap and water (OR = 0.02: 95% CI = 0.006 – 0.040) were negatively associated with *H. pylori* infection.

Conclusions: The prevalence of *H. pylori* amongst dyspepsia patients in Garki Hospital Abuja was found to be high. Interventions to increase awareness of *H. pylori* infection and prevent infection and transmission of *H. pylori* through good dietary and hygiene practices are vital.

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Abstract 514

Seroprevalence of anti-CCHF IgG in population in different districts of endemic region and Crimean-Congo haemorrhagic fever morbidity

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Background: 710 cases of Crimean-Congo hemorrhagic fever (CCHF). were recorded in the Rostov region of Russia from 2000 to 2019. This region is endemic for CCHF since the sixties of the last century.

Aim of study: to detect the level of seroprevalence in the 12 endemic for CCHF districts of the Rostov region and compare it with CCHF morbidity in the same areas.

Materials/methods: 522 serum samples of conditionally healthy individuals from 12 districts of Rostov region were checked on anti-CCHF-IgG by ELISA. Analysis of CCHF morbidity from 2015 to 2019 in the same districts was implemented

Results: Within 4 years (2015-2018) the decrease of CCHF morbidity was observed. 77 CCHF cases were recoded in this area in 2015, 51 - in 2016, 37 in 2017, 24 in 2018 . In 2019 CCHF morbidity raised up to 48 cases. The largest number of cases (72%) were registered in 8 endenic districts. anti-CCHF-IgG were found in individuals from 6 districts. On average, the proportion of seropositive individuals for CCHF was 1.2%. 10 years ago, this level was 0.4%. This indicator ranged from 0% (in Dubovsky, Martynovsky, Kamensky, Peschanokopsky and Tselinsky, Proletarsky districts) to 1.4-1,7 % (in Zavetinsky, Remontnensky Orlovsky, Bagaevsky districts) and 2.2% - 2.3% in Salsky and Zimovnikovsky districts. In areas with a high incidence of CCHF we have observed positive correlation with a level of seroprevalence (r = 0.8, p=0,04). But in districts with the high prevalence of anti-CCHF-IgG, the level of morbidity (5-9 cases of CCHF annually) was more less than 10 years ago (13-14 cases). From other side, In the 1/3 of districts with 0% seroprevalence (Dubovsky and Martynovsky districts) the incidence of CCHF was higher than 10 years ago (4-5 versus 0-1). Increasing the level of seropositive individuals in the region as a whole is inversely related to the incidence rate (r = -0,8, p=0,04).

Conclusions: These data allow to predict a further increase the incidence of CCHF in the districts with low level of seroprevalence and annual registration of cases of CCHF and should be used in the CCHF epidemiological forecast.

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Abstract 517

Prevalence and serotype distribution of *Streptococcus agalactiae* colonisation among pregnant women in Taiwan

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Background: Group B *streptococcus* (GBS), also known as *Streptococcus agalactiae*, is a prevailing pathogen that leads to neonatal bacteremia, sepsis, meningitis, and even mortality. The study was aimed to investigate the antennal GBS colonization in pregnant women at the gestational age of 35-37 weeks in Taiwan, including prevalence, serotype distribution, antimicrobial resistance profiles, and molecular characters.

Materials/methods: A total of 977 vaginal swabs were collected throughout the 2016 calendar year at single hospital in Taiwan. All GBS isolates were tested for capsule serotypes by using multiplex polymerase chain reaction (PCR) assay. Multilocus sequence typing (MLST) was carried out on selective representative isolates. Antimicrobial susceptibility profile to penicillin, ampicillin, erythromycin, clindamycin, levofloxacin, and ceftriaxone was determined in accordance with CLSI guideline. PCR targeting the major virulence gene, *HvgA*, was performed in isolates of clonal complex (CC) 17.

Results: Of the 977 swab cultures, 219 were positive for GBS (22%). In total, seven serotypes were identified, and serotype III was the leading capsular type (25.1%) followed by VI (22.4%), V (14.6%), Ia (13.7%), II (11.9%). Serotype IV was not detected in the present study. MLST analysis was carried out in 105 isolates and depicted 14 sequence types (ST). The leading three sequence types in order were ST1 (50, 47.6%), ST12 (10, 9.5%), ST17 (8, 7.6%). Of 105 MLST tested isolates, 21 were serotype VI and fully were ST1 (100%). For ST12, serotype II was the dominant type (9/10, 90%). In addition, a total of 8 isolates were identified as CC17 strain and all were serotype III. All these 8 ST17-III isolates harbored *HvgA* gene. Four clonal complexes were found in this study and the predominant clonal complexes were CC1 (51, 48.6%), followed by CC23 (19, 18.1%). Regarding of antimicrobial resistance, all the isolates were susceptible to penicillin (100%). Resistance rates of erythromycin and clindamycin were 41.1% and 39.3%, respectively.

Conclusions: In this present study, GBS colonization rate of pregnant women in Taiwan is 22%. Serotype III and VI are the two leading capsule types and the CC1 is the predominant clonal complex. Penicillin was still the first choice for treating GBS infection.

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Abstract 519

Interim pharmacokinetic analysis of a multi-centre randomised open label phase IIb study in neonates to validate the meta-analysis population pharmacokinetic model used to simulate an optimised dosing regimen in neonates and infants aged < 90 days: the NeoVanc trial

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Background: Vancomycin remains one of the most widely prescribed antibiotics for Gram-positive neonatal late onset sepsis (LOS), however, a consensus on optimal vancomycin dosing and duration is lacking. Robust neonatal clinical pharmacokinetic (PK) data comparing different vancomycin dosing regimens remain sparse. NeoVanc (NCT02790996) is a European, randomised controlled, non-inferiority trial comparing an optimised and standard vancomycin regimen in infants aged ≤90 days with suspected/proven Gram-positive LOS. The optimised regimen was determined through pre-clinical studies including a population PK meta-analysis of individual data from >1600 babies.

Materials/methods: Babies with clinical sepsis (≥3 clinical/laboratory criteria) or confirmed sepsis (Gram-positive blood culture and ≥1 clinical/laboratory criterion) were recruited. Participants were randomised 1:1 to the optimised regimen (vancomycin loading dose (25 mg/kg) followed by 5±1 day course) or a standard regimen (no loading dose;10±2 day vancomycin course). An interim PK analysis was performed; the validation dataset was collected from 8 centres in 5 European countries. Data collected included demographic variables (gestational and postnatal age, birth and current weight), vancomycin administration (dose, time of start and end of infusion, exact sampling time), creatinine concentrations (Jaffe, enzymatic), vancomycin concentrations (ultraperformance liquid chromatography-tandem mass spectrometry).

Results: 68 babies recruited between March 2017 and April 2018 were included in the interim analysis. Gestational age was <29 (n=16), 29–36 (n=22), >35 (n=30) weeks. Median (IQR) birthweight was 1258 (455–4040)g with median weight at randomisation being 1525 (590–4156)g. Median post-menstrual age at randomisation was 33.8(25.1–47) weeks. Median serum creatinine was 41.5(8.84–96.36) µmol/L. 240/255 PK and scavenged PK samples were evaluable. Vancomycin concentrations were used to confirm the reliability of the meta-analysis model where clearance (CL) was dependant on current weight, method used to quantify creatininaemia, renal maturation (RM) and renal function (RF) according to $CL = \theta 6 \times (CW/1350)^{\theta 7} \times RM \times RF \times F_{Jaffé\text{-}Enzymatic} \times F_{race}$

Conclusions: External validation with NeoVanc trial PK data confirmed the predictive performance of the model developed from the PK meta-analysis.

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Abstract 523

Unravelling the mechanism of virulence of M1 protein of *Streptococcus pyogenes*

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Background: Most pathogenic bacteria form complex extracellular protein-protein interaction networks (PPINs) with host proteins on the bacterial surface. The dynamic PPIN and the way they are formed and regulated, can deepen our understanding of bacterial infection and host immune response. However, it still remains a challenge to quantitatively determine the dynamics, structure and function of such host-pathogen interactions in a systems-wide manner.

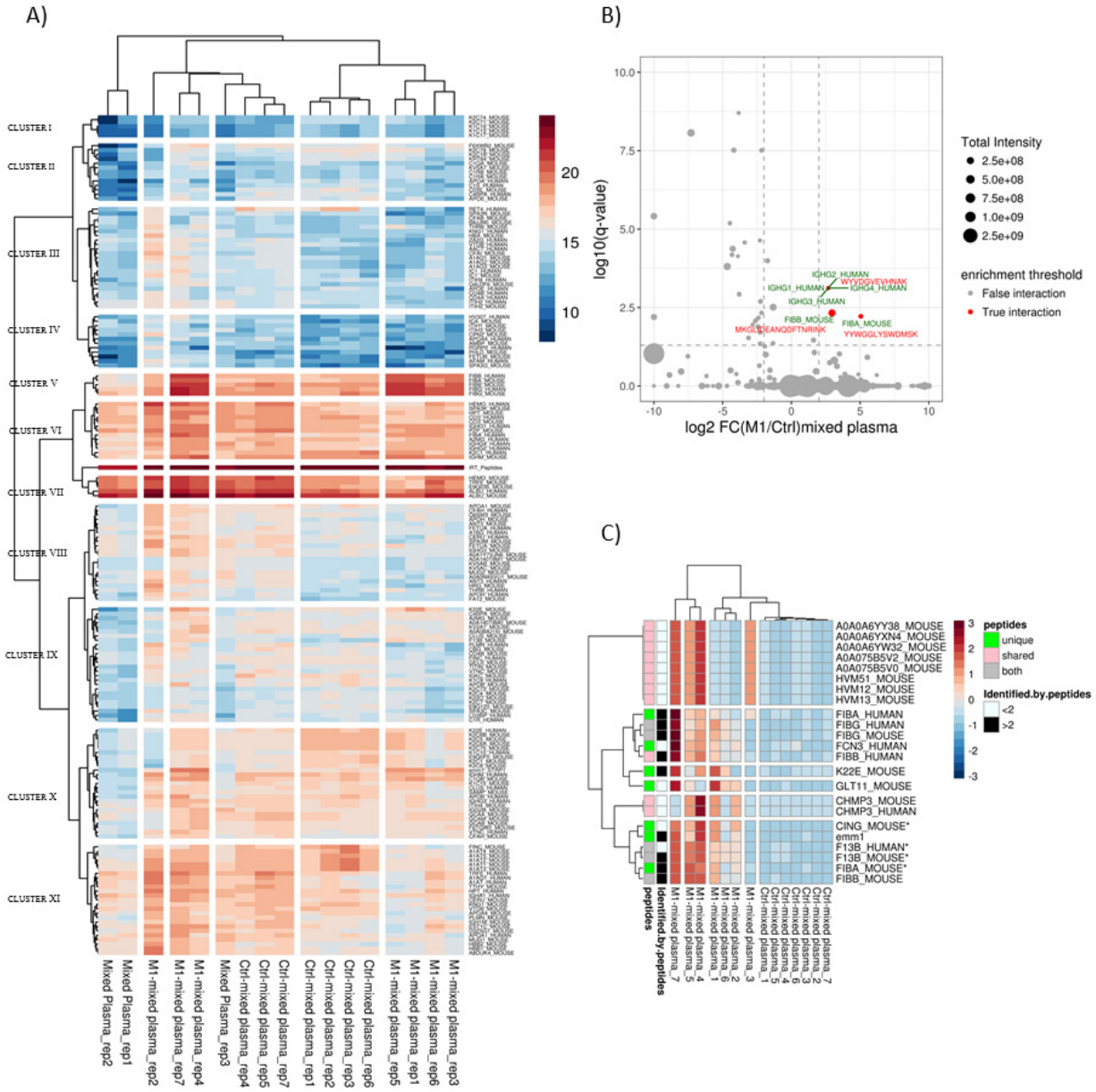
Materials/methods: To enable quantitative analysis of PPINs we have established a generic affinity-purification mass spectrometry-based proteomics strategy (AP-MS)[1] to investigate bacterial pathogen-host PPINs at a grand scale. We have applied the AP-MS strategy to determine how human host and mouse (BALB/c) plasma proteins competitively interact with main virulence factor - the M1-protein – of the human pathogen *Streptococcus pyogenes*.

The experimental workflow includes isolation of interacting proteins using affinity-enrichment followed by highly quantitative MS techniques including sequential window acquisition of all theoretical fragment ion spectra analysis MS (SWATH-MS)[2].

[1]Happonen L., *et al. Nat Commun* 2019; [2]Gillet, LC. *et al. Mol Cell Proteomics,* 2012.

Results: The dynamic regulation of the PPINs was assessed using a mixture of human and BALB/c mouse (50/50 vol/vol dilution) plasma to measure any inherent competition between both mammalians' protein interactions. Eleven different clusters of proteins with different binding patterns were identified, being human and mouse albumin, fibrinogen, C3 protein of complement system or mouse IgM and human IgGs, enrichment proteins (clusters V, VI and VI, Figure 1A). A full peptide-level analysis unraveled several common peptides among human and mouse proteins (Figure 1B), of which fibrinogen was the most conserved protein among mammalians, showing a high homology human to mouse. (Figure 1C).

Conclusions: These results demonstrate how M1 protein assembles a complex PPIN in plasma which could modulate the host immune response. Excitingly, the M1-protein is shown to be a ligand for human and mouse fibrinogen, but also for human IgGs or heavy chain variable domains of mouse Igs.



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Abstract 525

Characterisation of internalin genes in *Listeria monocytogenes* food strains, and their association with invasiveness *in vitro*

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Background: *Listeria monocytogenes* (*Lm*) is a facultative intracellular pathogen and the causative agent of a food-borne disease listeriosis. The bacterium colonizes niches in food processing environments due to ability to survive in a variety of stress conditions. Internalization enables *Lm* to invade non-phagocytic cells like intestinal epithelium. The process is mediated mainly through a group of proteins called internalins (Inl), of which InlA and InlB have been shown to play a critical role. In this study, 16 strains of *L. monocytogenes* collected from food samples in Poland were tested for the hemolytic activity and invasiveness in cultured cells. Data from phenotypic analysis were integrated with genomic approach to assess the biodiversity of the pathogen and reveal genetic variants of internalin genes.

Materials/methods: Invasiveness was tested in gentamycin protection assays using epithelial (HeLa), placental (JEG-3), and neuronal (Neuro-2a) cell lines. Simultaneously, the isolates were subjected to Illumina MiSeq whole genome sequencing (WGS). *In silico* multi-locus sequence typing (MLST) and core genome MLST were performed using Institute Pasteur *Lm* MLST database. Sequence search for the presence of virulence genes, manual annotation etc. were performed with UGENE program. Sequences of LIPI-1 pathogenicity island and internalin clusters were aligned using MAUVE software.

Results: The isolates were differentiated into 2 phylogenetic lines (I, n=9; II, n=7), and 8 sequence types (ST), with ST580 (5/16) being the most common. Five internalin profiles were distinguished: I (CC9), II (ST1413), III (CC2, CC3, CC5), IV (ST517) and V (CC1). Premature stop codon mutation (AA 685) in *inlA* were identified in all line II isolates, of which only one exhibited unimpaired invasion to placental epithelial cells.

Conclusions: Comparative analysis revealed the presence of globally distributed sequence types along with differences among the isolates at a genomic level. Two strains exhibit unique features. LM-UW02, classified as the second known representative of ST1413, uniquely does not encode Vip protein and carries the A117T mutation in LRR region of *inlB* gene. LM-UW11 from phylogenetic line I, encodes InlG previously attributed to line II strains only and harbors LIPI-4 pathogenicity island characteristic mainly for clinical strains with increased CNS and placenta invasion capacity.

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Abstract 529

Regulation of intestinal bacterial translocation by intestinal lamina propria dendritic cells expressing TLR5 after trauma/haemorrhagic shock

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Background: Enterogenous infection is a major cause of death induced by traumatic/hemorrhagic shock (T/HS). Specific toll-like receptors (TLR5$^+$) lamina propria dendritic cells (LPDCs) are critical antigen presenting cells (APCs) for modulating the intestinal mucosa-related immunological state to defend against bacterial translocation. We aimed to investigate LPDCs' responses after T/HS, which would deeply affect the subsequent local immunity of the intestinal mucosa as well as bacterial translocation.

Materials/methods: Wild-type (WT) and Tlr5$^{-/-}$ mice were divided into T/HS and sham groups. After T/HS, TLR5$^+$ LPDCs were sorted. Hemodynamic parameters and intestinal mechanical barriers were determined. Th1 differentiation was analyzed in mouse intestinal lamina propria (LP) or in a co-culture system of LPDCs and naïve T cells. Moreover, intestinal bacterial translocation and mouse survival were also monitored.

Results: CD11c$^+$ MHCII$^+$ LPDCs specifically expressed TLR5. No differences were observed between WT and Tlr5$^{-/-}$ mice regarding hemodynamic parameters and intestinal mechanical barriers after T/HS. LPDCs sourced from T/HS WT mice induced decreased Th1 polarization and more bacterial translocation, however, Tlr5 knockout conferred LPDCs with abilities to induce increased Th1 polarization and remain stable under T/HS hit. Moreover, retinoic acid (RA) released by TLR5$^+$ LPDCs might play a key role in modulating Th1 polarization. Finally, RA treatment clearly increased the quantity of Th1 cells in LP and attenuated bacterial translocation after T/HS in WT mice but not Tlr5$^{-/-}$ mice (Figure 1), though mouse survival after T/HS was not prolonged by RA enteral supplementation.

Conclusions: Disordered LPDC TLR5-RA downregulation-induced Th1 differentiation might be an immunological mechanism of intestinal bacterial translocation and enterogenous infection after T/HS, and a TLR5-RA-independent mechanism that is relatively stable and rarely affected by T/HS may exist for LPDCs to polarize Th1 cells. In summary, both TLR5-RA-dependent and TLR5-RA-independent pathways within LPDCs may be therapeutic targets for interfering with Th1 differentiation and intestinal bacterial translocation.

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Abstract 532

Are residual waters vehicles of transmission of resistance mechanisms? DARWIN JPI AMR-2016 study

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Background: One of the biggest health problems is antimicrobial resistance (AMR) complicating the treatment of infections and community health. In 2016, DARWIN project (Dynamics of Antimicrobial Resistance Project in the Urban Water Cycle in Europe) emerges with the objective of developing a dynamic predictive model to assist in wastewater management, analyzing and quantifying resistant microorganisms and their genetic determinants, from their excretion in hospital and urban sources, to the water receiving surface (http://www.amr-darwin.eu/)

Materials/methods: Sampling has been carried out in 3 cities simultaneously, Copenhagen, New Castle and Santiago de Compostela, by 8 different points of the wastewater treatment system: hospital and urban effluent, wastewater treatment plant, relevant plant compartments, and in the Sar River up- and down-stream of the WWTP (purification plant), in Santiago de Compostela (ES). CHROMID®ESBL and CHROMID®CARBA (BioMeriuex) were the chromogenic medias used for detection of ESBLs and carbapenemases respectively, plus a non-commercial MBQ medium supplemented with antibiotics. Isolates were identified by MALDI Biotyper Bruker and sequencing of the 16S rRNA gene.

Results: A total of 504 resistant strains were isolated from the different sampling points in Santiago de Compostela city. MALDI Biotyper showed a correlation index with respect to 16S sequencing up 0.9 at genus level, because of the identification of environmental isolates non-associated with infection. The isolates with greater clinical relevance and resistance were isolated in the hospital effluent, highlighting the isolate of *Klebsiella pneumoniae* producing BLEEs and carbapenemases, and being *Escherichia* spp the most ubiquitous Enterobacteria. The greatest confluence of *Aeromonas* spp came from the residential effluent, although they were isolated at all points. After the treatments carried out in the wastewater, the resistant bacteria decreased by 80%. Downstream of the Sar River the largest isolates producing BLEEs were *Aeromonas* caviae complex, and resistant to carbapenems were *Pseudomonas* spp

Conclusions: The isolates with greater clinical relevance and resistance, especially to carbapenems, were isolated at hospital effluent. WWTPs could act as a vehicle for transmission of resistance mechanisms to environmental strains. Therefore, current wastewater treatments could be insufficient to eliminate resistant strains, especially those resistant to carbapenems.

TREEMAP OF ISOLATES COLLECTED

HOSP= HOSPITAL; RESD=RESIDENTIAL; ENTR= ENTER; BioT=Biological Treatment; RVUP= UP RIVER SAR; RVDW= DOWN RIVER SAR. CAR CARBAPENEMASES RESISTANCE; ESBL= EXTENDED SPECTRUM BETALACTAMASES RESISTANCE. W18= WINTER FEBRUARY 2018; S18= E SUMMER SEPTEMBER 2018

DISTRIBUTION OF ISOLATES COLLECTED FROM DIFFERENT SAMPLING POINTS IN SANTIAGO COMPOSTELA CITY

	CARBAPENEMASES								ESBL							
	CHROMID			MBQ					CHROMID			MBQ				
	W18	S18		A18	S18				W18	S18		W18	S18			
HOSPITAL	17	7	24	5	3	8	32		27	7	34	4	3	7	41	73
RESIDENTIAL	13	4	17	5	3	8	25		22	7	29	5	3	8	37	62
ENTER	13	7	20	9	5	14	34		29	8	37	11	7	18	55	89
DEC1	11	2	13	6	5	11	24		30	6	36	7	5	12	48	72
BioTREATMENT	1	5	6	7	3	10	16		4	8	12	8	7	15	27	43
DEC2	0	2	2	2	0	2	4		2	2	4	6	4	10	14	18
UPRIVER	21	2	23	1	7	8	31		25	8	34	2	11	13	47	78
DOWNRIVER	11	5	16	2	5	7	23		20	11	31	5	10	15	46	69
	87	34	121	37	31	68	189		160	57	217	48	50	98	315	504

DISTRIBUTION OF ISOLATES BY PHYLOGENETIC GROUP-FAMILY

	CARBAPENEMASES							ESBL								
	CHROMID			MBQ				CHROMID			MBQ					
	W18	S18		W18	S18			W18	S18		W18	S18				
Aeromonas	21	2	23			0	23	73	16	89			0	89	112	
Citrobacter-Serratia		2	2	1		1	3	8	4	12			0	12	15	
Enterobacter-Pantoea	7	1	8	1		1	9	3	0	3			0	3	12	
Escherichia-Shigella			0			0	0	6	1	7		1	1	8	8	
Klebsiella-Raoultella	1	3	4			0	4	2	5	7	1		1	8	12	
Proteus-Providencia			0			0	0	6		6			0	6	6	
Salmonella			0		1	1	1			0			0	0	1	
Actinomycetales			0		1	1	1			0	1		1	1	2	
Arcobacter			0			0	0	1	1	2			0	2	2	
Acinetobacter	1		1	8	3	11	12	6	4	10	17	2	19	29	41	
Balneatrix			0			0	0			0	1		1	1	1	
Brevundimonas			0	9	7	16	16			0	3	1	4	4	20	
Burkholderiales	1		1	7	3	10	11	1	2	3	1		1	4	15	
Chryseobacterium-Elizabethkingia		2	2	3	1	4	6		3	3	1		1	4	10	
Flavobacterium	1		1			0	1	12		12		1	1	13	14	
Methylobacterium			0		2	2	2			0		3	3	3	5	
Ochrobactrum			0		1	1	1		1	1	14	16	30	31	32	
Pseudomonas	51	14	65	2	3	5	70	39	17	56	7	22	29	85	155	
Sphingobacterium	1		1			0	1	1	2	3			0	3	4	
Sphingomonadaceae			0		3	3	3			0			0	0	3	
Stenotrophomonas	3	10	13	6	6	12	25	2	1	3	2	4	6	9	34	
	87	34	121	37	31	68	189	160	57	217	48	50	98	315	504	

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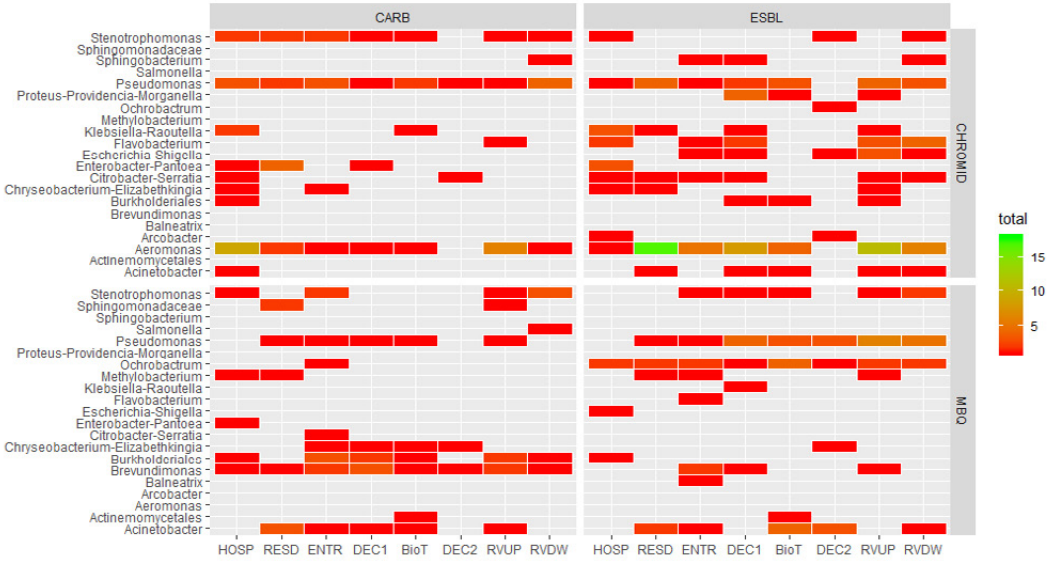

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Abstract 538

Hepatosplenic bartonellosis in immunocompetent adults: a case series and literature review

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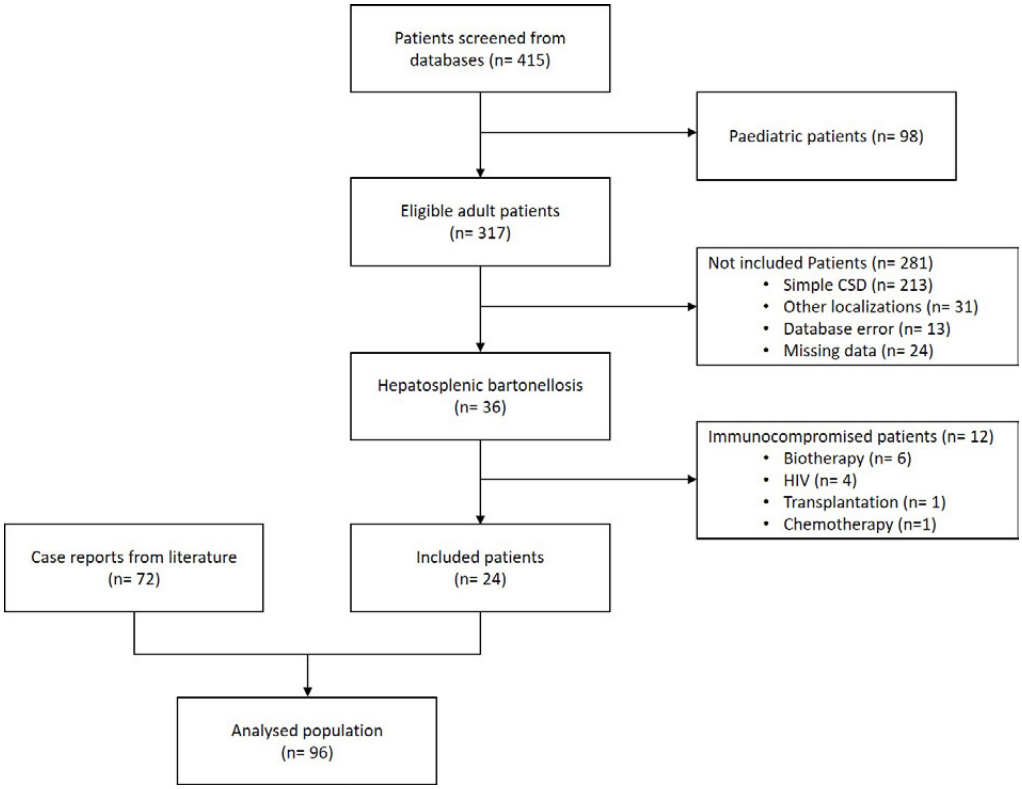
Background: *Bartonella henselae*, agent of cat-scratch disease (CSD) is rarely responsible from visceral granulomatosis, reported by few case series with low numbers. The objective was to better characterize hepatosplenic bartonellosis (HSB) in immunocompetent adults, a rare complication of *B. henselae* infection.

Materials/methods: Retrospective study of all HSB diagnosed in 4 french tertiary care university hospitals in 2001-2018. Inclusion criteria were i) radiological lesions in liver and/or spleen; ii) *B. henselae* infection documented by PCR, or serology. We excluded patients <15-year-old or immunocompromised. A literature review was performed using Medline, Embase, and Scopus database, with no language or time restriction.

Results: Of 414 cases of bartonellosis documented during the study period in the 4 centres, 24 (5.8%) were HSB in immunocompetent adults (estimated incidence, 0.19/million inhabitants-year). Literature review identified 72 additional cases. Overall, there were 53 men and 43 women, median age was 41 years [IQR 27-52], 79 (82.3%) reported contact with cats. Main symptoms were fever (n=80, 83.3%), weight loss (n=56, 58.3%), abdominal pain (n=45, 46.9%), and peripheral lymphadenopathy (n=45, 46.9%). Median duration of symptoms before diagnosis was 30 days [15-60]. Abdominal imaging found round-shaped lesion(s) in liver (n=16, 16.7%), spleen (n=28, 29.2%), or both (n=52, 54.2%), multiple in 82 patients (85.4%). *B. henselae* infection was documented by serology (n=80), and/or PCR (n=38). Antibacterial treatment was prescribed for 81 patients (84.4%), mostly macrolides (n=38), cyclines (n=36), and quinolones (n=21), for a median duration of 30 days [14-60]. Surgery was performed in 12 patients (12.5%). Of the 89 patients with follow-up data, 85 were cured (95.5%).

Conclusions: HSB is a rare disease in immunocompetent adults, with favourable outcome in most cases, whatever the management.



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Abstract 565

Prophages, plasmid integration and lack of CRISPR-Cas elements underlie genome adaptation in European human-associated *Staphylococcus aureus* ST398

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Abstract third-party references: on behalf of COMBACTE-NET 6A & 6B working groups

Background: *Staphylococcus aureus* (SA) sequence type (ST) 398 causes both moderate livestock-associated and severe-to-fatal human-associated (HA) infections. HA-ST398 infections are common in Asia (AS) and are also gaining epidemiological importance in European (EU) hospitals. Due to geographic separation, we hypothesized divergent evolutionary trajectories among AS-HA-ST398 and EU-HA-ST398 and investigated these in ST398 isolated from hospitalized patients in both continents.

Materials/methods: EU-SA (n=868) obtained from mechanically-ventilated ICU or from surgical ward patients enrolled in ongoing clinical trials in COMBACTE-NET (NCT02413242, NCT02935244, NCT02296320) during 2014-2018 in 9 countries were whole genom -sequenced (short-read, Illumina-MiSeq; and long-read, n=2, Pacbio Sequel). Raw read processing and assembly, MLST-typing, resistance/virulence gene identification and genome annotation were performed with BacPipe (v1.2.6; https://github.com/wholeGenomeSequencingAnalysisPipeline/BacPipe) and SMRTLink v7.0.1. EU-HA-ST398 (n=44) were identified and genomic relatedness of 1 isolate/patient (n=26), together with AS-HA-ST398 sequences (n=8, hospitalized patients in China, 2010) obtained from NCBI, was studied using allelic-loci-comparison (cg/wgMLST) with a study-specific ST398-scheme (chewBBACA), comparative genome analysis (Mauve v2.4.0) and SNP calling (CLC v9.5.1).

Results: Analysed strains (n=34) formed three clades based on core-genome and whole-genome MLST (Figure A & B). EU-HA-ST398 segregated in 2 clades (average 341 allelic-loci-differences) differentiated by the presence and absence of the highly-conserved ϕST398_5 prophage that inserts in *smpB* which encodes a SsrA-binding protein. In both core and accessory genome analysis, EU-HA-ST398 Clade 2, containing primarily ST398 isolated from South-Eastern Europe, clustered closer to AS-HA-ST398 (n=6, Clade 1) than to Clade 3 that consisted of strains from Western Europe. All ST398 lacked CRISPR-cas elements and EU-HA-ST398 genomes harboured integrated plasmids and resistance-gene clusters (Figure C). On average, the accessory genome ratio determined for the 5 long-read-sequenced HA-ST398 (2 EU & 3 AS) was 6.5% which is higher than USA300-FPR3757 (ST8; 4.807%) but lower than TW20 (ST239; 11.088%).

Conclusions: Our data shows that HA-ST398 genomes are labile, easily acquire and integrate mobile elements that might underlie the emergence and success of the clone. The remarkable genome relatedness of the Chinese and the South-Eastern European clade indicates that an intercontinental spread of this clade might have been a recent occurrence.

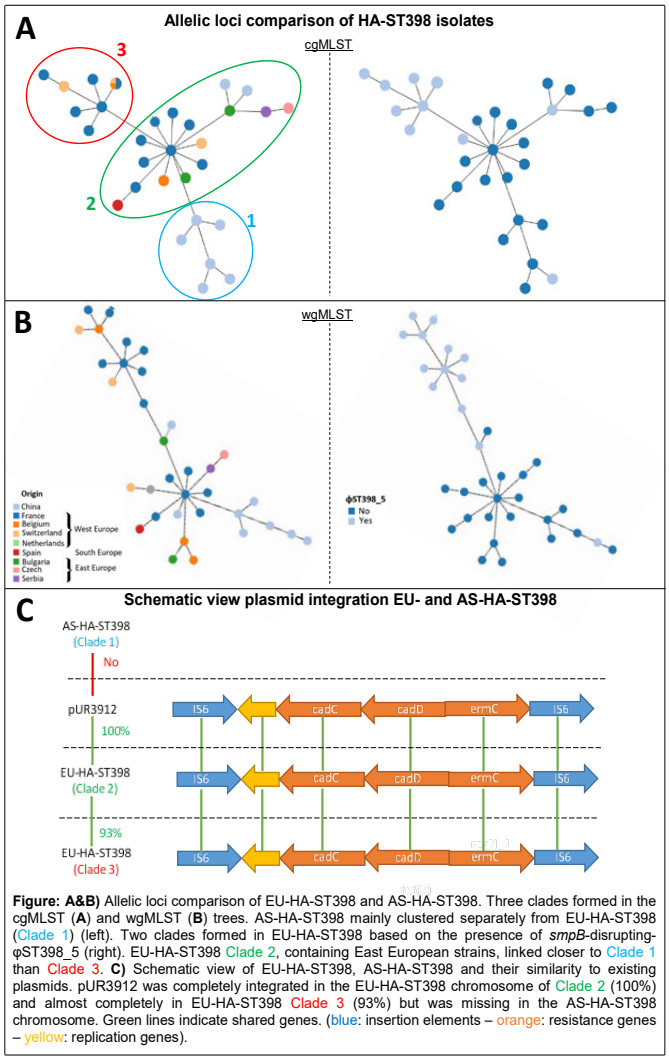

Figure: A&B) Allelic loci comparison of EU-HA-ST398 and AS-HA-ST398. Three clades formed in the cgMLST (**A**) and wgMLST (**B**) trees. AS-HA-ST398 mainly clustered separately from EU-HA-ST398 (Clade 1) (left). Two clades formed in EU-HA-ST398 based on the presence of *smpB*-disrupting-φST398_5 (right). EU-HA-ST398 Clade 2, containing East European strains, linked closer to Clade 1 than Clade 3. **C)** Schematic view of EU-HA-ST398, AS-HA-ST398 and their similarity to existing plasmids. pUR3912 was completely integrated in the EU-HA-ST398 chromosome of Clade 2 (100%) and almost completely in EU-HA-ST398 Clade 3 (93%) but was missing in the AS-HA-ST398 chromosome. Green lines indicate shared genes. (blue: insertion elements – orange: resistance genes – yellow: replication genes).

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Abstract 567

Can Rapid Antimicrobial Susceptibly Testing (RAST) improve the time to the optimal therapy for bloodstream infections?

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Background: Gram-negative bloodstream infections (BSI) remain an important cause of morbidity and mortality. Fast and reliable antimicrobial susceptibility assays ensure early adequate therapy and may reduce the prolonged use of empiric broad-range antibiotics. EUCAST has validated new breakpoints for short incubation disk diffusion testing directly from positive blood culture bottles, interpretable after 4, 6 and 8 hours (RAST). We aimed to evaluate the effect of RAST on BSI management in our hospital.

Materials/methods: RAST was implemented at the University Medical Center Hamburg-Eppendorf (Germany) in addition to standard of care (SOC; Vitek2), i.e. availability of AST results a day after blood culture positivity. For all interpretable results (zone diameter outside the area of technical uncertainty, ATU) categorical agreement (CA, concordant interpretation by SOC and RAST), very major error (VME, resistant by SOC, susceptible by RAST), major error (ME, susceptible by SOC, resistant by RAST) and minor error (mE, susceptible, increased exposure by SOC, resistant or susceptible by RAST) rates were calculated. The proportion of patients receiving optimal antimicrobial therapy after communication of RAST results was determined.

Results: For 97 blood cultures growing species for which RAST breakpoints are available, overall categorical agreement between RAST and SOC was 97.1 %; mE rate was 1.5 %, ME rate was 1.4 % and no VME were observed (Table1). A significant number of results within the ATU (158/879) was found. Clinical impact of RAST was evaluated for 51 patients from 1st May to 31th July 2019. In 90.2 % (46/51) of the cases RAST was available after 4h, in 7.8 % (4/51) after 6h and in 2 % (1/51) after 8h. Optimal treatment was achieved in 21/51 (41.2 %) patients according to the RAST results and among these, RAST allowed for early escalation to a broad-spectrum antibiotic in 6 cases related to multi-resistant isolates. An unnecessary escalation based on RAST occurred in 9/51(17.6%) patients.

Conclusions: Our findings suggest that the implementation of RAST may be especially helpful for early treatment escalation in BSI caused by multi-resistant bacteria. RAST result communication should be integrated into structured antimicrobial stewardship programs to prevent inadequate or premature treatment adjustments.

Table 1. RAST categorical agreement vs. Vitek2 per species and incubation time from 1st May to 30 September 2019.

Reported the antibiotics tested with breakpoints readable.

	E.coli (77 isolates) Piperacillin-tazobactam, cefotaxime, ceftazidime, meropenem, ciprofloxacin and gentamicin		***K. pneumoniae*** (10 isolates) Piperacillin-tazobactam, cefotaxime, ceftazidime, meropenem, ciprofloxacin and gentamicin		***P.aeruginosa*** (9 isolates) Piperacillin-tazobactam, ceftazidime, meropenem, ciprofloxacin and gentamicin		***A.baumanii*** (1 isolate) Meropenem, ciprofloxacin and gentamicin	**Total** (97 isolates)
Incubation time	4h	6h	4h	6h	6h	8h	4h	
Categorical agreement on the total of readable breakpoints (%).								
Correct	320 (97.3)	244 (97.2)	51 (96.3)	27 (96.4)	42 (95.5)	14 (100)	2 (100)	700 (97.1)
mE	7 (2.1)	4 (1.6)	0	0	0	0	0	11 (1.5)
ME	2 (0.6)	3 (1.2)	2 (3.7)	1 (3.6)	2 (4.5)	0	0	10 (1.4)
VME	0	0	0	0	0	0	0	0
Total	329	251	53	28	44	14	2	721
ATU	76	53	12	7	4	5	1	158

mE: minor error
ME: major error
VME: very major error
ATU: Area of Technical Uncertainty

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Abstract 571

Proton pump inhibitors increase the digestive carrying of OXA-48-producing *Enterobacteriaceae* in a mouse model

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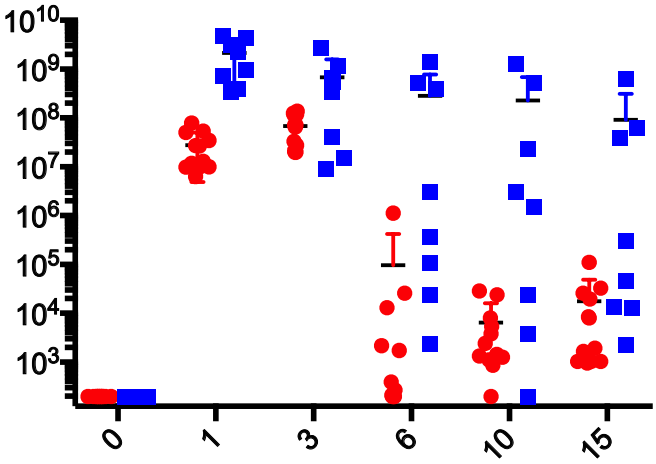
Background: Proton pump inhibitors (PPI) are responsible for altering the composition of the gut microbiota but little is known about their impact on the gut resistome. It would appear that PPI consumption is associated with extended-spectrum β-lactamase–producing Enterobacteriaceae rectal carriage at hospital admission. Our objective was to evaluate the effect of PPI on the digestive carriage of OXA-48-producing Enterobacteriaceae in a mouse model.

Materials/methods: C57BL/6J mice were initially treated orally with amoxicillin (0.5 $g.l^{-1}$ in drinking water) for 7 days before the bacterial challenge (10^7 CFU of OXA-48-producing Escherichia coli) by gastric gavage. PPI were added to drinking water (0.1 $g.l^{-1}$ of pantoprazole) for a group of mice (PPI group) throughout the experiment while the control group did not receive them. The stool was collected for 15 days after the bacterial challenge. The bacterial count was performed on selective chromogenic medium for the screening of OXA-48 type Carbapenemase-Producing Enterobacteriaceae. The mice were housed in individual cages to avoid inter-individual contamination.

Results: Height mice were analyzed in the PPI group and 12 in the control group. One day after the bacterial challenge the PPI group had a higher average concentration of E. Coli OXA-48 in the feces ($2.1x10^9$ $CFU.g^{-1}$ versus $2.8x10^7$; $P < 0.001$). Except for the 3rd day after the bacterial challenge, this concentration was higher in the PPI group than in the control group ($P < 0.001$ on days 6, 10 and 15). Indeed, there was a clear decrease in E. Coli OXA-48 colonization in the control group from the 6th day post-bacterial challenge (approximately 4 log $CFU.g^{-1}$), while the PPI group kept a high level of carriage (approximately 8 log $CFU.g^{-1}$) (Figure).

Conclusions: The use of PPI could be a factor promoting digestive colonization with resistant bacteria. These widely prescribed treatments should be evaluated in humans in order not to ignore a possible factor promoting the spread of this type of bacterium.



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Abstract 572

Time to positivity of blood cultures and its role in the diagnosis of bacteraemia

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Background: This study aimed to evaluate the time-to-positivity (TTP) of all bacteremia episodes (true and contaminations) isolated in a tertiary hospital in order to study to what extent the TTP can provide information on the type of microorganism isolated and its involvement in infection.

Materials/methods: From January to October 2019 a total of 1121 bacteremia episodes were recorded. Of them, 742 were considered true (698 monomicrobial, 44 polymicrobial) and 379 contaminations. TTPs of the first positive bottle of all monomicrobial episodes (n=698) and of the ones considered contaminants (n=379) were evaluated. Blood culture samples are routinely incubated at 35ºC until they yield a positive signal or for up to five days in a BD-BactecFX (BD®) automated instrument. Each new episode is daily discussed by the antimicrobial stewardship program team.

Results: Table 1. The average TTP for true cases was 17.3h (16.8h excluding yeasts) and 32.5h for contaminants. Bottles of true episodes flagged positive considerably faster ($p<0.001$) than the ones considered contaminations. Regarding true episodes, 44.3% (309/698) grew in ≤12h, 85.4% (596/698) in ≤24h and 95.7% (668/698) in ≤48h. 98.7% (309/313) of the microorganisms with a TTP≤12h were involved in a true episode. Regarding Enterobacterales, in 61.5% (122/343) the TTP≤12h. Considering coagulase negative staphylococci (CoNS), the isolates considered contaminants yielded a TTP significantly higher ($p<0.001$) than the ones involved in infection. No significant differences in TPPs were observed among *Staphylococcus aureus* and significant CoNS, or among Enterobacterales and non-fermenting Gram-negative bacteria.

Conclusions: In hospitals with a high contamination rate, TTP can be especially useful in guiding towards the type of microorganism involved and its role in infection.

Table 1 Time-to-positivity (TTP) of isolates and its role in infection.

		Number of isolates	TPP (hours)	TTP≤12h
True bacteremia episodes		**698**	**17.3 (2.4-117.6)**	**44.3% (309/698)**
Gram-negative bacteria (n=391)	Enterobacterales	343	13.9 (2.43-94)	61.5% (211/343)
	Escherichia coli	253	13.3 (2.43-94)	65.2% (165/253)
	Non-Fermenting Gram negative bacteria	27	21.6 (10.8-59.2)	3.7% (1/27)
Gram-positive bacteria (n=296)	*Staphylococcus aureus*	63	17.6 (6.2-69.4)	33.3% (21/63)
	CoNs	95	20.8 (3.2-70.3)	12.6% (12/95)
Yeasts		11	46.7 (13.1-117.6)	0% (0/11)
Contaminations		**379**	**32.5 (10.6-118.4)**	**1.1% (4/379)**
CoNs		322	27.3 (13.0-103)	0% (0/322)

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Abstract 583

Treatment of latent tuberculosis infection based on the interferon-gamma releasing assay in allogeneic stem cell transplant recipients

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Background: The tuberculin skin test is being replaced by the interferon-gamma releasing assay (IGRA) for diagnosing latent tuberculosis infection (LTBI) in transplant recipients. However, there is limited evidence that IGRA-based LTBI treatment is effective in preventing TB in hematopoietic stem cell transplant (HCT) recipients. Therefore, we have evaluated its effectiveness.

Materials/methods: We retrospectively enrolled patients who underwent allogeneic HCT from January 2010 to December 2018 in a tertiary hospital in an intermediate TB-burden country, and observed TB development for at least 6 months of follow-up until 24 months after HCT. All patients underwent IGRA using QuantiFERON-TB Gold In-Tube (QFT-TB) to screen for LTBI before HCT. LTBI treatment was defined as taking isoniazid (INH) for at least 6 months. We classified the study population into three groups: the negative or indeterminate QFT-TB group, the positive QFT-TB with full LTBI treatment, and the positive QFT-TB without LTBI treatment (no treatment or early discontinued treatment).

Results: A total of 1,162 patients were followed- up for 1,550.4 person-years. 181 (15.6%) patients gave positive QFT-TB results. There were 981 (84.4%) in the negative (n=911) or indeterminate (n=70) QFT-TB group, 51 (4.4%) in the positive QFT-TB with LTBI treatment, and 130 (11.2%) in the positive QFT-TB without LTBI treatment, of whom 75 had no INH treatment and 55 stopped treatment prematurely. 21 (1.8%) patients developed active TB comprising 15 (1.5%) in the negative group, none in both the indeterminate group and in the positive QFT-TB patients with LTBI treatment, and 6 (4.6%) in the positive QFT-TB without LTBI treatment group. The median time from allogeneic HCT to TB diagnosis was 7.4 months (IQR 3.9-10.8). The incidence of TB in the positive QFT-TB without LTBI treatment group (3.58/100 person-years) was significantly higher than in the negative or indeterminate QFT-TB group (1.15/100 person-years) (p=0.01), and there was a trend towards it being higher than in the positive QFT-TB with LTBI treatment group (0/100 person-years) (p=0.09). The number needed to treat (NNT) was 22 (95% CI 12-99) with positive QFT-TB results.

Conclusions: IGRA-based INH treatment appears to lower the rate of post-transplant TB after HCT, with a reasonable NNT.

Table. Active tuberculosis based on QuantiFERON Gold In-tube assay and treatment of latent tuberculosis in allogeneic hematopoietic stem cell transplant recipients

	Confirmed or probable TB incidence rates				
	Number of total patients	Number of TB cases	Number of person-years	TB rate per 100 person-years	95% CI
Negative or indeterminate QFT-TB	981	15	1,303.2	1.15[a,c]	0.64-1.90
Negative QFT-TB	911	15	1,225.5	1.22[d]	0.69-2.02
Indeterminate QFT-TB	70	0	77.7	0	0-4.75
Positive QFT-TB with LTBI treatment	51	0	79.8	0[a,b]	0-4.62
Positive QFT-TB without LTBI treatment	130	6	167.4	3.58[b,c,d]	1.32-7.80

TB, tuberculosis; QFT-TB, QuantiFERON-TB Gold In-tube; LTBI, latent tuberculosis infection; CI, confidence interval

[a]P value = 0.34 between the negative or indeterminate group and the positive QFT-TB with LTBI treatment group

[b]P value = 0.09 between the positive QFT-TB with LTBI treatment group and the positive QFT-TB without LTBI treatment group

[c]P value = 0.01 between the negative of indeterminate QFT-TB group and the positive QFT-TB without LTBI treatment group

[d]P value = 0.02 between the negative QFT-TB group and the positive QFT-TB without LTBI treatment group

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Abstract 587

Next-generation infection prevention: integrated whole genome sequencing and clinical epidemiology analysis to detect actionable carbapenem-resistant *Acinetobacter baumannii* transmission hotspots

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Background: CRAB is a significant hospital-acquired pathogen. In our centre, previous infection prevention and control (IPC) resources were concentrated on other multidrug-resistant organisms other than CRAB as the rate of CRAB was stable with no evidence of outbreaks. We used WGS to uncover horizontal transmission of CRAB and established plausible routes of transmission for targeted IPC actions in an endemic setting.

Materials/methods: We prospectively collected epidemiological characteristics of patients with CRAB infection or colonisation, and identified genetic relatedness of CRAB isolates using a pairwise single nucleotide polymorphisms (SNP) threshold of ≤ 11. We investigated patients with genomically-linked CRAB isolates for either spatio-temporal overlap (sharing the same ward at the same time) or spatial only overlap (sharing the same ward at different times). Findings were regularly presented to IPC and intensive care unit (ICU) committees, and follow-up actions were documented.

Results: Of 141 CRAB isolates identified between May and November 2016, 70 (48.2%) from 61 patients were available for WGS. Including 22 clinical (from 12 patients) and 11 environmental CRAB isolates from a previous 2015 study, a total of 92 samples (73 patients) were analysed. WGS identified seven distinct CRAB clusters involving a total of 47 patients (cluster size 1 to 28 patients). Genomic transmissions were explained by spatio-temporal overlap in 14 patients (29.8%) and spatial overlap only in 13 patients (27.7%). The focus of transmission was deduced to be the ICUs (Figure 1). Dissemination of CRAB from the ICUs to general wards and onward horizontal transmission were demonstrated in 2 instances. Clusters were also found to be related to the environmental isolates from 2015 suggesting the environment as a possible site or source of the horizontal transmission. Discussion of the above findings at IPC and ICU meetings led to implementation of enhanced control measures, including terminal environmental cleaning supplemented by hydrogen peroxide vapour disinfectant for rooms occupied by CRAB patients.

Conclusions: This study showed that WGS could be utilised as a "tool-of-persuasion" for action in IPC by demonstrating presence of ongoing transmission of CRAB in an endemic setting and identifying actionable routes of transmission for directed IPC interventions.

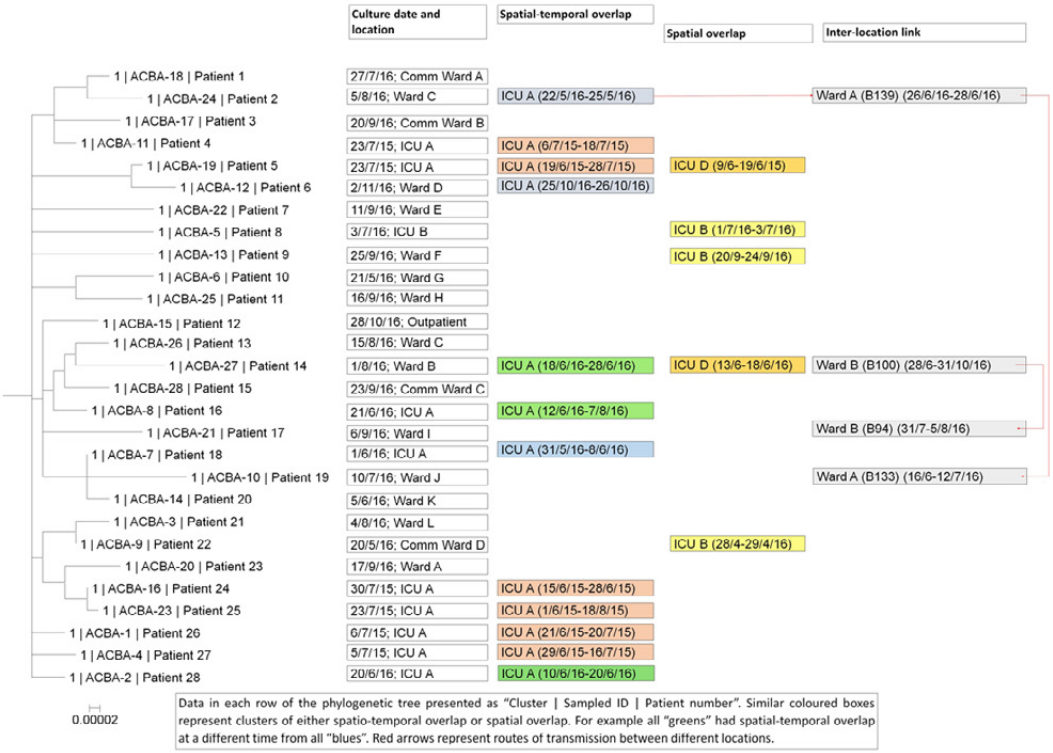

Figure 1: Phylogenetic tree (left) with concurrent epidemiologic information.

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Abstract 588

Correlation between antibiotic resistance of main Gram-negative pathogens and antibiotic consumption in a general hospital of China

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Background: Our hospital is a newly established hospital in China, which is located in the tropics. Better depicting antibiotic consumption and antibiotic resistance may help better develop and implement an antibiotic stewardship with regional characteristics.

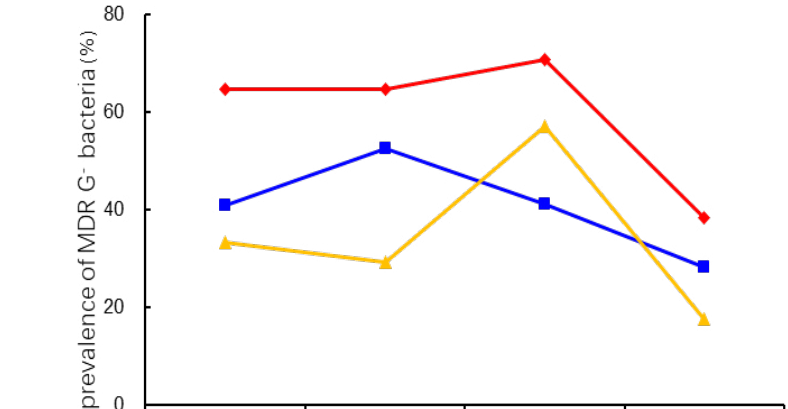
Materials/methods: Total antibiotic prescriptions, patient days and microbiological data from January 2014 to December 2017 were collected. Antibiotic use density (AUD) was expressed as daily defined dose (DDD) and normalized per 100 patient-days. The resistance rates of Gram-negative pathogens against commonly used antibiotics were calculated. The relationship between antibiotic consumption and bacterial resistance rate was described by Pearson's correlation coefficient.

Results: Different from mainland China, *Acinetobacter baumannii* was the leading Gram-negative pathogen, followed by *Klebsiella pneumoniae*, *Escherichia coli* and *Pseudomonas aeruginosa*. The AUD was gradually increased from 2014 to 2016, while it was slowly decreased in 2017. Ceftazidime/tazobactam, levofloxacin and meropenem were the top three consumed antibiotics. The proportion of multidrug resistant (MDR) Gram-negative bacteria was increased (>40%) before 2016, and it was decreased in 2017. The prevalence of MDR *A. baumannii* and MDR *P. aeruginosa* was correlated with the AUD of β-lactam/lactamase inhibitors, fluoroquinolones and carbapenems. The increased AUD of meropenem had positive effects on the incidence of carbapenem-resistant *A. baumannii* and *P. aeruginosa*.

Conclusions: Our study showed that there was an association between the resistance density of Gram-negative pathogens and the consumption of β-lactam/lactamase inhibitors, carbapenems and fluoroquinolones. Collectively, a multifaceted antimicrobial stewardship is necessary to decrease resistance density of available antibiotics.

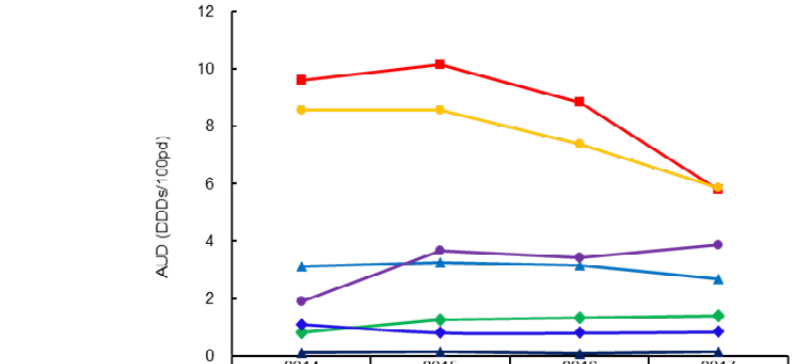
Figure 1. Changing pattern in prevalence of pathogens and AUD of antibiotics from 2014 to 2017. a) MDR Gram-negative bacteria, b) AUD of various antimicrobial agents, c) AUD of mainly used antibiotics. MDR-AB: Multidrug-resistant *A. baumannii*; MDR-PA: Multidrug-resistant *P. aeruginosa*; MDR-KP: Multidrug-resistant *K. pneumonia*. AUD: antibiotic use density; DDD: defined daily dose. pd: patient-day.

a



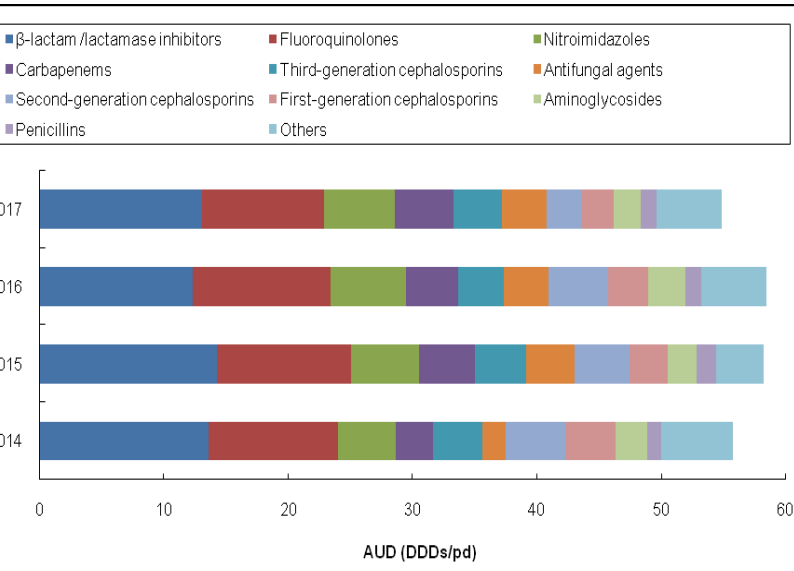
	2014	2015	2016	2017
MDR-AB	64.79	64.64	70.62	38.39
MDR-PA	40.91	52.65	41.06	28.31
MDR-KP	33.33	29.13	57.08	17.73

b



	2014	2015	2016	2017
Ceftazidime	0.82	1.26	1.34	1.40
Ceftazidime/tazobactam	9.62	10.16	8.82	5.78
Cefoperazone/sulbactam	3.11	3.26	3.14	2.66
Meropenem	1.90	3.68	3.43	3.87
Imipenem-cilastatin	1.10	0.82	0.81	0.84
Amikacin	0.12	0.16	0.06	0.13
Levofloxacin	8.58	8.57	7.38	5.85

c



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Abstract 592

Identification of individual risk factors for acquisition of vancomycin-resistant Enteroccocus faecium (VRE) during an outbreak in an university hospital and implication in prevention strategies

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Background: Erasme hospital is the 864 bed academic hospital of the Université Libre de Bruxelles (Brussels, Belgium). A sustained increase in vancomycin resistant *Enteroccocus faecium* (VRE) acquisition occurred in 2017 and involved several departments (mainly intensive care, haematology, and gastroenterology departments). We performed a case control study to identify individual risk factors for acquisition of VRE.

Materials/methods: The study involved the 10 concerned hospitalisation wards, where we had implemented a systematic screening for VRE carriage at admission and during hospitalisation, from 1/1/2017 until 30/9/2018. Isolated VRE were genotyped during a limited period to explore the clonality of the outbreak. For each case, a spatio-temporally matched control was selected among screened patients. Case and control files were reviewed retrospectively to collect 36 selected variables (previous hospitalisation, intensive care stay, prior antibiotic therapy, major co-morbidities and procedures). Variables associated with a *p*-value < 0.1 were integrated into a multivariate model (multiple logistic regression).

Results: 73 patients colonised with *vanA* (n=72) or *vanB* (n=1) VRE fulfilled inclusion criteria and were matched with 73 controls. Genotyping demonstrated a high proportion of monoclonality (71%VRE) among the isolated VRE. A recent previous hospitalisation, intensive care stay, solid organ transplantation, and previous exposure to any antibiotics, or to 8 specific antimicrobial agents were associated with acquisition of VRE in univariate analysis. Among 15 variables with univariate p value <0.10, 4 were identified as independent risk factors for VRE colonization using the multivariate model: prior antibiotic therapy (OR 5,5 [1,1-26,5]; $p = 0,04$), vancomycin (OR 10,2 [1,1 – 95,8]; $p = 0,04$) or metronidazole exposure (OR 24 [2,2-267]; $p = 0,01$) and recent solid organ transplantation (OR 5,8 [1,1-29,3]; $p = 0,03$).

Conclusions: Our results confirm the role of antibiotic exposure, especially vancomycin but also metronidazole, in the acquisition of VRE. More originally, solid organ transplantation appeared also independently associated with this risk. This last risk factor could have important consequences if confirmed by others, as, in addition to prudent use of antibiotics and infection control measures, it could be recommended to avoid hospitalisation of VRE colonised patients in the same ward than transplanted patients.

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Abstract 593

Evaluation of a new commercial assay for detection and characterisation of carbapenemase genes

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Background: The MAST ISOPLEX®*CRE-ART* is a loop-mediated isothermal amplification (LAMP) assay for detection of genes encoding carbapenemases in Enterobacterales, *Pseudomonas aeruginosa* and *Acinetobacter* species. We describe here the first evaluation of this assay with bacterial strains.

Materials/methods: The assay was evaluated with a diverse collection of 248 Gram-negative bacteria including Enterobacterales ($n = 203$), *Acinetobacter* species ($n = 37$) and *P. aeruginosa* ($n = 8$). A diverse range of carbapenemases were represented as well as a range of controls with other ß-lactamases. Isolates were sampled from Mueller-Hinton agar and DNA was extracted using an extremely simple protocol that involved heating at 95°C for 5 minutes in buffer. An internal process control was added at the point of extraction. The tests were performed on an ABI 7500 real time PCR instrument and the entire procedure (including sample preparation) required approximately 1 hour to generate results.

Results: 154 out of 155 (99.4%) carbapenemase-producing Enterobacterales (CPE) with VIM, NDM, IMP, KPC or OXA-48-like carbapenemases were successfully detected as well as 4/4 carbapenemase-producing *P. aeruginosa* (with VIM or NDM carbapenemases). One CPE isolate with NMC-A remained undetected. For *Acinetobacter*, the assay was able to successfully detect all isolates with OXA-23 ($n = 23$), OXA-24 / OXA-40 ($n = 2$) or NDM ($n = 3$). Eighteen other *Acinetobacter* isolates with carbapenemases (with OXA-51, OXA-58 or OXA-69) remained undetected as these genes are not targeted by the assay. The Ct values for isolates with carbapenemases ranged from 5.01 - 10.37 and provided clear distinction from 2/53 isolates without carbapenemases that generated a signal (Ct values > 20). Both of these isolates were negative on repeat testing. Applying a Ct cut-off value of 15 allowed successful detection of all genes that are targeted by the assay with 100% sensitivity and specificity.

Conclusions: The MAST ISOPLEX®*CRE-ART* is a simple and rapid assay that allows highly effective detection and differentiation of the most common carbapenemase genes including the 5 major carbapenemase genes found in Enterobacterales and OXA-23 in *Acinetobacter* species.

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Abstract 595

Longitudinal analysis of lung microbiota in intensive care unit patients undergoing mechanical ventilation

Laura Alagna*[1], Anna Maria Peri[1], Leonardo Mancabelli[2], Christian Milani[2], Federico Magni[3], Silvia Del Bianco[3], Alessia Vargiolu[3;4], Edoardo Picetti[5], Sara Rossi[5], Tommaso Tonetti[5], Roberto Fumagalli[4;6], Luca Galimberti[4;6], Marcello Guarnieri[4;6], Guglielmo Marco Migliorino[7], Liliane Chatenoud[8], Isabella Sala[8], Alessandra Bandera[1;9], Giuseppe Citerio[3;4], Andrea Gori[1;9]

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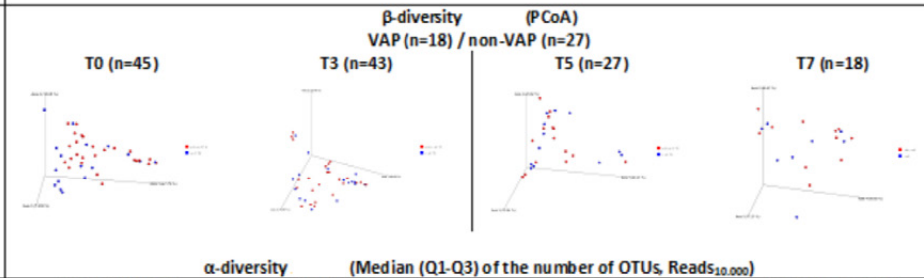
Background: A specific and distinct lung microbiota is present in healthy subjects; changes in commensal composition has been associated with various chronic respiratory diseases. Aim of this study was to explore and quantify the potential modification of lung microbiota during mechanical ventilation (MV), paying particular attention to patients developing within 15 days ventilator associated pneumonia (VAP).

Materials/methods: Pilot observational multicenter prospective study involving two neurological and one general Intensive Care Units. All adult patients admitted from 10/2017 to 03/2019 and intubated for extra-pulmonary reasons with expected duration of MV longer than 48 hours were enrolled. All patient were followed until day 15 or at estubation, when earlier. Tracheal aspirate was collected at intubation (T0), day 3 (T3), 5 (T5) and 7 (T7). Pulmonary microbiota analysis through 16S-rRNA gene sequencing was performed in all VAP patients and in a subgroup of non-VAP ones, comparable within center for reason and period of intubation, and antibiotic administration pre-intubation (48h). Microbiota results are presented according to selected indices of α-diversity and β-diversity, as operational taxonomic units (OTU_S) number and Principal Coordinates Analysis (PCoA), respectively.

Results: Sixty-nine patients were enrolled and microbiota of 18 VAP and 27 non-VAP was analysed. Groups were comparable for sex, Glasgow Coma Score (mean≈8), intubation days (mean=10) and diagnoses at intubation; although VAP patients were slightly younger (mean=46.8) than non-VAP (mean=57.6 years). When number of OTU_S was analyzed over time, despite a wide variability between patients, a significant U-shape was observed, with median values of 139.2, 83.9, 87.2 and 129.8 at t0, t3, t5 and t7, respectively (*p-value*= 0.03 after that age, days of intubation and VAP occurrence were considered into the repeated measures model). When the similarity between patients in terms of microbiota composition (β-diversity) was analyzed at each time point, no major differences emerged between VAP and non-VAP patients, as showed by PCoA figures.

Conclusions: This pilot analysis showed a U-shape time-pattern in the number of OTUs identified in pulmonary microbiota during MV. Considering its wide variability between-patients, larger samples are needed to analyze determinants of this time-pattern and to identify potential differences in microbiota species-composition.



	α-diversity (Median (Q1-Q3) of the number of OTUs, $Reads_{10.000}$)			
Total*	139.2 (77.7-239)	83.9 (38.7-141.9)	87.2 (56.7-177.4)	129.8 (86.1-261.2)
VAP (n=18)	115.3 (80.4-180.5)	62.2 (18.4-116.6)	64.9 (56.4-185.4)	156.2 (125.1-261.2)
Non-VAP (n=27)	193.7 (75.3-241.2)	87.2 (48.2-167.5)	89.6 (65.3-169.4)	125.8 (86.1-164.8)

** Multilevel repeated measures model: time effect p=0.03*

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Abstract 597

Occurrence of NDM-1-producing Morganella morganii and *Proteus mirabilis* in a single patient, Portugal: probable *in vivo* transfer by conjugation

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Background: Recent studies showed that KPC is the most common acquired carbapenemase identified among enterobacterial isolates in Portugal, where OXA-181 producers are also identified at low rate. Our study was initiated by the isolation of two carbapenem-resistant, carbapenemase-producing but KPC- and OXA-181 negative enterobacterial isolates from a single patient in Portugal.

Materials/methods: Carbapenemase genes were searched by PCR assays and mating-out assays were performed to further characterize the plasmid support of the carbapenemase genes. Genetic characterization of the plasmid supports was performed by whole plasmid sequencing using the Illumina technology.

Results: The two carbapenemase-producing isolates, namely a *Morganella morganii* and a *Proteus mirabilis*, were found to produce the NDM-1 carbapenemase. Surprisingly, both isolates shared the same bla_{NDM-1}-positive plasmid. This 154-kb in-size plasmid belonged to the IncA/C type and co-harbor two AmpC ß-lactamase genes, namely bla_{CMY-4} and bla_{DHA-1}, in addition to the 16S rRNA methylase gene *armA* encoding high-level resistance to aminoglycosides. Moreover, the *M. morganii* isolate produced the CTX-M-33 extended-spectrum ß-lactamase possessing weak carbapenemase activity, encoded by another plasmid.

Conclusions: We showed here that, apart from KPC-type and OXA-181 carbapenemases that have been identified as common, another concern is the emergence of NDM-1-producing enterobacterial isolate in Portugal. We demonstrated here the in-vivo plasmid transfer of bla_{NDM-1}-positive plasmid leading to dissemination of that carbapenemase gene within different enterobacterial species in a given patient.

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Abstract 600

Impact of a catch-up strategy of Tdap vaccination during hospitalisation on vaccination coverage among people over 65 years of age in Sarthe: the HOSPIVAC study

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Background: The Tetanus-Diphteria-Polio (Tdap) vaccination coverage of the elderly in France is insufficient and decreases with age. The main objective of this study was to evaluate the impact of a catch up strategy of Tdap vaccination during hospitalization among people over 65 years of age in Sarthe. The secondary objectives were to assess the Tdap vaccination coverage of this population and the factors independently associated with the vaccination status being up to date.

Materials/methods: This was a prospective, monocentric, randomized, clustered study. From 28/05/2018 to 27/05/2019, eligible patients over 65 years of age hospitalized in the general medicine ward at Le Mans General Hospital were included. The Tdap vaccination status of patients was collected at inclusion in both groups. In the intervention group, the vaccination update was performed during hospitalization. In case of temporary contraindication or refusal, a prescription was given to the patient upon discharge. The final vaccination status was collected during a call to the patient's general practitioner two months after discharge from hospital.

Results: 157 patients were included, 73 in the intervention group 84 in the control group. In the intervention and control groups, vaccination coverage increased by 24.6% and 2.4% respectively ($p<0.001$). The vaccine coverage at inclusion was 46.5%. The factor independently associated with the vaccination being up to date was having been sufficiently informed about vaccination by the general practitioner OR = 5.07 [2.45-10.51]. In terms of knowledge of immunization status, 27.4% of patients who thought they were up to date were not.

Conclusions: The Tdap vaccination coverage of patients over 65 years of age in Sarthe is low. A catch up strategy for Tdap vaccination during hospitalization is effective. The availability of vaccines in hospital should improve immunization coverage. The systematic collection of the vaccination status of patients at entry should be facilitated by new data collection tools. The general practitioner is a source of information on vaccination for the population over 65 years of age.

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Abstract 602

Faecal microbiota transplantation in the treatment of *Clostridioides difficile* infection

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Abstract third-party references: Supported by Ministry of Health, Czech Republic – conceptual development of research organization (FNBr, 65269705)

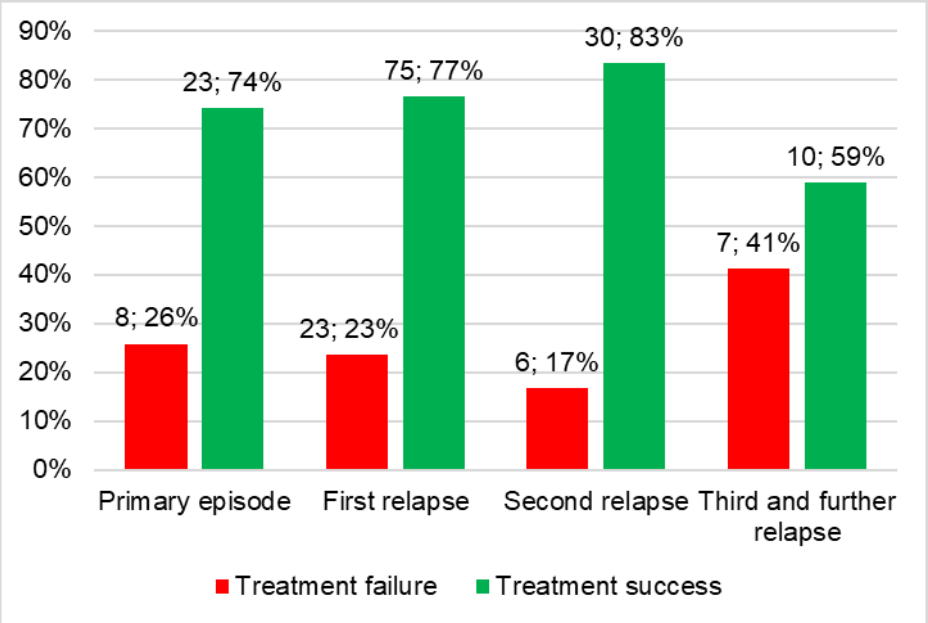
Background: Fecal microbiota transplantation represents a unique therapeutic procedure targeted to restore the natural diversity of intestinal microbiota and to prevent recurrence of one of the most significant nosocomial infections – *Clostridioides difficile* colitis. The aim of this prospective study was to assess the success rate and safety of fecal bacteriotherapy in the treatment of *Clostridium* colitis at a clinic that had been the first in the Czech Republic to perform this procedure as early as 2010, and still is the national leader in the number of realized transplantations to-date.

Materials/methods: Within the monitored four-year interval (2015–2018), 172 patients were treated by means of intestinal microbiota transplantation. The patients were followed up by means of personal visits or by phone after treatment. If colitis did not recur within eight weeks, the treatment was evaluated as successful.

Results: The overall success rate of FMT in the study period was 76 %. Advanced patient age was the only separate risk factor for treatment successful identified through subgroup analysis. No statistically significant difference in success rate was demonstrated based on patient sex, the way of fecal transplant application, initial antibiotic therapy or on the application of fresh or frozen donor stool. Two serious adverse events were observed in the study period; both cases were of rectal wall perforation, and occurred during stool suspension application via rectal enema. There was no lethality.

Conclusions: Fecal microbiota transplantation is a successful and safe therapeutic alternative for recurrent colitis caused by *Clostridioides difficile.*

Diagram 1: Dependence of FMT success rate on the number of previous CDI episodes



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Abstract 603

Nasopharyngeal viral load determinants among influenza-infected patients receiving primary care in France: 2010-2018

Romain Gueneau*[1], Sylvie Behillil[2], Enouf Vincent[2], Madec Yoann[1], Sylvie Van Der Werf[2]

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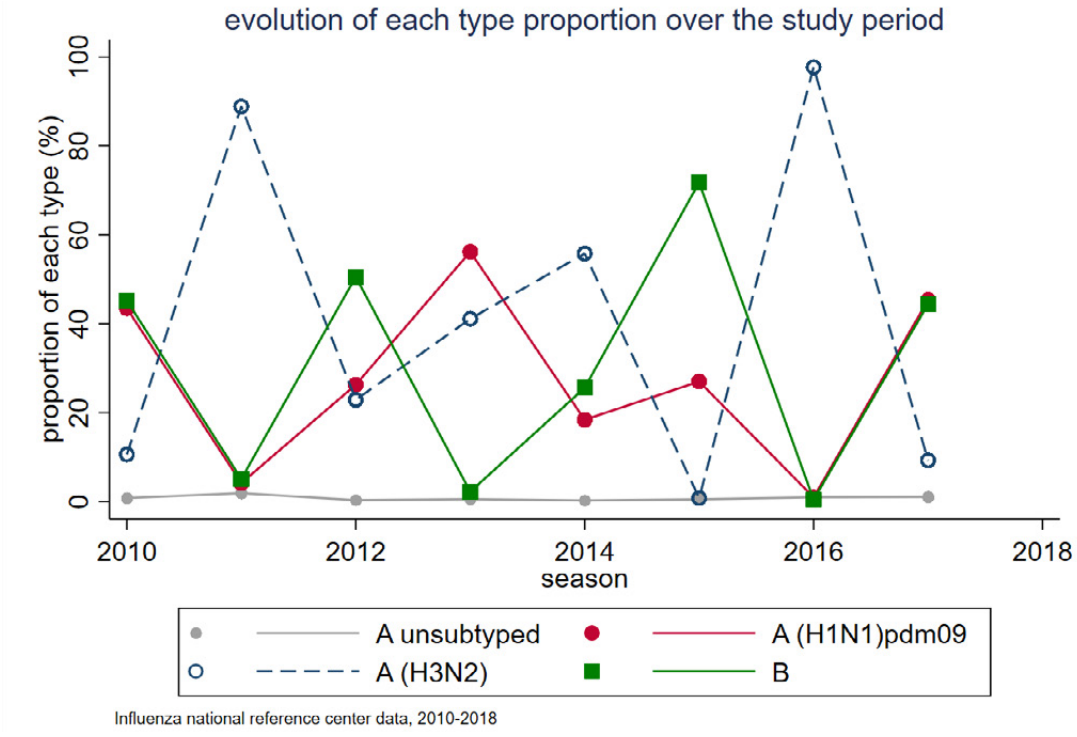
Background: Influenza, is a continuing major public health problem due to recurrent seasonal epidemics justifying epidemiological and virologic surveillance. Virus detection by RT-qPCR, widely used for surveillance, is mostly a qualitative diagnosis tool but also allows to estimate the viral load (VL). We analyzed factors associated with VL in nasopharyngeal specimens from patients attending primary care with confirmed influenza virus infection.

Materials/methods: Patients recruited by the French primary care surveillance networks in the Northern half of France during the 2010-2011 to 2017-2018 seasons for which a nasopharyngeal swab was found positive for influenza virus type A or B by RT-qPCR were included. For each patient, epidemiological and clinical data were collected. Analyses by RT-qPCR performed at the National Influenza Center also provided influenza A virus subtype and an estimated VL. Determinants of VL were identified using multivariate linear regression and severity (presence of dyspnea or hospitalization) determinants were identified using logistic regression.

Results: Overall, specimens from 6297 patients were included, ranging from 365 in 2013-2014 to 1179 in 2015-2016. Of these, 50.7% were men. Median (inter quartile range) age at diagnosis was 20 (6-43) years. Influenza virus was A(H1N1)pdm09 in 1722 (27.4%) patients, A(H3N2) in 2184 (34.7%) patients and B in 2345 (37.2%) patients. Mean (standard deviation) VL was 4.78 (1.43) log copies/µL. In multivariate analysis, patients infected with A(H3N2) and B viruses presented significantly higher VL then those infected with A(H1N1)pdm09 ($p<0.001$). The 2012-2013 and 2014-2015 seasons were characterized, in multivariate analysis by lower VL than all other seasons ($p<0.001$). The other factors associated with increased VL were younger and older ages (<2, 2-4, 4-15 and ≥65 years; $p<0.001$), male gender ($p=0.01$), presence of rhinitis ($p<0.001$), and being vaccinated in patients older than 65 years or immunocompromised ($p=0.04$). In multivariate analysis, higher VL was associated with increased severity, but the type of influenza virus was not associated with severity.

Conclusions: After adjusting for confounding factors among which the influenza virus, VL fluctuations remained between seasons, with no appropriate explanations today. However, we noted that the seasons exhibiting the lowest VL levels were always those when the three viruses co-circulated.



Influenza national reference center data, 2010-2018

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Abstract 607

Flu isolation wards: does medical specialty matter? Comparison of three specialties on outcome and antibiotic usage in hospitalised influenza A infected patients in Vienna during the season 2018/19

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Background: Diagnosis and care of influenza are often provided across several medical specialties. We compared patient outcomes at the infectious diseases (ID), rheumatology (Rheu) and the pulmonology (Pul) department.

Materials/methods: In this exploratory-prospective-observational multi-centre-study we included all influenza positive patients ≥18 years who were hospitalized for critical medical reasons and treated at flu-isolation-wards in three hospitals in Vienna during the season 2018/19. Diagnosis was made via Cobas®Liat®-POCT.

Results: 490 patients with a median age of 73 years (IQR 61-82) were included. 48.8% were female. No difference regarding age, sex and underlying diseases were present at admission.

The complications were different: pneumonia (ID 27.8%, Rheu 40%, Pulm 39.8%, p=0.031), acute kidney failure (ID 12.7%, Rheu 21.2%, Pulm 37.1%, p<0.001), acute heart failure (ID 4.3%, Rheu 17.1%, Pulm 14.4%, p<0.001), respiratory insufficiency (ID 45.1%, Rheu 41.5%, Pulm 56.3%, p=0.030).

Oseltamivir prescription was lower at the pulmonology flu ward (ID 79.6%, Rheu 90.5%, Pulm 61.7%, p<0.001).

176 patients (35.9%) had pneumonia. Antibiotic treatment differed between specialties (see table 1).

	Total N=176	Infectious diseases (n=45)	Rheumatology (n=80)	Pulmonology (n=51)	p-value
Amoxicillin/Clavulanic-acid	38.1%	28.9%	63.7%	5.9%	p<0.001
3rd-Generation-Cephalosporin	24.4%	4.4%	5%	72.5%	p<0.001
Piperacillin/Tazobactam	9.7%	6.7%	15%	3.9%	ns (p=0.092)
Levofloxacin	9.1%	4.4%	6.3%	17.6%	ns (p=0.053)
Cefuroxime	8.8%	28.9%	1.3%	0%	p<0.001
Macrolide	8.5%	2.2%	2.5%	23.5%	p<0.001
Doxycycline	4.5%	17.8%	0%	0%	p<0.001
Other antibiotic	4.0%	6.7%	2.5%	3.9%	ns
Antibiotic not known	4.5%	4.4%	7.5%	0%	ns
Combination therapy	9.7%	2.2%	2.5%	27.5%	p<0.001

The median length-of-stay was ID 6 days [IQR 5-8], Rheu 6 days [IQR 5-7] and at Pulm 7 days [IQR 5-9.5], p=0.034. In-hospital-mortality was 4.3%, increased to 9.5% during the 90-day follow-up-period and did not differ between specialties.

Conclusions: We detected differences in oseltamivir usage, length-of-stay and antibiotic choices for pneumonia. Influenza-associated-mortality was not affected by specialty.

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Abstract 614

Ursolic acid and its amide derivatives disrupt clinical *Acinetobacter baumannii* isolates and biofilm formation

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Background: Hospital acquired infections due to antimicrobial resistant ESKAPE pathogens have emerged globally with increased morbidity and mortality. *Acinetobacter baumannii* is a members of ESKAPE pathogens which acquired multiple drug resistance (MDR) even with the last resort drug colistin at rapid phase which hinder its treatment or management. World Health Organization (WHO) categorized *A. baumannii* among the list of pathogens for which new pharmacophore required on urgent basis. So, in this study Ursolic acid (UA) and its synthetic amide derivatives were screened against standard (ATCC: 19606) and clinical isolates of *A. baumannii* strains.

Materials/methods: In the first phase of this study clinical isolates were collected and identified as *A. baumannii* strains phenotypically as well as genotypically. Then the ursolic acid and its derivatives were screened for antimicrobial, biofilm inhibiting and eradicating potential.

Results: Out of tested compounds amide derivative of UA (KSUA-2,4) was found to possess better antimicrobial concentration at 77.87µg/ml against colistin resistant A. baumannii strains (Colistin MIC > 100µg/ml). Compound KSUA-2,4 significantly inhibited or eradicated >60% biofilm formation of tested standard and clinical isolates at MIC. Microscopic analysis further confirms the biofilm inhibition and eradication potential of this compounds. Atomic Force Microscope analysis (AFM) further confirms the antimicrobial properties KSUA-2,4 and suggesting that the antimicrobial action might be due the the membrane leakage. Considering this evidence, microbial membrane potential was determine by using FACS analysis which confirm the loss of membrane potential after compound treatment. Gene expression analysis further explained that this compound inhibit biofilm formation by reducing the gene expressionof *bap* (biofilm gene) and *abaR* (quorum sensing).

Conclusions: Urasolic acid amide derivative KSUA-2,4 significantly inhibit growth and biofilm formation of colistin resistant *A. baumannii* strains, so, might be used to tackle *Acinetobacter baumannii* related nosocomial infections and further evaluated as a drug candidate.

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Abstract 615

Survival outcome in allogeneic haematopoietic stem cell transplant recipients with multiple, sequential *cytomegalovirus*, Epstein-Barr virus, BK virus and respiratory viral infections

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Background: Reactivation of latent double-stranded DNA (dsDNA) viruses [Cytomegalovirus (CMV), Epstein-Barr virus (EBV) and BK polyomavirus (BKV)] as well as community-acquired respiratory viruses can lead to significant morbidity after allogeneic haematopoietic stem cell transplantation (allo-HSCT). The clinical burden of multiple, sequential viral infections in this population has not been well characterized. We aimed to assess the impact of cumulative viral infections on clinical outcome in recipients of allo-HSCT.

Materials/methods: All patients undergoing allo-HSCT between January 2015 to December 2017 at Royal Melbourne Hospital were included in a retrospective analysis. Episodes of viral infection with time to event were recorded for a minimum follow up period of 12 months or until death. Weekly quantitative CMV and EBV PCR to day 100 was performed and as clinically indicated thereafter. BKV PCR and respiratory virus PCR were tested as clinically indicated. An episode of infection was defined as first detectable CMV, EBV, BKV and/or respiratory virus. Statistical analysis evaluating time to multiple viral events was performed using Andersen-Gill and Cox proportional hazard models.

Results: Two hundred and fifty-five patients [median age=51, male (61%)] were included. Indication for HSCT was AML (41%), ALL (11%), MDS (11%), others (37%). Anti-thymoglobulin (ATG) conditioning regimens were used in n=117 (46%). 401 episodes of viral infection were identified in 206 patients. CMV reactivation = 139 (55%), EBV =131 (51%), BK = 53 (21%) and respiratory viral infections were identified in 78 (31%) patients. 19 patients (7.5%) had reactivation of all 3 dsDNA viruses; 9 patients (3.5%) had all 4 viral events. The 12-month all-cause mortality was 26.7%.

ATG use was associated with increased risk of viral infections overall [HR 1.5, 95% CI 1.2-1.8, p<0.001], and a longer median duration of both CMV viremia (79 vs 72 days, p=0.008) and EBV viremia (36 vs 28 days p=0.03). The risk of twelve-month all cause mortality was increased in patients with multiple, sequential viral infections (HR 1.36 95% CI 1.15-1.62, p<0.001).

Conclusions: Multiple episodes of latent dsDNA or respiratory viral infections occurring within the first 12 months of allogeneic HSCT was associated with an increase in overall mortality.

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Abstract 616

Immunogenicity and safety of a quadrivalent influenza vaccine (GC GLU) versus quadrivalent seasonal influenza vaccine (Fluarix Tetra) in Asian adults aged 20 to 50: a phase III prospective, open labeled, multi-centre study

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Background: The egg based quadrivalent vaccines (IV4) was suggested by WHO for use in the 2019-2020. Due to the high demand of IV4 globally, we conducted a non-inforior phase III clinical trial to evluate the Immunogenicity and safety of an IV4 (GC GLU), compared with active controlled (AC) (Fluarix Tetra, GSK).

Materials/methods: The randomized, open labelled, active controlled study was conducted in four sites in Taiwan (NCT03718468). Vaccinee aged 20-50 were enrolled. GC flu is an IV4 contained 60ug purified inactivated influenza virus antigen (15ug each), including A (H1N1), A (H3N2), B (Maryland), and B (Phuket). The primary end point was the non-inferior immunogeneicity of GC flu to AC as HAI titers against each virus strain on Day 22 (GMTac/GMTgcflu<=1.5).

Results: 842 vaccinee were randomized and received one dose of vaccination, and the baseline characteristic was similar in the 2 groups. 840 vaccinee fulfilled PP criteria, with 421 received GC Flu and 419 received AC. For both type A strains, there was no significant difference between GC FLU and the AC. The 95% CI upper bounds of GMTac/GMTgcflu are both 1.00. For both type B strain, the 95% CI upper bounds of GMTac/GMTgcflu are 1.41 (Table 1). Further analyzing GMT using ANCOVA incorporating baseline, study site, and/or age as factors if significant, the upper bounds of the 95% CI of GMTac/GMTgcflu of all 4 strains ≤ 1.5 in PP population. Safety analyses were performed on the 842 ITT population. The local solicited AEs was 80.3% (339/422) in GC flu group and 81.9% (344/420) in AC group. The systemic solicited AEs were 53.6% (238/422) and 45.2% (190/420) and unsolicited AE were 19.2% (81/422) and 16.7% (70/420), respectively.

Conclusions: GC flu exhibit comparable safety profile and immunogenicity non-inferior to Fluarix Tetra.

Table 1 GMT_{ac}/GMT_{gcflu} on Day 22 for PP population

Strain	GMT (Median, 95% CI)		GMT_{ac}/GMT_{gcflu}
	GC FLU	Fluarix Tetra	
A/H1N1	160.77	160.77	1.00
	(159.97, 159.97)	(159.97, 159.97)	(1.00, **1.00**)
A/H3N2	79.84	79.84	1.00
	(80.00, 80.00)	(80.00, 80.00)	(1.00, **1.00**)
B-Yamagata	79.84	79.84	1.00
	(56.54, 80.00)	(80.00, 80.00)	(1.00, **1.41**)
B-Victoria	113.30	160.77	1.41
	(80.00, 159.97)	(113.18, 159.97)	(1.00, **1.41**)

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Abstract 624

Clinical experience with isavuconazole in Chinese healthy volunteers and Chinese patients with invasive aspergillosis

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Abstract third-party references: Funded by Pfizer Inc. Submitted by Karen Miller from CMC Connect, a divison of McCann Health Medical Communications Ltd on behalf of the authors

Background: Invasive aspergillosis (IA) has an increasing incidence in China. We present experience with the antifungal isavuconazole in Chinese subjects from two clinical studies: a Phase I study in healthy volunteers (Study 9766-CL-0038 [NCT01555918]) and the global Phase 3 SECURE study (NCT00412893) in patients with IA.

Materials/methods: Healthy volunteers received an oral or intravenous dose of isavuconazole 200 mg on Day 1 of each 15-day period, followed by a 2-week washout (Part 1), and 200 mg three-times-daily for 2 days followed by once-daily for 10 days (Part 2). In SECURE, patients were randomised to isavuconazole 200 mg intravenously three-times-daily on Days 1 and 2, then either intravenously or orally once-daily, or voriconazole 6 mg/kg intravenously twice-daily on Day 1, 4 mg/kg intravenously twice-daily on Day 2, then intravenously 4 mg/kg twice-daily or orally 200 mg twice-daily from Day 3 to end of treatment [EOT] (up to 84 days). One patient was randomised to isavuconazole but received voriconazole intravenously for the first 7 days, then switched to oral isavuconazole until EOT and was included in the voriconazole safety population and the isavuconazole intent-to-treat population. Efficacy (SECURE), safety and pharmacokinetic measures were assessed.

Results: Sixty-two Chinese healthy volunteers/patients were included (46 received isavuconazole). Plasma exposure to oral isavuconazole was higher in Chinese than Western healthy volunteers (Studies 9766-CL-0041 [NCT01657890]) and 9766-CL-0017 [NCT01565720]) (Table). In SECURE, trough steady-state isavuconazole concentrations for three Chinese patients were higher (3844–8646 ng/mL) than for the global population (452–8646 ng/mL). The primary endpoint of all-cause mortality through Day 42 was 10% (1/10) in the isavuconazole group and 25% (4/16) in the voriconazole group. Overall, 88.9% (8/9) of Chinese isavuconazole-treated patients experienced ≥1 treatment-emergent adverse event, as did 94.1% (16/17) of those receiving voriconazole. Efficacy and safety trends were similar to the global population.

Global isavuconazole exposure-response modelling results revealed no statistically significant relationships of exposure with efficacy endpoints. Furthermore, the differences in exposure were not associated with differences in safety outcomes.

Conclusions: Safety/efficacy in Chinese patients was consistent with the global population. Higher exposure did not alter safety/efficacy outcomes in the global analysis.

Table. Comparison of isavuconazole exposure in Chinese healthy volunteers from Study 9766-CL-0038 and Western healthy volunteers after oral administration[a]

Parameter	Single-dose		Multiple-dose	
Mean (SD)	Chinese HVs	Western HVs	Chinese HVs	Western HVs
Study	9766-CL-0038	9766-CL-0041	9766-CL-0038	9766-CL-0017
n	12	24	12	37
C_{max} (µg/mL)	3.4 (0.5)	2.3 (0.5)	8.9 (1.7)	7.5 (1.9)
AUC (µg·h/mL)[b]	116.4 (36.3)	96.3 (27.7)	140.4 (32.8)	121.4 (35.8)

[a]Note: the pharmacokinetics of isavuconazole are linear and dose-proportional following both oral and intravenous administration.
[b]AUC is AUC_{inf} for single-dose results, AUC_{tau} for multiple-dose results.
AUC, area under the time–concentration curve; C_{max}, maximum concentration; HV, healthy volunteer; SD, standard deviation.

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Abstract 634

The potential benefit of a second C-reactive protein measurement in patients with Gram-negative bacteraemia presenting to the emergency medicine department

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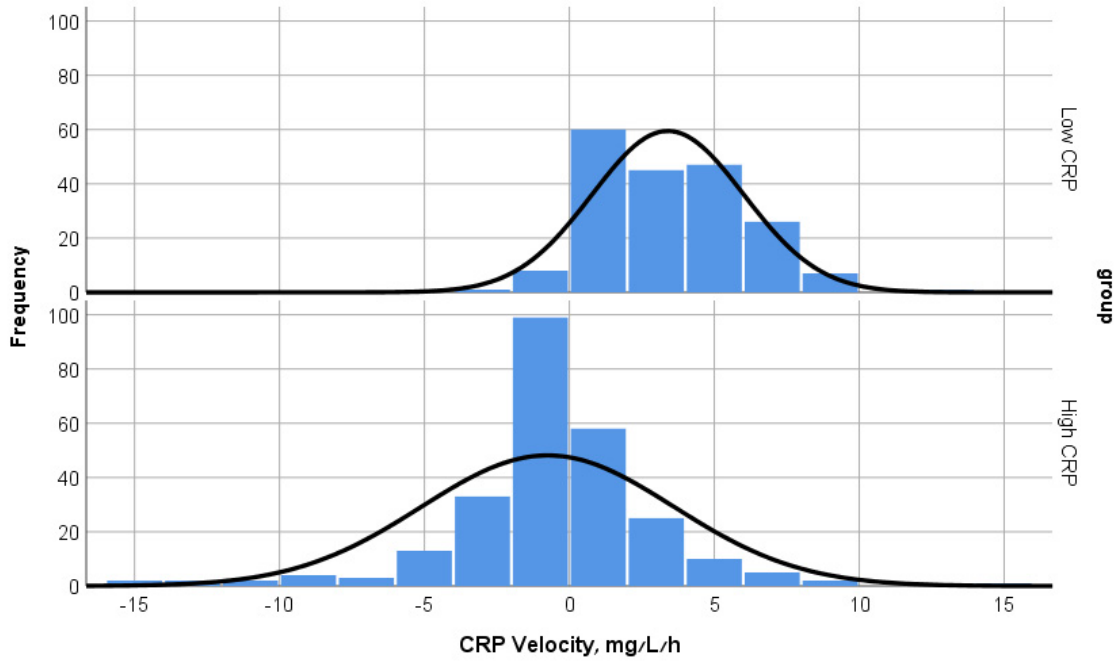
Background: Low concentrations of C-reactive protein (CRP) in patients presenting with acute bacterial infections to an emergency medicine department could convey the erroneous impression of a relatively mild infection. We focused on a group of patients with gram negative bacteremia, a phenomenon frequently seen in the emergency medicine department.

Materials/methods: Of the 2200 patients with gram negative bacteremia, we reviewed the medical records of 460 patients who presented with CRP <30mg/L and 460 patients with CRP>187mg/L. Following a series of exclusions, we finally investigated 229 and 289 patients with low and high CRP concentrations, respectively. The cut-off values of relatively low and high CRP were obtained by using a large (n=17,206) database of apparently healthy individuals.

Results: We divided our total cohort into low and high CRP groups. Patients were examined following a mean of 1 and 2.7 days (standard deviation of 2.6 and 3.7 days), respectively from symptom onset. Median first CRP was 13.6 and 219.9 mg/L (interquartile range 6.4-21.6 and 195-270.1) for low and high CRP groups, respectively. Compared to patients with first high CRP, patients with first low CRP concentrations had a significant 5-fold higher CRP level with their second test representing a higher CRP velocity

Conclusions: Patients with gram negative bacteremia can present with CRP concentrations that are within the range of those detected in apparently healthy individuals. A second CRP test obtained in those presenting with low CRP concentrations might prompt the physician to reevaluate the ongoing inflammatory response, thereby avoiding an eventual erroneous decision regarding the severity and prognosis of the infectious condition.

Figure: Frequency of CRP velocity in low and high baseline CRP groups.



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Abstract 638

Daptomycin decreased mortality in methicillin-resistant *Staphylococcus aureus* bacteraemia compared to vancomycin: a monocentric retrospective study of 96 cases

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Background: MRSA bacteraemia is a severe and frequent infection currently treated with Vancomycin as gold standard. However Vancomycin, has a slow bactericidal effect, a slow diffusion in tissue, and severe adverse effects that may alter prognosis. Daptomycin, a lipoglycopeptide, has less adverse effects and is more bactericidal. Currently data are missing to support the non-inferiority of Daptomycin against Vancomycin in MRSA bacteraemia on clinical outcomes. We aimed to demonstrate the non-inferiority of Daptomycin on mortality in this context.

Materials/methods: In a monocentric retrospective study, we included 96 patients with MRSA bacteraemia treated with Daptomycin or Vancomycin in a university hospital in Amiens, North of France between 2010 and 2019. We excluded patients with pneumonia or with polymicrobial bacteraemia. The primary outcome was survival after 30 days of antibiotic. The secondary outcomes were tolerance (acute renal failure or end of treatment for adverse events), blood culture (BC) negativation, time to BC negativation, time to apyrexia, length of stay and complications (secondary abscess, endocarditis, septic arthritis or spondylodiscitis).

Results: Both groups were similar in terms of age (mean ± SD in vancomycine group vs daptomycine group) (70.5 ± 13 vs 70.2 ± 11.6) and severity (evaluated by SOFA score, median [interquartile range]) (3 [2-4.5] vs 4 [2-5.5]). There was more men treated with Daptomycine (sex ratio H/F=32/7) than with vancomycine (35/22). Mortality was 40% (23/57) and 13% (5/39) in Vancomycin and Daptomycin group respectively (odd ratio (OR) = 0.22, Confidence Interval (CI) 95% = [0.06; 0.69], p<0,005). There were 11 and 4 cases of acute renal failure in Vancomycin and Daptomycin group, respectively (OR = 0.48, IC95% [0.14; 1.65]; 2 and 1 premature end of treatment due to adverse events in Vancomycin and Daptomycin group, respectively. No difference was found regarding length of stay, BC negativation at day 3, time to BC negativation, time to apyrexia or complications.

Conclusions: Daptomycin drastically decreased mortality in MRSA bacteraemia compared to Vancomycin in our cohort but larger study are warranted to confirm these results.

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Abstract 643

A systematic analysis of the direct antiglobulin test in post-artesunate delayed haemolysis during severe imported *Plasmodium falciparum* malaria: a multi-centre retrospective study

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Background: Post-artesunate delayed haemolysis (PADH) is a frequent adverse effect of artesunate treatment for severe *Plasmodium falciparum* malaria. Cases of PADH with positive direct antiglobulin tests (DATs) have been reported, but systematic analyses of the DAT and its responsibility in the late haemolytic event during severe imported malaria are lacking.

Materials/methods: In this multicentre retrospective study, we reviewed medical data from all patients with severe imported *Plasmodium falciparum* malaria in 5 infectious diseases departments over an 8-year period, and included all patients for whom at least one DAT had been performed (DC-Screening I or II, Biorad©) . We further analysed parameters of anaemia and haemolysis from day 0 to day +28 of treatment initiation in patients for whom sufficient follow-up data was available. We defined PADH as a 10% drop in haemoglobin levels and a 10% rise in lactate dehydrogenase levels occurring after day 7 of treatment initiation.

Results: Out of 355 patients with severe imported malaria, 46 patients with at least one DAT evaluation were included (including 7 with 2 separate DAT evaluations). The median age of patients was 44.5 years, and median parasitaemia was 6.4%. Overall, 53 DATs were performed at a median (min-max) of 10 (1-35) days after treatment initiation, which coincided within 7 days of a patient's haemoglobin nadir in 74% of cases. The DAT was positive in 50.9% (27/53) of cases. Most were positive for IgG (22/27, 81%), among which 63% (17/27) were weakly positive. Among 40 patients with sufficient follow-up data, 17/40 (42.5%) experienced PADH. Compared to patients without PADH, those who experienced PADH had significantly higher median haemoglobin levels (12.4g/dL vs 10.6g/dL, p = 0.021) and parasitaemia (11.4% vs 6%, p = 0.046) at admission. DAT positivity was not significantly associated with the occurrence of PADH (p = 0.36). No patient received systemic corticosteroids, 41% required one or more erythrocyte transfusions, and outcomes were favourable in all cases.

Conclusions: DAT positivity is frequent during severe imported malaria. Auto-immune haemolysis does not appear to be a significant pathophysiological mechanism in most cases of PADH, although it may be involved in some rare cases.

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Abstract 645

Interplay between inflammation and infection in a single-centre cohort of patients with X-linked agammaglobulinemia

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Background: X-linked agammaglobulinemia (XLA) is a rare primary antibody deficiency associated with increased susceptibility to early-life infections. Various inflammatory manifestations have been reported during XLA but they are less well-characterised than in other primary immune deficiencies (PID), and are sometimes difficult to distinguish from cases of atypical infections.

Materials/methods: We carried out a retrospective cross-sectional analysis of the medical records of all patients with XLA referred to our hospital between 2009 and 2019. We reviewed data on all inflammatory manifestations, including clinical, biological, histological features, and link to a pathogen. In addition, we reviewed data on all infections before XLA diagnosis, at ages 16 to 18, and at last follow-up. Only infections that led to hospitalisation or that were documented were considered. We also retrieved data regarding use of antibiotic prophylaxis, immunosuppressive treatment, and last residual immunoglobulin level.

Results: Sixty patients with definite XLA were included. Median age (range) at last follow-up was 22.5 (4-59) years. Forty-seven inflammatory flares were reported in 14 patients (23.3%). The most frequently affected organ was the gastro-intestinal tract, presenting as inflammatory bowel disease or coeliac-like enteropathy in 8 patients (13%). Eight/14 (57%) patients received systemic corticosteroids and 4 received tumour necrosis factor inhibitors. A total of 188 infections were recorded, including 95 after initiation of immunoglobulin replacement therapy (IgRT). The most common sites of infection were the lungs and the gastro-intestinal tract. Of note, we recorded 13 cases of Giardia intestinalis infections and 12 cases of Campylobacter spp. infections. Overall, 53% of patients experienced either inflammatory or infectious manifestations despite IgRT during a total follow-up of 1470 patient-years. These occurred more frequently during adulthood than before the age of 16. Having a history of at least one inflammatory manifestation was significantly associated with experiencing more infections (0.14 vs 0.04 infections per person-year, p = <0.001) and more hospital admissions (6.29 vs 1.09 admissions, p = <0.001), as well as receiving higher mean monthly IgRT doses (0.74 vs 0.54 g/kg/month, p = 0.014) in adulthood.

Conclusions: Inflammatory manifestations are of increasing importance in XLA patients reaching adulthood and are associated with increased susceptibility to infection

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Abstract 646

Investigating the sexual protective behaviour among HIV-positive women in Tehran, Iran

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Abstract third-party references: Iranian research center of HIV/AIDS/For validation of data not for fund

Background: The third wave of human immunodeficiency virus (HIV) is rising due to high-risk sexual behaviours in Iran. In spite of launching programs to combat HIV in Iran, condom use frequency has not yet reached the optimal level, especially in high-risk groups. The aim of this study was to assess the sexual protection behaviours and awareness among HIV-positive women.

Materials/methods: This descriptive study was performed on 100 HIV-positive women who referred to the Voluntary and Counselling Centre (VCT) in Tehran and were recruited using a purposive sampling method. Data collection was carried out using HIV/acquired immunodeficiency syndrome (AIDS) awareness and sexual protection behaviour questionnaires.

Results: Condom use was practiced only by 22.2% in all their vaginal and anal sexual intercourse during the three months, and 77.8% of the women never used condoms or failed to use them continuously. Their sexual partners were HIV-positive in 71% of cases. The mean ± SD of awareness score about HIV/AIDS was 7.60 ± 3.31, indicating average awareness of the subjects in the study. A totalof 49.1% of the participants stated that their sexual partners' reluctance was the most important reason for non-use of condoms, while women were not willing to use condoms in 18.2% of cases.

Conclusions: The results of the present study indicated poor sexual protection behaviours in HIV-positive women. As a result, gender-based harm reduction programs to promote safe sexual behaviour, awareness level, and negotiation power for condom use in HIV-positive women is more important than ever.

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Abstract 652

Correlation between serum C-reactive protein levels and CURB-65 in elderly patients with community-acquired pneumonia

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Background: : CURB-65 is an important clinical score for severity in community- acquired pneumonia (CAP). C-reactive protein (CRP) an acute phase protein marker for bacterial infection or tissue inflammation. Serum CRP levels are well correlated with the severity of CAP. We aimed to investigate whether serum levels of CRP correlates with CURB-65 ranking in hospitalized patients with CAP.

Materials/methods: 858 patients aged 18 - 90 years who were hospitalized with CAP during a period of two years in the departments of Internal Medicine at Ziv Medical Center in Safed, Israel, were collected. Five hundred patients who met the inclusion and exclusion criteria were included. CURB-65 and serum levels of CRP within 24 hours of admission were collected for each paricipant. The correlation between serum CRP levels and CURB-65 were analyzed by Spearman's rank correlation test.

Results: The mean age of all study group was 64±19 years, and the means CRP levels and CURB-65 score were 114 ± 100 mg/dl, 1.4±1.1points, respectively. No significant correlation was found between CRP and CURB-65 for all study group (R=-0.014, P=0.768). Nevertheless, we found a significant correlation between CRP and CURB-65 in 320 patients aged ≥ 65 years (R=0.126,P=0.024)

Conclusions: In this study we found a significnat correlation between CRP and CURB-65 among elderly patients aged ≥65 years but not among patients bellow the age 65 years. We believe that CRP measurments could be used as adjuvant marker to CURB-65 for assessment CAP severity in elderly patients.

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Abstract 656

Genome-based epidemiology and antimicrobial susceptibility of a nation-representative collection of clinical isolates of *Acinetobacter baumannii* obtained from Saudi Arabia

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Abstract third-party references: King Abdullah International Medical Research Center, King Abdulaziz University

Background: *Multidrug-resistant Acinetobacter baumannii has emerged as one of the most troublesome pathogens for health care institutions worldwide. However, limited information is collected on the antimicrobial resistance rates among clinical isolates in Saudi Arabia. Here we characterized a nationally representative collection of isolates.*

Materials/methods: Isolates (n=200) were collected between March-2018 and March-2019 from five National Guard-Health Affairs hospitals covering the east, west and centre of Saudi Arabia. Identification was confirmed by species-specific PCR. Susceptibility testing were obtained with the VITEK II system and broth microdilution. β-Lactamase genes were sought by PCR. Selected (n=114) isolates were further characterized by multi-locus sequence typing (ST) (n=71) using the Oxford scheme or by whole genome sequencing (n=43) on the MiSeq instrument. Phylogeny was defined by single nucleotide polymorphism (SNP) analysis.

Results: Majority (122/200, 61%) of the isolates were resistant to carbapenems among which 118/122 (96.8%) encoded Oxa-23-like; the remaining (4/122, 3.2%) produced Oxa-24-like. Isolates were variably resistant to gentamicin (36.5%) and tobramycin (42.4%) but remained mostly susceptible to colistin (93.7%) and tigecycline (78.8%). MLST and genome sequences identified 26 and 21 different STs among carbapenem-resistant (n=90) and -sensitive (n=24) isolates, respectively. STs of carbapenem-sensitive isolates were highly diverse whereas most (88.9 %, 80/90) of those identified in resistant isolates were single or double locus variants of each other and comprised ST557 (n=25), ST218 (n=23), ST195 (n=13), ST1286 (n=8), ST451 (n=4), ST208 (n=2), ST444 (n=2), ST214 (n=1) and ST1050 (n=1), all of which belonged to ST2 (Pasteur scheme). Overall, phylogenetic analysis clustered carbapenem-resistant ST2 isolates according to their Oxford STs, but these were hundreds of SNPs apart. Among most common STs, SNP analysis identified close relatedness between isolates collected from the same or different hospitals suggesting inter- and intra-hospital transmission.

Conclusions: Our results showed a high prevalence rate of carbapenem resistance among A. baumannii in Saudi Arabia that was mainly associated with the acquisition of Oxa-23-like carbapenemase. Majority of carbapenem-resistant isolates belonged to ST2 (Pasteur scheme) but these were highly diverse at the whole-genome level. Spread of resistance was partially explained by clonal dissemination.

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Abstract 657

Feasibility, reproducibility and first results of a multimodal prevention approach for KPC-Kp in a high prevalence hospital setting

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Background: Targeted actions of infection control on hospital institutions' local epidemiology and resources are required to contain carbapenemase-producing *Klebsiella pneumoniae* (KPC-Kp).

Materials/methods: An interchange protocol with the Infectious Diseases Unit of Modena Polyclinic was started to verify the feasibility of "Anti-KPC-Kp bundle" in the setting of S.M. Goretti Hospital of Latina (a tertiary university care centre with a high endemicity of KPC-Kp). A dedicated multidisciplinary working group was set up. Standardized indexes were defined to evaluate setting modifications and proposed targets in 3 high-risk wards (Intensive Care Unit (ICU), Emergency Medicine, Neurosurgery):

-active surveillance of rectal colonization;

-handwashing adherence assessments;

-alcohol solution consumptions, L/1000patient-days (PD);

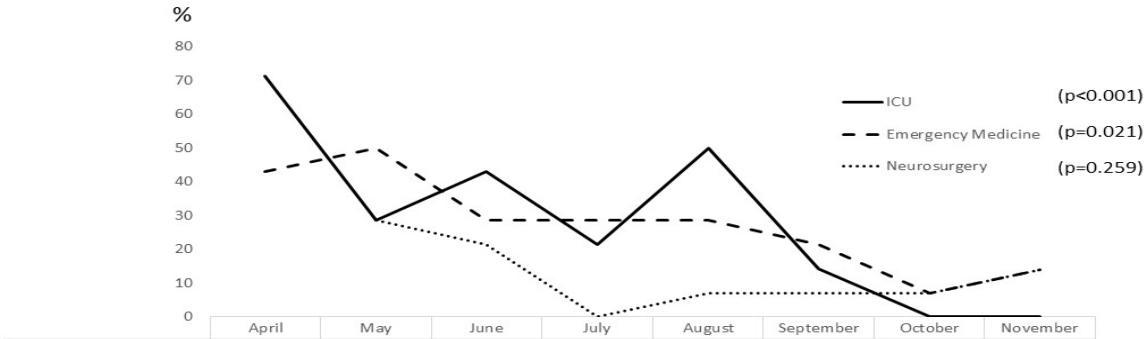
-meropenem Defined Daily Dose (DDD)/100PD;

Statistical analysis:Indexes modifications are shown in percentages or changes in level (average±SD). A Poisson regression model was applied to analyse the trend of KPC-Kp prevalence in ICU, Emergency Medicine and Neurosurgery. Only for ICU, a Poisson regression model was applied also to analyse the trend of the incidence density rates, considering the total hospitalization days as an offset in the model. Active control by participative focus groups among healthcare workers ensured the continuous implementation of the bundle.

Results: At baseline carbapenem resistance in all Kp hospital's blood cultures was 71,4% (in ICU 87,5%).

KPC-Kp prevalence reported monthly on the first day showed a dramatic reduction (Figure 1).

Figure 1: KPC–Kp colonization prevalence



	April	May	June	July	August	September	October	November
ICU	71,4	28,6	42,9	21,4	50	14,3	0	0
Emergency Medicine	42,9	50	28,6	28,6	28,6	21,4	7,1	14
Neurosurgery		28,6	21,4	0	7,1	7,1	7,1	14

Results from the Poisson regression models showed a statistically significant negative trend of prevalence in ICU (p<0.001) and Emergency Medicine (p=0.021), but not in Neurosurgery (p=0.259). A statistically significant negative trend was also found for incidence density rates in ICU (p=0.007). At basal, handwashing adherence in ICU was 59,3%. Further assessments are scheduled after starting a structured training program. An increase of alcoholic hand rub consumption was ob-

served from 14,2(SD±7,56)to 33,59(SD±13,11). A slight decrease of meropenem DDD was observed from 19,53(SD±16,98) to 14,09(SD±9,72).

Conclusions: After 8 months, an improvement of the indexes was observed. The exported model based on a multimodal approach exerted a rapid effect on Kp-KPC diffusion in the intensive area of the hospital, also in a different situation of high basal prevalence. A longer follow-up is necessary to confirm these data together with a more detailed carbapenem resistance rates' analysis.

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Abstract 663

Matched-paired analysis of patients treated for invasive mucormycosis with isavuconazole versus standard treatment

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Background: Isavuconazole (ISAV) is a novel, broad-spectrum triazole antifungal, available as both an intravenous and oral water-soluble prodrug, for the treatment of adult patients with invasive aspergillosis and mucormycosis. It was first approved for mucormycosis in 2015 based on data from 37 patients enrolled in a single-arm open-label trial (VITAL study) and 33 matched controls from the FungiScope® registry.[1] Additional real-world data documenting the effectiveness of isavuconazole are obtained from an ongoing retrospective study within FungiScope®.

Materials/methods: FungiScope® proven and probable invasive mucormycosis cases treated with ISAV between 2016 and 2018 were matched with amphotericin B-based treatment controls from 1997 to 2018. Case-matching criteria included disease severity (i.e. central nervous system or disseminated disease), hematological malignancy and surgery. Baseline patient characteristics, key outcomes of clinical response according to the European Organization for Research and Treatment of Cancer/Mycoses Study Group (EORTC/MSG) criteria and all-cause mortality (ACM) were compared descriptively.

Results: 17 ISAV cases (16 proven, 1 probable) and 44 controls (41 proven, 3 probable) were identified. In the majority of cases (n=14, 82%), ISAV was administered as treatment for invasive mucormycosis in patients who had received prior lipid formulations of amphotericin B. In the remaining cases, ISAV was administered after prior posaconazole (n=2) or as primary therapy (n=1). In the control group, all patients received an amphotericin B-based therapy at some point, with 70% (n=31) as their initial or primary documented therapy.

Baseline patient characteristics and causative pathogens were similar between ISAV cases and controls. The overall response (complete or partial response) rates at the final assessment were 47% (8/17) for ISAV cases and 45% (20/44) for controls. ACM was 47% (8/17) in ISAV cases as compared to 59% (26/44) in controls.

Conclusions: In this analysis from FungiScope®, ISAV showed similar overall treatment response and improved mortality as compared to amphotericin B-based treatment in patients with invasive mucormycosis.

[1]Marty FM et al, Lancet Infect Dis. 2016;16:828-837.

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Abstract 664

Anal human papilloma virus infection and disease in HIV-positive and -negative men and woman

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Background: Determining the forms of sexual behavior risk factors for various types of HPV infection is the basis for both understanding the natural courses of different HPV types and designing comprehensive strategies The aim of this study was to evaluate the prevalence of HPV infections in patients with clinical anal lesions and in patients with risky factor of sexual intercourse.

Materials/methods: The analysis involved samples from patients who consecutively came to the Virology laboratory of the Department of Sciences for Health Promotion and Mother and Child Care (Policlinico University of Palermo, Italy), between February 2017 and May 2019 with clinicians' requests for HPV tests Routine laboratory diagnosis of HPV infection was performed on all samples using routine laboratory procedures as previously reported. HPV genotypes were identified using the INNO-LiPA HPV Genotyping Extra II kit (Fujirebio). All cytology, HPV testing, and histological examination was assessed in enrolled population.

Results: we enrolled 113 pts (74 of men and 39 of women), 64 reported anal lesions suggestive of HPV etiology and 49/113 patients showed sexual intercourse as sexual behavior risk factors. 43/113 enrolled pts showed HIV infections (37/74 males and 6/39 females). Among 113 anal sampling investigations we found HPV infection in 74/113 patients. HPV infection was confirmed in 44/64 patients 'with anal lesion suggestive of HPV etiology. HPV infection was confirmed in 30/49 pts with sexual intercourse Oncogenic types were found in 48/74 positive samples: 31 were males and 17 were females. Among 74 HPV positive infections we founded multiple HPV genotype positive analysis in 38/74 cases. 36/38 multiple HPV genotype infection showed high risk genotypes. Overall of these were male with sexual intercourse as risk factors. Please copy and paste the corresponding text here

Conclusions: Our study shows that the presence of HPV and multiple HPV infections in the anal district is high especially in subjects with sexual intercourse risk factors and male gender. Anal HPV lesion should be involved the clinicians to HPV analysis to found multiple and HR HPV infection to prevent cancer evolution and stressed preventive strategies

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Abstract 666

Cost-benefit analysis of rapid influenza testing in German emergency rooms

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Background: Seasonal influenza causes significant morbidity worldwide and has a substantial economic impact on the health-care system. The objective of this study was to assess the cost-benefit by implementing two influenza tests that provides rapid testing results in emergency rooms (ER) of German hospitals.

Materials/methods: A deterministic decision-analytic model was developed simulating the incremental costs of using the Solana Influenza A+B real time molecular assay or the Sofia Influenza point-of-care A+B antigen assays, as compared to those of using conventional clinical judgement alone to confirm or exclude influenza in adult ILI (influenza-like illness) patients, in German ER, prior to hospitalization. Direct costs were evaluated from the hospital perspective, considering resource use directly related to influenza testing and treatment, as well as indirect costs incurred by nosocomial influenza transmission. Univariate sensitivity analysis was performed to examine the extent to which our calculations were effected by varying the parameters considered in our model between plausible extremes. To capture the interactions between multiple inputs, we also provided a probabilistic sensitivity analysis (PSA) by drawing values at random out of the distributions of the respective parameters in a second order Monte Carlo simulation with 10.000 repetitions.

Results: Through base-case analysis and assuming an influenza prevalence of 42.6%, influenza testing with the Solana and the Sofia assays reduced average costs of hospitalized ILI patients by € 132.61 and € 52.16 per tested patient, respectively. Moreover, utilizing the Solana assay, but not the Sofia assay saved € 6.9 per tested patient in favor of the hospital. In PSA, under all reasonable assumptions, implementing the Solana assay reduced hospital costs on average by €144.13 as compared to the clinical-judgement-only strategy, thus, it was found to be constantly less expensive. In PSA, the Sofia assay also resulted in constantly lower expenditures, but of € 119.89 per tested patient compared to the symptom-based approach.

Conclusions: Using highly specific influenza tests that provides a fast testing result in ILI patients at German ER may significantly reduce hospital expenditures.

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Abstract 667

The clinical and molecular epidemiology of non-carbapenemase-producing carbapenem-resistant *Enterobacteriaceae*: a case-case-control matched analysis

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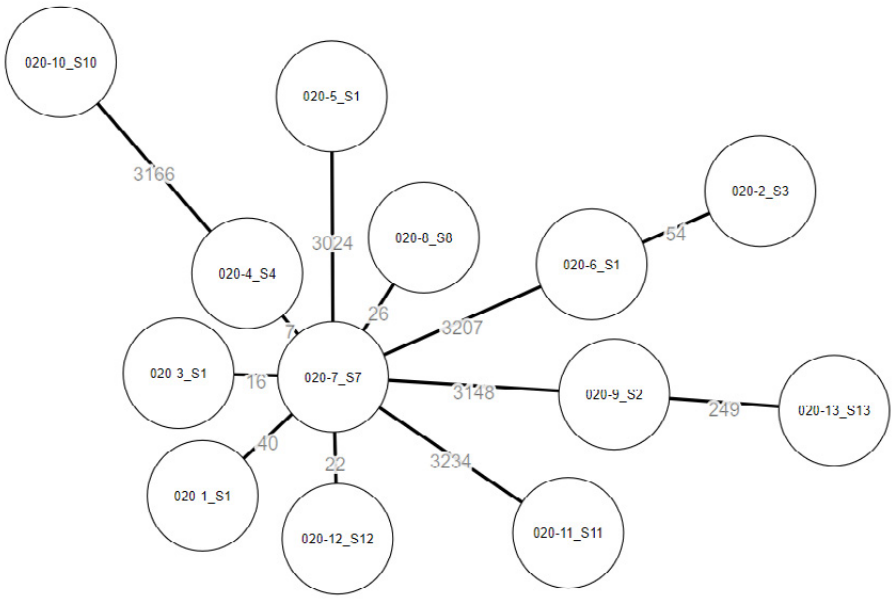
Background: Risk factors and outcomes associated with CRE acquisitions, are derived primarily of cohorts consisting of carbapenemase-producing (CP) strains, but CRE-non-CP are understudied. Study aims were to analyze the clinical and genomic epidemiology of CRE-non-CP.

Materials/methods: A case-case-control matched analysis was conducted at Shamir (Assaf Harofeh) Medical Center, Israel, 11/2014 to 12/2016. Isolates were *Klebsiella* spp., *Escherichia coli* or *Enterobacter* spp. showing meropenem MIC≥ 2 µg/dL and negative for CP detection by multiplex PCR. CRE-non-CP patients (infected and asymptomatic carriers) were matched to patients with non-CRE Enterobacteriaceae carriage, and to un-infected controls (1:1:1 ratio). Matching criteria (in order of importance) included the 1) bacterial species 2) colonization vs. infection status, 3) age group, 4) calendar year, and 5) time at risk (days from admission to culture). Matched multivariable regression models were constructed to analyze risk factors for CRE non-CP acquisition, and its independent impact on multiple outcomes. Thirteen representative isolates were whole genome sequenced using Illumina and analyzed for resistome and phylogeny (MLST and cgMLST).

Results: The study included 327 patients: 109 CRE-non-CP carriers (94% asymptomatic) who were perfectly matched to susceptible cases and uninfected controls. Despite multiple associations per univariable analyses, matched logistic regression revealed that the independent predictors of CRE-non-CP acquisition remained: 1) recent (≤ 3 months) exposure to antibiotics (to any class, of at least 2 days' duration); 2) ICU admission; and 3) chronic skin ulcers. CRE-non-CP isolation was not independently associated with worse outcomes. Genomic analyses revealed multiple clones (figure), and confirmed the lack of carbapenemases and co-existence of multiple genes contributing to carbapenem-resistance phenotype (multiple beta-lactamases and efflux pumps).

Conclusions: CRE-non-CP acquisitions were almost exclusively associated with asymptomatic carriage. Both the independent predictors (i.e., exposure to antibiotics), and what could be deduced from the genomic analyses (i.e., polyclonality and presence of various resistance mechanisms), imply that the major mode of acquisition is "emergence of resistance", not "patient-to-patient transmission", although this needs to be further explored in designated trials. CRE-non-CP remains an epidemiological threat due to the therapeutic challenge it imposes, and directed efforts (i.e., stewardship) should be invested in order to curb its continued spread.



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Abstract 668

Analysis of the vaccination coverage in a dispensary in Mayotte, an oversea department and region of France

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Background: Mayotte has been the 101st French County since April 2011. It has a high-density population explained by a high birth rate and a high immigration population coming from the Comoro islands. The aim of this study was to compare the mandatory vaccine coverage rate in dispensaries for native versus migrants.

Materials/methods: The vaccine status was collected during general practice consultations in the dispensaries of the north of the island of Mayotte from the 12th to the 28th of June 2019. Patients were interrogated by a general practitioner and a translator about their vaccine status written in their health care notebook (carnettis). We noted the number of injections received of each mandatory vaccine, place of birth, age and gender. We considered that the vaccine status was complete if all the mandatory vaccination for their age was written on their health care notebook.

Results: We included 162 patients (54% (87) children <18-year-old and 57% (93) women. Migrants represented 22% (36/162) of patients and 78% (126/162) were native (French mahorais). In this population, 23% (37/162) were up to date on their mandatory vaccinations, 45% (73/162) were not and 32% (52/162) of vaccine status were unknown. The health care vaccine notebook of children was better filled in than those of the adults with only 4,60% (4/87) of unknown vaccine status (2 of those were migrant children) against 64% (48/75) of unknown vaccine status for adults. Among children 25.3% (22/87) were up to date on their mandatory vaccinations compared to 20% (15/75) of adults. In total 21% (27/126) of natives versus 21.6% (35/162) of migrants were up to date on their vaccinations (p=0,14).

Conclusions: In this study the vaccination coverage was not affected by the origin of patients whether they are native or migrants. The causes of limitation to health care access for the overall population are multiple: lack of transportation, cost and high waiting time of consultation, lack of social welfare and health insurance, cost of vaccine if they are not realized in a Mother and Children Health care center and for migrants, the fear of being arrested on their way to consultation.

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Abstract 669

Incidence rate of health care associated infection in tertiary care children's hospital in Ukraine

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Background: Health care associated infections (HAI) are the most frequent adverse event in health care delivery worldwide. At any given time, the prevalence of HAI in developed countries varies between 3,5% and 12%. In low- and middle-income countries the frequency of HAI in intensive care units (ICU) is at least 2-3 fold higher than in high-income countries and for device-associated infections the frequency is up to 13 times higher.

Previously, health care facilities were not encouraged to use standardized approach for registration and notification of HAI which resulted in lack of data and understanding of the burden of HAI and affect planning on HAI response in Ukraine.

The aim of the study was to calculate the baseline incidence rate (IR) of HAI in ICU and surgical wards of tertiary care children hospital in Ukraine

Materials/methods: Data on HAI was obtained using standardized notification forms that were filled by the doctors from March 1st till October 1st 2019. The case definitions of HAI outlined in EU Commission implementing decision 2018/945 were used. Data verification and calculations of HAI incidence rates were conducted by department of infection control and risk assessment.

Results: The incidence rate of central line-associated bloodstream infections (CLABSIs) was 10,3 per 1000 device-days, the most common causative pathogens were Gram-negatives (60%). The IR of ventilator-associated pneumonia (VAP) was 49,7 per 1000 device-days, the most common causative pathogens were *A. baumannii* (38,8%), *K.pneumoniae* (22,2 %). The IR of catheter-associated urinary tract infections (CAUTIs) was 18,3 per 1000 device days. The average length of catheterization was – 6 days for urinary catheters, 18 days for central line catheters and the average length of ventilation was 16 days.

Conclusions: The incidence rates of device-associated infections that were obtained are comparable to the HAI rates in low- and middle-income countries. Further surveillance on HAI, reducing the length of device use and implementation of core components for infection control are essential for reducing the burden of HAI.

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Abstract 671

Trachoma between schoolchildren: epidemiological situation in an endemic region of north-east Brazil

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Background: Trachoma is a chronic relapsing keratoconjunctivitis caused by Chlamydia trachomatis that remains a public health problem and a major cause of morbidity, visual impairment and preventable blindness in Brazil. This study aimed to characterize the epidemiological situation of trachoma in the state of Ceará, northeastern Brazil.

Materials/methods: A cross-sectional study was conducted with data from school surveys conducted from 2013 to 2017 in 78 of 184 municipalities in the state of Ceará. The population comprised schoolchildren aged 5 to 14 years old. External ocular examination with 2.5X magnifying binocular loupe and flashlight was performed by reference examiners trained by the Brazilian Ministry of Health for clinical diagnosis of trachoma according to World Health Organization simplified trachoma classification system. Secondary data were obtained from the official Epidemiological Surveillance System of the Health Secretary of the State of Ceará.

Results: 936,916 schoolchildren were examined and 32,948 cases of trachoma detected. The proportion of cases decreased in the period with a reduction from 4.49% in 2013 to 2.04% in 2017. Most (72.6%) of the municipalities had a percentage below 5%. However, 42 (13.7%) municipalities still had a case rate above 10%.

Conclusions: The epidemiological profile of trachoma in Ceará shows a reduction in the proportion of cases of the disease among schoolchildren. The extension and distribution of trachoma in the state of Ceará is still of great magnitude and demonstrates the need for more effective actions to control the disease among schoolchildren.

Year	2013	2014	2015	2016	2017
Schoolchildren examined	73.408	200.839	300.104	169.076	193.489
Schoolchildren with trachoma (%)	3.300 (4.49)	9.183 (4.57)	10.695 (3,56)	3.453 (2.04)	6.317 (3.26)

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Abstract 672

Clinical manifestations of hospitalised chikungunya fever cases during epidemic in the state of Ceará, Brazil, from 2017 to 2019

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Background: Chikungunya fever is a viral illness transmitted by hematophagous arthropods and occurs mainly in tropical and subtropical areas. Chikungunya virus spread to America in late 2013. Autochtonous transmission was confirmed in Brazil in 2014. Chikungunya fever presents typically with fever and joint pain and may also develop severe and atypical manifestations.

Materials/methods: This was a retrospective study which analysed data from patients' charts in a reference hospital in infectious diseases in Brazil. The study period was from January 2017 to April 2019. São José Hospital of Infectious Disease is located in state of Ceará, in the northeastern region of Brazil. Medical records of patients admitted to this hospital with Chikungunya fever confirmed by serological test were reviewed.

Results: Medical records from 71 patients with confirmed Chikungunya fever were analyzed. The average age was 22 years (±26). Comorbidities were found in 26 patients (36.6%). The most frequent clinical manifestations on admission were fever (68; 95.7%), nausea and vomiting (57; 80.3%), rash (49; 69%), arthralgia (35; 49.3%), and headache (27; 38%). Dermatological manifestations with bullous rash were observed in 13 cases (18.3%), of which 12 (92.3%) were children, and 9 (69.2%) younger than 1-year old. During hospitalization, 25 patients (35.2%) presented complications, especially neurological manifestations (15; 21.1%), of which 7 were meningitis, 5 encephalitis, 1 Guillain-Barré syndrome, 1 myelitis and 1 meningoencephalitis. Other frequent complications were acute kidney injury, hydroelectrolytic disorders, myocarditis, and sepsis. 64 patients (90.1%) were discharged, 2 (2.8%) died and 5 (7.1%) were transferred to another hospital.

Conclusions: Great variability in the clinical manifestations of patients with Chikungunya fever admitted to a reference hospital in northeastern Brazil was observed. A significant percentage of complications, atypical manifestations, and unfavorable outcomes underscore the importance of early clinical recognition of Chikungunya fever to ensure adequate clinical support and reduce the risk of complications.

Clinical manifestations of Chikungunya fever	n(%)
Fever	68(95.7)
Nausea and vomiting	57(80.3)
Rash	49(69)
Arthralgia	35(49.3)
Headache	27(38)
Abdominal pain	22(31)
Diarrhea	16(22.5)
Dermatological manifestations with bullous rash	13(18.3)
Hepatomegaly	11(15.5)

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Abstract 677

Pan-genome analysis supports the differentiation of Bacteroides fragilis in division I and the potentially carbapenem-resistant cfiA+ division II into two species

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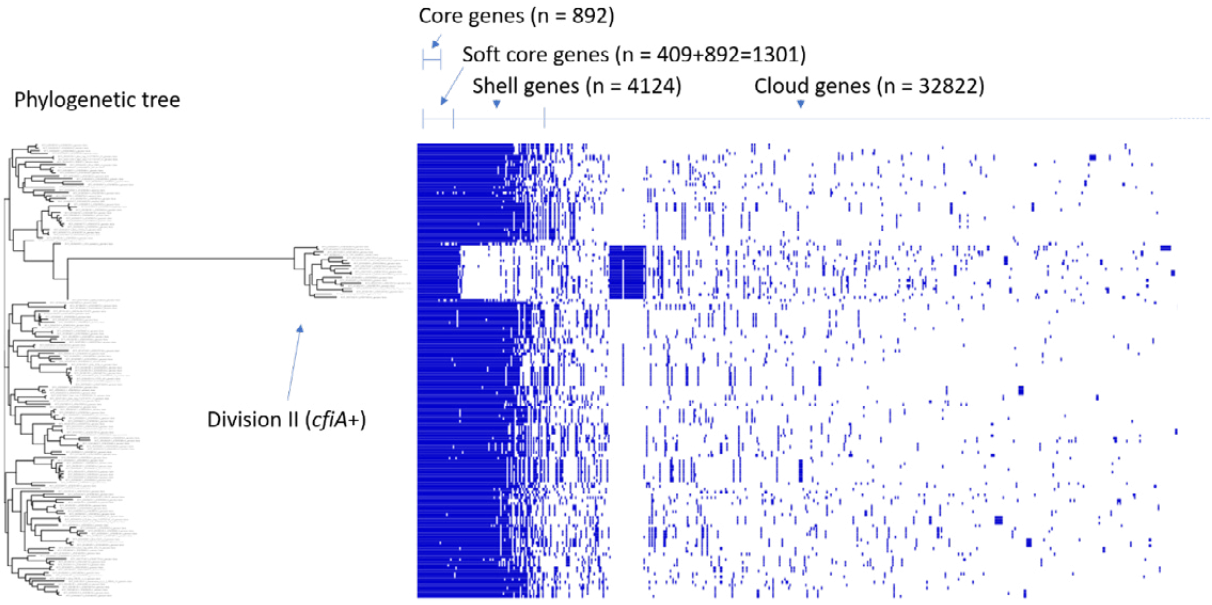
Background: The commensal, opportunistic pathogen *B. fragilis* comprises at least two DNA homology groups. Division I carry the chromosomal *cepA* cephalosporinase gene and division II carry the *cfiA* carbapenemase gene. 5-30% of clinical isolates are *cfiA*+ and of these 30-50% display phenotypical resistance to carbapenems. The *cepA* and *cfiA* carrying isolates can be distinguished using routine MALDI-TOF-MS, but not by 16S rRNA gene sequencing. To investigate the differentiation of core genes between the two divisions we performed preliminary pangenome analysis.

Materials/methods: *B. fragilis* genomes were identified and downloaded from NCBI RefSeq using *ncbi-genome-download* (https://github.com/kblin/ncbi-genome-download) and re-annotated using Prokka. Roary with MAFFT was used for pangenome alignment phylogeny analysis. ABRicate (https://github.com/tseemann/abricate) was used for identification of antimicrobial resistance genes.

Results: Genome assemblies of 161 *B. fragilis* isolates were available on October 15, 2019. For the 161 isolates a total of 38,247 genes were annotated of which 892 were core genes present in 99-100% of strains (Figure 1). 19 isolates were *cfiA*+ (division II) isolates. *Cfia+* and *cepA*+ strains respectively, contained a large set of genes not present in the other. Division II isolates shared a core genome of 2602 genes of a total of 14216 genes. For *cepA*+ (division I) isolates a total of 31415 genes were annotated of which 1627 were core genes.

Conclusions: Of the 161 *B. fragilis* genome assemblies 19 are division II strains. The core-genome of the 161 isolates is only 892 genes which is much lower than the core-genome of *E. coli*, which has a comparable genome size to *B. fragilis*. 97% of *E. coli* strains share a core-genome of 2,613 genes (Ambram *et al* bioRxiv 2019). The core-genome of the 19 division II isolates is 2,602 genes. The current results support further work towards describing *B. fragilis* division II as a separate species.

Figure 1. Visualisation of the pan-genome of 161 *B. fragilis* strains from NCBI RefSeq using phandango (https://jameshadfield.github.io/phandango/). The 19 *B. fragilis* division II (*cfiA*+) are clearly differentiated from the remaining strains. A large set of genes are present in one division but not the other.



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Abstract 679

Potential benefit of the new pneumococcal conjugate vaccines in Navarra, Spain

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Background: the 13-valent pneumococcal conjugate vaccine (pcv13) was introduced in navarra in 2010. in 2020 two new pcvs are expected to be manufactured. pcv15 includes pcv13 serotypes plus 22f and 33f. pcv20 includes pcv13 serotypes plus 8, 10a, 11a, 12f, 15b, 22f and 33f. monitoring of serotype distribution is necessary for surveillance and evaluation of vaccines. we aimed to monitor the circulating serotypes before the possible introduction of pcv15 and/or pcv20 in navarra.

Materials/methods: we included the cases of invasive pneumococcal disease (ipd) diagnosed in navarra between 2010-2019. an ipd case was defined as isolation of *s. pneumoniae* or detection by pcr from a normally sterile body site.

Results: 608 ipd were included: 67 (11%) patients were <5 years old, 239 (39.3%) patients were 5-64 years old and 302 (49.7%) patients were >=65 years old. 55 ipd could not be serotyped. among the 553 serotyped ipd, the 3 most frequent serotypes were: serotype 3 (17.5%), serotype 8 (9.2%) and serotype 19a (7.4%). other detected serotypes (between 4-5%) were: 9n, 7f and 22f. the detected serotypes according to the group of age were: in children < 5 years old serotypes 19a (14.1%), 24f (14.1%) and 3 (10.7%); in patients between 5-64 years old serotypes 8 (16.4%), 3 (12.6%) and 9n (7.9%); in patients >= 65 years old serotypes 3 (22.9%), 19a (6.9%) and 8 and 6b (5.5% each).

the rate of antibiotic resistance and the related serotypes was: 3.5% of penicillin resistance related to serotypes 11a, 14 and 19a; 0.7% of cefotaxime resistance related to serotypes 14 and 19a; 21.2% of erythromycin resistance related to serotypes 24f, 33f and 19a; 0.8% of quinolones resistance related to diverse serotypes.

Conclusions: the most prevalent serotypes causing ipd in navarra were 3, 8 and 19a. in the last 9 years, in all ages 48.3% and 67.1% of ipd in navarra were caused by serotypes included in pcv15 and pcv20 respectively. it would be critical to assess the effectiveness of the new vaccines against serotype 3. serotype 24f caused 3.8% of ipd and is not covered by any of these 2 new products.

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Abstract 681

Generation of protective antibodies against heterologous Acinetobacter baumanni isolates

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Abstract third-party references: Medical Research Council (MRC), Global Challenges Research Fund (GCRF), Respiratory Department, CITR, University College London

Background: Opportunistic nosocomial infections by multi-drug resistant *Acinetobacter baumanni* (*A. baumanni*) are associated with high morbidity and mortality rates. The increase in the incidence of infections caused by pan-drug resistant isolates further highlights the urgent need for novel therapeutics. We report on the generation of cross-reactive antibodies that are protective against homologous and heterologous strains *in vivo* and *in vitro.*

Materials/methods: We immunized CD1 mice with sub-lethal doses of Ab3879 (st215/kl10) and Abapsp-515 (st164/kl47) clinical *A. baumanni* isolates. We measured *in vitro* IgG binding to the bacterial surface and lysate by flow cytometry and Western blot analysis. Growth inhibitory/ bactericidal activity of antibodies were measured by comparing bacterial growth in the presence anti-sera. Neutrophil phagocytosis of *A. baumanni* was measured following bacterial opsonisation with either homologous or heterologous sera, followed by incubation with neutrophils isolated from healthy human blood donors. The efficacy of antibodies *in vivo* was evaluated using a bacteremia mouse model of *A. baumanni* infection by either passive or active immunization prior to challenge.

Results: Flow cytometry and growth impairment assays demonstrated that antibody in sera recovered from mice previously infected with *A. baumanni* recognized homologous and heterologous isolates but to different degrees. Anti-Ab3879 antibodies recognized the surface of the homologous isolate to a greater extent when compared to heterologous isolate (Ab3879, 93% versus Abapsp-515, 67%). Similarly, anti-Abapsp-515 bound its homologous isolates to a greater extent than Ab3879. Western blot analysis showed the recognition of both isolate-specific high molecular weight capsule, and multiple proteins. Survival following intraperitoneal challenge with lethal doses of Ab3879 was 100% in both homologous (Ab3879) and heterologous (Abapsp-515) immunized mice compared to 50% in controls, and the bacterial burdens in the lungs, spleen and liver of immunized mice were significantly lower compared to control mice (p-value < 0.05).

Conclusions: We demonstrate the generation of cross-reactive antibodies that recognize heterologous isolates both through recognition of structurally-related capsular polysaccharide and/ or conserved proteins. Protective antibodies to specific conserved protein targets could potentially be used for future monoclonal antibody passive immunization therapies.

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Abstract 685

Pharmacokinetic/Pharmacodynamic benefit of prolonged ceftazidime/avibactam infusion

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Background: Cystic fibrosis patients are prone to bacterial pulmonary infections, mainly with *Burkholderia cepacia* complex. These bacteria are associated with severe complications.

Ceftazidime is currently combined with avibactam (CZA) as a first-line antibiotic. No studies have evaluated the CZA infusion time in patients with cystic fibrosis to date, although this population is known to have its own pharmacokinetic (PK) characteristics. The aim of this study was to evaluate different dosage regimens and to identify those that guarantee microbiological efficacy.

Materials/methods: From the population pharmacokinetic models published by Bulitta & *al.* and Bensman & *al*., 10 000 PK profiles were simulated. The MIC distribution of *Burkholderia cepacia* complex bacteria was determined at the Burkholderia Observatory (Toulouse University Hospital) from strains isolated from 46 different hospitals. Based on the simulated kinetic profiles and the MIC distribution, the Probability of Target Attainment (PTA) and the Cumulative Fraction Response (CFR) were calculated. The critical values of the pharmacokinetic/pharmacodynamic (PK/PD) criterion were 65% fT>MIC and 50% fT>1mg/L for ceftazidime and avibactam, respectively.

Results: The CFR have shown that a minimum infusion time of 6 h is required to reach the critical value of the PK/PD criterion in more than 99% of patients. The infusion time can then be adapted after determining the MIC of the offending germ. For example, for a germ with a MIC equal to 8 mg/L, an infusion time of 4 h is necessary to guarantee microbiological efficacy in more than 99% of patients.

Conclusions: This work shows that the infusion time of CZA depends on the type of treatment (probabilistic antibiotic therapy or adapted secondarily to the antibiogram) and the sensitivity (MIC) of the causative pathogen.

This simulation-based work must be validated for use in hospital practice. Nevertheless, this approach was adopted for one patient (Toulouse University Hospital). As a result, the critical value of the PK/PD criterion was reached on the one hand and, on the other hand, clinical improvement was quickly obtained.

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Abstract 687

Role of deoxyribonucleic acid content in the composition of microbial biofilm in the pathogenesis of severe respiratory infections

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Background: It has been known about possibility of microorganisms to create specific multi-layered structures called biofilms. Non-cellular deoxyribonucleic acid actively participates in regulation of properties of biofilms. Thus, in biofilms transfer of genetic information including genes responsible for sensitivity to antibacterial drugs occurs much more often than in single-living bacterial cells. However, despite the involvement of extracellular deoxyribonucleic acid in adhesive processes and intercellular interactions, its role has not been fully understood.

Materials/methods: 238 isolates isolated from sputum and pharynx of 175 patients during 2016-2019 were studied. Patients were divided into two groups: the 1st group of 139 people (79,4%) had severe respiratory infections, the 2nd of 36 people (20,6%) - respiratory infections of moderate severity.

Results: A method was developed for determining percentage of deoxyribonucleic acid in microbial community using 4'6-diamidino-2-phenylindole dihydrochloride. Average age of the 1st group was higher than the second ($p<0,05$). Pseudomonas aeruginosa had the largest mass of biofilm and percentage of deoxyribonucleic acid in group 1, 48,25 [30,5-70,1] mcg/ml and 5,21 [2,17-7,67] %, $p = 0,04$. A strong relationship was found between percentage of deoxyribonucleic acid in Pseudomonas aeruginosa and severity of disease, $r = 0,73$, $p<0,05$. The incidence of adverse outcomes in isolating antibiotic resistant isolates was higher than in antibiotic sensitive ($p<0,05$). Analysis of results made it possible to propose fatal outcome when mass of microbial biofilm is > 47,5 mcg/well and percentage of deoxyribonucleic acid is >2,33% ($p<0,01$).

Conclusions: Method for determining percentage of deoxyribonucleic acid in biofilm has been proposed. With age there is a decrease in immune system which contributes to adherence of more pathogenic, antibiotic resistant microflora which has high biofilm weight and deoxyribonucleic acid percentage leading to disease progression and death.

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Abstract 689

Enterovirus D68 subclade B3 in children with acute flaccid paralysis in west Africa: evidence of spread of outbreaks reported in US and Europe, 2016

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Background: Since 2014, several outbreaks due to Enterovirus D-68 (EV-D68) have been reported, and it was confirmed that the virus can cause upper and lower respiratory tract diseases and be associated with the neurologic syndrome of acute flaccid myelitis (AFM). However, in African countries, the circulation and the molecular epidemiology of EV-D68 is poorly documented particularly on children with AFM. Our study aims to understand the extent of EV-D68 AFP in West Africa but also to know its genetic diversity and molecular epidemiology.

Materials/methods: To investigate the circulation of EV-68 in West Africa in AFP during the 2016 outbreak, we retrospectively screened 567 stools sample collected through routine poliomyelitis surveillance activities in seven countries of West Africa including Cape Verde, Gambia, Guinea-Bissau, Guinea Conakry, Mauritania, Niger, and Senegal between June to September 2016. After EV-D68 detection, molecular characterization was performed by amplification of the VP1 regions, followed by nucleotide sequencing.

Results: Among the 567 stool specimens tested, EV-D68 was detected in sixteen samples (2.8%) from three countries whose Guinea Conakry (11/391), Niger (1/85) and Senegal (4/59). The majority (62.5%) of the EV-D68 cases were detected in July. Children under 5 years were more vulnerable to EV-D68 infection with a frequency of 87.5 %. Phylogenetic analysis of sequences of the VP1 region revealed that all West Africa strains sequenced belongs to the Subclade B3 variant of clade B. Additionally, the Subclade B3 strains of West Africa clustered with several other strains circulating during the same period in Spain and Sweden.

Conclusions: This study allowed to understand the extent of EV-D68 AFP in West Africa but also evidence of spread of outbreaks reported in US and Europe in 2016. These findings warrant implementation of enhanced surveillance of EV-D68 in confirmed case of AFM in African countries for a better understanding the disease and it burden.

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Abstract 690

Dissemination of a blaNDM-1-carrying IncA/C2 plasmid in a broiler flock: a possible real-life scenario

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Background: Emergence of carbapenemase-producing Enterobacteriaceae (CPE) in livestock animals poses a worrying concern for public health safety. The sporadic detection of CPE in livestock suggests their low prevalence and a knowledge gap on the spread potential of plasmids carrying carbapenemase-encoding genes. In the frame of an international research project EFFORT, *in vivo* broiler chicken infection experiments were performed, aiming to understand spread and adaptation potential of a *S*. Corvallis native bla_{NDM-1}-carrying broad-host range IncA/C_2 plasmid in the absence of antibiotic pressure.

Materials/methods: Broiler chicken infection model was selected as an *in vivo* model for the investigation of spread and adaptation of a public health relevant broad MDR-encoding bla_{NDM-1}-carrying IncA/C_2 plasmid. Following oral inoculation of NDM-1-producing *S*. Corvallis strain, selection of *S*. Corvallis re-isolates and enterobacterial transconjugants were in-depth analysed by S1-PFGE and by Illumina and Nanopore whole-genome sequencing for a deeper insight into variants of the bla_{NDM-1}-carrying IncA/C_2 plasmid at genome level.

Results: The conducted *in vivo* study revealed rapid and broad host range dissemination of the bla_{NDM-1}-carrying IncA/C_2 plasmid to commensal *E. coli* strains (ST-117, ST-156, ST-2040, ST-2485) and a *K. pneumoniae* strain (ST-1106). Beside plasmid transfer, a transposition event of the bla_{NDM-1} gene onto another ff30 kb plasmid of an *E. coli* transconjugant strain was detected. Three types of structural deletions of the bla_{NDM-1}-carrying IncA/C_2 plasmid were detected (ff10 kb deletions, ff70 kb deletions as a co-integrate formation). Despite structural deletions, loss of the bla_{NDM-1} gene was not observed.

Conclusions: Conducted *in vivo* study revealed broad dissemination of the bla_{NDM-1}-carrying IncA/C_2 plasmid. This occurrence is worrying as such entrance scenario might lead to broader dissemination of this plasmid in environments with mixed bacterial population. Another concerning observation is the transposition event of bla_{NDM-1} gene onto another plasmid which might facilitate further dissemination of this gene. Few structural alterations of bla_{NDM-1}-carrying IncA/C_2 plasmid indicate adaptation and persistence potential of this plasmid in the absence of antibiotic pressure. With the aim of preventing this scenario, entrance of a NDM-1-producing *S*. Corvallis strain into a broiler flock should be prevented, as broad dissemination of its MDR-encoding bla_{NDM-1}-carrying IncA/C_2 plasmid is inevitable.

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Abstract 693

Comparing clinical outcomes in Gram-negative bloodstream infections with desirability of outcomes ranking: focus on non-fermenting organisms

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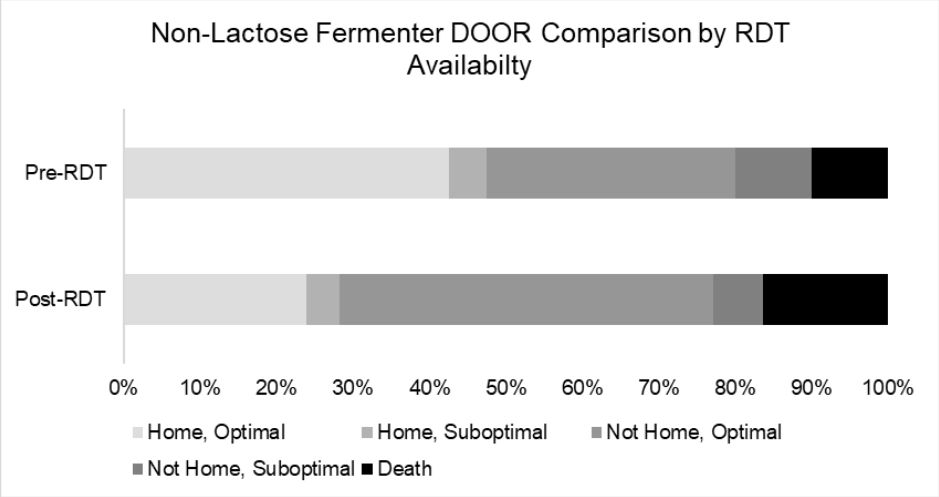
Background: Rapid diagnostic testing (RDT) for the management of bloodstream infections (BSIs) has the potential to decrease time to organism identification and effective antibiotic therapy. These findings are primarily driven by data in gram-positive organisms, with less known regarding the benefits among gram-negatives, especially non-lactose fermenting organisms, where antibiotic resistance is complex and rarely detected by current RDTs.

Materials/methods: Subgroup analysis of retrospective quasi-experimental study of adult patients with gram-negative BSI from 9/2014 to 08/2018, with Verigene intervention in 9/2015. Inverse probability of treatment weighting (IPTW) controlling for Charlson Comorbidity Index and critical illness was used to balance patients. To further analyze risk/benefit IPTW-adjusted desirably of outcomes ranking (DOOR) was derived combining patient disposition and optimal antibiotic therapy. The DOOR designation was as follows; 1 = home, optimal antibiotics; 2 = home, suboptimal antibiotics; 3 = not home, optimal antibiotics, 4 = not home, suboptimal antibiotics, 5 = death.

Results: The original cohort consisted of 832 patients; 700 with *Enterobacteriaceae*, 99 with *P. aeruginosa* and 33 *Acinetobacter spp.* BSI. Among *Enterobacteriaceae*, median time to optimal therapy significantly decreased with RDT (54.7 vs 25.9 hours, $P = 0.02$); however there was no change among non-lactose fermenters (24.5 vs 25.2 hours, $P = 0.34$). For subgroup analysis, 132 met inclusion; 40 pre-RDT, 92 post-RDT. Among the IPTW subgroup there were no significant differences in time to optimal antibiotics (24.6 vs 25.4 hours, $P = 0.3$) or in-patient all-cause mortality (10.9% vs 16.7%, $P = 0.54$) with the introduction of RDT. Additionally controlling for source of infection there was no difference in in-patient all-cause mortality (adjusted OR = 0.77, 95% CI 0.14, 4.2). DOOR was similar between groups; the probably of a lower DOOR among the pre-RDT group (Figure 1) was marginally higher (10%, 95% CI 9.6%, 10.5%).



Conclusions: Compared to patients with gram-negative BSI caused by *Enterobacteriaceae*, among BSI caused by non-lactose fermenting organisms the addition of RDT did not confer significant benefits. This is likely due to the complex, multifactorial mechanisms of resistance rarely detected by available RDT platforms.

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Abstract 708

Detection of echinocandin resistance in *Candida glabrata* in the microbiology laboratory using commercial methods: interpret with caution!

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Background: Echinocandin resistance in *C. glabrata* can be detected in the clinical microbiology laboratory by using EUCAST and CLSI reference broth microdilution methods. Reference methods are time-consuming and most of microbiology laboratories lie on commercial methods such as Sensititre Yeast One® (SYO) or ETest to perform antifungal susceptibility testing. We assessed the ability of the ETest and SYO to accurately detect echinocandin resistance in *C. glabrata* clinical isolates.

Materials/methods: We studied micafungin- or anidulafungin-resistant *C. glabrata* isolates (n=29) according to EUCAST EDef. 7.3.1 methodology and harbouring the following *FKS2* gene mutations: Δ658 (n=14), S663P (n=7), W715L (n=3), S663Y (n=1), E655A (n=1), and none (n=3). Echinocandin susceptibility using CLSI M27-ED4, ETest, and SYO (the latter using CLSI breakpoints) was further performed. Agreement between methods and very major errors (false susceptibility) were assessed.

Results: Essential agreement (1± two-fold dilutions) between EUCAST and CLSI for anidulafungin and micafungin was 86% and 79%, respectively, and all mutants were correctly classified as resistant using both procedures (Figure). SYO yielded 6 isolates with very major errors to only micafungin (n=2, Δ658 and W715L), only anidulafungin (n=2, Δ658), or both (n=2, *FKS* wild type); the EUCAST MIC ranges against the isolates were 0.06-0.5 mg/L (micafungin) and 0.25-2 mg/L (anidulafungin). All isolates showed an MIC of micafungin and anidulafungin ≥0.06 mg/L and ≥0.03 mg/L, respectively.

Conclusions: Micafungin and anidulafungin MICs against *C. glabrata* obtained by SYO should be interpreted with caution because up to 20% of very major errors (false susceptibility) may come out. In the absence of clinical breakpoints for MICs obtained by ETest, values ≥0.06 mg/L and 0.03 mg/L for micafungin and anidulafungin, respectively, could be used to detect echinocandin resistance. Isolates with suspicion of phenotypic echinocandin resistance using SYO or ETest should be confirmed by CLSI or EUCAST and by further *FKS* gene sequencing.

Drug	Method	Number of isolates at each MIC (in mg/L)									
		0.03	0.06	0.125	0.25	0.5	1	2	4	8	16
Micafungin	EUCAST	0	2	3	0	3	3	11	4	0	3
	CLSI	0	0	0	1	2	7	6	10	1	2
	SYO	0	**2**	**2**	1	4	8	3	6	1	2
	ETest	0	3	4	7	5	3	4	3	0	0
Anidulafungin	EUCAST	0	0	0	1	4	2	15	5	2	0
	CLSI	0	0	0	0	4	2	5	18	0	0
	SYO	0	0	**2**	**2**	5	7	11	1	0	1
	ETest	2	2	0	5	6	3	7	1	0	3

Cells in grey indicate phenotypic resistance. CLSI breakpoints were adopted for SYO.

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Abstract 710

Five-day versus ten-day oseltamivir chemoprophylaxis to prevent hospital influenza transmission: a non-inferiority randomised open-label study

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Background: Based on the evidence of a protective effect of antivirals against influenza as well as their generally benign safety profile, some hospital infection control authorities recommend oseltamivir prophylaxis for vulnerable patients who were in close contact with influenza. Given the short incubation period of influenza, the recommended oseltamivir post-exposure prophylaxis for 7 to 10 days after the last known exposure may be too long.

Materials/methods: In an open-label randomized clinical trial, performed in a single-centre university hospital, the effectiveness of a 5-day versus 10-day post-exposure oseltamivir prophylaxis was compared in an intention to treat (ITT) and per protocol (PP) analyses and on a noninferiority premise in adult patients who were exposed as close contacts to influenza. Breakthrough influenza rate was assessed up to 10 days after discontinuation of oseltamivir prophylaxis.

Results: Among 222 randomized contact patients (median age 75 years; male 119 [53.6%]; median Charlson comorbidity index 5), 110 patients (49.6%) were assigned to receive oseltamivir post-exposure prophylaxis for 5 days, and 112 patients for 10 days. Patients in the two prophylaxis groups did not differ regarding basic demographic and clinical characteristics. Because single-patient rooms and cohorting capacities were in short supply, the median duration of exposition to influenza was two days (IQR 1–3 days). All of 137 identified influenza patients, who served as index cases for 202/222 (91.0%) exposed contact patients, were prescribed oseltamivir treatment for 5 days. Rates of breakthrough influenza were 2/110 (1.8%) with 5-day regimen and 0/112 (0%) with 10-day regimen in the ITT study population (difference, 1.8 percentage points [1-sided 95% CI, −1 to 4.9 percentage points]; *P*=0.765) and 2/102 (2.0%) and 0/95 (0%), respectively, in the PP study population (difference, 2.0 percentage points [1-sided 95% CI, −1 to 5.3 percentage points]; *P*=0.745).

Conclusions: In patients, exposed to influenza as close contacts within hospital environment, 5-day post-exposure oseltamivir prophylaxis was noninferior to 10-day regimen with respect to preventing influenza transmission, assuming the predetermined noninferiority margin of 7 percentage points. Both prophylactic regimens were effective even if the exposed contact patients could not have been separated from index patients with influenza.

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Abstract 711

Association of statin use and microbiological and clinical characteristics of early Lyme borreliosis

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Background: *Borrelia burgdorferi* sensu stricto, the causative agent of Lyme borreliosis (LB) possesses a functional 3-hydroxy-3-methyl-glutaryl-coenzyme A reductase (HMGR), which is a rate limiting enzyme of the mevalonate pathway that contributes to cell wall synthesis. Statins are HMGR inhibitors and have been shown to reduce bacterial burden and alter the immune response to favour clearance of spirochetes in a mouse model of LB.

Materials/methods: The association between background statin use and prospectively collected clinical and microbiologic characteristics was investigated in 1220 adult patients with early LB manifesting as erythema migrans (EM) at a single-centre university hospital in Ljubljana, Slovenia. Patients were assessed at enrolment and followed-up for 12 months.

Results: Statin treatment was associated with age and prevalence of other comorbidities besides hyperlipidemia, but not with borrelial skin culture positivity rate, serological response to infection, or presence of LB-associated symptoms at enrolment. The proportion of patients taking statins was lower among patients with disseminated disease manifested as multiple EM than among those with solitary EM, but the difference was not significant (10/195, 5.1% vs 84/1025, 8.2%; P=0.19). The time to resolution of EM after starting antibiotic treatment was comparable in patients on statins and in those without statins (median 7 days, IQR 4–14). At 12 months, 59/989 (6.0%) patients showed incomplete response. The odds for incomplete response decreased with time from enrolment (odds ratio (OR) 0.49, 0.50, and 0.48 for 2-month vs. 14-days, 6-month vs. 2-month, and 12-month vs. 6-month follow-up visits, respectively), were higher in patients who reported LB-associated constitutional symptoms at enrolment (OR 8.10, 95% CI 5.69–11.55; P<0.001), but were not affected by statin use (OR 1.09, 95% CI 0.61–1.98; P=0.76).

Conclusions: In our study of European patients with EM, most of whom were infected with *B. afzelii*, statin use was not associated with selected clinical and microbiological parameters of infection.

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Abstract 715

Excluded versus included patients in a randomised controlled trial of infections caused by carbapenem-resistant Gram-negative bacteria: relevance to external validity

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Background: Population external validity is the extent to which an experimental study results can be generalized from a specific sample to a defined population. In order to apply the results of a study, we should be able to assess its population external validity. We performed an investigator-initiated randomized controlled trial (RCT) (AIDA study), which compared colistin-meropenem combination therapy to colistin monotherapy in the treatment of patients infected with carbapenem-resistant Gram-negative bacteria. In order to exam the study's population external validity and to substantiate the use of AIDA study results in clinical practice, we performed a concomitant observational trial.

Materials/methods: The study was conducted between October 1st, 2013 and January 31st, 2017 (during the RCTs recruitment period) in Greece, Israel and Italy. Patients included in the observational arm of the study have fulfilled clinical and microbiological inclusion criteria but were excluded from the RCT due to receipt of colistin for >96 hours, refusal to participate, or prior inclusion in the RCT. Non-randomized cases were compared to randomized patients. The primary outcome was clinical failure at 14 days of infection onset.

Results: Analysis included 701 patients. Patients were infected mainly with Acinetobacter baumannii [78.2% (548/701)]. The most common reason for exclusion was refusal to participate [62% (183/295)]. Non-randomized and randomized patients were similar in most of the demographic and background parameters, though randomized patients showed minor differences towards a more severe infection. Combination therapy was less common in non-randomized patients [31.9% (53/166) vs. 51.2% (208/406), p=0.000]. Randomized patients received longer treatment of colistin [13 days (IQR 10-16) vs. 8.5 days (IQR 0-15), p=0.000]. Univariate analysis showed that non-randomized patients were more inclined to clinical failure on day 14 from infection onset [82% (242/295) vs. 75.5% (307/406), p=0.042]. After adjusting for other variables, non-inclusion was not an independent risk factor for clinical failure at day 14.

Conclusions: The similarity between the observational arm and RCT patients has strengthened our confidence in the population external validity of the AIDA trial. Adding an observational arm to intervention studies can help increase the population external validity and improve implementation of study results in clinical practice.

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Abstract 716

Investigation of the prevalence of Verocytotoxigenic *Escherichia coli* (VTEC) contamination of private groundwater wells in Ireland

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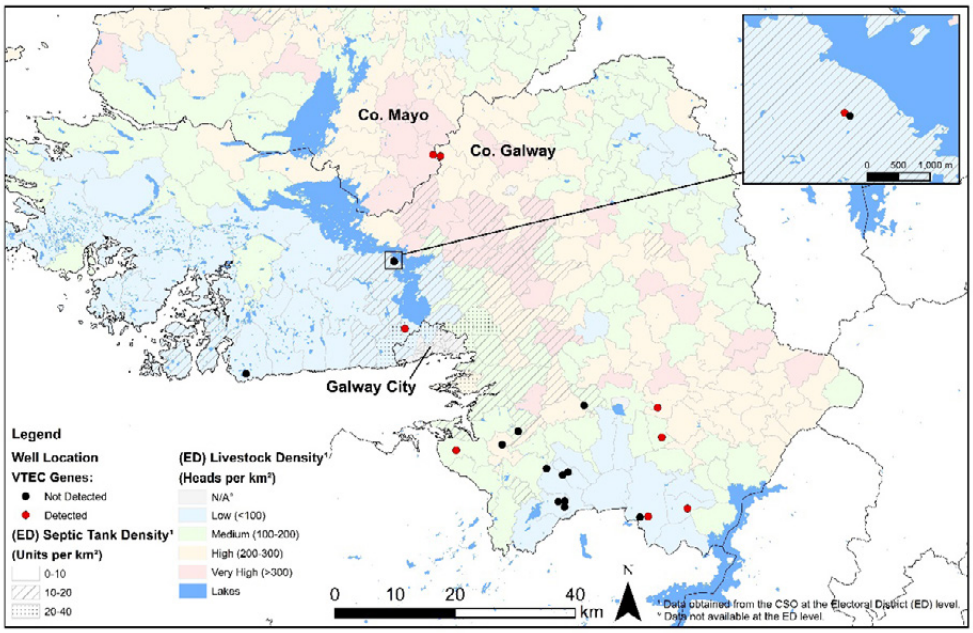
Background: Approximately 750,000 people in Ireland obtain their drinking water from a private well. Wells are unregulated and quality testing by users is infrequent. Waterborne transmission of Verocytotoxigenic *Escherichia coli* (VTEC) through private wells has emerged as an important transmission route. Cattle manure and septic tanks are possible contamination sources, with persistent heavy rainfall contributing to microbial ingress. Ireland has the highest incidence of human VTEC infection, at almost ten times the EU average in 2017. The aim of this study was to investigate the prevalence of VTEC contamination in domestic private wells in Ireland.

Materials/methods: Groundwater wells (n=21) were sampled during October 2019 (Figure 1). Raw and/or treated well water samples (30 L) were collected and analysed using the "CapE" method (Morris, 2016). Filters were enriched overnight in buffered peptone water, DNA was extracted from enrichment broths and tested by multiplex real-time PCR for *eae, vtx1* and *vtx2* genes. Positive samples were tested for genes associated with serogroups 0157, 026, 0153, 0145, 0111 and 0104. All samples were assessed for total coliforms and total *E. coli* using the Colilert-18 system (IDEXX). Data relating to groundwater vulnerability were geospatially linked to each well and assessed for univariate association with VTEC presence/absence.

Results: Verocytotoxin genes were detected in 9/21 wells (43%), 7 of which were also positive for *eae*. One or more of six serogroup gene targets were identified in all positive samples. Multiple serogroups were detected in 4/9, with 0145 (n=6), 0157 (n=5) and 0103 (n=4) the most prevalent. Presence of live *E. coli* in well water samples (Colilert-18) was associated with detection of verocytotoxin genes (P=.0075, Fisher's Exact test). No significant associations were noted between the groundwater vulnerability variables analysed and presence of VTEC (significance level P<.05).

Conclusions: Private wells in Ireland are at risk of contamination with pathogenic strains of *E. coli* capable of causing human disease. This research represents preliminary data from the DESIGN (Detection of Environmental Sources of Infectious diseases in Groundwater Networks) study. Data generated from more widespread sampling may lead to policy development to protect private well users in Ireland from waterborne infectious diseases.



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Abstract 721

Genomic analysis of carbapenemase-encoding plasmids from *Klebsiella pneumoniae* across Europe highlights three major patterns of dissemination

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Background: The incidence of *Klebsiella pneumoniae* infections that are resistant to carbapenems, a last-line class of antibiotics, has been rapidly increasing. The primary mechanism of carbapenem resistance is production of carbapenemase enzymes, which are most frequently encoded on plasmids by $bla_{\text{OXA-48-like}}$, $bla_{\text{VIM-like}}$, $bla_{\text{NDM-like}}$ and $bla_{\text{KPC-like}}$ genes. Using short-read sequence data, we previously analysed genomes of >1700 isolates from the *K. pneumoniae* species complex submitted during the European survey of carbapenemase-producing *Enterobacteriaceae* (EuSCAPE). Here, we investigated the diversity, prevalence and transmission dynamics of carbapenemase-encoding plasmids in this sample collection.

Materials/methods: All carbapenemase-carrying contigs from short-read assemblies (n=696) were clustered into gene context (GC) groups, based on the order and nucleotide similarity of coding sequences flanking each carbapenemase gene. We performed long-read sequencing on 79 isolates including one isolate per GC group. These encoded a total of 14 $bla_{\text{OXA-48-like}}$, 11 $bla_{\text{VIM-like}}$, 15 $bla_{\text{NDM-like}}$ and 44 $bla_{\text{KPC-like}}$ genes. Long- and short-read sequence data were assembled together using Unicycler. Short-read mapping to the newly-obtained reference plasmids indicated how much of the reference sequence was present amongst all remaining isolates from the collection.

Results: We identified three major patterns by which carbapenemase genes have disseminated via plasmids. First, $bla_{\text{OXA-48-like}}$ genes have spread across diverse lineages primarily via the highly conserved, epidemic pOXA-48-like plasmid. Phylogenetic analysis of pOXA-48-like plasmid sequences demonstrated substantial horizontal transmission amongst co-localised chromosomal lineages but also indicated prolonged vertical transmission upon acquisition by high-risk lineages (ST11, ST15, ST101). Second, $bla_{\text{VIM-like}}$ and $bla_{\text{NDM-like}}$ genes have spread via transient associations of diverse plasmids with numerous lineages, albeit with high-risk lineages also playing a primary role in geographic spread. Third, $bla_{\text{KPC-like}}$ genes have transmitted predominantly by stable association with one successful clonal lineage (ST258/512), despite frequent mobilisation between pre-existing yet diverse plasmids within the lineage. These include pKpQIL-like plasmids which have co-evolved with the ST258/512 chromosome.

Conclusions: Here, we highlight three predominant modes of plasmid spread that have enabled widespread dissemination of carbapenemase genes. They can be summarised as using one plasmid/multiple lineages, multiple plasmids/multiple lineages, and multiple plasmids/one lineage. Despite these contrasts, all are underpinned by significant propagation along high-risk clonal lineages.

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Abstract 722

A prospective cohort study of Malawian children presenting with fever

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Background: Of an estimated 4.3 million cases of malaria in Malawi in 2017, the majority of malaria-related deaths occurred in children. Differentiating causes of childhood fever in rural clinics is challenging. Greater understanding of clinical features that differentiate malaria from other causes of fever may improve triage of febrile children in these settings. This study aimed to analyse clinical features associated with malaria and parental perceptions on causation of fever in a rural clinic in Malawi.

Materials/methods: This prospective cohort study included 313 children presenting with fever to a charity-funded clinic in rural Malawi between the months of March and June 2019. Children underwent tympanic temperature measurement and malaria rapid diagnostic testing (MRDT). Blood films were not routinely performed. Clinical assessment was performed, and brief interviews conducted with the child's parent or guardian.

Results: 47.3% of children had positive MRDTs and were treated for malaria as per WHO guidelines. Children with a history of vomiting were more likely to have a positive MRDT (Odds ratio 3.4773, Confidence Interval 1.98-6.10, p-value <0.0001). This association increased when combined with a history of headache (OR 11.44, CI 2.6-50.2, p-value 0.0012). Negative MRDTs were predicted by rash (OR 6.6776, CI 1.49-29.90, p-value 0.013) and upper respiratory tract symptoms (OR 9.9716, CI 5.13-19.38, p-value <0.0001). There was no significant difference in time to presentation between MRDT positive and negative children. The likelihood of a positive MRDT was not significantly different where parents predicted a diagnosis of malaria as the cause of symptoms. There was a strong correlation between recorded temperature up to 40˚c and likelihood of positive MRDT (R = 0.976, p-value 0.004). Temperature >40˚c did not predict positive MRDT.

Conclusions: A diagnosis of malaria was predicted by symptoms of vomiting and headache, and by objectively elevated temperatures up to 40˚c. Parents did not reliably differentiate the cause of symptoms at time of presentation, and children with malaria did not present earlier. This data should inform triage and malaria testing of febrile children and guide community education regarding malaria symptomatology.

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Abstract 723

Typing of MRSA isolates from bloodstream infections in the Dutch-German border region and Berlin

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Background: Recent surveillance data indicated that in hospitals located in the Northern Dutch part of the Dutch-German border area, the incidence of MRSA bloodstream infections (BSIs) was (although lower than in Germany) higher than expected and exceeded national levels (Jurke et al., 2019). It was speculated that this could be a result of an additive burden of BSIs due to livestock-associated (LA)-MRSA in the border area characterized by a high density of livestock production. In order to evaluate this, we investigated the MRSA isolates from BSIs by using molecular surveillance techniques.

Materials/methods: We retrospectively characterized all available MRSA bacteremia isolates from university hospitals in the Dutch and the German part of the Dutch-German border region, as well as (for comparison) a hospital in Berlin. Typing of the isolates collected between 2016-2018 was performed by using WGS and a gene-by-gene approach (cgMLST, Ridom SeqSphere+ v6.0.2). Antimicrobial resistance genes were detected using CLC Genomics Workbench v12.0.3 and the ResFinder database.

Results: A total of 31 MRSA isolates were characterized (n=6 from Groningen, n=10 from Berlin, n=15 from Oldenburg). Most of the isolates belonged to clonal complex (CC)22 (n=16), which was the most frequent CC in Groningen and Berlin but not in Oldenburg (Figure 1). Two isolates had new sequence types (STs 5702 and 5703, single locus variants of ST22). Several resistance genes were identified. None of the isolates was PVL-positive. MRSA ST398, indicative for LA-MRSA was not detected. Two possible direct transmission events could have occurred between two patients in Oldenburg and Berlin.

Conclusions: CC22 was the most commonly found clonal complex and none of the isolates belonged to the typical LA-MRSA STs, ruling out the additive burden that could have arisen from a high density of livestock production in this "Euregio".

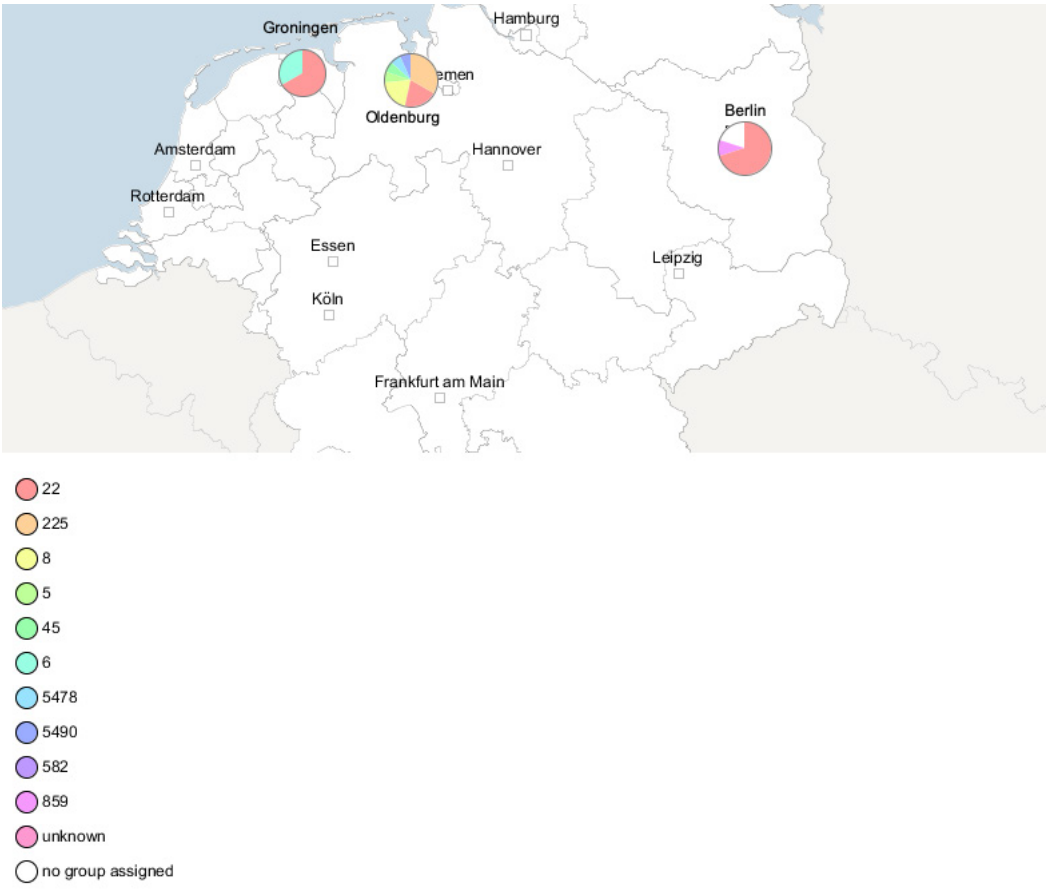

Figure 1. Most common STs found in the 3 different studied sites.

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Abstract 728

Ignatzschineria bacteraemia following maggot wound infestation

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Background: Myiasis is an infestation of live humans and other vertebrates by larvae of various flies of the order Diptera which feed on host's dead or living tissue. In humans, it is often associated with precarious living conditions. We describe a case of myiasis with subsequent *Ignatzschineria* sp. bloodstream infection as a complication of maggot wound infestation in a young male migrant.

Materials/methods: 18-year-old male patient was admitted to our hospital after being found in the river on the Slovenian border. On admission, he was febrile (39.6°C), normotensive with tachycardia (130/min). Since he was traveling by foot in the rural areas and woodlands of Balkans he had multiple superficial wounds on both legs with surrounding cellulitis and numerous small moving larvae on the skin and in the skin folds. His laboratory results revealed CRP 499, PCT 8,9 and leucocytosis of 25,9 $x10^9$ with a left shift (8% bands). Debridement of the wounds was performed and the patient was started on flucloxacillin and ciprofloxacin. The wounds were redressed two days later with numerous larvae observed and debrided.

Results: According to the shape and pattern of the posterior spiracles the larvae were identified as *Lucilia* sp. Rectal swab yielded *Enterobacter cloacae* ESBL and the skin swabs MRSA, therefore we changed antibiotics to imipenem and vancomycin. Blood cultures yielded *Ignatzschineria* sp., identified from subculture on blood agar only by 16S rRNA gene sequencing and sensitive to piperacillin/tazobactam, ceftazidim, imipenem and ciprofloxacin. After 10 days of antibiotic therapy the CRP levels decreased and clinical condition improved, he was afebrile and discharged. After second debridement there were no more larvae observed and the wounds were healing well.

Conclusions: This is the first human case of *Ignatzschineria* bacteraemia in Slovenia. *Ignatzschineria* spp. are emerging bacteria that have known association to myiasis in humans. Bacteraemia caused by these bacteria is rare. Given the increasing number of illegal border-crossers it could become an important migrant health issue. Therefore, it should be suspected by healthcare providers when experiencing maggot wound infestation.

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Abstract 758

Increasing trend of leptospirosis in an area of northern Spain (1986-2019)

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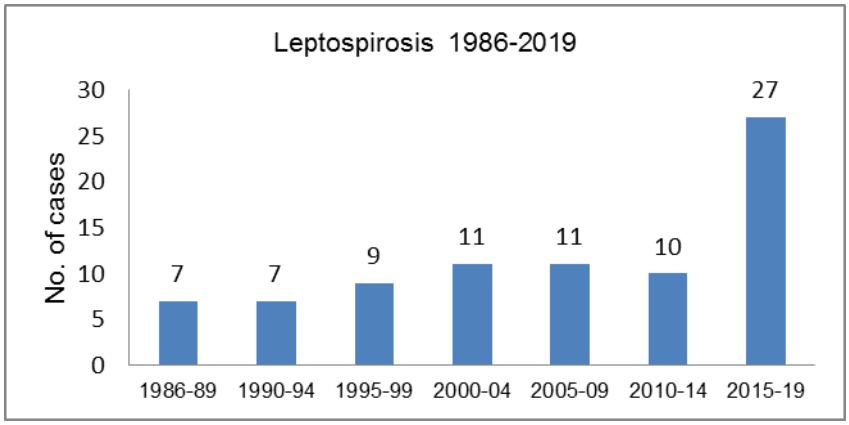
Background: Leptospirosis is a zoonotic disease more frequent in wet tropical and subtropical regions. Human infection results from indirect exposure to urine of carrier mammals, especially rodents. This work studies the incidence and epidemiological characteristics of leptospirosis in Gipuzkoa (Basque Country, Spain), 712119 inhabitants.

Materials/methods: Retrospective leptospirosis review of clinical and laboratory data, 1986-Sept2019. Laboratory tests: *Leptospira* agglutination (Diagnostics Pasteur) until 1991, IgM ELISA (Panbio or Novatek) since that year and *Leptospira* DNA detection using an "in house" PCR (JCM 2014;52:2011) in 2015-2016 and a commercial PCR (Tropical fever, Fast-Track Diagnosis) since 2017. Microscopic Agglutination Test (MAT) (reference laboratories) was used to confirm agglutination or IgM-positive cases. Cases were classified following CDC Leptospirosis 2013 Case Definition.

Results: Eighty-two cases were detected in the period of study, being 55 (67.1%) confirmed and 27 (32.9%) probable cases, 72 (88%) in males. PCR only contributed with one more case than serology but allowed to confirm 13 cases that otherwise would have been classified as probable cases. Thirty-one cases (38%) were detected in 1986-2002 and 51 (62%) in 2003-2019 (22 of them in the last three years). Fifty six cases (73% of the 77 with known age) were 30-69 years-old (group range 13-77 years). In 2017-2019, the incidence was 1.03 cases/100.000 inhabitants, being in males 30-69 years-old 2/100.000. An epidemiological linkage was known in 60 (73%) cases: job-related (sewer maintenance, agricultural activities, livestock farming) in 67% and recreational activities (immersion in water, hunting, trekking) in 33%. Most cases were autochthonous (93%) and occurred in summer and fall (81%). Ninety-eight percent of patients needed hospitalization and 50% were admitted in the Intensive Care Unit. There were no deaths. *L. icterohaemorrhagiae* (71%) and *L. canicola* (18%) were the most common serogroups. The increase of cases observed in the last period (2017-2019), could not be attributed to an increase in requests or a common epidemiologically source.

Conclusions: In Gipuzkoa, the incidence of leptospirosis increased in recent years without a known cause. The highest rate was detected in 30-69 year-old males. A plausible epidemiological exposure was detected in most cases and PCR allowed confirm many of them.



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Abstract 768

Linezolid-resistant strains of *Enterococcus faecium* in the Czech Republic from 2009 to 2018

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Background: Enterococci has become one of the most important opportunistic pathogens leading to nosocomial infections, *Enterococcus faecium* is the most clinical relevant. The treatment of infections caused by enterococci is limited since they exhibit intrinsic resistance to a broad spectrum of antibiotics (cephalosporins, sulphonamides, aminoglycosides, macrolides). However, linezolid was approved and is still used for treatment of vancomycin-resistant enterococci infections, the incidence of linezolid resistant enterococci is worldwide on the rise. Therefore, the aims of this study was to determine mechanism of resistance and to map epidemiology of this pathogen within the Czech Republic since 2009 to 2018.

Materials/methods: The minimum inhibitory concentration (MIC) of 571 strains of *E. faecium* was examined according to the EUCAST recommendations. Molecular tools, PCR (plasmid carrying genes *cfr, optrA*), sequencing (23S rRNA, L3, L4 proteins) as well as multilocus sequence typing (MLST) were used to elucidate the mechanisms of resistance of linezolid resistant strains and to determine epidemiological relationship between linezolid resistant enterococci widespread in the Czech Republic within 9 years. Software Bionumerics 7.6.3 was used for sequence and consequently BURP analysis.

Results: All linezolid resistant isolates (n=75, 13%) had MIC for linezolid above 4mg/L. Altogether, 83 % (n=62) of strains were resistant also to vancomycin and/or to aminoglycosides (77%, n=58). Totally, 71 strains were linezolid resistant due to the mutation G2576T in 23S rRNA of 50S ribosomal subunit. The presence of gene *cfr* was confirmed just once. MLST analysis revealed the presence of only one clonal complex, CC17 (ST18, 78, 80, 117) of linezolid resistant *E. faecium* in the Czech Republic.

Conclusions: The high risk hospital associated clone CC17 confirmed all around Europe was also observed in the Czech Republic. The main mechanism (95%) of resistance to linezolid among *E. faecium* was the mutation in 23S rRNA (G2576T).

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Abstract 771

RESTORE-IMI 2: randomised, double-blind, phase III trial comparing efficacy and safety of imipenem/cilastatin (IMI)/relebactam (REL) versus piperacillin/tazobactam (PIP/TAZ) in adult patients with hospital-acquired or ventilator-associated bacterial pneumonia (HABP/VABP)

Ivan Titov[1], Richard G Wunderink[2], Antoine Roquilly[3], Daniel Rodriguez Gonzalez[4], Aileen David-Wang[5], Helen W. Boucher[6], Keith S. Kaye*[7], Maria C. Losada[8], Jiejun Du[8], Robert Tipping[8], Matthew L. Rizk[8], Munjal Patel[8], Michelle L. Brown[8], Nicholas Kartsonis[8], Joan Butterton[8], Amanda Paschke[8], Luke F. Chen[8]

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Abstract third-party references: Funding for this research was provided by Merck Sharp & Dohme Corp., a subsidiary of Merck & Co., Inc., Kenilworth, NJ, USA.

Background: Due to rising carbapenem resistance, new HABP/VABP treatment options are needed. IMI/REL, a combination of IMI and the class A and class C β-lactamase inhibitor REL, is active against many carbapenem-resistant gram-negative pathogens. We conducted a phase 3 clinical trial evaluating efficacy and safety of IMI/REL in HABP/VABP.

Materials/methods: RESTORE-IMI 2 was a randomized, controlled, double-blind, multinational, phase 3, non-inferiority trial in adult patients with HABP/VABP. Lower respiratory tract specimens were obtained ≤48 hours prior to screening. Patients were randomized 1:1 to IMI/REL 500mg/250mg or PIP/TAZ 4g/500mg, given intravenously every 6h for 7-14d. Patients also received empiric linezolid until baseline cultures confirmed absence of MRSA. The primary endpoint was Day 28 all-cause mortality and the key secondary endpoint was clinical response at early follow-up (7-14d after completing therapy) in the modified intent-to-treat (MITT) population (randomized patients with ≥1 dose of study drug, excluding patients with only gram-positive cocci present on baseline Gram stain). Non-inferiority margins for these endpoints were 10% and -12.5%, respectively. The safety population comprised all patients who received study drug.

Results: The MITT population comprised 531 of 537 randomized patients (264 IMI/REL, 267 PIP/TAZ); 48.6% had ventilated HABP or VABP, 42.9% were ≥ 65 years old, 66.1% were in the ICU, 47.5% had APACHE-II scores ≥15, and 24.7% had moderate/severe renal impairment. The most common causative pathogens in the microbiologic MITT population (MITT patients with confirmed, eligible causative pathogens) were *K. pneumoniae* (25.6%), *P. aeruginosa* (18.9%), *A. calcoaceticus-baumannii* complex (15.7%), and *E. coli* (15.5%). IMI/REL was non-inferior ($p < 0.001$) to PIP/TAZ in both primary and key secondary efficacy endpoints (Table). Rates of adverse events (AEs) in the safety population (IMI/REL 226/266 [85.0%] vs PIP/TAZ 233/269 [86.6%]), and therapy discontinuations due to both overall AEs (IMI/REL 15/266 [5.6%] vs PIP/TAZ 22/269 [8.2%]) or specifically due to drug-related AEs (IMI/REL 6/266 [2.3%] vs PIP/TAZ 4/269 [1.5%]) were similar in both groups. The most frequently reported (>5 patients) drug-related AEs in the IMI/REL arm were diarrhea, increased alanine aminotransferase, and increased aspartate aminotransferase (6/266 [2.3%] each).

Conclusions: IMI/REL is an efficacious and well-tolerated treatment option for HABP/VABP.

Table. Primary and key secondary efficacy outcomes (MITT population)

	IMI/REL n/N (%)	PIP/TAZ n/N (%)	Adjusted difference[a] (95% CI)
Primary endpoint			
Day 28 all-cause mortality	42/264 (15.9%)	57/267 (21.3%)	-5.3% (-11.9, 1.2)[b]
Key secondary endpoint			
Favorable clinical response at EFU	161/264 (61.0%)	149/267 (55.8%)	5.0% (-3.2, 13.2)[c]

CI, confidence interval. EFU, early follow-up visit. IMI/REL, imipenem/cilastatin/relebactam. N, total number of MITT patients in treatment arm. n, number of patients who died or had unknown survival status (primary endpoint) or number of patients with favorable clinical response (key secondary endpoint). PIP/TAZ, piperacillin/tazobactam.

[a]Adjusted differences and confidence intervals stratified by pneumonia type (non-ventilated HABP vs. ventilated HABP/VABP) and baseline Acute Physiology and Chronic Health Evaluation II (APACHE II) score (<15 vs. ≥15) using the Miettinen & Nurminem method. [b]The upper bound of the CI is less than the pre-defined non-inferiority margin of 10 percentage points, indicating success for the non-inferiority hypothesis. [c]The lower bound of the CI is greater than the pre-defined non-inferiority margin of -12.5 percentage points, indicating success for the non-inferiority hypothesis.

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Abstract 772

Mycobacterium tuberculosis drives expansion of low-density neutrophils equipped with regulatory activities

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Background: In human tuberculosis (TB) neutrophils represent the most commonly infected phagocytes, however their role in TB protection and pathology remained contradictory, with some data implicating neutrophils in the TB control and others associating them with TB pathology and progression. Moreover, a subset of low-density neutrophils (LDNs) has been identified in TB, but until now, despite several studies have described the diversity of neutrophil subpopulations, their plasticity in playing different functions is still not fully elucidated.

Materials/methods: We have compared the *ratio* between neutrophils and lymphocytes (N/L) in Active TB patients Cured TB patients and Healthy donors (H.D.). Moreover, in active TB patients, we have analyzed total neutrophils and their low-density (LDNs) and normal-density (NDNs) subsets, in terms of frequency, phenotype, functional features and gene expression signature. Data collection, emocytometer, flowcytometry and confocal microscopy were used in order to evaluate the absolute count of neutrophils and lymphocytes cells, the phenotypical and functional properties of the subsets of neutrophils and their transcriptomic profile for cytokines, chemokines and transcription factors of the innate immunity compartment.

Results: Biological properties of the two isolated neutrophil populations suggest their dual role during TB: NDNs provide a mechanism for bacteria killing, through oxidative burst and NETosis, by upregulating transcription factors involved in the release of cytokines and activation of innate and acquired immune cells, LDNs instead exert suppressive activities on T cell response.

Conclusions: The balance between these two subsets of neutrophils might influence either the initial steps of innate immune responses or the subsequent development of the adaptive immune response to *M. tuberculosis*, ultimately influencing the outcome of infection.

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Abstract 777

Susceptibility of β-lactam-resistant *Pseudomonas aeruginosa* to last-line antibiotics stratified by carbapenemase production

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Background: Carbapenem-resistant *Pseudomonas aeruginosa* is a global critical threat. There are various mechanisms of resistance to carbapenems including carbapenemase production. Clonal spread of NDM-producing-*Pseudomonas aeruginosa* has previously been demonstrated in our local population. An investigation was conducted to determine the distribution of carbapenemase production and antimicrobial susceptibility among β-lactam resistant *Pseudomonas aeruginosa*.

Materials/methods: Polymerase-chain-reaction (PCR) for gene-encoding NDM, KPC, OXA-48, GES, VIM, IMP, and OXA-23 was performed on β-lactam-resistant *Pseudomonas aeruginosa* isolates from a tertiary hospital in Singapore between 1/1/2019 and 30/6/2019. Only isolates that were non-susceptible to ceftazidime, cefepime, piperacillin-tazobactam, imipenem, and meropenem from routine susceptibility testing (Vitek 2) were included. Extended antimicrobial susceptibility testing to aztreonam, ceftazidime-avibactam, ceftolozane-tazobactam, and colistin was also performed using Sensititre broth-microdilution (ThermoFisher) and interpreted according to EUCAST breakpoints.

Results: Twenty-nine (54.7%) of the 53 *Pseudomonas aeruginosa* isolates were found to carry carbapenemase genes. Of these, fifteen (28.3%) were NDM-positive, eleven (20.8%) were IMP-positive, and three (5.7%) were GES-positive. The overall susceptibility results are present in Table 1. Metallo-β-lactamase-positive-isolates (NDM and IMP) were all resistant to ceftazidime-avibactam and ceftolozane-tazobactam, while GES-positive-isolates (class A carbapenemase) were susceptible to ceftazidime-avibactam but resistant to ceftolozane-tazobactam. Susceptibility to colistin was variable. All colistin-resistant isolates had a minimum-inhibitory-concentration (MIC) of 4 mg/L.

Table 1: Susceptibility of *Pseudomonas aeruginosa* isolates stratified by resistance mechanism

Drug	NDM	GES	IMP	Carbapenenamase negative	Overall
Aztreonam	86.7% (13/15)	33.3% (1/3)	45.5% (5/11)	25% (6/24)	47.2% (25/53)
Ceftazidime-avibactam	0% (0/15)	100% (3/3)	0% (0/11)	58.3% (14/24)	32.1% (17/53)
Ceftolozane-tazobactam	0% (0/15)	0% (0/3)	0% (0/11)	62.% (15/24)	28.3% (15/53)
Colistin	80% (12/15)	0% (0/3)	72.7% (8/11)	62.% (15/24)	66.0% (35/53)

Conclusions: High rates of carbapenemase production was demonstrated among our β-lactam-resistant *Pseudomonas aeruginosa* isolates. High rates of resistance to various last-line antimicrobials were also demonstrated. The antibiogram varied based on carbapenemase-genes. Overall susceptibility was highest for colistin at 66.0%, and less than 50% for other drugs. All colistin resistant isolates had MICs within the area-of-technical-uncertainty (ATU) for colistin, the impact of which is unclear. Further work is needed to control spread of these multi-drug-resistant-organisms and to develop better treatment options.

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Abstract 780

Effectiveness of implementing a locally developed antibiotic use guideline for community-acquired cellulitis at a large tertiary care university hospital in Thailand

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Background: Cellulitis is a common infection among both ambulatory and hospitalized patients. A study conducted in 970 adult patients with cellulitis at Siriraj Hospital revealed that broad-spectrum antibiotic or antibiotic combination was inappropriately prescribed in most of these patients even though only a narrow-spectrum agent and a single agent was needed in most patients. The objective of this study was to determine the effectiveness of implementing a locally-developed clinical practice guideline (CPG) for antibiotic use in adults with community-acquired cellulitis who receive medical care at Siriraj Hospital in Bangkok, Thailand.

Materials/methods: The CPG for antibiotic treatment of community-acquired cellulitis was developed based on data from 970 adult patients treated for cellulitis at Siriraj Hospital during June to December 2016. The CPG is a one-page Thai language document. The CPG was introduced via multiple methods, including posters, brochures, circular letters, social media, conference, classroom training, and interactive education during January to September 2018. Medical records of adult patients with cellulitis were collected and analyzed for demographic and clinical characteristics, antibiotic regimens, clinical outcomes, cost of treatment, and CPG compliance.

Results: Among 360 adult patients with community-acquired cellulitis, 84.4% were ambulatory, and 15.6% were hospitalized. The median age of patients was 62 years, and 59.4% were female. Antibiotic prescription according to CPG (CPG-compliant group) was observed in 251 patients (69.7%), and CPG non-compliance was found in 109 patients (30.3%) (CPG-noncompliant group). The demographics and characteristics of patients were comparable between groups. Patients in the CPG-compliant group had a significantly lower rate of intravenous antibiotics (18.7% vs. 33.9%, p=0.007), lower prescription rate of broad-spectrum antibiotics (14.7% vs. 78.9%, p<0.001) and antibiotic combinations (6.4% vs. 13.8%, p=0.022), shorter median duration of antibiotic treatment (7 vs. 10 days, p<0.001), lower median cost of antibiotic treatment (3 vs. 7 USD, p<0.001), and lower median hospitalization cost (601 vs.1,587 USD, p=0.008) than those in the CPG-noncompliant group. Treatment outcomes were not significantly different between groups.

Conclusions: Adherence to the CPG could reduce inappropriate prescription of broad-spectrum antibiotics or antibiotic combinations and lower treatment costs in adults with community-acquired cellulitis without differences in favorable outcomes or adverse events.

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Abstract 784

Launch of a new faecal molecular external quality assessment scheme by UK NEQAS Parasitology

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Background: Protozoan infections still cause significant morbidity and are responsible for a large portion of infectious gastroenteritis. They are even believed to be twice as common as bacterial infections. These commonly recognized pathogenic protozoa include *Giardia lamblia*, Cryptosporidium species and *Entamoeba histolytica*.

Because of the clinical importance of these protozoa, rapid plus sensitive detection and standardised diagnostic procedures are needed in order to allow for specific and rational treatment. As a result, recent times have seen increased use of molecular methods for detection.

Various molecular methodologies exist each with their own specific and general pitfalls and limitations.

Thus, the need for a fit-for-purpose qualitative External Quality Assessment (EQA) or Proficiency testing scheme for these parasites is very timely.

Materials/methods: We sent out a questionnaire to all participants within our microscopy-based Faecal Parasitology EQA scheme in order to determine level of interest for a molecular EQA scheme.

Freeze dried specimens were prepared using clinical and/or cultured specimens spiked in negative faeces.

The homogeneity and stability of these specimens at various temperatures and time points were analysed.

A pre-pilot survey was performed with 10 labs (UK plus non-UK) and results analysed.

Results: 100% of participants were able to identify faecal parasites in our EQA challenge. No false positive or false negatives were observed in the mini-pilot.

Freeze dried faeces is a suitable matrix due to the following:

- Intended matched participant results.
- Samples travelled well.
- Samples worked well under all DNA extraction and amplification methods used by participants.
- Samples were homogeneous and stable under the tested conditions.

Conclusions: We have produced a fit for purpose EQA scheme for molecular detection of faecal parasites.

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Abstract 785

Forecasting of Crimean-Congo haemorrhagic fever outcome

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Background: During providing medical care to seriously ill patients with Crimean-Congo hemorrhagic fever (CCHF), the risk of Health care-associated infections (HCAIs) increases in first and second level hospitals. A unified assessment of the severity of the patient's condition which allow to identify the patients at high risk of death and indications for transfer to a third-level hospital is requied.

Aim: to develop a methodology for assessment the risk of death in patients with CCHF based on the clinical and laboratory parameters at the day of hospitalization, which are available in the hospitals of first / second level.

Materials/methods: Based on the analysis of 4 methods of assessment the severity of patients with CCHF (Swanepoel R. et al., 1989; Bakir M. et al., 2012; Dokuzoguz B., 2013; Bakir M. et al., 2015) a mortality risk prediction scale was developed. It based on 12 clinical and laboratory parameters (age, alanine transaminase, aspartate transaminase, leukocyte count, liver size, organ disorders, bleeding, thrombocyte count, prothrombin time, international normalized ratio, fibrinogen) and 2-4 gradations of each parameter, which were reflected in 32 criteria of the scale. The scale was tested on the retrospective analysis of case records of 52 patients with CCHF who were treated in hospitals of the Turkestan region in Kazakhstan in 2000-2018.

Results: Clinical and laboratory parameters of the patients were evaluated in accordance with the developed point scale for assessing the risk of death in patients with CCHF. Each evaluated parameter was assigned a certain number of points and their total amount was determined. With a patient score of ≥11, a high probability of an adverse outcome was predicted. With a score of <11, the probability of an fatal outcome of CCHF was estimated as low. The sensitivity of the proposed method is 100%, specificity - 98%, predicted value - 90%.

Conclusions: The proposed metodology with a high probability allows to predict the development of an unfavorable outcome of CCHF and is suitable for use in hospitals of the first and second levels to optimize the medical care of patients with this pathology and the prevent of HAIs.

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Abstract 787

A pathogen and a non-pathogen spotted fever group Rickettsia trigger differential proteome signatures in macrophages

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Background: Spotted fever group *Rickettsia* are recognized as important agents of human tick-borne diseases worldwide such as Mediterranean spotted fever (*R. conorii*) and Rocky Mountain spotted fever (*R. rickettsii*). Reductive genome evolution in obligate intracellular *Rickettsia* has resulted in the loss of many metabolic pathways, which culminates with *Rickettsia* species being strictly dependent on host cells to survive and proliferate. Several efforts have been made to identify host and bacterial determinants that allow bacteria to proliferate inside host cells. We have reported a differential tropism of pathogenic and non-pathogenic *Rickettsia* species in macrophages, further strengthening the complexity of host-rickettsiae interactions and raising questions on how pathogenic *Rickettsia* manipulate host pathways to their advantage.

Materials/methods: We have herein employed a quantitative high-throughput proteomics approach (SWATH-MS) to profile alterations in THP-1 macrophages upon infection with the highly pathogenic *R. conorii* and the non-pathogenic *R. montanensis*.

Results: Our results revealed that *R. conorii* is able to substantially reprogram several host signaling pathways, modulating host cells to a niche apparently more adapted to its needs. Specifically, *R. conorii* induced the accumulation of several enzymes of the tricarboxylic acid cycle, oxidative phosphorylation, fatty acid β-oxidation, and glutaminolysis, as well as of several inner and outer membrane mitochondrial transporters. These results suggest a profound metabolic rewriting of macrophages by *R. conorii* toward a metabolic signature of an M2-like, anti-inflammatory activation program. Moreover, several subunits forming the proteasome and immunoproteasome are found in lower abundance upon infection with both rickettsial species, which may help bacteria to escape immune surveillance. *R. conorii*-infection specifically induced the accumulation of several host proteins implicated in protein processing and quality control in ER, suggesting that this pathogenic *Rickettsia* may be able to increase the ER protein folding capacity.

Conclusions: Our results unfold the intricate pattern of modulation triggered by a pathogenic *Rickettsia* to control macrophage homeostasis and to maintain a viable intracellular niche. By illuminating the still very poorly studied aspects of macrophage-*Rickettsia* interactions, our work provides an essential framework for a deeper understanding of the link between rickettsial pathogenicity and host manipulation.

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Abstract 792

Feasible alternatives to dried blood spot in the retrospective diagnosis of congenital *cytomegalovirus* infection

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Background: Retrospective diagnosis of CMV infection (cCMV) cases plays a crucial role in the management of late-onset symptomatic infants and it is usually achieved by CMV DNA detection in dried blood spot (DBS) cards. However, there is a lack of consensus about the most reliable extraction and PCR protocols to be used. In this study, we describe viral load (VL) results in various clinical samples from confirmed cCMV cases. The objectives were: (1) To compare CMV-VL values in samples obtained at birth from infants with cCMV. (2) To evaluate dried umbilical cord (DUC) samples as an alternative to dried blood samples (DBS).

Materials/methods: Saliva and/or urine, peripheral blood, and DBS from 15 infants with confirmed cCMV infection were collected at birth. CMV-VL was determined by real-time polymerase chain reaction (rt-PCR). In two cases, VL was determined from available DUC samples. The Mann–Whitney U test was used to compare VL values.

Results: Five (33.3%) of the 15 infants were symptomatic, and 10 (66.6%) were asymptomatic. The CMV-VL found in saliva and in urine were both higher than those found in peripheral blood (*p*-value: 0.0001). Symptomatic infants presented 100% of detectable VL in peripheral blood and 40% in DBS. Asymptomatic infants showed 75% of detectable VL in peripheral blood and 40% in DBS.

Conclusions: When VL was detectable in peripheral blood, the values were lower than in saliva or urine, in both symptomatic and asymptomatic cases of cCMV. The low sensitivity in DBS samples could be due to low blood volume content, making CMV-VL undetectable even when using optimised extraction and PCR protocols. Based on our experience and on published data, DUC could be a reliable alternative to DBS.

	n	Detectable-VL	Median Log [IQR]	Median IU/ml [IQR]
Saliva-VL	10	10 (100%)	Log 6.3 [5.8-6.5]	1,958,525 [597,683-3,483,843]
Urine-VL	12	12 (100%)	Log 5.8 [5.5-6.5]	691,865 [188,489,5-3,175,696]
Peripheral blood-VL	12	10 (83,3%)	Log 3.0 [2.6-3.6]	1,019 [364-4,002]
DBS-VL	15	6 (40%)	Log 2.8 [2.6-2.9]	604,5 [415-858]
DUC-VL	2	2 (100%)	Log 4.2 [4.0-4.3]	16,05 [9,754-22,341]

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Abstract 793

Kingella endocarditis in children: a distinct entity or not ?

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Background: *Kingella,* a gram-negative coccobacillus, causes various invasive pediatric diseases, including life threatening infective endocarditis (IE). Data on pediatric *Kingella* endocarditis are scarce. Our aim is to describe the clinical features of pediatric *Kingella* IE patients and compare them to other causative agents of IE, determining whether they have unique clinical characteristics.

Materials/methods: We retrospectively analyzed patients, aged 0-18 years, admitted with IE between the years 1994-2019, in a tertiary pediatric center in Israel.

Inclusion criteria was fulfillment of Duke's criteria for diagnosis of IE. We compared the epidemiologic, clinical, laboratory, imaging and cardiac features of the patients with Kingella to Streptococcus species and Staphylococcus Aureus IE.

Results: 60 patients were included in the study. In 19 the causative pathogen was kingella, 25 had Streptococcus and 16 had Staphylococcus aureus IE. Nine (47%) patients with Kingella endocarditis had no known previous heart defect. The mean age of the patients with Kingella was younger than the Streptococci and Staphylococci groups (16±10 months, 106±70, 68±76 respectively, P< 0.001). A male predominance was noted (69.4% compared with 40.0%, 37.5% respectively). The Kingella IE patients had higher temperature on admission, history of oral aphthae prior to the diagnosis of IE (29.4% compared with 0%, 0% respectively, P<0.002)and higher lymphocyte count (4.27K±3.04, compared with 2.09K±1.36, 2.40K±2.38 respectively, P<0.002) .

Conclusions: Kingella IE pediatric patients have some unique features compared to those with S. aureus and Streptococci IE; Young healthy children (<36 months), especially males, with or without congenital heart defect, with recent history of oral aphthae, that present with prolonged fever should raise the suspicion for Kingella IE.

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Abstract 794

Stenotrophomonas maltophilia bloodstream infections in umbilical cord blood transplant recipients

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Background: Limited data are available on *Stenotrophomonas maltophilia* bloodstream infection (SM-BSI) in umbilical cord blood transplant (uCBT) recipients who exhibit a higher risk of delayed neutrophil engraftment relative to other types of allogeneic hematopoietic stem cell transplant recipients. Additionally, the therapeutic efficacy against SM-BSI and hemato-toxicity of trimethoprim-sulfamethoxazole (SXT) are still unknown in uCBT settings.

Materials/methods: The medical and microbiological records of patients who received uCBTs between December 2008 and December 2015 were reviewed. Identification and drug susceptibility testing were performed using the WalkAway 96 SI system. The current CLSI breakpoints for *S. maltophilia* were used. Evaluation of SXT was performed only for recipients who received ≥ 7 days of intravenous SXT as treatment for SM-BSI (the evaluation cohort).

Results: Of 561 uCBT recipients, 34 developed SM-BSI. Diabetes mellitus, severe neutropenia for ≥ 21 days, and age ≥ 60 years were significant independent risk factors for SM-BSI. The hazard ratio for all-cause mortality up to 100 days after transplantation was 10.5 (95% CI, 6.79 – 16.1) for patients with SM-BSI, compared to patients without SM-BSI. Of the 34 recipients with SM-BSI, 25 developed SM-BSI during the pre-engraftment phase (neutrophil count < 500/μL) and 24 were treated with an intravenous SXT-based regimen (iSXT-BR). The 7-day- and 30-day-crude-mortality-rates of the recipients with SM-BSI were 64.7% and 73.5%, respectively. Additionally, 7-day-crude-mortality-rate of the recipients with SM-BSI with pneumonia (11/12) was significantly higher than that for recipients without pneumonia (11/22) (P=0.04). The susceptibility rates of the 34 causative strains for SXT and levofloxacin were 97% and 79%, respectively. Nine recipients were included in the evaluation cohort. The doses of iSXT ranged from 2.4 to 6.9 mg/kg/day of the trimethoprime component. Five of the nine recipients developed SM-BSI during the pre-engraftment phase. The 30-day-crude-mortality-rate and the clinical cure rate of the cohort were 22% and 77%, respectively. In addition, only one of the nine recipients experienced significant neutrophil toxicity.

Conclusions: The epidemiology of SM-BSI in uCBT recipients was determined and its negative impact on survival was demonstrated. The iSXT-BR was a tolerable and important therapeutic option for SM-BSI in the uCBT setting, including during the pre-engraftment phase.

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Abstract 797

Impact of a routine molecular Point-of-Care test-and-treat strategy for influenza in adults hospitalised with acute respiratory illness: a pragmatic, multi-centre, randomised controlled trial (FluPOC)

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Background: Influenza infections often remain undiagnosed in patients admitted to hospital due to lack of routine testing. When tested for, the diagnosis of influenza is often delayed due to the long turnaround times of laboratory PCR, leading to inappropriate and late antiviral and isolation facility use. Molecular point-of-care tests (mPOCT) for influenza can deliver results in under 1 hour but high quality evidence for impact on clinical management and outcomes is lacking.

Materials/methods: In this pragmatic, multicentre, randomised controlled trial we enrolled adults admitted to hospital with acute respiratory illness (ARI) during influenza season. Patients were randomised (1:1) to receive mPOCT for influenza or routine clinical care. The primary outcome was the proportion of influenza infected patients who received antivirals. Secondary outcomes included; the detection rate of influenza, turnaround time of results, time to antivirals, isolation facility use, antibiotic use, length of stay, time on supplementary oxygen, critical care admission and mortality.

Results: 613 patients were recruited and randomised, 307 to POCT and 306 to routine care. All were analysed in the intention-to-treat (ITT) analysis. 100/307 (33%) patients in the POCT group and 102/306 (33%) patients in the control group were influenza infected. The median [IQR] turnaround time for results was 1.2 [1.1-1.4] hours in the POCT group and 23 [16-29] hours in the control group, p<0.0001. 100/100 (100%) influenza-infected patients were diagnosed in the POCT group but only 55/102 (54%) were diagnosed in the control group, p<0.0001. 99/100 (99%) influenza-infected patients received antiviral treatment in the POCT group versus 63/102 (62%) in the control group, relative risk 1.6 (95%CI 1.4 to 1.9); p<0.0001. 70/100 (70%) of influenza infected patients in the POCT group were correctly nursed in single room accommodation versus 39/102 (38%) in the control group, p<0.0001. Admission to critical care units or death occured in 1/100 (1%) patients in the POCT group versus 8/102 (7.8%) in the control group, p=0.035.

Conclusions: A routine mPOCT strategy for influenza in adults hospitalised with ARI improved the detection of influenza and the appropriate and timely use of antivirals and isolation facilities. It was also associated with improvements in clincal outcome.

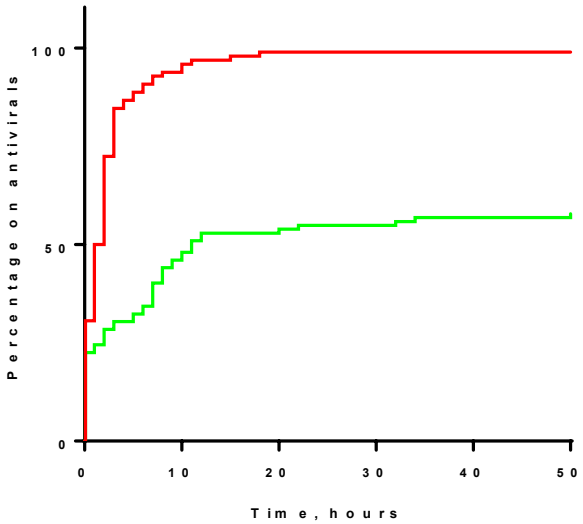

Figure 1. Kaplan-Meier curve showing time to the administration of antivirals in the point-of-care testing group (red) and the control group (green) in influenza-infected patients. Log rank test, p<0.0001.

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Abstract 802

In vitro activity of ceftazidime-avibactam (CAZ-AVI) and comparators against Gram-negative pathogens isolated from patients in Canadian hospitals in 2009-2018: CANWARD surveillance study

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Background: Ceftazidime-avibactam is used for the treatment of infections caused by multi-drug-resistant organisms. We determined the in vitro activity of ceftazidime (CAZ) with and without avibactam and comparators versus Gram-negative pathogens recovered from January 2009 to December 2018 from patients in medical and surgical wards, intensive care units, clinics, and emergency rooms in 15 Canadian hospitals.

Materials/methods: Antimicrobial susceptibility testing was performed using broth microdilution panels following CLSI recommendations (M07, 11th edition). Susceptibility was determined using EUCAST breakpoints (where available) or CLSI breakpoints (M100, 29th edition). Cephalosporin-resistant *Escherichia coli* and *Klebsiella* spp. isolates were genetically characterized for ESBL production using PCR and DNA sequencing.

Results:

	MIC_{90} (µg/mL) /% susceptible					
	CAZ-AVI	Ceftazidime	Meropenem	TZP	TOL-TAZ	Ceftriaxone
Escherichia coli (6902)	0.25/99.9	2/89.2	≤0.03/100	4/95.8	0.5/98.8	2/89.9
E. coli CRO-R (676)	0.5/99.3	>32/5.6	0.06/99.7	16/82.4	1/91.1	>64/0
E. coli ESBL (566)	0.5/99.8	>32/6.7	0.06/99.8	16/83.9	1/93.7	>64/1.8
Pseudomonas aeruginosa (3511)	8/93.3	32/80.0	8/79.9	64/82.3	2/97.4	>64/NA
P. aeruginosa (CAZ-R) (704)	>16/67.1	>32/0	32/46.7	512/21.5	8/87.9	>64/NA
P. aeruginosa (TZP-R) (620)	>16/68.1	>32/10.8	32/43.9	512/0	8/88.3	>64/NA
P. aeruginosa (MER-R) (279)	>16/54.8	>32/25.1	>32/0	512/29.0	8/82.8	>64/NA
Klebsiella pneumoniae (2289)	0.5/100	1/92.1	0.06/99.6	8/91.3	0.5/96.1	1/92.1
K. pneumoniae CRO-R (141)	2/99.3	>32/6.4	0.5/92.9	>512/44.7	64/57.1	>64/0
K. pneumoniae ESBL (127)	2/100	>32/8.7	0.25/95.3	>512/44.9	32/62.9	>64/5.5
Enterobacter cloacae (991)	1/99.7	>32/71.6	0.12/99.8	64/79.9	8/79.5	>64/72.9
E. cloacae CRO-R (249)	2/98.8	>32/2.0	0.25/99.2	128/25.5	16/25.5	>64/0
E. cloacae ERT-R (97)	2/99.0	>32/2.1	0.5/97.9	256/11.3	32/12.4	>64/2.1
Serratia marcescens (584)	0.5/99.7	1/95.4	0.06/99.8	4/94.9	1/93.6	1/93.5
Klebsiella oxytoca (617)	0.5/99.8	1/95.3	≤0.03/100	128/88.0	0.5/96.9	1/90.1
Proteus mirabilis (522)	0.12/100	≤0.25/96.9	0.12/100	≤1/99.4	0.5/99.9	≤0.25/98.1
Acinetobacter baumannii (161)	>16/55.3*	32/77.0	2/94.4	64/80.8	4/93.6‡	32/47.8

CAZ-AVI: ceftazidime-avibactam, TOL-TAZ: ceftolozane-tazobactam; CRO-R: ceftriaxone-resistant; CAZ-R: ceftazidime-resistant; TZP: piperacillin-tazobactam, ERT-R: ertapenem-resistant, MER-R: meropenem-resistant, *MIC ≤ 4 µg/mL, ‡MIC ≤8 µg/mL.

Conclusions: CAZ-AVI demonstrated *in vitro* activity against clinical *Enterobacterales* isolates, including those with resistance to oximinocephalosporins by a variety of mechanisms. 93.3% of *P. aeruginosa* were susceptible to CAZ-AVI while CAZ, MER and TZP-resistant *P. aeruginosa* were moderately susceptible to CAZ-AVI. Activity against *A. baumannii* was not improved compared to CAZ alone.

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Abstract 805

Evaluation of the FebriDx host response Point-of-Care test to differentiate viral from bacterial aetiology in adults hospitalised with acute respiratory illness during influenza season

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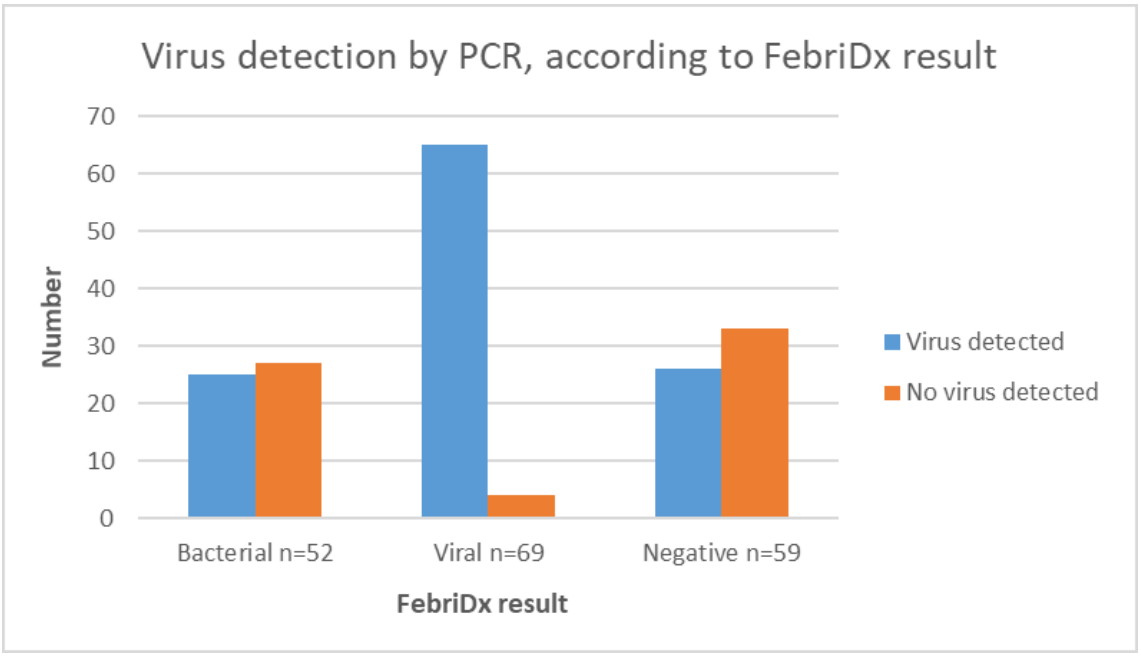
Background: Diagnostic uncertainly regarding microbial aetiology in patients hospitalised with acute respiratory illness (ARI) contributes to antibiotic overuse. A host response test distinguishing between viral or bacterial infection may reduce unnecessary antibiotic use. The FebriDx is a low cost, rapid, host response point-of-care test that uses fingerpick blood samples to distinguish between viral or bacterial infection by detection of MxA and/or CRP.

Materials/methods: We took fingerpick blood samples from adults with ARI, hospitalised during influenza season, and tested them using the FebriDx. Respiratory samples were tested for viruses on the Biofire FilmArray Respiratory Panel 2 plus. The FebriDx was evaluated for failure rate and accuracy of results (Viral, Bacterial, Negative). FebriDx results were not given to treating clinicians. All patients gave written consent.

Results: We took fingerpick blood samples from adults with ARI, hospitalised during influenza season, and tested them using the FebriDx. Respiratory samples were tested for viruses on the Biofire FilmArray Respiratory Panel 2 plus. The FebriDx was evaluated for failure rate and accuracy of results (Viral, Bacterial, Negative). FebriDx results were not given to treating clinicians. All patients gave written consent.

Conclusions: In this real-world evaluation FebriDx use in adults hospitalised with ARI was associated with a relatively high test failure rate and problems reading test lines. FebriDx had a high specificity (94%) and positive predictive value (94%) for the detection of viruses, especially influenza. Bacterial and negative FebriDx results were often associated with non-influenza virus detection which may represent colonisation, secondary bacterial infection or viral infection confined to the airways.



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Abstract 807

Impact of pharmacist-driven antimicrobial stewardship interventions on multicomponent patient outcomes

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Background: Prospective audit and feedback (PAAF) is a core antimicrobial stewardship (AS) strategy recommended to improve antimicrobial use. While studies have demonstrated the benefit of PAAF on clinical outcomes in specific disease states or high-risk groups, few have reviewed the broader impact of this AS initiative. The purpose of this study was to determine the impact of pharmacist-driven AS interventions on multicomponent patient outcomes.

Materials/methods: Retrospective cohort included adult inpatients treated with antimicrobials for ≥ 72 hours from July 2015-December 2015. Patients with an ID consultation, on long-term antibiotics, or made hospice or comfort care during their admission were excluded. Patients were grouped according to the presence or absence of AS intervention performed by a pharmacist. Primary endpoint was a composite of 30-day all-cause mortality, 30-day readmission, 28-day emergence of antimicrobial resistance, and 90-day *Clostridioides difficile* infection (CDI). Secondary endpoints included hospital and intensive care unit (ICU) length of stay (LOS).

Results: 338 patients screened, 200 included: 100 with AS intervention, 100 without. Baseline characteristics were similar between groups except less chronic obstructive pulmonary disease (p=0.01), peptic ulcer disease (p=0.017) and diabetes with organ damage (p = 0.02) in the AS intervention group. Infection types were similar between groups, however more patients were ICU status in the AS intervention group (p = 0.003). Primary and secondary endpoints are listed in Table 1.

Table 1. Study Endpoints

Variable	No AS Intervention n = 100	AS Intervention n = 100	P-value
Composite	43 (43)	26 (26)	0.011
30-day Mortality	2 (2)	3 (3)	1
30-day Readmission	38 (38)	20 (20)	0.005
28-day Resistance	6 (6)	2 (2)	0.279
90-day CDI	5 (5)	3 (3)	0.721
Hospital LOS	6 (5-9)	9 (6-15)	< 0.001
ICU LOS*	9 (7-12)	12 (8-17)	0.077

Data presented as n (%) or median (IQR)

*n = 25 and 45, respectively

Conclusions: Patients with AS intervention performed by a pharmacist were found to have lower rates of 30-day readmission compared to those without. Overall, these results demonstrate a positive impact of pharmacist-driven AS intervention on long-term patient outcomes; however differences in LOS warrant further investigation.

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Abstract 810

A new perspective: microbiota, the role of Streptococcus gallolyticus in childhood colorectal cancer

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Background: Colorectal cancer in childhood is rare but usually associated with a higher incidence of unfavorable histotypes (high-grade,poorly differentiated subtypes) and more aggressive tumor behavior. The prognosis is poor due to delayed diagnosis and advanced stage at diagnosis. The tumorigenesis of childhood colorectal cancer, which necessarily occurs over a shorter period,is still unclear and most likely evolves through different steps. There has been limited knowledge about colorectal cancer in childhood.The aim of this study was to investigate the relationship between childhood colorectal cancer and *S. gallolyticus.*

Materials/methods: The clinical and pathologic characteristics, and outcomes of colorectal cancer in 21 children and adolescents referred to our Pediatric Oncology Department between 1974 and 2017 were reviewed. The control group (healthy colorectal tissue) was consisted of 40 pediatric patients who underwent colon surgery for other reasons. Demographic and clinical findings of the patients were evaluated. *S. gallolyticus* analysis was performed from cancerous and healthy colorectal tissues. DNA was isolated from paraffin tissue for *S. gallolyticus* analysis. The presence of *S. gallolyticus* was screened by the Real-Time PCR method using specific predetermined primers and probes. Positive isolates were confirmed by sanger sequence analysis.

Results: The median age of patients with colorectal cancer was 14 years (range:10 to 17 years). The male-to-female ratio was 2.5:1. Tumor localization was mostly in the rectum and/or sigmoid region (n=14, 66.7%).The most common stage was stage D (61.9%, n=13).There wasn't any patient in stage A. The most common histologic subtype was mucinous adenocarcinoma (61.9%, n=13). None of the pediatric patients with colorectal cancer had documented *S. gallolyticus* in blood culture. *S. gallolyticus* was detected in 8 (38.1%) colorectal cancer patients and 2 (5%) children in the control group (p= 0.002).

Conclusions: Childhood colorectal cancer has distinct features with poor prognosis despite multidisciplinary approaches and new therapies. In our study, *S. gallolyticus* was found to be significantly higher in colorectal cancer tissues in our patients. This is the first study in the literature. Our study provides a new perspective for early diagnosis and understand risk groups for childhood colorectal cancer that may have a different pathophysiology than adults.

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Abstract 812

Determination of pentraxin 3 levels in cerebrospinal fluid during central nervous system infections

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Background: Pentraxin 3 (PTX3) is an acute phase protein; its plasmatic levels significantly raise during severe infections. Data on PTX3 levels in cerebrospinal fluid (CSF) of patients with central nervous system (CNS) infections are lacking. We aimed: a) to assess the diagnostic potential of measuring CSF PTX3 levels in patients with CNS infections; b) to establish CSF PTX3 cut-offs to distinguish between bacterial and aseptic meningoencephalitis (ROC curve).

Materials/methods: In this retrospective observational study, PTX3 levels were measured in CSF from 19 patients admitted to Trieste Hospital, Italy, with CNS infection from January 2016 to September 2018. CSF was collected by lumbar puncture performed within two hours from hospital admission. For each patient four samples of CSF were collected for obtaining these data: (1) leukocyte count, glucose and total protein levels, (2) culture and molecular amplification, (3) real-time PCR for virus (HSV 1-2, CMV, EBV, VZV, WNV, enteroviruses, TBEV and Mumps virus) and (4) PTX3 levels. The latest samples were first stored at -80°C and then analysed in duplicate using a home-made sandwich ELISA. The assay has a lower limit of detection of 100 pg/ml, with 8–10% inter-assay variability.

Results: A diagnosis of bacterial infection and aseptic meningoencephalitis was made in 7 (37%) and 12 (63%) patients, respectively. Subjects with bacterial infections showed significantly higher PTX3 levels (13.5 vs 1.27 ng/mL in aseptic meningoencephalitis, p=0.010). We identified two different CSF PTX3 levels cut-offs. 1) The best cut-off to maximize Youden's J was 9.6 ng/mL with a sensitivity, specificity, positive predictive value and negative predictive value (NPV) of 71.4%, 91.4%, 83.3%, 84.6%, respectively; 2) The cut-off with higher NPV (100%) was 3.6 ng/mL: a diagnosis of bacterial infections was obtained in 0% patients with CSF PTX3 levels <3.6 ng/mL vs 58% of those with CSF PTX3 levels ≥ 3.6 ng/mL (p=0.017).

Conclusions: CSF PTX3 levels are higher in bacterial meningitis than aseptic meningoencephalitis. A cut-off of 3.6 ng/mL of CSF PTX3 has a high NPV and can be used to exclude bacterial CNS infections.

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Abstract 813

Physicochemical characterisation of aluminium hydroxide and aluminium phosphate and their potential adjuvant function in combination with squalene emulsion for EV71 vaccine development

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Background: Aluminum phosphate and aluminum hydroxide (generally called Alum) are two conventional adjuvants acceptable for human vaccines. Yet, the physicochemical properties as well as the adjuvanticity associated with the structure of the two forms of gel suspensions are poorly defined.

Materials/methods: We designed vaccine formulations based on aluminum phosphate and aluminum hydroxide as adjuvants, and investigated respective mode of action linking the physicochemical properties and the adjuvanticity.

Results: The SEM microscopy indicated that aluminum phosphate gel solutions are amorphous, whereas aluminum hydroxide gel solutions have a crystalline structure consistent with boehmite. At very low concentrations, the adsorption of model protein (BSA) onto both aluminum-containing adjuvants followed Langmuir adsorption isotherm, i.e. the antigen adsorption percentage was functional to the antigen/adjuvant ratio. As the protein concentration increases, the adsorbed BSA reduced as less vacant sites were offered on the surface of adjuvants. Notably, 100% of adsorption could be achieved in aluminum hydroxide, whereas a maximal 30% of adsorption was observed in aluminum phosphate, probably due to the presence of the same charge on the adjuvant and antigen. For the investigation of biological interactions, the prepared aluminum salts were tested for their properties to drive the activation/maturation of murine bone marrow-derived dendritic cells (DCs). Flow-cytometry analysis showed that aluminum hydroxide may be an efficient regulator of DC activation, compared with aluminum phosphate. For immunogenicity study of an enterovirus (EV) 71 formalin-inactivated whole virus vaccine, we found that a single-dose intramuscular injection of 0.2 μg inactivated virus could not elicit a forceful EV71 virus neutralized antibody titer. When the same amount of antigen was co-administered with single adjuvant, aluminum phosphate or squalene emulsion, enhances protective EV71-specific serological immunity in mice; moreover, the adjuvant potency of their combination was more potent than individual to induce high levels of antigen-specific antibodies.

Conclusions: It was concluded that aluminum hydroxide, rather than aluminum phosphate, is suitable to be adjuvanted in vaccine candidate according to the results from morphology, antigen adsorption efficiency and DCs activation/maturation; in addition, it will be of great interest for co-administrating Alum together with an emulsified vaccine delivery system against the emerging infectious diseases.

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Abstract 821

Introducing end-of-life considerations into a computerised decision support system for antibiotic treatment: effects on the system's recommendations and comparison to physicians' behaviour

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Background: TREAT is a previously developed and validated computerized decision support system for antibiotic treatment, in clinical use. Currently, it does not address end of life (EOL) considerations, when antibiotic treatment does not offer a benefit but inflicts high collateral damage.

Materials/methods: Based on a causal probabilistic network, TREAT advises antibiotic treatment using a cost-benefit calculation. Costs, expressed as life years loss, comprise of drug, adverse events and ecological costs. The latter considering the clinical significance of resistance selection following specific antibiotics in the individual treated and among contacts. We developed an individualized ecological costs model, addressing the higher ecological impact of patients at EOL. The main individualized ecological cost components were patients' risk for harboring resistant bacteria at baseline, their risk for experiencing a subsequent infection and their potential to transmit resistant bacteria. After implementation into TREAT's cost-benefit calculation, we compared TREAT's baseline advice to its individualized ecological costs advice and physicians' prescribed treatment. Broad-spectrum treatment included piperacillin-tazobactam, carbapenems, vancomycin and colistin.

Results: In a previously collected cohort of 1232 patients with suspected or proven sepsis, a significant difference in ecological costs between 30-day survivors and fatalities was observed. Implementation of individualized ecological costs in TREAT resulted in change of advice for 44.7% (551/1232) patients. Among all patients, the individualized ecological cost TREAT advised significantly less 3rd generation cephalosporins, quinolones and broad-spectrum antibiotics compared to baseline TREAT and significantly more frequently ampicillin, ampicillin-clavulanate and chloramphenicol. Among 30-day fatalities (18.9%, 233/1232), no treatment was advised by individualized TREAT for 11.1% (26/233) patients vs 8.1% (19/233) by baseline TREAT and 16.3% (38/233) by physicians. When prescribing antibiotics, TREAT recommended ampicillin significantly more frequently and ceftriaxone significantly less frequently than physicians. Broad-spectrum treatment and ceftriaxone were advised for 21% (49/233), 44.2% (103/233) and 58.4% (136/233) by individualized TREAT, baseline TREAT and physicians.

Conclusions: Individualization of the ecological costs and EOL considerations are necessary in a decision support system for antibiotic treatment, to approximate physicians' behavior and to avoid aggressive futile antibiotic treatment. Physicians limited treatment at EOL more frequently than individualized TREAT, but used more broad-spectrum therapy when prescribing antibiotics at EOL.

Figure 1: Top 3 treatments for respiratory and urinary infections

Baseline advice	Individualized advice	Prescribed
Respiratory tract infections (N= 528)		
Ceftriaxone IV 157 (29.7%)	Doxycycline IV 131 (24.8%)	Ceftriaxone IV 101 (19.1%)
Doxycycline IV 128 (24.2%)	Ampicillin IV 130 (24.6%)	Ceftriaxone IV + Azithromycin PO 84 (16%)
Quinolone 50 (9.5%)	No treatment 59 (11.2%)	No treatment 55 (10.4%)
Urinary tract infections (N= 383)		
Amikacin IV 198 (51.7%)	Amikacin 165 (43%)	Amikacin 73 (19%)
Quinolone 45 (11.7%)	Amoxicillin-clavulanate IV 54 (14%)	Ceftriaxone IV 82 (21.4%)
No treatment 32 (8.3%)	No treatment 40 (10.4%)	No treatment 57 (14.9%)

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Abstract 822

Pinpointing the genetic intra-host diversity of *Mycobacterium tuberculosis* and its determinants

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Abstract third-party references: on behalf of the Lyon TB study group

Background: Tuberculosis (TB) caused by *Mycobacterium tuberculosis* (Mtb) complex results in a variety of disease manifestations and epidemiological success. Recently, studies based on Whole Genome Sequencing (WGS) have revealed micro-diversity in isolates composition. However this diversity and its dynamics have not yet been considered as a source of information to highlight the process leading to adapt and respond to a changing environment. Here we characterized the variability of the composition of pulmonary and extrapulmonary Mtb isolates and its relations with various host factors

Materials/methods: We explored by WGS Mtb genomic micro-diversity within hosts, by comparing pairwise isolates obtained from both pulmonary and extra-pulmonary sampling in 37 TB patients. Firstly we determined the frequency of single nucleotide polymorphisms (SNP) called at heterozygous sites, then variants were defined as assemblies harboring SNP with similar frequencies. Diversity was assessed by alpha and beta diversity measures based on the variant assemblies. Clinical data resuming the immune and nutritional status of patients were also recorded.

Results: We observed differences between pulmonary and extra-pulmonary isolates from the same patient for 68% of cases, supporting Mtb micro-diversity within the same host. Differences in variant distribution between the pulmonary and the extra-pulmonary isolates, with overall lower extra-pulmonary diversity, indicates Mtb compartmentalization in different body sites. Moreover, we observed a variability involving gene functions specifically associated with either pulmonary or extra-pulmonary TB. Our analysis revealed a correlation between Mtb micro-diversity within pulmonary compartment and low patient body mass indexes. Conversely, Mtb micro-diversity within extra-pulmonary compartment inversely correlated with patient CD4 T cells count, supporting the selective pressure of the immune response on Mtb infection spreading.

Conclusions: These results confirm that close-related but still different Mtb variants coexist rather than a clonal population. This micro-diversity is shaped by the interactions between Mtb and various host factors. Compartmentalization could rely on the higher ability of variants to disseminate and adapt to extra-pulmonary tissues, but more in-depth analysis is required to correlate with some clinical presentations. Taking into account this diversity of Mtb variants, its intra-host dynamics should lead to a better understanding of the dynamics of this disease.

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Abstract 823

Evaluating the predictive performance of ID-ODS software in critically ill patients for piperacillin: a comparison using IV bolus and continuous infusion data

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Background: Piperacillin displays high interindividual variability in critically ill patients. PKPD Model based dosing software can optimize antibiotic exposure and improve treatment outcome. Our objective is to evaluate and compare the accuracy of the individualized dosing program ID-ODS™ (Individually Designed Optimum Dosing Strategies) in predicting piperacillin concentrations a priori in critically ill patients for both continuous infusion and bolus injections.

Materials/methods: The data used for the validation comes from a prior publication in critically ill patients. Samples were collected on days 1 and 2 in 16 patients, with 8 patients receiving bolus dosing and 8 patients receiving continuous infusion. All patients in the continuous infusion group received a loading dose of 4 g. Patient demographics and dosing information were input into the IDODS software and concentrations were predicted in 0.1 hour increments. To assess the predictability of the software, we compared the observed VS predicted concentrations and estimated the R^2, bias and precision. Statistical analysis was performed using the R software.

Results: In total we had 116 observations from the 8 patients on continuous infusion and 113 observations from the 8 patients on bolus dosing. For the continuous infusion group, the R^2 was 0.54, bias was - 25 % and precision was 74 %. For the bolus dosing group, the R^2 was 0.67, bias was - 38 % and precision was 72 %. For both groups, we noticed the software is biased and under predicts the early concentrations after dose administration, while bias approaches zero at later time points.

Conclusions: The IDODS software demonstrated reasonable accuracy in predicting piperacillin concentrations. Predictive performance was similar across the two dosing groups indicating it can be applied for either administration method. The software tended to under predict concentrations at early time points after drug administration. Given piperacillin has time dependent activity and the focus is on achieving therapeutic trough concentrations, this is not likely to impact dose selection. Overall, IDODS software can be used to optimize initial dosing of piperacillin and decrease the likelihood of suboptimal concentrations compared to standard dosing. Further clinical trials are needed to assess its impact on clinical outcome.

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Abstract 824

International survey on diagnosis and management of human herpes virus-8 infection in solid organ transplant recipients

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Abstract third-party references: ESGICH Escmid Study Group of Infections in Immunocompromised Host

Background: HHV8/KSHV infection is associated with uncommon but potentially fatal neoplastic and non-neoplastic diseases in Solid Organ Transplant (SOT) recipients. Screening and follow-up protocols are not established.

We aimed to define the current approach of transplant centers worldwide to screening and management of HHV-8 in transplant recipients.

Materials/methods: We conducted a survey (June-October 2019) on behalf of Escmid Study Group of Infections in Immunocompromised Host (ESGICH). Study group members received an email containing an introduction and a link to our survey, 12 questions about screening and follow-up for HHV-8 (www.surveymonkey.com/r/ESGICH-HHV8).

Results: 51 transplant centers filled out the survey (23 Italy, 8 Spain, 8 other European countries, 4 USA, 1 Canada, 3 Latin America, 1 Israel, 3 anonymous.)

34 centers (67%) do not perform screening for HHV-8; routinely screening is performed in 14 centers (27%) mainly for recipients. Centers where serology is performed use IFA or ELISA in equal proportion. Transplant suitability is not influenced by HHV8 serology in any center.

29 centers (57%) do not monitor HHV8 after transplant, while 10 (20%) perform it only in symptomatic patients, 3 (6%) perform universal follow-up, 9 (17%) use different risk-based approaches. The most used test for monitoring is quantitative commercial PCR (52%). Frequency of monitoring differs widely. Only 2 centers perform HHV8 specific T-cell response.

The most common approach in case of elevated viremia is reducing immunosuppression (n=29, 57%) and/or switching from CNI to m-TOR inhibitor (n=23, 45%) with or without antivirals; (val)ganciclovir is the most used agent.

67% of the centers registered HHV-8-related diseases in SOT in the last five years: cutaneous (n=16) and visceral (n=16) Kaposi Sarcoma, non-malignant disease (i.e. KICS like syndrome, n= 14), MCD (n=8) and PEL (n=4).

Conclusions: There is no uniform approach for screening and management of HHV-8 in SOT recipients. 67% of centers do not screen for HHV-8 serology, but the same proportion registered HHV-8 associated diseases: these are probably underestimated in the transplant setting. Considering potentially fatal complications and the possibility to screen and perform prompt diagnosis, collaborative studies to establish the best screening and prevention strategies of HHV8-related diseases in SOT are needed.

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Abstract 828

Performance of a PCR-based syndromic panel compared to routine culture and microscopy in patients suspected of pneumonia

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Background: Syndromic testing for lower respiratory tract infections with Biofire® Filmarray® Pneumonia Panel (BF) consists of a multiplex PCR with 27 pathogens and a turn-around-time of two hours. Routine diagnostic of bacterial pneumonia in the Capital Region of Denmark consist of culture preceded by microscopy for quality assessment of sputum. Turn-around-time and sensitivity of culture can be a limiting factor for targeted antimicrobial treatment. Hence, we evaluated BF against culture for analytical and clinical performance.

Materials/methods: from January to May 2019 298 samples (sputum or endotracheal aspirates) were collected consecutively from hospitalized patients with suspected pneumonia. Samples were referred routinely to the Department of Clinical Microbiology (Copenhagen University Hospital Hvidovre) for culture and additional testing by BF.

Retrospectively, patients were categorized into 'pneumonia' according to IDSA definition, 'probable pneumonia' for patients without lung infiltrate but otherwise meeting the pneumonia criteria, and "not pneumonia". Analytical performance was evaluated by bacterial pathogen concordance between the two methods. Clinical performance was determined regarding pneumonia/not pneumonia and detection of a positive/negative bacterial pathogen, and evaluated by sensitivity, positive predictive value (PPV), negative predictive value (NPV) and efficacy.

Patients with probable pneumonia were excluded in clinical performance calculations.

Results: 98 patients had pneumonia, 71 had probable pneumonia and 129 had not pneumonia.

Overall positive agreement between culture and BF was 42%. The rate increased to 67% when pathogens in lowest quantity (10^4 and 10^5 copies/mL) in BF were excluded.

Overall sensitivity of BF was improved from 73% to 89%, and for culture from 50% to 72%, when only high-quality samples as judged by microscopy were included in the analysis. For BF, PPV: 50%, NPV: 69% and efficacy: 57% were comparable to culture (PPV: 49%; NPV: 62%; efficacy: 56%); this increased slightly for both BF (PPV: 55%; NPV: 76%; efficacy:61) and culture (PPV: 53%; NPV: 62%; efficacy: 56%), when only high-quality samples were included.

Conclusions: PPV and NPV of both BF and culture were low. Both tests are therefore best used in patients in whom the pneumonia diagnosis has been established clinically. Indiscriminate use may be diagnostically misleading and a cause of inappropriate use of antibiotics.

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Abstract 831

Correlation of central line-associated bloodstream infections with employee turnover: continuity in nursing staff matters!

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Background: Understaffing has been previously reported as a risk factor for central line-associated bloodstream infections (CLABSI). No previous study addressed the question whether fluctuations in staffing have an impact on CLABSI incidence. We analyzed prospectively collected CLABSI surveillance data and data on employee turnover of health care workers (HCW) to address this research question.

Materials/methods: In January 2016, a semi-automatic surveillance system for CLABSI was implemented at the University Hospital Zurich, a 950 bed tertiary care hospital. Source data including presence of a central venous catheter (CVC), length of hospital stay, and microbial results of blood cultures are prospectively extracted from our patient data management system into Caradigm Intelligence Platform®. In case of positive blood culture results in a patient with a CVC in place at time of sampling, an infection control nurse differentiates between bacteremia of other origin and CLABSI. Monthly incidence rates (IR, CLABSI/1000 catheter days) were calculated and correlated to human resources management-derived monthly data on employee turnover of HCWs (defined as number of HCWs who left the hospital divided by the number of employed HCWs in that month).

Results: Over a period of 24 months, we detected a positive correlation of CLABSI incidence and nursing personnel turnover (Spearman rank correlation, r=0.467, P=0.022) (Figure). In more detailed analyses on the professional training of nursing personnel, a correlation of CLABSI incidence rates and turnover of nurses with advanced training was confirmed (Spearman rank correlation, r=0.471, P=0.021). Physician turnover did not correlate with CLABSI incidence (Spearman rank correlation, r=-0.058, P=0.787).

Conclusions: Prospectively determined CLABSI incidence correlated positively with the degree of turnover of nurses overall and nurses with advanced training, but not with the turnover of physicians. Efforts to maintain continuity in nursing staff might be helpful for sustained reduction in CLABSI rates.

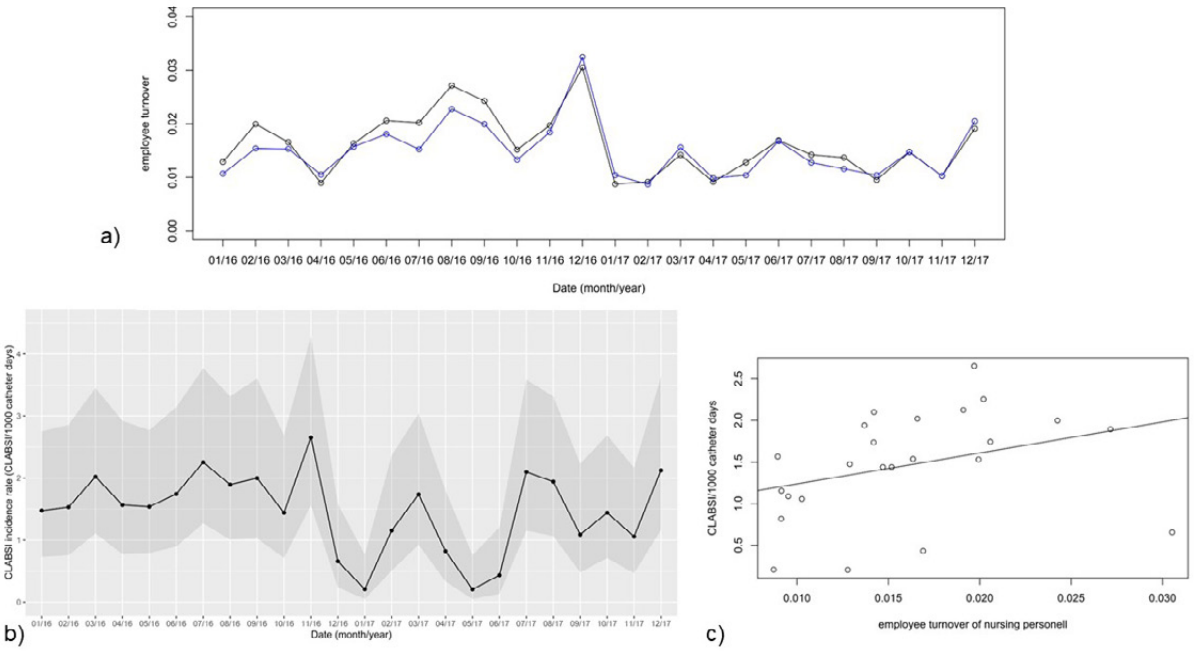

Figure: a) Employee turnover of nursing personnel (black line) and nurses with advanced training (blue line)

b) Incidence rates of central line-associated bloodstream infections

c) Correlation of central line-associated bloodstream infection rates and turnover of nursing personnel

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Abstract 832

Can gentamicin concentrations be used to estimate glomerular filtration rate in intensive care unit patients?

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Background: Acute kidney injury is common in critical ill intensive care unit (ICU) patients. Accurate assessment of kidney function is vital to correct dosing of important drugs such as antibiotics in sepsis patients. Kidney function can be assessed using plasma creatinine or cystatin C to calculate estimated glomerular filtration rate (eGFR). However, both of these markers are endogenous and require steady-state conditions. As gentamicin is freely filtered in the glomerulus, it is a potential exogenous marker for eGFR when used in ICU patients. The aim of the study was to investigate whether serum gentamicin concentrations correlates to standard estimates of eGFR in an ICU setting.

Materials/methods: All adult patients (≥18 years) in the ICU of Uppsala University Hospital treated with gentamicin and with at least one serum gentamicin measurement between January 1, 2009 and December 31, 2013 were included in this retrospective study. Patients on renal replacement therapy, and those with missing gentamicin dose information were excluded. Data on age, sex, weight, gentamicin administration time and dose, serum gentamicin, plasma creatinine and cystatin C were collected. eGFR for creatinine and cystatin C were calculated from the LM-rev and CAPA equations, respectively. Gentamicin clearance was estimated with a population pharmacokinetic model (Hodiamont et al 2017). Correlation, bias and agreement for the two eGFRs compared to gentamicin clearance were calculated.

Results: 254 patients were included. The correlation coefficient for gentamicin clearance vs. eGFR creatinine was 0.69, with a mean difference between the methods 4.6 (1.9-7.3; bias (95% CI)) and limits of agreement -43.7-52.9 mL/min. The correlation coefficient for gentamicin clearance vs. eGFR cystatin C was 0.67, with a mean difference of -1.9 (-5.1-1.3) and limits of agreement -58.3 to 54.5 mL/min.

Conclusions: In the comparison of the two eGFR methods and gentamicin clearance we found low agreement despite low bias. However, cystatin C and creatinine are suboptimal markers of kidney function in the ICU. Gentamicin clearance for estimating GFR in ICU patients cannot be dismissed and should be compared to other exogenous GFR markers.

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Abstract 835

Epidemiology of carbapenemase-producing *Klebsiella pneumoniae* in Northern Portugal: predominance of KPC-2 and OXA-48

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Background: Carbapenemase-producing *Klebsiella pneumoniae* are increasingly reported in Portugal, but data from the northern region of the country (Trás-os-Montes and Alto Douro) are missing. The aim of the present study was to provide information on the molecular epidemiology of carbapenemase-producing *K. pneumoniae* isolates currently circulating at the tertiary and university hospital of Vila Real, Portugal.

Materials/methods: A total of 106 carbapenemase-producing *K. pneumoniae* isolates recovered between January 2018 and March 2019 were included in this study. All isolates were characterized by antimicrobial susceptibility, identification of resistance determinants, pulsed-field gel electrophoresis (PFGE), multilocus sequence typing (MLST), and plasmid analysis.

Results: The most common carbapenemase identified was KPC-2 (91%), followed by OXA-48 (9%). The bla_{KPC-2} gene was mainly carried onto IncN (53%) and IncF (29%) plasmid types, whereas the bla_{OXA-48} gene was mainly located on the IncL (80%) incompatibility group. Molecular characterization distributed the 106 isolates into 29 PFGE types and 26 STs, but three clones included 50% of the isolates: PFGE A-ST147-KPC-2 (n=31; 29%), B-ST15-KPC-2 (n=16; 15%), and C-ST11-OXA-48 (n=6; 6%). Antimicrobial resistance rates were the followings: ciprofloxacin (76%), trimethoprim-sulfamethoxazole (75%), tobramycin (62%), gentamicin (34%), amikacin (25%), tigecycline (21%), fosfomycin (10%), and colistin (7%). None of the colistin-resistant isolates harbored *mcr-1*. All isolates remained susceptible to ceftazidime/avibactam, but 10% presented elevated MICs (3 and 4 mg/L).

Conclusions: KPC-2 was found to be the predominant carbapenemase among *K. pneumoniae* isolates currently circulating at this hospital from northern Portugal, followed by OXA-48. These data actually contrast with those obtained from the rest of the country, where KPC-3 predominates. Moreover, this study showed a high diversity of KPC-2-producing *K. pneumoniae* isolates with a predominance of the ST147 and ST15 clones.

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Abstract 836

Faecal carriage of extended-spectrum beta-lactamase producing *Enterobacteriaceae* at hospital admission in Portugal: a prospective survey

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Background: Among Gram-negative bacteria, the wide spread of extended-spectrum β-lactamases (ESBL) producing isolates is considered as a global threat. This study aimed to prospectively evaluate the prevalence of ESBL-producing Enterobacteriaceae fecal carriers at admission in a Portuguese hospital and to determine the epidemiology and antimicrobial resistance pattern of ESBL-producing isolates.

Materials/methods: Between December 1st, 2018 and February 2nd, 2019, rectal swabs were collected within the first 48h from 151 patients admitted to the hospital. In addition, a total of 48 rectal swabs were obtained from weekly screenings of 37 patients hospitalized for more than 48h. All ESBL- and/or carbapenemase-producing enterobacterial isolates were tested for antimicrobial susceptibility, and characterised by PFGE and MLST.

Results: The prevalence of ESBL producers was 17% at hospital admission and 24% among patients hospitalized for >48h, while the prevalence of carbapenemase producers was 3% in both cases. Most of the isolates were *Escherichia coli* (54%) and *Klebsiella pneumoniae* (41%).The most common ESBL identified was CTX-M-15 (n=17/34; 50%), followed by CTX-M-14 (n=10; 29%), CTX-M-33 (n=4; 12%), SHV-12 (n=2), and CTX-M-55 (n=1). The 20 *E.coli* isolates were distributed into 16 pulsotypes and nine sequence types (ST), out of which ST131 included 60% of the isolates. The 15 *K. pneumoniae* were grouped in 12 PFGE types and nine STs, out of which three (ST17, ST449, and ST147) included 60% of the isolates. A high proportion of isolates showed resistance to ciprofloxacin (86%), SXT (68%), tobramycin (57%), and gentamicin (43%). All isolates remained susceptible to fosfomycin.

Conclusions: A high prevalence of ESBL-producing Enterobacteriaceae was found at hospital admission and more than 50% of the isolates showed resistance to first-line antibiotics for the treatment of uncomplicated lower urinary tract infections. The choice of empiric drugs in the community should be cautious, leaving fosfomycin as a safe alternative.

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Abstract 837

Focus on nuclear imaging and other complementary exams for bacteraemia in early post-operative cardiac surgery

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Background: In cardiac surgery, the occurrence of bacteremia after cardiac surgery is common (1). European Society of Cardiology introduced nuclear imaging in the diagnostic management of endocarditis but post-operative inflammation could be false positive diagnosis (2–4)the European Association of Nuclear Medicine (EANM. The aim of this study is to describe the impact of imaging complementary exams in the management of early post-operative bacteremia.

Materials/methods: Our study is a monocentric retrospective study included any patient over 18-year-old with bacteremia within 30 days of cardiac surgery hospitalized at Bichat Claude Bernard Hospital from January 2013 to December 2016. We included all the patients who had imaging complementary exams during their hospital stay. Every diagnostic and therapeutic decision was decided with a multidisciplinary expert staff. We excluded the blood cultures considered as contamination.

Results: Overall, among the 128 patients who had positive blood culture occurring after cardiac surgery, the different complementary exams exploring infectious complications (echocardiography, CT-scan, 18F-FDG-PET CT (PET/CT) and White blood cell scintigraphy (WBC) scintigraphy) are represented in the Table 1. PET/CT was performed in 18.3% (n=19) of the patients in a median time to scan was 53 days (22.8-105). It led to diagnosis while TTE was negative for 6 patients positive on valve and 8 other diagnosis and while TOE was negative for 5 patients positive on valve and 8 other diagnosis. WBC scintigraphy was performed in 11.5% (n=12) of the patients in a median time to WBC was 60 days (17-105). WBC scintigraphy did not give a better sensibility without any patient positive for WBC scintigraphy and negative for PET/CT. WBC scintigraphy seemed more specific as it confirmed prothesis infection in 2 patients and infirmed it in 1 patient.

Conclusions: In our cohort, we found a positive impact of nuclear imaging with better diagnostic performance on positive blood culture occurring after cardiac surgery. Prospective studies could lead to further responses.

Table 1: Focus on nuclear imaging

Transthoracic echocardiography (TTE)	**108 (84.4)**
Suspicion of endocarditis on TTE (%)	**8 (7.7)**
PET/CT scan done	**0**
WBC scintigraphy done	**1**
Positive	0
Transesophageal echocardiography (TOE)	**64 (50.0)**
Suspicion of endocarditis on TTO (%)	**14 (13.5)**
PET/CT scan done	**4**
Positive	1
WBC scintigraphy done	**4**
Positive	1
Conventional CT scan (%)	**44 (42.3)**
Positive	**30 (68.2)**
Sternal wound infection	5 (11.4)
Septic embolism	5 (11.4)
Other infection	7 (15.9)
Non septic embolism	4 (9.1)
Other	9 (20.5)
While PET/CT scan negative	**1 (1.0)**
While White blood cell scintigraphy negative	**1 (1.0)**
Negative	14 (31.8)
PET/CT scan (%)	**19 (18.3)**
Positive	**10 (52.6)**
Positive on valve	5 (4.8)
Sternal wound infection	2 (1.9)
Other infection	1 (1.0)
Cancer	2 (1.9)
While conventional CT-scan negative	**1 (0.8)**
While White blood cell scintigraphy negative	**2 (1.6)**
Negative	8 (42.1)
Time to PET/CT scan in days (median (IQR))	**42 (28-67)**
White blood cell scintigraphy (%)	**12 (11.5)**
Positive	**4 (33.3)**
While conventional CT-scan negative	2 (1.6)
While PET/CT scan negative	0 (0)
Time to White blood cell scintigraphy in days (median (IQR))	**64 (34-105)**

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Abstract 840

Epidemiology and antimicrobial resistance of methicillin-resistant *Staphylococcus aureus* isolates colonising pigs with different exposure to antibiotics

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Background: In 2016, very high rates of methicillin-resistant *Staphylococcus aureus* (MRSA)-ST398 (99%) were found in different Portuguese pig farms that used colistin, amoxicillin, and zinc oxide as feed additives. Since then, farms A and B banned the use of colistin, and farm C banned the use of both antibiotics. The aim of the present study was to evaluate the impact of the ban of colistin and amoxicillin on pig MRSA carriage rates, clonal types and antimicrobial resistance, and compare data with those obtained in 2016.

Materials/methods: In 2018, 103 pigs (52 from farm B using amoxicillin only as a feed additive and 51 from farm C where no antibiotics were included in the feed regimen) were nasally swabbed for MRSA colonization. Isolates were tested for antimicrobial susceptibility, and characterised by *spa* typing, SCC*mec* typing and MLST. Whole genome sequencing (WGS) was performed for representative isolates.

Results: Overall, 96% of the pigs swabbed in 2018 carried MRSA, mostly ST398-SCC*mec* V-*spa* types t011/t108. MRSA from pigs not receiving antibiotics in the feed regimen showed susceptibility to a higher number of antibiotics, namely erythromycin, ciprofloxacin, gentamicin, and chloramphenicol. Notably, most of these isolates (n=52) presented an unusual erythromycin-susceptibility/clindamycin-resistance phenotype. WGS showed that these isolates lacked the *erm* and the *lnu* genes encoding resistance to macrolides and lincosamides, respectively, but carried the $vgaA_{LC}$ gene encoding resistance to lincosamides, which is here firstly identified in *S. aureus* ST398.

Conclusions: Two years of ban of colistin and amoxicillin as feed additives did not significantly impact the MRSA nasal carriage rates. Nevertheless, the MRSA strains circulating in those farms showed resistance to a lower number of antibiotic classes.

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Abstract 843

Impact of coagulase-negative staphylococci positive blood culture occurring in early postoperative cardiac surgery

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Background: The occurrence of bacteremia after cardiac surgery is common (1). It often involved coagulase-negative Staphylococci bacteremia (CoNS) but with difficulties to distinguish contamination to real infections (2–4). The objectives of this study are to describe CoNS bacteremia after cardiac surgery.

Materials/methods: This monocentric retrospective study included any patient over 18-year-old with bacteremia within 30 days of cardiac surgery hospitalized at Bichat Claude Bernard Hospital from January 2013 to December 2016. We excluded all the other identified germ in blood cultures. We divided into 2 groups, one with a diagnosis of infection and the others considered as contamination. We defined contaminant as clinical presentation and laboratory criteria (13). These criteria included a unique positive blood culture, >2 days until the first blood culture became positive, the isolated microorganisms (CoNS, Corynebacterium species, Bacillus species other than anthracis and *P. acnes*) and clinical risk score including negative blood cultures and a favorable evolution without antibiotics. Sepsis was defined by Sepsis 3.0 criteria (14). Every diagnostic and therapeutic decision was decided with a multidisciplinary expert staff.

Results: Among the 211 patients screened, 41.2% (n=87) had CoNS bacteremia. 80.4% (n=70) were considered as contamination and 19.6% (n=17) were not considered as contamination. The details of the comparison are shown on Table 1. In the group of CoNS infection, the germ the most represented was *Staphylococcus epidermidis* (n=10 (58.8%)) with same proportion of the others CoNS in the 2 groups. 2 were considered as an endocarditis based on nuclear imaging and treated as so. The patients with infection by CoNS had significantly more surgical treatment related to the wound sternal infection diagnosis. The hospital length of stay and mortality was significantly higher in the group with infection by CoNS.

Conclusions: Positive blood culture by CoNS occurring after cardiac surgery is a common complication but not always as a contaminant with a high rate of mortality with wound sternal infection as a leading cause and some cases of endocarditis. Prospective studies could lead to further responses.

Table 1: CoNS bacteremia: contamination vs infection

Type of surgery	Infection	Contamination	p
n	17	70	
Age (mean (SD))	65.4 (10.1)	64.6 (14.8)	0.835
Male gender (%)	12 (70.6)	57 (81.4)	0.512
Body mass index (mean (SD))	28.80 (8.1)	27.62 (5.6)	0.483
EuroSCORE (mean (SD))	6.1 (9.2)	9.17 (16.9)	0.648
IGS2 score (mean (SD))	62.7 (22.9)	53.29 (23.9)	0.488
Diabetes (%)	8 (47.1)	22 (31.4)	0.351
Type of surgery (%)			0.932
Coronary bypass	5 (29.4)	23 (32.9)	
Valvular surgery	7 (41.2)	27 (38.6)	
Time to surgery (%)			0.225
Emergency (<48h)	0 (0.0)	11 (15.7)	
Scheduled	12 (75.0)	42 (60.0)	
Urgent (within 3-7 days)	4 (25.0)	17 (24.3)	
Redux (%)	2 (7.4)	17 (22.1)	0.139
Duration of CPB, minute (mean (sd))	90.3 (30.1)	85.11 (44.3)	0.662
Duration of aortic clamping (mean in minutes (sd))	68.2 (25.1)	60.7 (31.1)	0.372
Delay of positive blood culture from surgery in days (mean (SD))	18.2 (17.7)	9.2 (8.2)	0.002
Superficial wound sternal infection (%)	4 (26.7)	0 (0.0)	0.003
Deep wound sternal infection (%)	6 (37.5)	4 (8.9)	0.024
Temperature (%)			0.820
Hypothermia (<36°C)	0 (0.0)	1 (3.7)	
Normothermia	6 (60.0)	15 (55.6)	
Fever (>38.5°C)	4 (40.0)	11 (40.7)	
Intensive care			
Catecholamines (%)	16 (100.0)	51 (77.3)	0.080
Invasive ventilation duration (mean (SD)) in days	297.6 (446.4)	223.6 (327.1)	0.474
Transfusion (%)	6 (35.3)	37 (53.6)	0.279
Septic shock (%)	9 (52.9)	12 (17.6)	0.007
Complementary exams			
Suspicion of endocarditis on TTE (%)	2 (11.8)	3 (4.3)	0.543
Suspicion of endocarditis on TOE (%)	2 (11.8)	2 (2.9)	0.354
PET/CT scan done (%)	3 (17.6)	3 (4.3)	0.157
Positive on valve	1 (33.3)	1 (33.3)	0.513
WBC scintigraphy done (%)	2 (11.8)	4 (5.7)	0.727
Positive on valve	2 (100.0)	0 (0.0)	0.050
Final diagnosis and outcomes			
Surgical treatment (%)	12 (75.0)	13 (20.0)	<0.001
Death (%)	6 (37.5)	9 (12.9)	0.048
Hospital death (%)	4 (23.5)	2 (2.9)	0.013
30 days death (%)	1 (5.9)	5 (7.1)	1.000
Survival time (mean (SD))	55.60 (28.6)	63.12 (95.4)	0.869
Hospital length of stay (mean (SD))	42.47 (33.9)	27.69 (25.3)	0.047
ICU length of stay (mean (SD))	12.27 (10.8)	18.22 (25.4)	0.451

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Abstract 844

Investigation of a nosocomial pulmonary tuberculosis in a French university hospital

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Background: Nosocomial pulmonary tuberculosis (TB) remains nowadays poorly known. Healthcare workers (HCW) are at increased risk for TB infection and disease due to a higher risk of TB exposure in a hospital setting. Pulmonary TB infection control measures are a key component to minimize the risk of transmission and to prevent a further spread of the disease, in particular in healthcare facilities. The aim is to describe two cases of nosocomial TB.

Materials/methods: Following the diagnosis of a pulmonary TB in a HCW in an Ear Nose Throat ward in a French university hospital, a retrospective descriptive review was performed to understand the route of acquisition.

Results: In August 2018, 6 patients and 107 HCWs were identified as contact subjects following a delayed pulmonary TB diagnostic and delayed airborne precautions implementation in the index patient, a 74-year-old male with an oropharynx cancer. Subsequent to a TB screening, two secondary cases were identified in HCWs. The first HCW, a 30-year-old man developed a nosocomial pulmonary TB three months after exposure, verified by culture. The ongoing whole genome sequencing (WGS) molecular survey implemented in our center confirmed that the isolate was identical to the one of the index case. Moreover, WGS analysis ruled out any possibility of transmission to an 18-year-old woman admitted to the unit concomitantly with the index case and developing pulmonary TB 4 months later. Further contact-tracing resulted in 79 contacts patients from hospital exposure. The second HCW, a 37-year-old female developed a nosocomial latent tuberculosis infection (LTI) following a positive QuantiFERON-TB Gold® test. No further investigation was conducted given the low risk of transmission of LTI and that the HCW was treated right after the diagnostic.

Conclusions: HCWs have to rigorously follow TB infection control measures in order to prevent the occurrence of TB nosocomial cases. They have also to comply with TB screening and testing in case of exposure and should receive TB education regularly.

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Abstract 845

Characterisation of *Staphylococcus aureus* in soft tissue infections: relevance of PVL producers

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Background: Methicillin-resistant *Staphylococcus aureus* (MRSA) is a group of bacteria able to resist to beta-lactamic antibiotics: This profile is mainly due to the presence of the *mecA* gene present in SSCmec cassette. MRSA, due to different characteristics, have been distinguished in community-acquired (CA-MRSA) and hospital-acquired (HA-MRSA) strains. The pathogenicity of *S. aureus* and the production of virulence factors are responsible for severe infections. PVL is an exotoxin produced by *S. aureus*, able to lyses the defense cells. The genes that encode this enzyme can integrate the SCCmec, mainly the types IV/V, common in CA-MRSA, causing infections with more difficult and prolonged treatment.

Materials/methods: 139 *S. aureus* isolates responsible to skin and soft tissue infections were identified and characterized according to its antibiotic susceptibility profile, in Centro Hospitalar e Universitário de Coimbra. DNA extraction was done and the *mecA* and *lukSF* genes detection were performed by PCR.

Results: The 139 isolates of *S. aureus*, according to the phenotype for oxacillin, were classified as MRSA 47 (34%) and as MSSA 92 (66%). All MRSA presented *mecA* gene and, among the MSSA, 49 (53.3%) were positive and 43 (46.7%) negative. The vancomycin phenotype was sensitive for all isolates and higher MIC levels were found in superficial infections (80.3%, n = 53), with more methicillin-sensitive isolates (MSSA). The gene that encodes the PVL was found in 2.2% (3) of the isolates: 2 from pediatric samples (abscess and non-surgical wound exudate (NSWE)) and 1 from a non-pediatric sample (NSWE).

Conclusions: The prevalence of PVL was 2.2%. The 3 isolates carrying-PVL were MRSA/MSSA and probably were acquired in the community, all had *mecA* gene. 2 isolates were found in pediatric samples, in a total of 13 isolates; the other was found in a non-pediatric sample, from a total of 126 isolates. PVL shown to have a high prevalence within *S. aureus*, causing skin and soft tissue infections in children with statistical significance, suggesting that this screening should be done for the better treatment and avoid prolonged infections.

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Abstract 846

Outcomes in ventilated patients with hospital-acquired/ventilator-associated bacterial pneumonia (HABP/VABP) treated with imipenem/cilastatin (IMI)/relebactam (REL) versus piperacillin/tazobactam (PIP/TAZ): subgroup analysis of the RESTORE-IMI 2 randomised, controlled trial

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Background: In the RESTORE-IMI 2 phase 3 trial, IMI/REL was non-inferior to PIP/TAZ for treatment of HABP/VABP in both primary and key secondary endpoints. Since ventilated HABP (vHABP) and VABP are associated with higher mortality than non-ventilated HABP, we specifically evaluated efficacy and safety outcomes in ventilated patients.

Materials/methods: RESTORE-IMI 2 was a randomized, controlled, double-blind, non-inferiority trial in adults with HABP/VABP. Lower respiratory tract (LRT) specimens were obtained ≤48 hours prior to screening. Patients were randomized to 7-14d of IMI/REL 500mg/250mg or PIP/TAZ 4g/500mg. Primary endpoint: Day 28 all-cause mortality (ACM) in the modified intent-to-treat (MITT) population (randomized patients with ≥1 dose of study drug, excluding patients with only gram-positive cocci present on baseline Gram stain). Key secondary endpoint: clinical response at early follow-up (7-14d after end-of-therapy). Another secondary endpoint was Day 28 ACM in the microbiologic MITT population (MITT patients with baseline pathogen species against which IMI/REL is known to have activity). The safety population included all patients who received study drug. Efficacy and safety endpoints were prospectively evaluated in the sub-population of ventilated patients (i.e., primary diagnosis of vHABP or VABP).

Results: In the MITT population, 122/264 (46.2%) IMI/REL and 136/267 (50.9%) PIP/TAZ patients had a primary diagnosis of vHABP or VABP. Of these, 39.9% were ≥65 years old, 66.3% had APACHE-II scores ≥15 (median score: 17.5 IMI/REL, 18.0 PIP/TAZ), and 19.4% had moderate/severe renal impairment. Baseline characteristics in ventilated patients were generally balanced between treatment arms. Most frequent baseline LRT pathogens (assessed in ventilated patients of the microbiologic MITT population) were *A. calcoaceticus-baumannii* complex (23.0% of patients), *K. pneumoniae* (21.5%), *P. aeruginosa* (20.1%), and *E. coli* (15.8%); baseline pathogens were balanced between arms. IMI/REL was associated with lower ACM than PIP/TAZ and comparable clinical response rates in the ventilated sub-population (Table). In the safety population of ventilated patients, rates of overall adverse events (AEs) (IMI/REL 114/124 [91.9%] vs PIP/TAZ 126/136 [92.6%]) and therapy discontinuations due to any AEs (IMI/REL 10/124 [8.1%] vs PIP/TAZ 14/136 [10.3%]) were similar in both groups.

Conclusions: IMI/REL is an efficacious and well-tolerated treatment option for mechanically ventilated patients with nosocomial pneumonia.

Table. Primary and secondary efficacy outcomes in patients with ventilated HABP/VABP

	IMI/REL n/N (%)	PIP/TAZ n/N (%)	Difference[a] (95% CI)
Primary endpoint			
Day 28 all-cause mortality (MITT)	24/122 (19.7%)	42/136 (30.9%)	-11.2% (-21.6, -0.5)
Key secondary endpoint			
Favorable clinical response at EFU (MITT)	66/122 (54.1%)	62/136 (45.6%)	8.5% (-3.7, 20.5)
Other secondary endpoints			
Day 28 all-cause mortality (mMITT)	19/102 (18.6%)	33/107 (30.8%)	-12.2% (-23.7, -0.5)

CI, confidence interval. EFU, early follow-up visit. IMI/REL, imipenem/cilastatin/relebactam. MITT, modified intent-to-treat population. mMITT, microbiologic modified intent-to-treat population. N, total number of patients with vHABP or VABP in that particular analysis population and treatment arm. n, number of patients who died or had unknown survival status or number of patients with favorable clinical response (depending on endpoint). PIP/TAZ, piperacillin/tazobactam.

[a]Differences (i.e., IMI/REL minus PIP/TAZ) and confidence intervals were calculated using the Miettinen & Nurminem method.

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Abstract 849

Baseline microbiology, susceptibility, molecular characterisation, and emergence of non-susceptibility in a recent randomised, controlled trial (RESTORE-IMI 2) comparing imipenem/cilastatin (IMI)/relebactam (REL) versus piperacillin/tazobactam (PIP/TAZ) for hospital-acquired or ventilator-associated bacterial pneumonia (HABP/VABP)

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Abstract third-party references: Funding for this research was provided by Merck Sharp & Dohme Corp., a subsidiary of Merck & Co., Inc., Kenilworth, NJ, USA.

Background: RESTORE-IMI 2 showed IMI/REL to be non-inferior to PIP/TAZ for treatment of HABP/VABP. Here we present key microbiologic data from that study.

Materials/methods: Randomized, controlled, double-blind, multinational, non-inferiority, phase 3 trial comparing IMI/REL 500mg/250mg versus PIP/TAZ 4g/500mg in HABP/VABP. Baseline lower respiratory tract (LRT) specimens were obtained ≤48h prior to screening, at end-of-therapy (EOT), and early follow-up (7-14d after EOT). Identification and susceptibility of all pathogens were confirmed at a central laboratory. LRT non-Morganellaceae Enterobacterales and *Pseudomonas aeruginosa* isolates underwent molecular characterization for β-lactamase genes if they were either imipenem-nonsusceptible isolates or imipenem-susceptible baseline isolates from patients with an imipenem-nonsusceptible isolate of the same species collected subsequently during treatment. The microbiologic modified intent-to-treat (mMITT) population included all patients with ≥1 dose of study therapy, without only gram-positive cocci on their baseline LRT specimen, and with baseline pathogen species known to be potentially susceptible to imipenem/REL.

Results: The mMITT population comprised 215 and 218 patients randomized to IMI/REL and PIP/TAZ, respectively. The most frequent baseline LRT pathogens were Enterobacterales, *P. aeruginosa*, and *Acinetobacter calcoaceticus-baumannii* complex; 84.0% of pathogens in the IMI/REL versus 70.4% in the PIP/TAZ arm were susceptible to randomized study drug according to EUCAST criteria (Table). In both treatment arms, the baseline LRT pathogens' imipenem/REL minimum inhibitory concentration (MIC) range, MIC_{50}, and MIC_{90} were similar. Across pathogens, PIP/TAZ had higher MIC values than imipenem/REL. Imipenem/REL MIC distributions in Enterobacterales and *P. aeruginosa* were like those previously reported in global and European 2016-2018 surveillance. Among molecularly characterized study isolates (n=59, 71.2% imipenem/REL, 30.5% imipenem, 33.9% PIP/TAZ susceptible), 8 were KPC-producing Enterobacterales (100% imipenem/REL, 0% imipenem, 0% PIP/TAZ susceptible); 6 OXA-48-like-producing Enterobacterales (66.7% imipenem/REL, 66.7% imipenem, 0% PIP/TAZ susceptible); 4 metallo-β-lactamase-producing Enterobacterales (0% imipenem/REL, imipenem, and PIP/TAZ susceptible); 3 carbapenemase-negative, ESBL-producing Enterobacterales (100% imipenem/REL, 100% imipenem, and 66.7% PIP/TAZ susceptible); and 29 metallo-β-lactamase-negative *P. aeruginosa* (79.3% imipenem/REL, 20.7% imipenem, and 44.8% PIP/TAZ susceptible).

Conclusions: In RESTORE-IMI 2, pathogen and MIC distributions were comparable to recent surveillance data and other recent HAPB/VABP trials. Most pathogens were susceptible to imipenem/REL. REL restored imipenem susceptibility in KPC-producing Enterobacterales and most metallo-β-lactamase-negative *P. aeruginosa*.

Pathogen	IMI/REL		PIP/TAZ	
	Patients with pathogen, n (%)[a]	Susceptibility, m/M (%)[b]	Patients with pathogen, n (%)[a]	Susceptibility, m/M (%)[b]
All pathogens	215 (100.0)	194/231 (84.0)	218 (100.0)	140/199 (70.4)
Aerobic Gram-Negative Bacillus	192 (89.3)	172/207 (83.1)	194 (89.0)	140/185 (75.7)
Acinetobacter calcoaceticus-baumannii complex	32 (14.9)	4/32 (12.5)	36 (16.5)	*ND*[c]
Enterobacter cloacae	8 (3.7)	8/8 (100.0)	19 (8.7)	16/19 (84.2)
Escherichia coli	30 (14.0)	30/30 (100.0)	37 (17.0)	30/35 (85.7)
Klebsiella pneumoniae	58 (27.0)	57/58 (98.3)	53 (24.3)	30/48 (62.5)
Pseudomonas aeruginosa	34 (15.8)	31/35 (88.6)	48 (22.0)	34/50 (68.0)
Serratia marcescens	13 (6.0)	12/13 (92.3)	4 (1.8)	4/4 (100.0)
Aerobic Gram-Negative Coccobacillus	13 (6.0)	12/14 (85.7)	12 (5.5)	*ND*[d]
Haemophilus influenzae	13 (6.0)	12/14 (85.7)	12 (5.5)	*ND*[d]

EUCAST = European Committee on Antimicrobial Susceptibility Testing. IMI/REL = imipenem/cilastatin/relebactam. LRT = lower respiratory tract. M = number of isolates with susceptibility interpretation (based on EUCAST, Version 9.0) available. m = number of isolates with a susceptibility interpretation of 'susceptible'. mMITT = microbiologic modified intent-to-treat. ND = not determined. n = number of mMITT patients with the pathogen. PIP/TAZ = piperacillin/tazobactam.

Susceptibility interpretation by broth microdilution testing for PIP/TAZ was based on the European Committee on Antimicrobial Susceptibility Testing breakpoint tables for interpretation of minimum inhibitory concentrations, Version 9.0. Imipenem/relebactam susceptibility was determined using the provisional EUCAST breakpoints. For pathogens without IMI/REL breakpoints, the corresponding imipenem interpretive criteria were applied to determine imipenem/relebactam susceptibility.

[a]Percentage calculated as number of mMITT patients with the pathogen divided by total number of patients in the mMITT population, within that treatment arm. [b]Percentage calculated as number of pathogen isolates with a susceptibility interpretation of 'susceptible' divided by total number of pathogen isolates with susceptibility interpretation available, within that treatment arm. [c]PIP/TAZ is assumed to not have any activity against this pathogen. [d]The lowest PIP/TAZ concentration tested (2 µg/mL) is greater than the EUCAST susceptibility breakpoint (0.25 µg/mL) for *H. influenzae*, so PIP/TAZ susceptibility according to EUCAST criteria could not be categorized for this pathogen.

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Abstract 856

Treatment of flaviviruses in solid organ transplant recipients with intravenous immunoglobulin and interferon alpha-2b: a Mayo Clinic Arizona experience

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Background: We present a case series of 10 solid organ transplant (SOT) recipients treated for either neuroinvasive West Nile virus (WNV) or St Louis Encephalitis virus (SLEV) at the Mayo Clinic in Arizona between 2011 and 2019.

Materials/methods: Data were queried using the integrating Biology and the Bedside clinical data analytics platform.

Results: All patients were treated with both intravenous immunoglobulin (IVIG) and interferon alpha-2b (IFN alpha-2b). 80% survived with 50% of those recovering completely. On average, recovery occured on illness day 23, 9 days after treatment initiation. 2 of 4 organ rejections recovered.

Conclusions: Flaviviruses present significant morbidity for SOT patients often requiring ICU admission. IVIG combined with IFN alpha-2b appears to show clinical benefit and is well tolerated in SOT recipients, profering a more standardized role in this population's treatment for neuroinvasive disease. Future prospective studies are needed to confirm these findings.

Table 1. Treatment regimens with outcomes

ID	Diagnosis	Treatment	Outcome	Days to response/ death after treatment initiation	Organ Rejection
1	WNV	500 mg/kg/d IVIG x 5 3 million units/d IFN α-2b x 4	Deceased	8	No
2	WNV	500 mg/kg/d IVIG x 4 3 million units/d IFN α-2b x 10	Partial recovery – mild cognitive impairment	5	No
3	WNV	1000 mg/kg/d IVIG x1 then 400 mg/kg/d x 6 3 million units/d IFN α-2b x 15	Partial recovery – paralysis persists	6	Yes
4	WNV	400 mg/kg/d IVIG x 5 3 million units/d IFN α-2b x 4	Partial recovery – weakness persists	14	Yes
5	SLEV	400 mg/kg/d IVIG x 5 3 million units/d IFN α-2b x 14	Recovered	8	No
6	WNV	400 mg/kg/d IVIG x 2 3 million units/d IFN α-2b x 15	Recovered	26	No
7	SLEV	400 mg/kg/d IVIG x 6 3 million units/d IFN α-2b x 10	Recovered	4	No
8	WNV	500 mg/kg/d IVIG x 5 3 million units/d IFN α-2b x 9 1 dose WNV enriched product	Recovered	4	No
9	WNV	400 mg/kg/d IVIG x 5 3 million units/d IFN α-2b x 11	Partial recovery – later died of pneumonia	7	Yes
10	WNV	400 mg/kg/d IVIG x 5 3 million units/d IFN α-2b x 3	Deceased	15	Yes

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Abstract 859

Deaths of emerging and re-emerging infectious diseases outbreaks, epidemics and pandemic in the last 10 years: a systematic review

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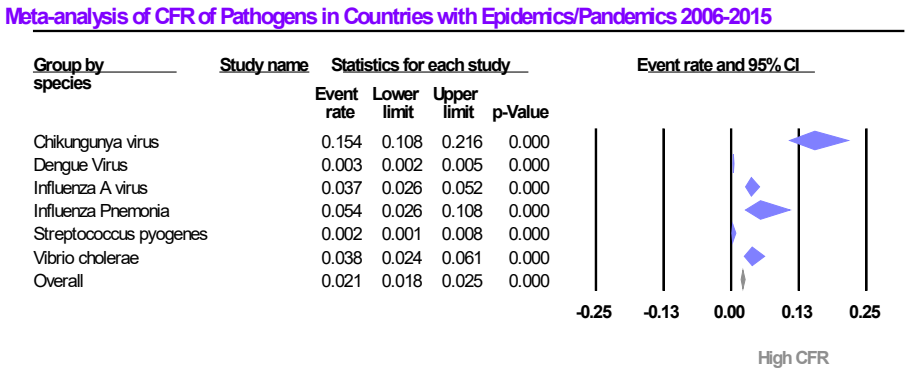
Background: The emergence and re-emerge of infectious diseases in the last decade has heightened concerns about the possibility of global outbreaks of disease and the ability of national and international health systems to respond and to overcome such infections successfully with the least possible number of victims. This study aimed to determine the death of the recent major emerging and re-emerging infectious disease outbreaks, epidemics, and pandemics.

Materials/methods: We searched 10 electronic databases: PubMed, Scopus, Ghl, Vhl, Popline, Isi, Google Scholar, Sigle, Nyam to assess the death of major emerging and re-emerging infectious disease outbreaks from 2006 to 2015. We used Strobe Statement for assessing the risk of bias in our included observational studies. The study protocol was registered on Prospero, number crd42016038138.

Results: Out of the total included 8315 studies,187 articles were eligible for analysis. Overall case fatality rate (Cfr) was 6.6.%. Cfr was the highest with outbreaks (11.3%) followed by pandemics (3.7%) and epidemics (3.2%). South East Asia was the most affected region in outbreaks with Cfr (21.3%). Burkholderia pseudomallei and Nipah virus had the highest outbreak Cfr (80%, and 78.6%). Cfr increased notably in the last two years of our review at 2014 and 2015 with Cfr 25.4%, and 30.1% respectively Significant risk of bias found with p-values of (0.001) using Egger's regression intercept.

Conclusions: South East Asia Region had the most death cases of infectious disease outbreaks. Burkholderia pseudomallei and Nipah virus were the causative pathogens that caused the highest number of cases of death.



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Abstract 861

Comparison of immune function between T, B lymphocytes, Th17, Th22 and Treg cells in children with hand, foot and mouth disease caused by EV71 and other *enterovirus* infections

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Background: Hand, foot and mouth disease is a global infectious disease caused by enterovirus, which occurs mostly in children under 5 years of age. There are more than 20 enteroviruses causing hand, foot and mouth disease, mainly Coxsackie A group 16 and enterovirus 71. HFMD caused by EV71 infection progresses rapidly, and it is prone to severe cases and even death. The pathogenesis of severe EV71 infection is still not fully understood. To investigate the difference of cellular immune function between enterovirus 71 (EV71) and other enterovirus infections in children with hand, foot and mouth disease, and to provide clinical diagnosis and treatment for hand, foot and mouth disease.

Materials/methods: The data of 94 children with hand, foot and mouth disease admitted to Hangzhou Children's Hospital from November 2016 to June 2017 were analyzed. Among them, 45 cases were in EV71 infection group and 49 cases were non-EV71 other enterovirus infection group. Determination of serum total T lymphocytes (%), cytotoxic T cells (%), helper T cells (%), total B lymphocytes (%), CD4+/CD8+ ratio, NK cells (%), Th17 cells%), Th22 cells (%), Treg cells (%), Treg/Th17 ratio, and comparison between different groups by cytometry.

Results: The levels of Th17 cells (%), Th22 cells (%) and total B lymphocytes (%) in the EV71 infection group were significantly higher than those in the non-EV71 other enterovirus infection group (t=5.672; t=4.934; t=2.074; P<0.05), and the ratio of Treg cells (%) and Treg/Th17 was lower than that of non-EV71 other enterovirus infection group (t=-5.817; t=-6.351; P<0.05).

Conclusions: Compared with other enterovirus infections, EV71 is more likely to cause cellular immune function disorder, especially the changes of Th17 cells, Th22 cells, Treg cells and total B lymphocytes.

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Abstract 862

Multiplex detection of meningitis and encephalitis pathogens: a study from laboratory to the clinical

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Background: Infectious Meningitis and Encephalitis as the potentially life-threatening conditions are mostly caused by bacterial, mycobacterium, fungus and viral agents. As the most devastating disease that results in nearly 150,000 deaths per year, early diagnosis and prompt initiation of treatment offer the chance of better prognosis. However, current laboratory testing projects do not meet demand for clinical diagnosis. Therefore, we come up with utilizing Multiplex detection for Meningitis and Encephalitis of 18 pathogens (MME-18) to help physicians achieve rapid and accurate diagnosis in infectious encephalitis and meningitis.

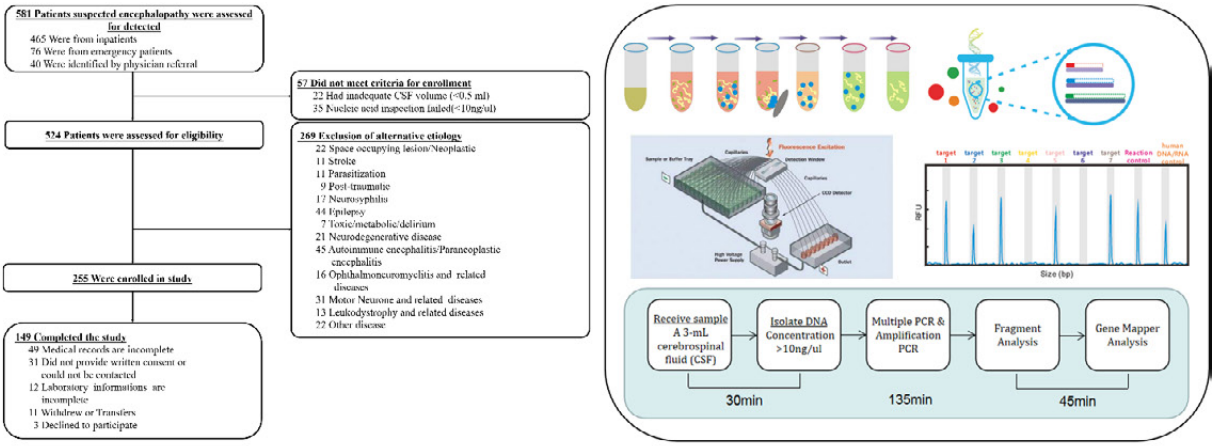
Materials/methods: The hospitalized patients with suspected intracranial infection were analyzed retrospectively between May and July in 2019 in West China Hospital of Sichuan University. MME-18 was designed to detect 18 pathogens in cerebrospinal fluid (CSF) of enrolled patients, including *N.meningitis, M.tuberculosis, L.monocytogenes, S.pneumonia*, Mycoplasma pneumoniae, *S.agalactiae, A.baumannii, H.influenzae, E.coli K1, C.neoformans*, enterovirus (EV), mumps virus (MuV), herpes simplex virus type 1 (HSV-1), herpes simplex virus type 2 (HSV-2), Epstein-Barr virus(EBV), varicella zoster virus(VZV), cytomegalovirus (CMV), human herpes virus type 6 (HHV-6). After using the GeneXpert and RT-qPCR to review the consistency of the results of 3 methods, we further informed clinician of the results and collected the feedback information of diagnosis and treatment.

Results: Among a total of 581 tested patients, 149 eligible individuals were enrolled in study. 85(57.05%) of the patients were positive for at least one of the 18 target pathogens. *M.tuberculosis*, *C.neoformans* and virus were the most common causative agents, including separate and multiple infections. According to the feedback of diagnosis and treatment provided by clinicians, 66(77.64%) patients were confirmed by clinical diagnosis and targeted treatment. 9(10.58%) patients results had not been supported by clinicians, but they were still willing to seek further information. At the same time, 10(11.76%) results were rejected or ignored.

Conclusions: MME-18 has much wider and accurate range of pathogenic spectrum while it is able to complete detection within 4.5 hours. Moreover, the MME-18 results may help diagnose and provide clinical treatment suggestion about encephalitis/meningitis.

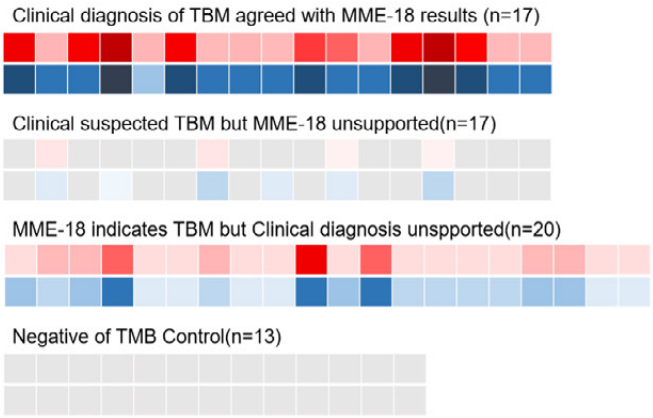
Table 1 Demographic and clinical Characteristic of the 149 Patients.

Characteristic	Value
Age	
Mean — yr	44.9
10 - 19yr	7(4.7)
20 - 39yr	47(31.8)
40 - 59yr	56(37.6)
>60yr	39(25.9)
Male sex — no.(%)	90(59.2)
Syndrome — no. (%)	
Meningitis alone	58(38.9)
Encephalitis with or without meningitis	87(58.4)
Myelitis with or without meningitis	4(2.7)
Exacerbation of chronic condition — no. (%)	29(19.5)
Immunocompromised — no. (%)	6(4.0)
HIV-1	4(2.7)
Solid-organ transplant	2(1.3)
Immunosuppression for non-neoplastic condition	6(4.0)
ICU admission — no. (%)	17(11.4)
Death within 30 days — no. (%)	1(0.8)
Median no. of days after hospital admission that CSF was collected for MME-18 assay(range) — days	2.2(1—8)

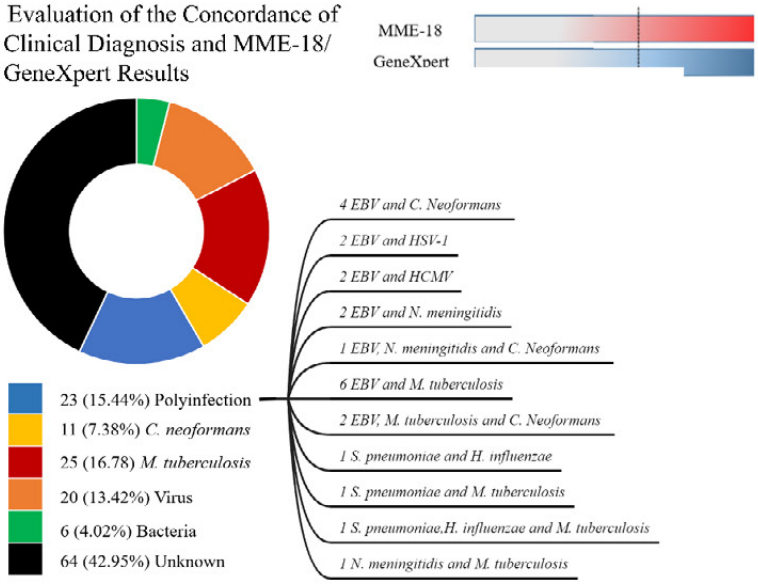


A Screening, Enrollment, and Follow-up

B Protocol for MME-18 Assay



C Evaluation of the Concordance of Clinical Diagnosis and MME-18/ GeneXpert Results



D Multiplex PCR Assessment for Meningitis and Encephalitis of 18 pathogens Analyses(149 cases discussed)

Figure 1 Figure 1 Results of MME-18 Testing and Clinical Effect
Panel A illustrates the flow of patients through the study. Panel B shows the protocol for multiplex PCR assessment for meningitis and encephalitis assay.Following receiving samples of cerebrospinal fluid(CSF), nucleic acid is isolated. The multiplex PCR is performed while the fragment was analyzed with the use of capillary electrophoresis.Panel C shows the concordance between clinical diagnosis and MME-18 results while the similarity of the red and blue illustrates the consistency of MME-18 and GeneXpert results. The positive results of Myocobacterium tuberculosis were detected in 54 of 149 paitents(36.2%). a propotion of 31.4% among 54 patients showed concordant results between clinicians and test results. The discoance rate was 68.5%. There were 2 different conditions, one was that clinical suspected tuberculous meningitis(TBM) with negative MME-18 results, the other is that clinical diagnosis of TBM is negative with positive MME-18 results. Panel D shows the pathogens distribution of 149 patients that was enrolled in the study.

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Abstract 865

Bacteriophage therapy against multidrug-resistant *Acinetobacter baumannii* infections

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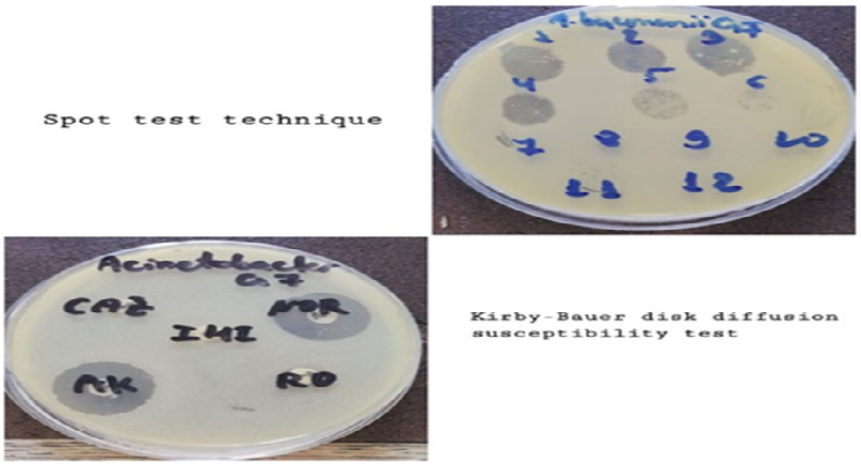
Background: *Acinetobacter baumanniis* is very powerful superbug and ranked 1st among the world deadliest superbugs. These superbugs are killing about 700,000 people per year. All the drug including the last resort drugs is resistant to this type of bacterial strain. The infections which are caused by these superbugs are hard to treat and are too expensive. In the past, we don't have any proper ways to treat Acinetobacter infection but nowadays we found one therapy which can treat such infections and we called it "Phage Therapy". A virus is used to treat the infections caused by bacteria. A bacteriophage is a virus which infects bacteria only and is harmless to the human cell, they also have high therapeutic ratio and they are better than any of the antibiotics because they can penetrate biofilm easily and are the future for multidrug-resistant bacteria's.

Materials/methods: In our study we used *A. baumannii* G7 strain, isolated from the wound of a soldier injured during the war in 2008. For antibiotic sensitivity were used five different antibiotics – Amikacin (30µg), Norfloxacin (10µg), Imipenem (10µg), Ceftazidime (10µg) and Rifampicin (5ug) by using Kirby-Bauer Disk Diffusion Susceptibility Test for antibiotics sensitivity fig.1 (picture2). Bacteriophage sensitivity was done towards 5 specific Acinetobacter monophages and 6 phage lysates by using Spot-test technique fig.1 (picture1).

Results: Disk diffusion susceptibility test revealed that *A. baumannii* strain used in our study was sensitive to norfloxacin and amikacin antibiotics, but showed resistance to ceftazidime, rifampicin and also to imipenem. Bacteriophage sensitivity showed that from the 11 phages 2 of fig. 1(1,2) had complete lysis, fig. 1(3,4) bacteriophages had Semi-confluent lysis. Fig. 5 and 6 bacteriophages had opaque lysis; Five of eleven phages showed resistance.

Conclusions: Bacteria are becoming immune to all drugs. Alternatives to antibiotics could be considered bacteriophages. They have many characteristics that make phages as potentially attractive therapeutic agents. And in the future, the only solution for all the bacteria is the phage therapy as one day all the bacteria will become resistant to every drug and in this situation phages will work and become our future.

Fig1.



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Abstract 866

Application of a multiplex polymerase chain reaction test for diagnosing bacterial enteritis in children in a real-life clinical setting

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Background: Although a variety of multiplex polymerase chain reaction (mPCR) tests have been used for diagnosing bacterial enteritis as a syndromic approach, few studies determined diagnostic accuracy of mPCR tests based on patients' symptoms and clinical diagnosis in a real-life clinical setting.

Materials/methods: Medical records of 710 inpatient pediatric patients (<19 years of age), in whom an mPCR test for 10 bacterial pathogens was performed, were retrospectively reviewed. Based on the clinical diagnosis on discharge, the enrolled patients were divided into two groups: acute gastroenteritis (AGE) group and non-AGE group. Clinical and laboratory characteristics and the mPCR test result were compared between the two patient groups.

Results: Among the enrolled patients, 467 (65.8%) and 243 (34.2%) patients were included in the AGE and non-AGE groups, respectively. Upper (37.9%) and lower (21.8%) respiratory tract infections were most common final diagnoses in the non-AGE group. The mPCR test revealed bacterial pathogens in 199 (28.0%) patients: 163 (34.9%) in the AGE group and 36 (14.8%) in the non-AGE group (P<0.001). *Campylobacter* spp. (n=64, 32.2%), *Clostridium difficile* (n=52, 26.1%), *Salmonella* spp. (n=46, 23.1%), and *Clostridium perfringens* (n=41, 20.6%) were most commonly identified. *Campylobacter* spp. (38.7% vs 2.8%, P<0.001) and *Salmonella* spp. (26.4% vs 8.3%, P=0.020) were more frequently identified in the AGE group; whereas, *C. difficile* (18.4% vs 61.1%, P<0.001) and *C. perfringens* (18.4% vs 30.6%, P=0.103) were more frequently identified in the non-AGE group. Among the 199 patients with positive mPCR test results, patients in the AGE group were older (median 7 years vs 2 years, P=0.002), more likely to have gastrointestinal symptoms (100% vs 86.1%, P<0.001), and less likely to have respiratory symptoms (8.0% vs 44.4%, P<0.001) compared to those in the non-AGE group.

Conclusions: More detailed history taking and physical examination can reduce performing unnecessary mPCR tests in patients with gastrointestinal symptoms. In pediatric patients suspected to have AGE, the clinical significance of each bacterial pathogen identified by an mPCR test should be determined individually. *Campylobacter* spp. and *Salmonella* spp. can be considered true pathogens; however, *Clostridium* spp. may be a bystander.

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Abstract 873

Development of a routine laboratory test enabling the detection of dermatophytes as well as the identification of Trichophyton rubrum by means of duplex real-time PCR from mycological samples and cultures

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Background: Dermatophytes are responsible, in majority, for fungal infections of the skin, hair and nails and *Trichophyton rubrum* is the most frequently isolated dermatophyte. The time of growth in culture and microscopic morphology identification (the "gold standard") requires a total of two to four weeks. Molecular methods were developed to improve time for diagnosis and treatment. We will present and demonstrate here the suitability of an in-house method enabling at the same time the detection, through duplex real-time PCR analysis, of dermatophyte positive samples and the direct identification of *Trichophyton rubrum.*

Materials/methods: Prior to real time PCR, nucleic acid extraction and purification steps are crucial. Different sample pre-treatment conditions were tested: with and without agitation and/or heating at 95°C (203°F). The highest yield of nucleic acid was obtained with a complete pre-treatment combining agitation and heating. After the pre-treatment, the samples were processed on the NucliSENS® EasyMAG® (bioMérieux) according to the manufacturer's recommendations. Finally, the extracted nucleic acids were performed on the CFX-96™ (Bio-Rad) with specific probes and primers. All positive samples for dermatophytes were identified by sequencing (ITS1-5.8S-ITS2).

Results: One hundred ninety-nine mycological samples were studied (one hundred forty-four nails and fifty-five skin samples) according to conventional methods and DERTR PCR. The sensitivity, specificity, positive and negative predictive values of each target were calculated and are respectively: 97,9%, 76,8%, 57,3% and 99,1% for dermatophytes; 95,2%, 87,9%, 67,8% and 98,6% for *Trichophyton rubrum*. These results demonstrate that the duplex DERTR PCR is a suitable method for rapid diagnosis of dermatophytosis and identification of *Trichophyton rubrum*.

Conclusions: We developed an in-house duplex real-time PCR able to detect dermatophytes and identify at the same time *Trichophyton rubrum* from mycological samples and cultures. This method routinely used as enable a diagnosis within four hours in contrast to the two to four weeks required with the conventional methods. This real time PCR has been submitted for accreditation ISO 15189 in November 2019.

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Abstract 892

The effect of mesenchymal stem cells on the mortality of severe sepsis and septic shock: a promising therapy

Emine Alp Mese[1], Zeynep Burcin Gonen[2], Kursat Gundogan[3], Aliye Esmaoglu[3], Leylagul Kaynar[4], Aysun Cetin[5], Musa Karakukcu[3], Mustafa Cetin[3], Gamze Kalın Ünüvar*[3], Mehmet Doganay[3]

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Background: The aim of this study is to assess the effect of mesenchymal stem cells on the mortality of sepsis and septic shock.

Materials/methods: During two years, 10 patients with severe sepsis and septic shock were included into the study from Medical and Anesthesiology and Reanimation Intensive Care Units.Mesenchymal stem cells (MSCs) treatment was added to standard therapy of sepsis.Patients received $1*10^6$/kg MSC on the 1st, 3rd, 5th, 7th and 9th days of ICU admission. Peripheral blood samples from patients were obtained before MSCs treatment and on the day of MSCs treatment for the measurement of cytokine (TNF-α,IFN-γ,IL−2,IL−4,IL−6,IL−10) levels.Outcomes of the patients were compared with the previous observational study conducted in the same ICUs.

Results: In the study group, 6 of 10 patients were male, whose ages were ranged from 22 to 68. Their APACHE II scores were ranged between 14-29. In the control group, 8 of 10 patients were male whose ages were ranged from 29 to 80. Their APACHE II scores were between 18-29. Survival rate for the 7th and 14th days of the 10 patients who were administered stem cell is 100%, survival rate for the 28th day is 70%. Except the patients who had advanced malignancy and uncontrolled source, there were improvements at the laboratory findings (CRP, procalcitonin, leukocyte, etc.) during the times when stem cells were administered to the patients.In the stem cell treatment group, decrease in the SOFA score of the analyses, which were adjusted by age and APACHE II, was statistically significant. A statistically significant change was not observed at the cytokine levels, which was compared the basal measurement of cytokine levels to the days of 1, 3, 5 and 7.In the control group, the survival rate of 10 patients was 60%. The deaths were observed at the control group before the 5^{th} and 7^{th} day of the treatment, no deaths were observed at the stem cell treatment group for the first two weeks and the period of mesenchymal stem cell administration.

Conclusions: Mesenchymal stem cell treatment had positive impact on survival rates of sepsis during the early phase.

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Abstract 893

Incidence of influenza-like illness among HIV-positive patients: an outpatient clinic survey-based study

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Background: HIV infection has been associated with increased susceptibility to Influenza and Influenza-like illness (ILI), as well as to worse clinical outcomes within this disease spectrum. We aimed to assess the incidence and predictors of ILI in a cohort of HIV-infected outpatients.

Materials/methods: A survey about the occurrence of ILI symptoms during the previous winter season was applied between January and May 2018 on three HIV outpatient clinics in a tertiary care centre. ILI case was defined according to the European Center for Disease Control. The survey was complemented with the clinical and laboratory features retrieved from Hospital electronic data records. An explanatory model for ILI was explored by multivariate regression analysis. The study was approved by the institutional ethics committee.

Results: The study included 232 patients (68% males), aged 47±12 years. Most of the patients were on anti-retroviral therapy (97%) and had supressed viremia (88%). Median CD4 cell count was 684 cells/µL [interquartile range 455-907]. The cumulative incidence rate was 38.4% (95%CI 30.8-47.2). Influenza vaccination on the concerned season was reported by 45.7% of patients. On multivariate analysis, lower ILI incidence was associated with higher CD4/CD8 ratio (aOR 0.38; 95%CI 0.16-0.94; p=0.04) adjusting for CD4 cell counts. This association was observed only for patients with CD4 counts below 500 cells/µL (aOR 0.10; 95%CI 0.01-0.66; p=0.02). Influenza vaccination and absolute CD4 cell counts were not significantly associated with differing incidence.

Conclusions: A high incidence of seasonal ILI was found. A higher risk of ILI may be associated with lower CD4/CD8 ratio, already described as indicator of an immunosenescent phenotype and increased immune activation. CD4/CD8 ratio may contribute on targeting subsets of patients for vaccination.

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Abstract 894

Safety of temporary interruption of anti-platelets in dengue fever with thrombocytopenia

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Background: Thrombocytopenia commonly occurs in dengue and may be complicated by bleeding. Dengue can occur in adults who may be on longterm anti-platelet therapy for comorbidities including myocardial infarction or ischemic stroke. In these cases, clinicians may temporarily discontinue antiplatelet therapy to minimize the risk of bleeding, however this may subject these patients to risk of further ischemic events.

Materials/methods: We conducted a retrospective cohort study of laboratory-confirmed adult dengue patients on antiplatelet therapy and evaluated participants whose anti-platelet therapy was continued versus discontinued. Primary outcome was a composite outcome of major adverse cardiac and cerebrovascular events (MACCE), and all-cause mortality in-hospital and for 1-year post discharge. Secondary outcomes were occurence of platelet and blood transfusion, and occurrence of dengue hemorrhagic fever (DHF), dengue shock syndrome, dengue with warning signs and severe dengue according to World Health Organization criteria.

Results: In total, 66 patients admitted for dengue fever were on anti-platelet therapy, of which 15 patients were continued on the anti-platelet therapy. We found discontinuation of antiplatelet therapy did not result in higher MACCE and mortality, with 4 (2 non-fatal strokes and 2 mortalities) occuring in the continuation group and 5 (3 non-fatal strokes and 2 mortalities) occuring in the discontinaution group (p=0.192). On the other hand, continuation of antiplatelet therapy did not result in more platelet or blood transfusion (p=0.489 and p=0.567 respectively), DHF (p=0.923) or bleeding manifestations.

Conclusions: Our results suggest that discontinuation or continuation of antiplatelet therapy based on clinical judgement in dengue with thrombocytopenia, is largely safe but further studies are needed.

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Abstract 895

Species identification and antifungal resistance of yeasts causing fungaemia at a tertiary care hospital in Madrid, Spain: the coast is clear

Judith Diaz-Garcia*[1;2], Carlos Sanchez Carrillo[1;2;3], Elena Reigadas Ramirez[1;2], Patricia Muñoz[1;2;3;4], Pilar Escribano[1;2;2], Jesus Guinea Ortega[1;2;3]

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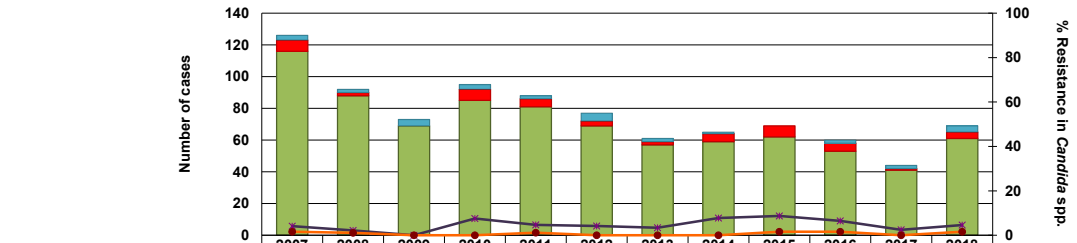
Background: Recent reports alert on an increase of fungaemia episodes caused by either echinocandin resistant *C. glabrata* isolates or multi-resistant species such as *C. auris*. We assessed the aetiology and antifungal susceptibility of agents causing fungaemia at a tertiary care hospital in Madrid (Spain) for 12 years.

Materials/methods: Isolates causing fungaemia in patients admitted to Hospital General Universitario Gregorio Marañón from 2007 to 2018 were tested for molecularly identification and *in vitro* susceptibility to amphotericin B, azoles, anidulafungin, and micafungin according to EUCAST EDef 7.3.1. Fluconazole and echinocandin resistance were assessed using the updated clinical breakpoints v.10.0. Multiple positive blood cultures in a single patient were considered different episodes when separated ≥1 week. Mutations in *FKS* and *ERG11* genes were sought in either echinocandin-resistant isolates or *C. albicans* fluconazole-resistant isolates, respectively.

Results: We studied 921 episodes from 805 patients (90% of patients developed a single episode). Episodes were caused by *C. albicans* (45.4%, n=418), *C. parapsilosis* complex (27%, n=248), *C. glabrata* complex (12.2%, n=112), *C. tropicalis* (6.8%, n=63), *C. krusei* (2.3%, n=21), other *Candida* spp. (3.1%, n=29), and non-*Candida* yeasts (3.3%, n=30). Overall, 4.7% (n=42) of *Candida* isolates were fluconazole-resistant (*C. krusei* [n=19], *C. glabrata* [n=11], *C. albicans* [n=3], *C. parapsilosis* complex [n=2], and other *Candida* spp. [n=7]). Echinocandin resistance involved only 0.8% (n=7) of *Candida* isolates (*C. tropicalis* [n=3], *C. krusei* [n=2], *C. albicans* [n=1], and *C. glabrata* [n=1]). One out of three fluconazole-resistant *C. albicans* isolates harboured *ERG11* mutations (A114S/G464S). *FKS* mutations were found in 5/7 echinocandin-resistant isolates (*C. tropicalis* [R647G *FKS1*, S645F *FKS1*]; *C. krusei* [L701M *FKS1*, n=2]; and *C. glabrata* [F659S *FKS2*]). Non-*Candida* yeasts showed intrinsic echinocandin resistance and decreased fluconazole susceptibility. Antifungal resistance rate proved steady over the years and was mainly affected by the presence of intrinsically resistant isolates (Figure). Resistance to amphotericin B was not detected.

Conclusions: Our fungaemia epidemiology did not differ from that previously reported in Spain and *C. auris* has not been detected in our hospital. Fluconazole and/or echinocandin resistance rates were low and dramatically impacted by species with intrinsic diminished antifungal susceptibility, and did not show signs of increase.



	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018
Other yeast (No.)	3	2	4	3	2	5	2	1	0	2	2	4
Candida spp. resistant (No.)	7	2	0	7	5	3	2	5	7	5	1	4
Candida spp. susceptible (No.)	116	88	69	85	81	69	57	59	62	53	41	61
Candida spp. Fluconazole-R (%)	4,1	2,2	0	7,6	4,7	4,2	3,4	7,8	8,7	6,5	2,5	4,6
Candida spp. Candins-R (%)	1,6	1,1	0	0	1,2	0	0	0	1,6	1,6	0	1,6

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Abstract 896

Nationwide azole resistance survey in clinical *Aspergillus fumigatus* isolates: a snapshot of the situation at 30 Spanish hospitals

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Background: Azole-resistant *Aspergillus fumigatus* isolates, though relatively common in the North of Europe, have been sporadically reported in Spain. We report the largest survey conducted in Span to assess the burden of azole resistance in *A. fumigatus*.

Materials/methods: The 30 participating hospitals, covering the majority of Spanish regions, stored all morphologically identified *A. fumigatus* complex clinical isolates – regardless their clinical significance – from the 15th of February to the 14th of May, 2019. Identification was confirmed by MALDI-TOF and antifungal susceptibility testing performed according to EUCAST 9.3.1 methodology. Resistant isolates were molecularly identified and *cyp51A* gene was sequenced in *A. fumigatus* sensu stricto isolates (itraconazole and/or voriconazole MIC ≥ 2 mg/L).

Results: A total of 848 *A. fumigatus* complex isolates of 726 patients were collected in 29/30 participating hospitals: *A. fumigatus* sensu stricto (n=828) and cryptic species (*A. lentulus* [n=6], *A. fumigatiaffinis* [n=6], *Neosartoria tsurutae* [n=3], *N. udagawae* [n=2], *A. novofumigatus* [n=2], *A. thermomutatus* [n=1]). Isolates were mostly (94%) from the lower respiratory tract. The vast majority of patients yielded either *A. fumigatus* sensu stricto (n=711) or cryptic species (n=10) exclusively, but 5 patients had coexistence of *A. fumigatus* sensu stricto + cryptic species. Amphotericin B resistance was found exclusively in cryptic species. A total of 64 (7.5%) isolates were resistant to ≥1 azoles. Azole resistance was higher in cryptic species than in *A. fumigatus* sensu stricto (95%, 19/20 vs. 5.5%, 45/828; Figure), with isavuconazole showing the lowest number of non-wild type isolates. Most of *A. fumigatus* sensu stricto resistant isolates showed *cyp51A* gene mutations (TR34-L98H, n=24; G54R, n=5; TR46/Y121F/T289A, n=1; other mutations, n=5; WT, n=10). *A. fumigatus* sensu stricto harbouring either the TR34-L98H (n=20) or TR46/Y121F/T289A (n=1) mutations were found in patients cared at hospitals located at 7/24 studied cities. We found 50 (7%) patients carrying either cryptic species (n=15) or *A. fumigatus* sensu stricto (n=35; 4.9%) resistant isolates.

Conclusions: We found 7% of patients carrying azole resistant *A. fumigatus* complex isolates in clinical samples in Spain. TR34-L98H or TR46/Y121F/T289A were the dominant *cyp51A* gene mutations in patients (60%) carrying resistant isolates although their presence was not widespread.

	MIC distributions (number of isolates at each MIC, in mg/L)												
	0.016	0.03	0.06	0.125	0.25	0.5	1	2	4	8	≥ 16	No. (% R)	No. (% Non WT)
***A. fumigatus* sensu lato (n=848)**													
Amphotericin B	0	1	5	70	407	306	46	7	5	1	0	13 (1.53)	13 (1.53)
Itraconazole	0	0	0	26	427	328	21	2	2	2	40	46 (5.42)	46 (5.42)
Voriconazole	0	0	0	3	82	529	177	19	28	7	3	57 (6.72)	57 (6.72)
Posaconazole	2	46	441	279	43	27	3	0	1	0	6	47 (5.54)	37 (4.36)
Isavuconazole	0	0	0	0	13	440	333	27	14	17	4	49 (5.78)	35 (4.13)
***A. fumigatus* sensu stricto (n=828)**													
Amphotericin B	0	1	5	68	407	305	42	0	0	0	0	0 (0)	0 (0)
Itraconazole	0	0	0	26	426	326	15	2	1	1	31	35 (4.22)	35 (4.22)
Voriconazole	0	0	0	3	82	529	176	13	19	3	3	38 (4.58)	38 (4.58)
Posaconazole	2	46	440	278	32	20	3	0	1	0	6	34 (4.10)	30 (3.62)
Isavuconazole	0	0	0	0	13	440	327	18	10	16	4	35 (4.22)	30 (3.62)
Cryptic species (n=20)													
Amphotericin B	0	0	0	2	0	1	4	7	5	1	0	13 (65)	13 (65)
Itraconazole	0	0	0	0	1	2	6	0	1	1	9	11 (55)	11 (55)
Voriconazole	0	0	0	0	0	0	1	6	9	4	0	19 (95)	19 (95)
Posaconazole	0	0	1	1	11	7	0	0	0	0	0	13 (65)	7 (35)
Isavuconazole	0	0	0	0	0	0	6	9	4	1	0	14 (70)	5 (25)

R: Resistant. **Non WT**: Non-wild type. Underlined values indicate non-wild type isolates and values in bold indicate resistant isolates according to ECOFFs (EUCAST Breakpoints table v 10.0, November, 2019).

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Abstract 898

Aetiologies, management and outcome of non-traumatic coma in small children: a prospective study in Benin

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Background: Malaria morbidity and mortality have declined since year 2000 and viral central nervous system infections have been reported as an important cause of hospital admission with coma in malaria-endemic Eastern Africa. Our objectives were to describe the etiologies, management and outcome of non-traumatic comas in small children in Benin.

Materials/methods: This study took place in 2 teaching hospitals. All HIV negative children between 2 and 6 years of age, with a Blantyre Coma Score below or equal to 2 were included. Along with a workup screening for malaria severity signs, a blood culture, a Tropical Fever PCR test (Fast-track diagnostics) and a cerebrospinal fluid (CSF) analysis, including a multiplex PCR (Biofire, Mérieux) were performed. All children with malaria were treated with intravenous artesunate. Patients also had free access to other drugs, including transfusions, prescribed at the study physician's discretion.

Results: Between March and November 2018, 84 children were included with a M/F sex ratio of 0.68 and a mean age of 43 months. A history of fever was declared in all children, with a mean duration of 4 (1-14) days and 90% (76/84) of them had received care provided by a health professional before admission, but only 11 children were given an adequate antimalarial oral therapy. Malaria was the only identified cause of coma in 86% (73/84), 5 had an associated infection (1 aseptic meningitis, 1 *Staphylococcus aureus* bacteremia, 1 *Streptococcus* bacteremia, 1 West Nile virus infection, 1 HHV6 CSF infection) and 6 had a non-malarial coma (1 dengue, 1 *E. coli* bacteremia, 4 unknown). Most (58/84) children received blood transfusions and 23% (20/84) ceftriaxone at admission ; the lethality rate was 30 % (26/84).

Conclusions: Cerebral malaria remains by far the most common cause of non-traumatic coma in the study area, with a high lethality rate despite an access to standardized care. For most children, missed opportunities to receive an early and effective antimalarial treatment have been declared. Severe malaria needs to be prevented, but efforts to struggle against malaria should not overlook the capacity building for providing care to life-threatening forms of the disease.

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Abstract 901

The progress towards achieving the UNAIDS ambitious 95% viral suppression target among adults living with HIV in South-Western Nigeria

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Background: In sub-Saharan Africa where genotypic drug resistance testing is rarely performed and poor adherence is blamed for the inability to achieve viral suppression and treatment failure, programmatic approaches to preventing & handling these are thus essential. Hypothesis tested was antiretroviral therapy adherence effect on viral load outcome. This study was aimed at determining and monitoring HIV/AIDS disease progression using viral load to provide prognostic information and evaluate patients for viral suppression.

Materials/methods: This study was an observational study of subjects living with HIV already initiated on antiretroviral therapy for at least six months, enrolled in health facilities across Ondo State, South-Western Nigeria, during a 12-month observation period starting October 2018 till September 2019. Quantitative viral load analysis was done using Polymerase Chain Reaction, Roche Cobas Taqman 96 Analyzer. All data were statistically analyzed, using Statistical Package for the Social Sciences (SPSS), with multiple comparisons done using Post Hoc Bonferonni test.

Results: A total of 8124 adults living with HIV eligible for the study were recruited. Most of them are in the age range of 35 – 39 years, with a mean age of 42.02 ± 10.88 years. 7162 (88.2%) & 1771 (21.8%) of the subjects had viral suppression of <1000 RNA and <20 RNA copies per ml respectively. The unsuppressed subjects went through enhanced adherence counselling (EAC) for three months and viral load test repeated thereafter. 192 patients who had completed the three sessions of EAC and repeated viral load increased the entire suppression numbers to 7339 (90.3%) & 1824 (22.5%) <1000 RNA copies per ml and <20 RNA copies per ml respectively during the period of observation. ART adherence has significant effect on viral load outcome (χ^2 = 7.63, df = 1, P = 0.001).

Conclusions: Current ART regimen & HIV treatment enhanced adherence counseling are key to the achieving viral suppression, thus, routine viral load monitoring will ultimately help in HIV/AIDS disease progression follow up and reduce treatment failure tendencies. This will help more patients stay on first line regimen and prolong their life expectancy, indicating that the UNAIDS last 95 target is achievable.

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Abstract 902

Characterisation and virulence of fibronectin-binding protein of Streptococcus intermedius

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Background: *Streptococcus intermedius*, a member of the anginosus group of streptococci, is a common commensal organism found in the human oral cavity and gastrointestinal and urogenital tracts. Furthermore, *S. intermedius* is associated with purulent infections, abscesses and infectious endocarditis. The organism secretes the human-specific cytolysin intermedilysin that is highly homologous to the cholesterol-binding cytolysin streptolysin O from *S. pyogenes*, pneumolysin from *S. pneumoniae*, and listeriolysin O from *Listeria monocytogenes.* In this study, we identified other pathogenic factors and described a fibronectin-binding protein (FBP) homolog of *S. intermedius* (FbpI) that mediated bacterial adhesion to epithelial cells and virulence in mice.

Materials/methods: *S. intermedius* GAI 1157 (wild-type (WT)) and isogenic mutant Δ*fbpI* prepared by homologous recombination were used. The binding activities of *S. intermedius* strains to fibronectin and epithelial cells were determined using (methyl-^{3}H)-thymidine-labelled bacteria. The fibronectin-binding domain was analysed using recombinant full-length (rFbpI) and N- and C-truncated forms of FbpI. The pathogenicity of FbpI was assessed using a mouse infection model. These mice were subcutaneously injected in the back with suspensions of *S. intermedius* WT or Δ*fbpI.* The abscesses were removed and weighed.

Results: The amino acid sequence of FbpI was similar to that of atypical FBPs that do not possess a conventional secretion signal and an anchorage motif. rFbpI was bound to immobilised fibronectin in a dose-dependent manner. The fibronectin-binding activity of the N-terminal construct of rFbpI comprising the translation initiation codon methionine of the open reading frame to Lys265 (rFbpI-N) bound immobilised fibronectin to a much lesser extent than rFbpI. In contrast, a construct comprising the C-terminal domain (Ala266 to Met549; rFbpI-C) bound immobilised fibronectin equivalently to rFbpI. Moreover, the adherence of isogenic mutant Δ*fbpI* to cultured epithelial cells and immobilised fibronectin was significantly lower than that of the WT strain. Furthermore, the abscess formation of Δ*fbpI* reduced in the mouse infection model compared with that in the WT strain.

Conclusions: Thus, FbpI may play a role in bacterial adhesion to host cells and represent a critical pathogenic factor of *S. intermedius*.

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Abstract 906

Staphylococcus aureus inhibits opsonophagocytosis and modulates neutrophils extracellular traps formation efficiently during the early stages of biofilm formation

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Background: Despite our versatile host immune responses with proven ability to eliminate Staphylococcus aureus invasion. Infection with this bacterium are still still a serious problem and can be frequently found in clinics, worldwide. Along with acute infection, *S. aureus* is also associated with biofilm-related chronic infections. In mature biofilms, encapsulated *S. aureus* cells are well known for their ability to resist the immune system and antibiotic treatment. Contrary, little information is available on immune evasion of *S. aureus* during the early stages of biofilm formation. Therefore, we studied if *S. aureus* developed mechanisms to overcome the host innate immune responses during these stages of biofilm development.

Materials/methods: S. *aureus* strains from various genetic background were grown *in vitro* to form biofilms. The production of immune modulators was studied during the early stage of biofilm formation using mass spectrometry, fluorescence resonance energy transfer (FRET) assay, and Luminex® based competitive ELISA. The detected immune modulators where studied for their ability to modulate the host innate immune response using several *ex vivo* setups, like co-incubation of biofilm with complement and study the complement activation. Furthermore, the interactions between biofilm and neutrophils were monitored with confocal microscopy and isothermal microcalorimetery.

Results: Contrary to the previous finding, during the early stages of biofilm formation, *S. aureus* actively releases 87 different proteins which include several immune modulators. Potent immune modulators CHIPS, FLIPr, Map, Sbi, SCIN, thermonuclease (nuc), and Staphylococcal Protein A (SpA) were among the prominent proteins found. We observed that biofilms produce enough SCIN to hinder human complement activation and in this way obstruct C5a release. Furthermore, SpA was found to stimulate NETosis, leading to death of neutrophils. Finally, the thermonuclease produced during the early stages of biofilm formation, broke down these NETs.

Conclusions: The main mechanisms of neutrophils to eliminate bacteria, Opsonophagocytosis and NETs formation, can be jeopardized by *S. aureus* during the early stages of biofilm formation; opsonization and phagocytosis are inhibited by SCIN, while NETs formation and destruction are modulated by SpA and thermonuclease. ensuring the survival of these young *S. aureus* biofilms.

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Abstract 907

Using mechanisms of action to assess new antibiotics against Gram-negative bacteria

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Background: In our previous study, a strategic system for testing antibiotics against specific resistance mechanisms has been constructed by using *Klebsiella pneumoniae* (J Antimicrob Chemother 2017; 72: 3302-16), which can facilitate the development of antibiotics that are robustly effective against multidrug-resistant bacteria. Given that the genetic background of several bacterial pathogens with high resistance rates is quite different from that of *K. pneumoniae*, specific resistance genes can be found in these pathogens. In this study, the strategic system has been constructed by using *Acinetobacter baumannii*.

Materials/methods: In-frame deletion, site-directed mutagenesis and plasmid transformation were used to generate genetically engineered strains with various resistance mechanisms from two fully susceptible *A. baumannii* strains. Antimicrobial susceptibility testing was used to test antibiotics against these strains *in vitro*.

Results: A total of 50 engineered strains with various resistance mechanisms from *A. baumannii* KAB1544 and ATCC 17978 were constructed. These strains included 31 strains with chromosome-mediated resistance and 19 strains with plasmid-mediated resistance, and each of the 50 resistance mechanisms showed similar effects on the MICs for KAB1544 and ATCC 17978. Compared to the parental strains, the engineered strains related to some efflux pumps showed a significant (≥4-fold) difference in the MICs of β-lactams, quinolones, aminoglycosides, tetracyclines, folate pathway inhibitors and/or phenicols, while no significant (≥4-fold) effects on the MICs were found for the engineered strains lacking OmpA, CarO, Omp25, Omp33, OmpW or OprD. Mechanisms due to GyrA/ParC mutations, β-lactamase, aminoglycoside-modifying enzyme, 16S rRNA methylase and *tet* resistance gene contributed their corresponding resistance as previously published.

Conclusions: Strains constructed in this study have clear resistance mechanisms and can be used to screen and assess compounds against specific resistance mechanisms for treating *Acinetobacter*. In addition to our previously published system for *Enterobacteriaceae* and our under-construction system for *Pseudomonas*, the combination of these three systems could increase the coverage of bacterial types for drug assessment and facilitate the selection process of new candidates in the drug development against superbugs.

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Abstract 908

Using machine learning for improving MLST analysis of nanopore sequenced bacteria

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Background: Due to the inherently high random and systematic error rates in Oxford Nanopore sequencing data, bacterial typing methods such as MLST are not easily implemented in a long read bioinformatic workflow. To account for the high error rates, different polishing tools have been developed. Here, we investigate if polishing with Racon and Medaka can improve MLST analysis for Nanopore data assembled with the Flye assembler.

Materials/methods: We have trained recurrent neural networks for polishing long read assemblies with the Medaka software from Oxford Nanopore Technologies. One of the pre-trained Medaka models was individually fine-tuned on three different datasets consisting of *Enterococcus faecium*, *Klebsiella pneumoniae* and *Staphylococcus aureus*. We evaluated both Flye assemblies polished by Racon and non-polished Flye assemblies.

Quast and DNAdiff were used to analyze the quality of the polishing and all assemblies were also subjected to a BLAST based MLST analysis where the number of correctly predicted STs and alleles were counted.

Results: By training a model on a subset of a specific dataset and evaluating on the remaining samples, we saw a substantial increase in sequence identity for the test samples. The results also show that polishing with Racon prior to polishing with Medaka can actually decrease the performance compared to using Medaka directly on a draft assembly.

Running MLST analysis on the draft assemblies (48 test samples in total) resulted in zero correct STs. However, using the fine-tuned Medaka models, we could correctly predict 42 STs, with an allele prediction rate of 97.6%. The model trained on the *K.pneumoniae* dataset was also evaluated on a larger, unseen *K.pneumoniae* dataset. The MLST analysis for this dataset, consisting of 36 samples, resulted in zero correct STs for the draft assemblies and 26 correct STs after polishing with Medaka. The allele prediction rate increased from 69.4% for the draft assemblies to 96.0% after polishing with Medaka.

Conclusions: This study shows that using machine learning for polishing assemblies enables MLST analysis of Nanopore data. However, a more diverse training set is needed in order to build a more robust polishing model.

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Abstract 909

Performance of the urine flow cytometer Sysmex UF-5000 in rapid diagnosis of urinary tract infections

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Background: Urinary tract infection (UTI) is one of the most common bacterial infections worldwide. Urine culture is the gold standard method to diagnose UTI, but is time consuming and tedious. Urine flow cytometry (FCM) can differentiate and quantify particles in urine, and is an alternative method for ruling out UTI. The aim of this study was to evaluate FCM as a rapid screening method to predict urine samples with negative or mixed culture growth.

Materials/methods: We performed standard microbiological analysis and FCM with the Sysmex flow cytometer UF-5000 on 3919 urine samples from both outpatients and hospitalized patients. 2565 (65%) samples were from women and 1354 (35%) were from men. Positive urine culture was defined as growth $\geq 10^4$ cfu/mL. Results from 17 FCM parameters and culture were evaluated to identify a) positive culture versus no culture and b) mixed culture (>2 organisms) versus pure culture (≤2 organisms) by the use of FCM.

Results: Positive culture ($\geq 10^4$ cfu/mL) was found in 2257/3919 (57%) urine samples; 1351 were pure and 906 were mixed cultures. ROC curve analyses comparing results from culture growth with different FCM parameters identified bacterial count (BACT; area under the curve [AUC] 0.939) and leucocyte count (WBC; AUC 0.809) as possible independent predictors for bacterial growth. Subpopulation analyses (men/women/inpatients/outpatients/immunocompromised/pregnant) revealed little association between FCM results and culture growth in pregnant women, leading to exclusion of this subpopulation (n=452). Investigation of different cut-offs for BACT and WBC, separate and in combinations, indicated that WBC marginally improved the outcome in combination with BACT (sensitivity 96.6%; negative predictive value [NPV] 92.3%), compared to BACT alone (sensitivity 95.2%; NPV 91.2%) using BACT/WBC cut-off 30. There was no difference between urine from in- or outpatients. Analyses comparing FCM parameters squamous epithelial cells (SquaEC) and epithelial cells (EC) with mixed culture indicated that neither were predictors for mixed culture.

Conclusions: FCM cannot predict mixed culture growth (ie, indication of contamination of specimen), but it can predict negative culture growth in both men (NPV 94.7%) and non-pregnant women (NPV 84.7). This reduces time-to-negativity compared to gold standard, which could potentially reduce unnecessary usage of antibiotics.

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Abstract 911

High prevalence of antimicrobial resistance in community-acquired urinary tract infections in Harare, Zimbabwe

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Background: Antimicrobial resistance (AMR) is compromising our ability to successfully treat infections. The Global Action Plan on AMR proposed by the WHO emphasizes the importance of strengthening surveillance in the attempt to limit the effects of AMR. There are few data on gram-negative AMR prevalence in sub-Saharan Africa especially from the outpatient setting. First-line treatment for urinary tract infections (UTIs) as recommended by Zimbabwe National Guidelines is amoxicillin or a fluoroquinolone which may not be optimal in the context of increasing AMR.

The aim of this study is to estimate the prevalence and risk factors for AMR in isolates from outpatients presenting with suspected UTIs to primary care clinics in Harare.

Materials/methods: Adult outpatients presenting with symptoms of UTI to six clinics in southern Harare between July and November 2019 were recruited. A urine sample was collected and inoculated on chromogenic agar. Cultures were considered positive if a growth of $>10^3$ CFU/ml of a known pathogen was obtained. Antimicrobial susceptibility testing (AST) using disc diffusion and EUCAST breakpoints was performed.

Results: Of the 383 adult participants recruited into the study, 256 (66.8%) were female. HIV infection was present in 90/337 (26.7%) patients who knew their status. 125 (32.6%), 222 (58.0%), and 36 (9.4%) cultures yielded an organism at $>10^3$ CFU/ml, no growth, and contamination respectively. The most common pathogen was *E. coli*, identified in 106/125 (84.8%), followed by other Enterobacteriaceae in 12/125 (9.6%) and enterococci in 6/125 (4.8%). Among Enterobacteriaceae prevalence of resistance was 100 (85%) to ampicillin, 94 (82%) to cotrimoxazole, 22 (19%) to ciprofloxacin, and 21 (18%) to third generation cephalosporins. No carbapenem resistance was recorded. HIV infection and a previous UTI were associated with the presence of third-generation cephalosporin resistance (Table).

Conclusions: The prevalence of resistance to first-line antibiotic treatment for uncomplicated UTI in this setting was high, emphasizing the need for AMR surveillance to inform setting specific guidelines. HIV infection may be a driver for AMR in this setting highlighting the need to give special consideration to this group when making empirical treatment decisions.

Table. Risk factors for resistance to third generation cephalosporins in Enterobacteriaceae

	Total (N=118)	3rd GC resistance (N=21)	No resistance to 3GC (N=97)	OR (95% CI)	aOR (95% CI)
Female, n (%)	98 (83%)	17 (81%)	81 (84%)	0.83 (0.25-2.84)	-
Age (years), median (IQR)	29 (22-42)	31 (22-38)	28 (23-46)	0.98 (0.94-1.01)	-
HIV positive, n (%)*	25 (25%)	7 (41%)	18 (21%)	**2.61 (0.85-7.98)**	**2.68 (0.82-8.8)**
Pregnancy, n (%)*	12 (13%)	2 (13%)	10 (13%)	1.00 (0.19-5.15)	-
Prior antimicrobial use, n (%)	44 (37%)	10 (53%)	34 (36%)	**1.99 (0.73-5.45)**	**0.95 (0.28-3.20)**
Prior hospital admission, n (%)	7 (6%)	0 (0)	7 (7%)	-	-
Prior UTI	23 (20%)	6 (33%)	17 (18%)	**2.29 (0.74-7.08)**	**2.58 (0.69-9.80)**

*HIV status was unknown for 16, 8 women did not know their pregnancy status; 3GC third-generation cephalosporin

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Abstract 913

Lassa fever infection and prevention control availability and use at healthcare facilities in South-Western Nigeria

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Background: Lassa fever is a zoonotic infection caused by arenavirus contracted primarily through contact with the contaminated excreta of Mastomys natalensis rodents. Secondary transmission of the virus between humans occurs through direct contact with infected blood or bodily secretions. The objective of this study was to assess the availability of infection & prevention control measures, consumables & their use in healthcare facilities in Western Nigeria.

Materials/methods: This study was a cross sectional study. Data was collected by trained volunteers and supervised by appointed supervisors and investigators, by a face-to-face interview using a pre-tested structured questionnaire on Lassa Fever. Frequency count was generated for all variables and statistical test of significance was performed with Chi-Square test.

Results: Eighty five healthcare facilities & workers were surveyed**,** out of which 80 (94.1%) had wash hand basins but only 48 (56.5%) had running water or any kind of water supply. Most, 55 (64.7%) & 49 (57.6%) of the healthcare workers do not practice hand washing before/after patient contact & had not been trained on infection control while only 48 (56.5%) were regularly using personal protective equipment such as white coat & gloves. There was no association between availability of personal protective equipment & its use ($\chi^2 = 3.02$, df = 1, P = 0.403).

Conclusions: Healthcare facilities do not meet the minimum standard for infection prevention & control measures. It is therefore recommended that government at all levels should immediately prioritize the infection prevention & control programs its health facilities to curb future spread of infectious diseases even in hospital premises among healthcare workers.

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Abstract 917

Achieving the third 95: Keeping adolescents living with HIV virally suppressed in rural Nigeria in test and treat era using continuous quality improvement model of peer counseling & support group

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Background: In 2016, Nigeria transitioned to "Test & Treat", a policy where all people living with HIV (PLHIV) are treated with lifelong antiretroviral therapy (ART). There are unique challenges achieving viral suppression in ALHIV mainly due to increased stigma, discrimination & lack of social support. Hypothesis tested was antiretroviral therapy adherence effect on viral load outcome. We examined viral suppression among adolescents living with HIV in rural Western Nigeria.

Materials/methods: This study was an observational study of adolescents living with HIV (ALHIV) already initiated on antiretroviral therapy for at least six months, enrolled in health facilities in rural parts of Western Nigeria, during a 12-month observation period starting October 2018 till September 2019. Quantitative viral load analysis was done using Polymerase Chain Reaction, Roche Cobas Taqman 96 Analyzer. All data were statistically analyzed, using Statistical Package for the Social Sciences (SPSS).

Results: A total of 316 subjects eligible for the study were recruited. Most of them are in the age range of 10 – 19 years, with a mean age of 13.51 ± 2.86 years. 222 (70.3%) & 52 (16.5%) of the subjects had viral suppression of <1000 and <20 RNA copies per ml respectively. The 94 subjects went through peer counseling by trained ALHIV and enhanced adherence counseling (EAC) for three months and viral load test repeated thereafter. 22 patients who had completed the three sessions of EAC and repeated viral load increased the entire suppression numbers to 244 (77.2%) & 60 (19.0%) <1000 and <20 RNA copies per ml respectively during the period of observation. The ALHIVs in the process joined the institutionalized social-media driven support group & adolescent decentralized care model ensuring they achieve the third 95 at undetectable viral load level. ART adherence has significant effect on viral load outcome ($\chi^2 = 20.902$, df = 1, P = 0.001).

Conclusions: Antiretroviral therapy (ARV) treatment adherence counseling is key to the achieving viral suppression and determine infection prognosis, thus, developing robust continuous quality improvement (CQI) plans to address issues across the cascade ultimately helping in the monitoring of HIV/AIDS disease progression and decrease treatment failure tendencies.

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Abstract 922

Assessment of viral load suppression rates among paediatric patients living with HIV in South-Western Nigeria

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Background: In resource-limited settings, where genotypic drug resistance testing is rarely performed and unsuppressed viral load outcome is a function of poor drug adherence, programmatic approaches in scaling up optimal adherence is essential. The aim of this study was to assess the viral load suppression rates among pediatric patients living with HIV using ART multi-month scripting model in south-western Nigeria.

Materials/methods: This study was a longitudinal study conducted on 283 paediatric patients living with HIV (136 males and 147 females) enrolled into antiretroviral therapy from a selected health facilities across Western Nigeria, during a 12-month observation period starting October 2018 till September 2019. Quantitative viral load analysis was done using Polymerase Chain Reaction, Roche Cobas Taqman 96 Analyzer. All data were statistically analyzed, using Statistical Package for the Social Sciences (SPSS), with multiple comparisons done using Post Hoc Bonferonni test.

Results: Most of the respondent were within the age range of 6 – 9 years, with a mean age of 6.07 ± 2.08 years. 167 (59.0%) & 37 (13.1%) of the subjects had viral suppression of <1000 RNA copies per ml and <20 RNA copies per ml respectively. The unsuppressed subjects went through enhanced adherence counselling (EAC) for three months and viral load test repeated thereafter. 33 patients who had completed the three sessions of EAC and repeated viral load increased the entire suppression numbers to 200 (70.7%) & 60 (19.0%) <1000 RNA copies per ml and <20 RNA copies per ml respectively during the period of observation. ART adherence has significant effect on viral load outcome from the study hypothesis tested ($\chi^2 = 15.763$, df = 1, P = 0.001).

Conclusions: Current ART regimen & HIV treatment enhanced adherence counseling are key to the achieving viral suppression, thus, routine viral load monitoring will ultimately help in HIV/AIDS disease progression follow up and reduce treatment failure tendencies. This will help more paediatric patients stay on first line regimen and prolong their life expectancy, indicating that the UNAIDS last 95 target is though achievable but more work is still to be done.

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Abstract 927

Co-infection with *Staphylococcus aureus* after primary influenza virus infection results in endothelial damage

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Background: The seasonal influenza virus (IV)-associated bronchopneumonia is one of the infectious diseases with the highest population-based mortality. Beyond the virulence of the virus itself, epidemiological data suggest that bacterial co-infections are the major cause of increased mortality. In this context, *Staphylococcus aureus* (*S. aureus*) represents a frequent causative bacterial pathogen in secondary pneumonia. Post-influenza models of *S. aureus* pneumonia demonstrate the severe outcome of a coinfection associated with substantial morbidity and mortality. To date, investigations concerning microbial infections of the lung are usually carried out in animal models. However, lung anatomy and physiology, as well as composition of the immune system differ significantly between rodents and humans.

To investigate the interactions between epithelial, endothelial and immune cells after IV / *S. aureus* co-infection, we established a human alveolus-model that generated a reactive tissue-tissue interface between the vascular endothelium and the airway-facing epithelium.

Materials/methods: MOTiF biochips were seeded with human endothelial cells on the vascular site and with epithelial cells and macrophages on the airway site. This organoid was cultured for up to 14 days with a stable and stable air-liquid interphase under dynamic flow conditions.

Results: Dynamic conditions that maintain the air-liquid-interface allow a stable barrier with high transepithelial resistance and an intact vascularity. We provide evidence for an increase of barrier integrity after introduction of macrophages, as proven by TEER measurement and permeability tests. Our data indicate a stable surfactant production of alveolar epithelial cells type II. Subsequent infection has been successfully established and pathogenicity factors can be investigated.

Conclusions: We established a functional, biochip-based human *in vitro* alveolus model that is suitable for investigation of complex co-infections and immune functions. Separated airway and vascular chambers allow infections with pathogens from the airway site.

Inducing an immune response using this method, it is possible to observe migration of immune cells from the vascular site to the infection to study species-specific mechanism of pathogens. Our results suggest that the endothelium is disrupted earlier than the epithelium, and *S. aureus* is able to inhibit the IV-induced apoptotic cellular response on the level of procaspase 8 inhibition.

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Abstract 929

Pilot evaluation of machine learning for the classification of *Streptococcus pneumoniae* PCV-13 serotypes from non-PCV13 serotypes based on MALDI-TOF MS analysis

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Background: *Streptococcus pneumoniae* serotyping is limited to Reference Laboratory. Knowing the serotype is of great significance from an epidemiological and preventive perspective because it makes possible to define the distribution of serotypes causing invasive pneumococcal disease (IPD).The PCV-13 includes 13 serotypes (1,3,4,5,6A,6B,7F,9V,14,18C,19A, and 23F). The main aim of this work was to assess if the mass spectra obtained by MALDI-TOF MS showed specific discriminatory peaks, using machine learning algorithms, and if those peaks were able to differentiate PCV-13 serotypes from NON-PCV13 serotypes. Therefore using this methodology as screening tool in order to then, use the reference method in a more targeted way.

Materials/methods: The study included PCV-13 isolates and the top 10 of the most prevalent NON-PCV13 isolates (12F, 24F, 13, 8, 11A, 15B, 16F, 22F, 7C and 23B), which were selected according to the Argentina national epidemiology, all isolates were previously serotyped by Quellung reaction. Mass spectrum analysis was performed using a MicroFlex LT mass spectrometer (Bruker Daltonik GmbH) and the procedures were conducted according to the manufacturer's instructions. Classification models were generated using the machine learning (ML) algorithms in ClinProTools, namely QuickClassifier (QC), Supervised Neural Network (SNN), and Genetic Algorithm (GA). All the peaks in the spectra were used in model generation.

Results: In this first part of the pilot evaluation, we were able to discriminate two groups types, making it possible to differentiate PCV-13 from NON-PCV13 isolates. GA, showed the best cross-validation and recognition capacity values. (Table 1)

Conclusions: A combination of MALDI-TOF MS analysis and ML models may be a potentially efficient screening tool for *Streptococcus pneumoniae* serotipification, although an external validation must be done in a second part of the pilot evaluation and more isolates whose serotypes are unknown should be challenged with all the algorithms in order to evaluate the real use of this methodology.

Table 1.

CLASSIFICATION ALGORITHMS	RECOGNITION CAPABILITY	CROSS VALIDATION	PEAKS USED IN MODEL
GA	100%	88.0%	13561,3876,7054,2983,2397
SNN	100%	81.9%	4703,7054,7527,4794,9978,10785
QC- DAV	68,5%	67,3%	2035
QC- P-VALUE T-TEST/ANOVA.	96.1%	76.3%	4703,4794,10785
QC- P-VALUE W/K-W.	96.1%	77.9%	4703,4794

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Abstract 930

Factors influencing vaccination coverage among children age 12–23 months in Afghanistan

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Abstract third-party references: ICF

Background: Childhood vaccination plays a key role in reducing morbidity and mortality from vaccine-preventable diseases. Numerous studies have assessed the influence of demographic and socioeconomic factors on child immunization around the world. There are few such studies in Afghanistan, however. Therefore, this study aimed to identify factors influencing vaccination status among children age 12–23 months in Afghanistan.

Materials/methods: Nationally representative data from the 2015 Afghanistan Demographic and Health Survey were used for this study. A sample of 5,708 children age 12-23 months with a vaccine card and immunization history was analyzed. Multinomial logistic regression was used to identify significant relationships between cofactors and vaccination status.

Results: In the study, half of the subjects were boys (51%), almost half were born at home (48%), and about three-fourths were residents of rural areas (76%). Background characteristics positively associated with vaccination status included delivery in a health facility, maternal age 30-39, attending at least four visits for antenatal care (ANC), health facility visit in the past 12 months, paternal professional occupation, and family in the richer wealth index.

In bivariate analysis, the central region showed the highest prevalence of full vaccination among children age 12-23 months. Controlling for cofactors, however, children in the northeast region were more likely to be vaccinated compared with children in the central region, while children in the southern region were less likely to be fully vaccinated.

Conclusions: This study identified maternal age, ANC visits, place of delivery, health facility visits in past 12 months, paternal occupation, wealth quintile, and geographic region as the factors influencing child's vaccination status in Afghanistan.

Key words: vaccine; immunization; children age 12-23 months; influencing factors; Afghanistan.

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Abstract 931

A multi-site evaluation of antifungal prescribing and the use of fungal diagnostics in critical care

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Background: Critical care patients are at higher risk of invasive fungal infections (IFI). Understanding the utilisation of antifungal drugs and diagnostics in intensive care units (ICU) is essential for the development of antifungal treatment pathways and stewardship.

Materials/methods: A 6-month evaluation (May-November 2019) of all antifungal prescribing episodes in medical and surgical ICUs across three London Trusts (collectively 168 ICU beds). 'Antifungal prescribing episode' was defined as a period of continuous antifungal therapy for a specified indication. Drug; duration; indication; treatment rationale at initiation (prophylaxis, empirical (clinical suspicion alone), pre-emptive (suggestive radiology/positive biomarkers), targeted at IFI, targeted at non-invasive infection (eg.Oral candidiasis); fungal diagnostics and final IFI classification were reviewed. Analyses were conducted in Microsoft Excel and GraphPad PrismV7.

Results: There were a total of 353 prescribing episodes in 305 patients (16% patients ≥2 episodes). Prescribing rationale at the start of the episode was 21% prophylaxis (median (IQR) duration of treatment 8 (4-18) days); 48% empirical (7 (3-11) days); 9% pre-emptive (11 (7-21) days); 11% targeted for IFI (16 (11-22) days); 11% targeted for non-invasive infection (4 (2-7) days).

Overall, fluconazole was the most frequently prescribed (fluconazole 42%;echinocandins 38%; triazoles 11%;amphotericin 8%), however echinocandins accounted for the majority (52%) of all empiric/ pre-emptive/IFI targeted prescribing.

For empirical therapy, a blood culture was sent in 72% and non-culture based tests in 48%. Serum beta-d-glucan (BDG) turnaround time (TAT) was significantly shorter for the ICU with diagnostics available on-site (median (IQR) TAT of 1 (1-2) day) compared to the two sites processing BDG at external laboratories (14 (12-17) days, 10 (8-12) days)(p =0.001). There was no significant difference in duration of empirical treatment for those with a negative BDG versus no BDG sent (8 versus 7 days (p=0.37)).

Regarding final IFI classification; 43 (14%) patients had proven IFI (40 invasive candidiasis;3 invasive mould). Data on probable/possible/no IFI cases, clinical outcomes and antifungal defined daily dose/occupied bed days will be presented.

Conclusions: In the ICU setting, antifungal prescribing is predominantly empirical. Rapid non-culture based diagnostic tests regarded as robust by clinicians, are required to influence antifungal prescribing decision-making in this high-risk patient group.

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Abstract 932

Antibiotic prescribing decisions in intensive care: a qualitative study

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Abstract third-party references: On behalf of the INHALE WP2 study group

Background: Antimicrobial stewardship (AMS) is a key issue in intensive care units (ICUs) where antibiotics are widely prescribed for complex patients. However, there is limited research examining how antibiotic prescribing decisions are made and how antimicrobial resistance (AMR) concerns impact decision-making in this context. INHALE is a comprehensive research programme exploring the influence of molecular diagnostics on prescribing for hospital acquired pneumonia (HAP) in ICU. This study explored how prescriber perceptions and contextual factors influence antibiotic prescribing decisions in ICUs, prior to implementation of molecular tests.

Materials/methods: Four focus groups and 34 vignette-based interviews were conducted with clinicians involved in antibiotic prescribing in four UK ICUs. Focus groups explored clinicians' perceptions of factors influencing their prescribing decisions and semi-structured interviews explored decision-making processes using two clinical vignettes in the context of HAP. Data were analysed using inductive thematic analysis.

Results: Prescriber perceptions were key to decision-making. Most clinicians balanced the societal risks of AMR against the needs of the individual patient, with the latter generally given precedence. In situations of doubt, the default was to prescribe antibiotics on the basis that the antibiotics might prevent patient mortality, with clinicians viewing prescribing as more defensible than not prescribing. The side-effects of antibiotics were rarely mentioned. Clinicians were aware of AMR and strove to withhold potentially unnecessary antibiotics where possible. This aim was counter-balanced by their previous experiences of negative consequences, which motivated the prescribing of antibiotics 'just in case' of an infection.

Clinicians' perceptions interacted with the prescribing context. Examples include a lower perceived threshold to prescribe antibiotics out of hours, the influence of input from non-ICU team members, as well as antibiotic prescribing norms and varied adherence to guideline recommendations across ICUs.

Conclusions: When making prescribing decisions, clinicians' understandable fear of undertreating possible infection and worsening outcomes is often in direct conflict with AMS aspirations. Prescribers seem to be driven by perceived negative consequences for patients and themselves over more distal issues of AMR. Evidence-based support from faster and more effective diagnostics may help reconcile these competing priorities by allowing for earlier antibiotic de-escalation and refinement.

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Abstract 933

Resistant bacteria in retail meat

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Background: Surveillance of antimicrobial resistance in foodborne bacteria is part of the WHO "Global Action Plan on Antimicrobial Resistance". Often surveillance focuses on specific bacteria, resistance mechanisms or production animals. We wanted to investigate, with a broad-range culture approach and PCR, if retail meat could be a possible source of resistant bacteria.

Materials/methods: Personnel form the Department of Clinical Microbiology, Odense University Hospital, were asked to swab their non-frozen retail meat in the kitchen just before preparation. Samples of pork, chicken and beef (100 of each) distributed evenly over one year were swabbed (10 cm x 10 cm) with FecalSwab (Copan, Italy) and stored at -80°C. All samples were cultured with selective and non-selective media, including media to detect MRSA, VRE, ESBL, CPO and *Clostridioides difficile*. MALDI-TOF and disk diffusion were used for identification and susceptibility testing. Also, PCR with the Allplex Entero-DR kit (Seegene, South Korea), detecting NDM, KPC, OXA-48, VIM, IMP, CTX-M, VanA, VanB genes, was performed.

Results: Any growth was seen from 92% of the samples (276/300). *Staphylococcus aureus* was detected in 23 (8%) samples, mainly chicken (17), of which one was an MRSA from pork. *Enterococcus* spp. were detected in 46 (15%) samples of which one was a VRE from pork. Twenty-nine different species of *Enterobacterales* was identified and one or more species were detected in 48% of the samples. No ESBLs were detected with the culture method but several of the identified species harbor chromosomal AmpC. *Pseudomonas* spp. (non-*aeruginosa*) were detected in 44% (133) of the samples. In 124 samples *Pseudomonas* was detected on the CPO selective media. From a random sample of 40 isolates, only three was not fully susceptible to meropenem. *C. difficile* was not detected in any of the samples. With PCR OXA-48 was detected in four samples, CTX-M in two, and vanA (identical with culture) and vanB in one sample each.

Conclusions: Retail meat could be a possible source of resistant bacteria. However, sequence typing is needed to establish that the same bacteria from this study can be found in humans. Even so, good kitchen hygiene will prevent transmission to humans.

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Abstract 935

Is there an increased risk for *Clostridium difficile* infection months after hospitalisation in a room occupied previously by a patient with *C. difficile*?

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Background: *Clostridioides difficile* (CD) is the most common infectious cause of acquired diarrhoea in healthcare systems with significant morbidity and mortality. Several risk factors for *C. difficile* infection (CDI) exist; antibiotic use and environmental exposure are probably the most important modifiable risk factors.

Aims: to explore whether hospitalization in room that was previously occupied by a patient with CDI (r-CDI) and cleaned according to standardized protocol is a risk factor for CDI.

Setting: the Baruch-Padeh Medical Center in northern Israel, a 350-bed hospital with a relatively-high rates of acquired CDI (40-45/100,000 cases/patient-days during 2017-2018).

Materials/methods: A retrospective case-control study comparing patients with CDI to a matched control group (age, sex and ward of hospitalization) without CDI during 2017-2018. Clinical and demographic data were collected from electronic medical records, including data on known risk factors, patient-room-placement, and movements during hospitalization. For every participant we determined whether there has been an r-CDI exposure at different timeframes (1, 3, 6 and 12 months previously).

Results: Study population included 75 CDI patients and 75 control patients. The groups had similar performance status and Charlson's comorbidity index. Length of stay prior to inclusion was similar in both groups, but was on average 2.7 days longer after inclusion in patients with CDI. Thirty-day mortality was higher in patients with CDI (36% *versus* 16%). In multivariate analysis: the presence of a nasogastric tube, use of 3rd generation cephalosporins and macrolides were independently associated with CDI. Previous exposure to r-CDI was significantly higher in the CDI group through all timeframes examined, the difference was significant if exposure occurred 3, 6 and 12 months previously (p= 0.032, 0.006, and 0.011, respectively); the association was maintained after adjustment for other risk factors (p= 0.014, 0.006, and 0.011, respectively).

Conclusions: Hospitalization in a room previously occupied by a patient with CDI is a significant risk factor for CDI up to 12 months after exposure. This work may assist in planning interventions for reduction of CDI healthcare acquisitions, such as environmental cleaning, antibiotic stewardship and cohorting CDI patients when necessary. Typing of CD isolates is of paramount importance and is currently underway.

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Abstract 936

Risk factors and clinical characteristics of virus Infection after haematopoietic stem cell transplantation

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Background: BK polyomavirus is an important cause of morbidity and mortality in hematological patients after hematopoietic stem cell transplantation (HSCT). It is acquired in childhood and especially becomes latent in urothelial epithelial cells. Reactivation of virus after HSCT can be seen with asymptomatic viruria or hemorrhagic cystitis (HC). The aim of the study was to assess risk factors, clinical characteristics and treatment options of BK virus infection after HSCT.

Materials/methods: We retrospectively analyzed information about patients with HSCT and BK virus (BKV) disease between January 2017-August 2019. Data included; underlying hematological disease, transplantation type, associated graft versus host disease (GVHD) and recent use of immunosuppressive agent.

Results: In total fifty-eight patients with HSCT were evaluated and BKV disease occurred in 20 (34%). The median age was 40 (range, 20 to 68), 50% were male. The most underlying disease was Acute Myeloid Leukemia (n=11). Five patients had autologous and fifteen patients had allogeneic SCT. The median time to engraftment was 15 days (range, 10 to 20). GVHD was seen eleven patients (40% skin, 15% gastrointestinal GVHD). These patients received systemic glucocorticoid therapy or immunosuppressant agents. The median time elapsed to BK virus disease after HSCT was 60 days (range, 30 to 450). Sixteen patients with BKV disease had high grade (grade 3) HC and four patients had low-grade HC (grade 2). While BK viremia was positive in 17 patients (68%), viruria was positive for all patients. Eight patients (15%) were treated with ciprofloxacin and cidofovir combination, six patients (30%) with cidofovir and three patients (15%) with ciprofloxacin. Three of them (20 patients) was treated by intravesical cidofovir. The complete response to the viruria or viremia was obtained from 11 patients (55%).

Conclusions: HC associated with BKV is an emerging clinical problem after HSCT causing prolonged hospitalization and mortality. It can be severe because the treatment options are often ineffective. The main goal of treatment is to reduce the dose of immunosuppressive agents. Close monitoring of BK virus in high-risk patients can be an important method to improve the complication in the early period.

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Abstract 937

The optimal strategy of empirical antibiotic therapies for non-severe community-acquired pneumonia: a bayesian network meta-analysis of randomised controlled trials

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Background: The 2019 the American Thoracic Society and Infectious Diseases Society of America guideline described that β-lactam (BL) monotherapy should not be routinely used for inpatients with community-acquired pneumonia (CAP) over fluoroquinolone (FQ) monotherapy or β-lactam/macrolide (BL-ML) combination therapy. However, the controversy about empirical antibiotic therapies is still unresolved. We conducted a systematic review and network meta-analysis to assess comparative efficacy of empirical antibiotic treatment strategies for nonesevere CAP.

Materials/methods: A systematic search for randomized controlled trials (RCTs) was performed through MEDLINE, EMBASE, and the Cochrane Central Register. We classified patients into FQ, BL-ML, and BL groups. The clinical success rate at the end to study was the primary outcome of interest. A Bayesian network meta-analysis was conducted and treatments were ranked based on their effectiveness.

Results: Twenty-three articles were included in the qualitative and quantitative synthesis using pairwise and network meta-analyses. Forest plots from network meta-analyses showed that the clinical success rates of FQ monotherapy were higher than BL monotherapy (OR 1.23; 95% CI 1.04–1.48). The difference in the clinical success rates for FQ monotherapy versus BL-ML combination therapy was not statistically significant (OR 1.19; 95% CI 0.88–1.68). And there was no difference in treatment success between BL monotherapy and BL-ML combination therapy (OR 1.03; 95% CI 0.73–1.43). On node-splitting analysis, inconsistency between direct and indirect comparison did not exist. In the rank-probability test, FQ monotherapy had the highest rank for the clinical success rate, followed by BL-ML combination therapy.

Conclusions: Current evidence showed that FQ monotherapy had better treatment outcomes than BL monotherapy for patients with nonsevere CAP. And the efficacy of FQ monotherapy was similar to BL-ML combination therapy. Our findings provide support for the current guidelines recommendations to propose empirical antibiotic treatment strategies for nonesevere CAP.

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Abstract 942

Accelerated HIV case finding and bridging the gap in antiretroviral therapy enrolment among prison inmates: a break-even in achieving the 95-95-95 UNAIDS targets among key populations in Western Nigeria

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Background: The clock is steadily ticking towards 2020 when the UNAIDS 95-95-95 global target in the fight against HIV/AIDS is hoped to be achieved. The hypothesis tested is the significant association between youthful age and HIV test outcome. The aim of the study was to engage in an accelerated HIV case finding and ensure enrolment into care among key populations in Western Nigeria fulfilling the first & second 90 of the UNAIDS targets.

Materials/methods: Lay Adhoc Staff/volunteers were purposely selected and trained. Consenting prison inmates had their blood samples taken and tested following the country's HIV serology National testing algorithm, using the recommended HIV testing kits. Those who tested positive went through a retesting process in the laboratory and confirmed positive. Post-test counselling was then conducted.

Results: A total of 771 prison inmates were tested across the four prisons (Male 765, Female 6) with a mean age ± SD is 31.25 ± 9.47 years. Ten of them (Male 9, Female 1) were confirmed new positives with a mean age ± SD is 31.40 ± 6.24 years, yielding a positivity rate of 1.3%. Eight of the ten positives are in their youthful age (<35 years). Odd's ratio shows that youthful age have higher association with HIV test outcome (OR: 2.81, CI: 0.80 – 9.79). The linkage rate for the positives is 100% with good escort service while adherence is ≥ 95%. The patients after six months on tenofovir, lamivudine & dolutegravir achieved viral supression.

Conclusions: This mode of HIV testing service (HTS) has proved to reach a key population yielding more positives in much fewer numbers of people tested and in a short period of time with 100% linkage with better resource/health financing outlook. Community ART Differentiated Service Delivery (DSD) Model is in line for the patients to sustain the gains in the effort to achieve the 95-95-95 fast track UNAIDS targets.

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Abstract 943

HIV-related stigma and discrimination in Western Nigeria: experiences of people living with HIV and rights issues

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Background: HIV-related stigma and discrimination continue to be major social determinants driving the epidemic of HIV globally despite the advances in medical treatment and increases in the awareness. Hypotheses tested was right awareness of people living with HIV/AIDS influencing HIV-related stigma & discrimination. The study aimed at assessing the level of HIV/AIDS related stigma and discrimination, forms, effects, and internal stigma experienced by PLHIVs in South-Western Nigeria.

Materials/methods: This cross sectional study was carried out at eight PEPFAR supported primary, secondary and tertiary level hospitals in South-Western Nigeria. The target population was adult (18 years and above) male and female persons living with HIV (PLHIVs) including key population. Data was collected from 278 consenting respondents by trained volunteers by a face-to-face interview.

Results: The mean age ± SD of the respondents was 38.48 ± 11.48 years, 70.05% females, mostly married in a monogamous setting (48.6%), with a formal education (86.3%), traders (33.5%), live in rural area (88.5%) while people in the key populations accounted for 9.4% of the participants. 78.4% elicited negative feelings such as depression and shame after diagnosis. About one-third (33.1%) PLHIVs have ever experienced HIV-related stigma and discrimination mostly gossip, physical abuse, and verbal insult, of which about two-third (63.2%) occurred in the hospital setting, followed by home/community (25.0%). In addition, 8.6% have been refused a job while 5.0% have lost their job because of their HIV status. Rights awareness by PLHIVs does not rule out HIV-related stigma & discrimination experience ($\chi^2 = 5.29$, df = 1, P = 0.021).

Conclusions: A remarkable proportion of PLHIV still face stigma/discrimination with possible dramatic impact on their treatment and resultant quality of life. Efforts therefore, should be made to ensure PLHIV are not only aware of their rights, but are empowered to seek redress if these rights are violated.

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Abstract 947

Should a molecular bacterial syndromic approach totally replace culture for the diagnosis of gastrointestinal tract infections ?

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Background: Molecular panels are rapid and sensitive tools for the syndromic diagnosis of gastrointestinal (GI) infections. Whether they should totally replace traditional approaches or be combined to non-molecular approaches (enrichment step, culture for species/serotype identification/epidemiological investigations, antimicrobial susceptibility testing (AST)) remains questioned. We retrospectively evaluated the routine use of Seegene Allplex GI panel I (7 bacterial targets) in the Nîmes University Hospital, France, during the first 8 months of implementation.

Materials/methods: At laboratory receipt, diarrhoeal faeces from patients not hospitalized for more than 3 days were inoculated into a Selenite broth (subculture on Hektoën medium) and transferred to a FecalSwab seeded on selective medium upon positive PCR result availability. PCR was performed 3 times a week. We comparatively analyzed PCR and culture results, with a focus on the utility on maintaining a subculture after enrichment and on the rate of strain recovery.

Results: 119 PCR were positive (16%) (5 with >1 pathogen), *Campylobacter* spp. being the most frequently detected pathogens (47%, one third more than before PCR). Strains have been isolated in 82 cases of positive PCR (66%, 52 to 94% according to the pathogen, cycle threshold (Ct): 21 to 44, time to FecalSwab seeding: 1-3 days). In 5 cases, *Salmonella* were detected by culture only, discrepant results being reproducible in 3 cases (14% of *Salmonella* infection diagnoses). One *Plesiomonas shigelloides* (out of PCR panel) was cultured. *tcdB* gene was detected in 22 patients over 3 years, of whom 3 had not been diagnosed for *Clostridioides difficile* infection.

Conclusions: We confirmed the utility of syndromic approaches in increasing the diagnosis yield of GI infections. Detection of toxin B-encoding gene was also helpful when *C. difficile* infection was not suspected. The incomplete pathogen recovery from FecalSwab was independent of Ct value and time before seeding in our study, and impaired AST and epidemiological investigations. An adequate load of the FecalSwab, hardly standardizable even in case of inoculation in the lab, is confirmed as an important parameter of pathogen detection. Maintaining a culture medium appears necessary for a larger *Salmonella* recovery and the detection of pathogens not included in the molecular panel.

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Abstract 948

The influence of delivery mode in the oral mycobiome: from childhood to adulthood

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Background: Postnatal acquisition of microorganisms from maternal and environmental sources contributes to the microbiome development of the child, and can potentially influence the future adult microbiome maturation. The mode of delivery may impact oral bacterial colonization as it is observed in several studies; however, the influence of this early life event on oral fungal colonization is still poorly investigated. Therefore, our aims were to perform: 1) a systematic review on the impact of the delivery mode on oral fungi transmission in early age and 2) a cross-sectional study regarding the association between this early life event in oral yeast colonization in young adults.

Materials/methods: A PubMed search was performed from April 25 to June 18, 2019, with inclusion criteria being comparative studies in humans that investigated oral fungi transmission and colonization in relation with the delivery mode. Colonization by yeasts in the oral cavity was evaluated in unstimulated saliva in 185 healthy young adults and correlated with delivery mode. Yeast isolation and identification was performed using Sabouraud Agar medium supplemented with chloramphenicol, followed by ChromAgar Candida and 18S/ITS gene sequencing.

Results: From the 4256 articles retrieved, only 8 articles were included in this review. There was more evidence towards the impact of the delivery mode on the fungal acquisition than against: the majority of the studies (N=6) found a relation between fungal colonization and vaginal delivery and, in 2 of these studies the existence of vertical fungal transmission from mother to child was reported. *Candida albicans* was the most commonly isolated fungal species, followed by *Candida parapsilosis.* Non-cultivable methods of fungal identification were only applied in one of the selected studies. Regarding the cross-sectional study, *Candida* species were isolated from 37.5% of the participants, *Candida albicans* being the most prevalent species. The prevalence of oral yeasts was significantly higher in those who were vaginally delivered compared to those born by caesarean-section.

Conclusions: Together, our results suggest that vaginal delivery appears to promote oral yeast colonization and carriage throughout life, from childhood to adulthood. More longitudinal studies using molecular methods are needed to fulfil the lack of knowledge within this field.

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Abstract 951

Computerised Tomography (CT) as a risk factor for the acquisition of carbapenem-resistant *Acinetobacter baumannii*

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Background: Multiple inanimate objects have been implicated in the transmission of resistant bacteria in the hospital. We examined whether performance of a CT scan increased the risk for colonization.

Materials/methods: All patients undergoing CT and all patients colonized or infected with carbapenem-resistant *Acinetobacter baumanii* (CRAB) were identified for 5 years from 2014-2019. Active admission and weekly surveillance was carried out for this bacterium. Each CT visit was classified as either an "Index Case" (presence of resistant bacteria prior to CT visit), an "Acquisition case" (appearance of resistant bacteria within 14 days of CT in a patient without prior colonization/infection), or a "Null case" (uncolonized/uninfected throughout). The risk of colonization/infection was calculated for patients undergoing CT for the first hour, each subsequent 6 hour period, and for days 2 – 7 after an index case. The results were normalized per 1000 CT scans [Number of acquisitions/number of patients undergoing CT during the relevant period normalized to 1000 scans].

Results: CT was performed for 115,680 patients during the study period. There were 324 Index cases and 254 Acquisition cases. The normalized risk of CRAB acquisition for the first 7 days is shown in the table. The odds ratio for acquisition during the first hour after a previous CRAB patient compared to 1 to <6 hours thereafter was 2.4 (95%CI 1.3 – 4.3, p=0.003).

Time period	<1 hr	1 to <6 hrs	6 to <12 hrs	12 to <24 hrs	>1 to <7 days
No of Scans	1685	5510	4616	7082	50428
CRAB acquisitions	19	26	14	19	122
Normalized risk of acquisition	11.3 (95%CI 7 - 18)	4.7 (95%CI 3 - 7)	3.0 (95%CI 2 - 5)	2.7 (95%CI 2 – 4)	2.4 (95%CI 2 - 3)

Conclusions: Acquisition of CRAB following CT scan is more frequent during the first hour after a previous patient with this bacterium had been examined. This probably reflects inadequate environmental cleaning.

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Abstract 954

Individualised autovaccination is a promising strategy for managing recurrent urinary tract infections in women

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Background: more than 20% of patients with urinary tract infection are at risk of recurrence. rUTI are a pervasive condition that negatively impacts patients Quality of Life (QoL). Causes of recurrence are multifactorial and include non-modifiable risk factors (nmRF). Antibiotic prophylaxis is broadly used to treat rUTI. However, its use is not devoid of adverse effects and can lead to resistance. Efficacy of mono/polyvalent inactivated bacteria has only been demonstrated in selected patient cohorts. Here, we show preliminary results of an ongoing prospective study aimed at evaluating the efficacy of an individualized autovaccine for outpatient management of rUTI in real-life conditions.

Materials/methods: women with uncomplicated rUTI were offered participation in a prospective study involving daily administration of a sublingual autovaccine (Uromune®) during 3 months. Individualized vaccines were generated for each patient by isolating inactivated bacteria from their urine culture (UC) samples. Demographic variables and rUTI nmRF were recorded. UC results, number of relapses and QoL using two questionnaires (daily activities: QoLQAct; emotions: QoLQEm) were evaluated as outcomes.

Results: the first 18 patients that have finished treatment were evaluated. Age mean±SD was 72.3±7.2 years. Mean±SD nmRF was 5.1±1.6, mainly menopause 18(100%), urogenital surgery 16(88.9%), urinary incontinence 13(72.2%), and diabetes mellitus 9(50%). Autovaccines were mostly generated from *E. coli* [12(66.7%)] and *K. pneumoniae* [3(16.7%)] strains. UC negativity was reached in 61.1% of patients and 82.4% showed a decrease in number of relapses (mean number pre-post 2.9 vs. 1.1, p<0.01). Similarly, QoL parameters improved in 76.5% of patients in QoLQAct (mean score pre-post 3.7 vs 1.5, p=0.02) and 70.5% in QoLQEm (mean score pre-post 11.5 vs 6.5, p=0.01). Improvements were observed regardless of bacteria strain.

Conclusions: This is, to our knowledge, the first prospective study evaluating autovaccination for the management of rUTI. We observed promising rates of UC negativization, decrease in rUTI episodes and improvement QoL parameters in non-selected women. Our results suggest that Uromune® autovaccine may be a valid strategy for reducing antibiotic consumption and for improving QoL in women with rUTI.

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Abstract 957

Results of a schistosomiasis screening programme in an immigrant population

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Background: Schistosomiasis is one of the most prevalent tropical diseases in the world. If the infection progresses without treatment, it can produce long-term complications like liver cirrhosis and bladder tumors among others. The results of a schistosomiasis screening program in the sub-Saharan immigrant population are described.

Materials/methods: A prospective screening program of schistosomiasis in all sub-Saharan patients attending in a Tropical Medicine Unit, in Asturias, Spain was performed between January 2009 and December 2017. Three formalin-ether concentrated stool samples and an enzyme-linked immunosorbent assay for serum anti-*Schistosoma spp* antibodies were used as screening. If urinalysis showed hematuria, we perform three urine analysis for Schistosoma haematobium. We considered infection to be established if the microscopic visualization and / or the ELISA were positive

Results: We analyzed 481 patients (52% women; average age 34 years; mean age in Spain 1,043 days). The most frequent areas of origin were Central Africa (51.7%), West Africa (45.3%), and East Africa (2.9%). Fifty-nine patients (12.3%) had a positive serology for Schistosomiasis (59.3% were male; mean age of 29 years, mean time in Spain:641 days). Five patients had a *S. intercalatum* in stool and three had *S. haematobium* in urine. Most of them come from Central (45.8%) and West Africa (52.5%), although without significant differences. There is not significantly differences in sex, age or length of stay in Spain, although 62.7% of infections were significantly detected in patients who had been less than 1 year in Spain (37/22 versus 202/220 p = 0.023 OR 1.832 [1.045-3.210]. Twenty-one (35.6%) patients were asymptomatic in the rest the most frequent symptoms were hematuria (10 patients) and abdominal pain (5 patients) and diarrhea (5 patients). One patient with *S. intercalatum* infection has bloody stools. Twenty-two patients showed eosinophilia in blood

Conclusions: In our series, schistosomiasis was detected in 12.3% of our patients, most of them diagnosed by serology. It appeared more frequently in male patients from Central and West Africa who had been less than one year of residence in Spain, although without significant differences. A third of them were asymptomatic

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Abstract 959

An ultrasensitive rapid single molecule counting method detects Bacillus anthracis lethal factor directly in blood samples

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Background: Following a bioterrorism attack or infectious disease outbreak, large numbers of people will require a rapid diagnosis to ensure delivery of life-saving therapeutic treatment. We present data for a highly sensitive anthrax test that runs on a benchtop platform that can be deployed in hospitals, clinics, or physician office laboratories. The new anthrax test detects Lethal Factor (LF), the earliest detectable biomarker for *Bacillus anthracis* infection, from a fingerstick blood sample in 20 minutes. Sensitively detecting LF, which appears in the blood before PCR tests can detect the pathogen, offers the possibility of identifying infected victims early increasing the chances for successful treatment.

Materials/methods: The test uses non-magnified digital imaging to count target-specific magnetic and fluorescent particles that have been tethered together by single LF molecules. A novel dye-cushion eliminates the need for sample preparation. A blood sample (70 µL), either fingerstick or venous, is added directly to the disposable cartridge, minimizing sample handling. Once loaded onto the analyzer, the test proceeds automatically and generates a result in aproximately 20 minutes. Contrived clinical samples prepared with blood drawn by venipuncture or fingerstick were used to estimate the limit of detection (LoD), precision, and dynamic range.

Results: The LoD of the Anthrax Toxin Test, determined using whole blood samples spiked with pure LF protein, is 61 pg/mL (Figure 1). The dynamic range of the test covers 5 logs of LF concentration, an important performance metric given the broad range of LF concentrations observed over the course of anthrax infection. In a simulated clinical study, whole blood collected by fingerstick from 40 healthy individuls was tested either spiked with 150 pg/mL purified LF or unspiked. In this study, the test demonstrated 100% sensitivity and 100% specificity.

Conclusions: The performance data demonstrate that the new anthrax test is highly sensitive, rapid, and specific for the detection of *B. Anthracis* LF in whole blood. Valuable features for crisis surge testing include minimum sample handling, a 20 minute test turnaround, and the benchtop analyzer's throughput.

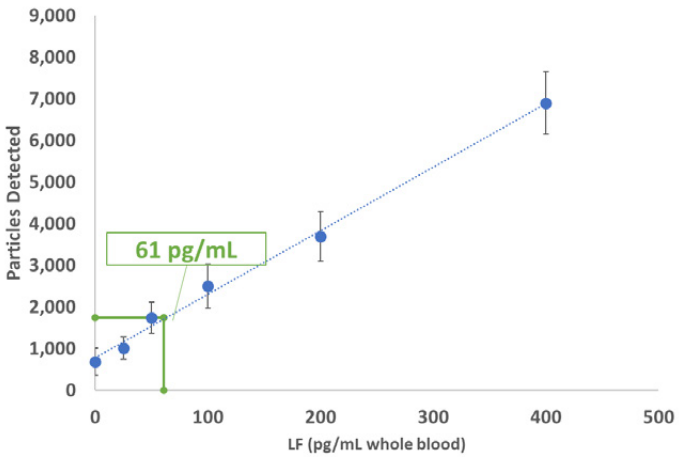

Figure 1. Analytical sensitivity of the LF test.

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Abstract 961

Multi-centre evaluation of the BIOFIRE FILMARRAY BCID 2 Panel for the detection of microorganisms and resistance markers in positive blood cultures

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Background: The BioFire® FilmArray® Blood Culture Identification 2 (BCID2) Panel is a rapid diagnostic test that provides results for 26 bacterial analytes, seven fungal analytes, and ten antimicrobial resistance (AMR) genes from positive blood culture (PBC) specimens in about an hour. The BCID2 Panel builds upon the existing BCID Panel with several additional assays that include *Bacteroides fragilis, Candida auris,* and additional AMR genes (CTX-M, IMP, *mcr-1*, *mecA/C* and MREJ, NDM, OXA-48-like, and VIM). Here, we summarize studies conducted to establish clinical performance using an Investigational Use Only version of the BCID2 Panel.

Materials/methods: A total of 1074 residual PBCs were enrolled at 7 US and 2 EU sites between October 2018 and May 2019. BCID2 Panel performance was compared to routine standard of care microbial culture, as well as molecular methods for AMR genes. In addition, BCID2 Panel MRSA results were compared to the FDA-cleared Xpert® MRSA/SA BC test (Cepheid, Inc).

Results: The BCID2 Panel identified at least one organism in 90.9% of enrolled PBCs. Among the 12.8% of positive specimens with multiple organism detections by the BCID2 Panel, combinations of gram-positive (GP) bacteria mixed with gram-negative (GN) bacteria, GP with yeast, GN with yeast, and combinations of all three were observed. The BCID2 Panel demonstrated an overall sensitivity of 99.2% and specificity of 99.6% for the identification of microorganisms compared to culture. Concordance between the BCID2 Panel and the Xpert MRSA/SA BC test for the identification of MRSA was 91.2% positive percent agreement (PPA) and 97.9% negative percent agreement (NPA); however, 100% concordance was observed when compared to phenotypic MRSA characterization by the laboratory. The overall PPA and NPA for the remainder of the BCID2 Panel AMR genes as compared to molecular methods was 98.9% and 99.9%, respectively. The overall success rate of obtaining valid results in initial specimen tests was 99.7%.

Conclusions: The new BCID2 Panel is a sensitive, specific, and robust test for rapid detection of microorganisms (including mixed polymicrobial samples) and a variety of AMR genes in PBCs.

Data presented are from assays that have not been cleared or approved for diagnostic use.

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Abstract 965

Shortened antibiotic treatments for Gram-negative bacteraemia in cancer patients: less is possible

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Background: There are no studies published evaluating 7-day treatment for Gram-negative bacilli (GNB) bacteraemia exclusively in cancer patients and neutropenia.

Materials/methods: Prospective observational study performed from May 2014 to August 2019. Adult cancer patients with GNB bacteraemia were included, with the following criteria: having received appropriate empirical antibiotic treatment (EAT), complete clinical response within 7 days with source control and having survived 48 hours after completion of treatment. According to the duration of the antibiotic treatment they were divided into: short, median 7 days (ST) or long, median 14 days (LT). A 30-day follow-up was performed to assess mortality and recurrence of bacteraemia. Categorical variables were analyzed by the Fisher exact test or the Chi-square test and continuous variables were analyzed by the U Mann-Whitney test.

Results: 74 patients were included (ST: 36 and LT: 38). No differences were observed in baseline characteristics between ST and LT respectively: age 57 years (47-68) vs 60 years (47-66) (p=0.70); hematologic malignancy 52.8% vs. 44.7% (p=0.48); chemotherapy: 97.2% vs 89.5% (p=0.18); neutropenia 58.3% vs 60.5% (p=0.84); Charlson score 2 (2-4) vs 2 (2-3) (p=0.69); Pitt score 1 (0-2) vs 1 (0-2) (p=0.22). ST patients had a higher APACHE II score: 21 (19-23) vs 17 (14-20) (p<0.0001). There were no differences in clinical presentation and microbiological characteristics between ST and LT respectively: bacteraemia with clinical source 72.2% vs. 76.3% (p= 0.68); hypotension 27.8% vs. 34.2% (p=0.55), *E. coli* 52.9% vs. 31.6% (p=0.065); *Klebsiella* spp. 27.8% vs. 39.5% (p=0.28); Multidrug-resistant GNB 27.8% vs. 21.1% (p=0.50). Treatment, outcome and recurrence between ST and LT were respectively: combined EAT 38.5% vs 44.7% (p=0.61); prolonged infusion 36.1% vs. 10.5% (p=0.012); ceftazidime-avibactam treatment: 22.2% vs 0 (p=0.002); overall mortality 2.8% vs. 7.9% (p=0.61); recurrence 2.8% vs. 0 (p=0.30). The length of hospitalization in days since bacteraemia and *Clostridiodes difficile* colitis between ST and LT were respectively: 7 (6-15) vs. 12 (7-19) (p=0.021) and 0 vs 8.9% (p=0.08).

Conclusions: In patients with cancer and GNB bacteraemia who receive appropriate EAT, with complete clinical response, 7-day duration may be adequate. They could also benefit from a shorter hospitalization.

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Abstract 966

Ceftazidime-avibactam for the treatment of carbapenemase-producing *Enterobacteriaceae* bacteraemia in oncohaematological patients: calm after the storm

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Abstract third-party references: On behalf of Argentinean Bacteraemia in Cancer and Hematopoietic Stem Cell Transplant Study Group

Background: There are no studies published demonstrating that treatment with ceftazidime-avibactam (CA) for carbapenemase-producing Enterobateriaceae bacteraemia (CPEB) improves survival in patients with hematologic malignancies and neutropenia.

Materials/methods: Prospective observational study performed from May 2014 to August 2019. Adult patients with hematologic malignancies or hematopoietic stem cell transplantation and KPC or OXA48-CPEB were included from 12 centers of Argentina. We compared patients who received definitive treatment with CA with patients treated with other antibiotics (OA). The 30-day mortality was examined by the Kaplan-Meier method with the log-rank test, and the Cox regression model was used to test statistical significance.

Results: 110 patients were included (CA: 22 and OA: 88). No differences were observed in baseline characteristics between CA and OA respectively: age 47 years (37-60) vs 50 years (39-64) (p=0.53); acute leukemia 68.2% vs. 59.1% (p=0.43); neutropenia 81.8% vs 84.1% (p=0.79); high risk by MASCC score: 100% vs 94.6% (p=0.31); neutropenia duration > 10 days: 81.8% vs 84.1% (p=0.79); Charlson score 2 (2-2) vs 2 (2-3) (p=0.27); Pitt score 0 (0-1) vs 1 (0-2) (p=0.11); APACHE II score: 13 (11-20) vs 12 (8-17) (p=0.092). There were no differences in clinical presentation and microbiological characteristics between CA and OA respectively: bacteremia with a clinical source: 68.2% vs. 62.5% (p=0.62); hypotension: 22.7% vs. 36.4% (p=0.31); KPC-CPEB: 95.5% vs 92% (p= 0.58); *Klebsiella* spp.: 90.9% vs. 90.9% (p=1); colistin-resistance: 27.3% vs. 31.8% (p=0.68); Meropenem MIC ≥ 16: 68.2% vs 69.9% (p=0.88). Treatment and outcome between CA and OA were respectively: appropriate empirical treatment: 81.8% (64% received CA) vs 52.3% (p=0.015); combined definitive treatment: 63.6% vs 92% (p=0.001); 7-day clinical response: 86.4% vs 52.3% (p=0.004); ICU admission: 18.2% vs 43.3% (p=0.048); 30-day mortality 18.2% vs. 50% (p=0.008). In the multivariate analysis the factors significantly associated with mortality were: Pitt score: OR 1.3, 95% CI, 1.1-1.45 (p=0.0001) and breakthrough CPEB: OR 2.1, 95% CI, 1.2-3.8 (p=0.011), while definitive treatment with CA was a protector factor for survival: OR 0.34, 95% CI, 0.12-0.9 (p=0.049).

Conclusions: Oncohematological patients with CPEB receiving definitive treatment with CA had clinical and survival benefit over OA treatments.

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Abstract 969

The dominant model analysis of Sirt3 genetic variants is associated with susceptibility to tuberculosis in a Chinese Han population

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Background: Tuberculosis (TB) is a complex infectious disease caused by the pathogen *Mycobacterium tuberculosis* (Mtb) which has coexisted with humanity since the Neolithic. Recent research indicated that SIRT3 plays a pivotal role in promoting the antimycobacterial response of mitochondria and autophagy during Mtb infection.

Materials/methods: A case-control study comprised 900 TB patients and 1534 heathy controls were retrospectively enrolled to assess the association between *Sirt3* gene polymorphisms and TB susceptibility. In total of five single-nucleotide polymorphisms (SNPs) (rs511744, rs3782118, rs7104764, rs536715, and rs28365927) which were selected through database 1000 Genomes Project and offline software Haploview V4.2, and genotyped by a customized 2×48-Plex SNPscanTM Kit.

Results: Our results suggested that the minor allele genotypes (A carriers) of rs3782118 confers the decreased risk of TB susceptibility (p Bonferroni = 0.032), and a similar but more significant effect was observed under the dominant model analysis (OR = 0.787, 95% CI = 0.666-0.931, $p_{Bonferroni}$ = 0.026). Haplotypes analysis showed that haplotype AGAAG (rs511744 / rs3782118 / rs7104764 / rs536715 / rs28365927) was associated with an increased risk of TB (p = 0.023, OR = 1.159, 95% CI = 1.019-1.317). In stratification analysis, we found that rs3782118 was associated with decreased risk of TB in female subgroup under the dominant model analysis ($p_{Bonferroni}$ = 0.016, OR = 0.678, 95% CI = 0.523-0.878). Moreover, functional annotations for three loci (rs7930823, rs3782116, and rs3782115) which are strongly linked to rs3782118 indicated that they may be responsible for the changes in some motifs.

Conclusions: Our study suggested that the SNP rs3782118 was associated with a lower susceptibility to TB, especially under the dominant model analysis, and that the haplotype AGAAG (contains the major allele G of rs3782118) was associated with an increased risk of TB. Further independent cohort studies are necessary to validate the protective effect of *Sirt3* genetic variants on the risk of TB.

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Abstract 970

Measles: clinical manifestations and complications during an outbreak in Bulgaria in 2019

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Background: *Measles* is causes by one of the most pathogenic viruses known to man. Almost every infections is manifested clinically and frequently leads to serious complications. The aim of the present study is to review the clinical presentation of measles during an outbreak in 2019.

Materials/methods: Between February and August 2019 in our Institution, a total of 341 cases of *measles* were hospitalized and verified through IgM antibodies and/or through molecular confirmation for the presence of the virus.

Results: 172 are male, 169 are female. In regards to the immunization status, 82 are under the age of immunization - 13 months. From the remaining patients, 106 have unknown status, 119 have not been immunized, 32 have received 1 dose of *measles* vaccine and 2 have received 2 doses.

In regards to the initial infection, in 77 cases this occurred through contact with a family member and in 49 cases-during a prior hospitalization.

Clinical manifestations and complications:

	<13 m. (n=82)	1-3 y. (n=67)	4-11 y. (n=140)	12-56 (n=52)	Total (n=341)
Rash	79	66	139	51	335
Conjuctivitis	72	58	124	41	295
Febrility	70	46	82	42	240
Koplik's spots	55	46	95	36	232
Diarrhea	54	48	90	27	219
Coryza	50	39	80	22	191
Vomitting	22	21	68	20	131
Bronchitis	15	17	49	23	104
Pneumonia	12	5	14	4	35

Conclusions: *Measles* affects primarily individuals who have not been immunized (90.02%), which leads to the necesity for implementation of further practices, aiming at increasing the procetantage of immunized individuals in Bulgaria. A significant number of Hospital-acquired infections (14.31%) were noted. This requires further evaluation of the methods for infection control in regards to highly contagious diseases.

Our data shows that generally clinical manifestations during the outbreak in Bulgaria correspond to those, described in literature. In regards to complications, bronchitis is more frequently noted in older patients (12-56 y. 44%), while pneumonia is more frequently seen in younger patients (<13 m. 14.0%).

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Abstract 971

Increasing influenza vaccination rates among healthcare workers and residents of long term care facilities for the elderly in Graz, Austria

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Background: Although annual vaccination against influenza is recommended in Austria for those over 50 years of age, all patients with chronic health conditions and health care workers (HCW) vaccination rates in Austria are as low as 20% according to OECD data. The aims of our study were (1) to evaluate the vaccination rate of residents and HCWs in long term care facilities (LTCF) in the season 2017/2018, (2) to explore motivations against vaccination, (3) to increase vaccination rates in the season 2018/2019 by a multi-modal intervention bundle.

Materials/methods: In January 2018, the rates of influenza vaccination of residents and HCWs of 4 LTCFs (Geriatric Health Centres Graz, Austria) were determined. Residents and HCWs were asked to respond to a survey anonymously asking for their motivation not to get vaccinated. In autumn 2018 an intervention bundle was conducted including: personal letters to all HCWs and residents, posters presenting peers in favour of vaccinations on display, meetings between local experts and residents, training sessions of influenza prevention for HCWs. Vaccination for HCWs was offered free of charge. Vaccination rates were again determined in January 2019.

Results: In the season 2017/2018, the vaccination rates were 6% (22/377) in residents and 1% (3/234) in HCWs. Following the interventions, there was a statistically significant increase in vaccination rates to 19% and 20% in residents and HCWs respectively ($p < 0.001$). 37% (141/377) of residents and 29% (67/ 234) of HCWs responded to the survey (table 1). 32% of HCWs questioned effectiveness of influenza vaccination.

Conclusions: A multi-modal intervention bundle was successful in significantly increasing influenza vaccination rates but vaccination rates were still low. The study revealed strong skepticism about the effectiveness of influenza vaccinations and vaccinations in general among HCWs.

Table 1: Reasons against influenza vaccination in HCWs and residents of 4 LTCFs in the season 2017/2018

	HCWs	Residents
Skeptical if influenza vaccination is effective.	32%	16%
Skeptical if vaccinations in general are effective.	15%	12%
Experienced side effects after previous vaccinations.	15%	8%
I did not get around to get vaccinated	8%	24%
I am scared of needles.	3%	3%
Other reasons	11%	38%

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Abstract 972

Radiologic features of Pneumocystis pneumonia differ between patients with and without HIV Infection

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Background: *Pneumocystis* pneumonia (PCP) is the leading opportunistic infection in patients with acquired immune deficiency syndrome in Taiwan. However, patients with hematologic diseases and under immunosuppressant use are also at a higher risk for PCP. Radiologic findings on chest computed tomography (CT) scan can be used to aid the diagnosis especially when invasive procedures to obtain tissue for the histopathologic diagnosis is often difficult in critically-ill patients. The aim of the study is to compare the differences in the radiologic features in PCP between patients with and without HIV infection.

Materials/methods: We retrospectively reviewed the chest CT findings in 101 patients diagnosed with *Pneumocystis* pneumonia with or without HIV infection from January 2014 to August 2019. Each image was reviewed by a radiologist and a chest medicine specialist and findings were recorded as diffuse consolidation, ground glass opacity, intralobular/interlobular lines, crazy-paving pattern, pulmonary cysts, pneumothorax, tree-in-bud pattern, pulmonary nodules, pleural effusion, intrathoracic adenopathy, architectural distortion and/or traction bronchiectasis. The distribution were recorded as peripheral or central distribution.

Results: The mortality rate was 15.4% (6/39) in HIV-infected patients and 43.5% (27/62) in non-HIV-infected patients in the study. Diffuse consolidation (30.6% vs 12.8%, p=0.04), pleural effusion (43.5% vs 5.1%, p<0.001) and intrathoracic adenopathy (27.4% vs 10.3%, p=0.04) were more often seen in non-HIV-infected patients and HIV-infected patients presented more frequently with ground glass opacity (94.9% vs 67.7%, p=0.001) and peripheral distribution (48.7% vs 29.0%, p=0.05).

Conclusions: This study showed that HIV-infected patients and non-HIV-infected patients presented differently on chest CT image; non-HIV-infected patients tend to have atypical presentations such as diffuse consolidation, pleural effusion and intrathoracic adenopathy. HIV-infected patients more often presented with ground glass opacity and peripheral distribution.

Table 1 Chest CT features in patients with and without HIV infection

Variables, n (%)	All N=101	HIV N=39	Non-HIV N=62	P value
Diffuse consolidation	24 (23.8)	5 (12.8)	19 (30.6)	0.04
Ground glass opacity	79 (78.2)	37 (94.9)	42 (67.7)	0.001
Tree-in-bud pattern	10 (9.9)	6 (15.4)	4 (6.5)	0.14
Pleural effusion	29 (28.7)	2 (5.1)	27 (43.5)	<0.001
Intrathoracic adenopathy	21 (20.8)	4 (10.3)	17 (27.4)	0.04

HIV: human immunodeficiency virus

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Abstract 975

Invasive pulmonary aspergillosis after heart transplantation

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Background: Mold infections are an important cause of morbidity and mortality in the solid organ transplant population. Invasive pulmonary aspergillosis (IPA) are an infrequent but major complication of heart transplantation (HTx). We sought to describe the frequency and determine risk factors of this mold infection at our centre.

Materials/methods: From January 2010 to October 2019 it was performed 133 HTx (46±14 year-old; male – 97). Immunosuppressive therapy was guided by transplant center protocol: methylprednisolone, tacrolimus, mycophenolate mofetil/everolimus plus induction (basiliximab - 80% (n=107), anti-thymocyte globulin - 15% (n=20)). We retrospectively analyzed early and long-term post-heart transplant results.

Results: During the whole follow-up 52 episodes of pneumonia were diagnosed, 16 (31%) of them were IPA (54±7 year-old), most cases (91%) were probable. Aspergillus fumigatus was the most common species isolated. All recipients were treated with voriconazole (from 2 to 6 months) with positive clinical outcomes in 81% (n=13) of them. Three patients (n=2 – in 1 month after HTx) died which was associated with sepsis and right ventricular heart failure. Adjunctive therapies included reduction of immunosuppressive therapy and colonystimulating factors for neutropenic patients. Risk factors of IPA were found: prolonged duration in ICU (n=8), neutropenia (n=8) and high doses of immunosuppression, such as triple-drug therapy including steroids (n=14), treatment for 2R/3A rejection (n=3) and 1 month after the conversion to everolimus (n=1).

Conclusions: IPA occurred in 31% of all post-HTx pneumonias. The development of IPA was associated with a combination of risk factors. Timely diagnosis of IPA allows initiating antimycotic therapy with positive clinical outcomes.

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Abstract 979

Globally intravenous dosing of antibiotics in infants and children clusters around a small number of strategies but is not completely uniform

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Background: Little is known about consistency of antibiotic prescribing in children.

Materials/methods: We investigated variation in dosing in mg/kg/day in the 16 most common antibiotics (with at least 90 doses recorded) prescribed for intravenous treatment (not prophylaxis or decolonization) across four years of data from the Global Point Prevalence Survey.

Results: Data consisted of 3,572 doses from 2,627 children in 62 hospitals in 23 countries. Almost half (46%) of doses were from the WHO European Region, 31% the Americas, 12% South-East Asia, 6% Western Pacific Region and 5% African Region; none were from Eastern Mediterranean Region. The median age of children was 36 months (IQR: 9–96 months, Range: 1 month–17 years).

The three most common antibiotics were ceftriaxone (14% of doses), meropenem (12%) and vancomycin (11%). Approximately half of antibiotic doses (56%) were for community-acquired infections. The most common diagnoses were bacterial LRTI (24%), sepsis (18%) and Febrile neutropenia/Fever (13%); 16 other diagnoses comprised the remaining 45% of diagnoses but each represented less than 7% doses individually.

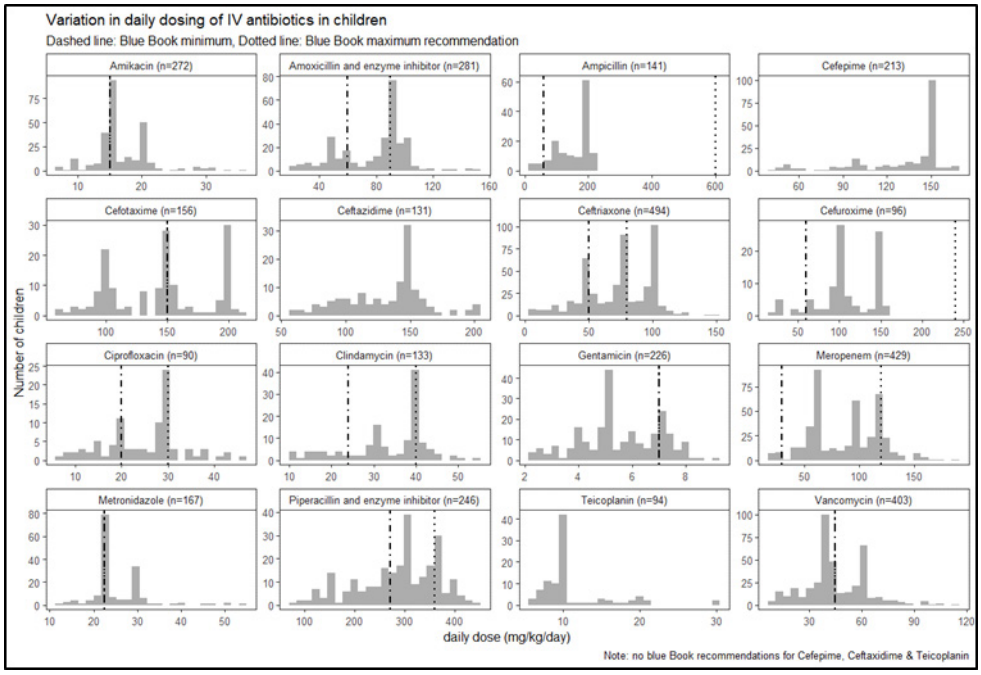

Figure 1: Daily dosing in 16 IV antibiotics in children. Vertical lines show minimum and maximum Blue Book recommendations.

The spread of dosing in mg/kg/day for each antibiotic ranged widely: from two-fold (ceftazidime) to more than 20-fold (ceftriaxone; figure 1). Dosing in mg/kg/day clustered around a small number of peaks, and all antibiotics had at least one dose used in at least 10% of children. Five antibiotics (amikacin, ampicillin, cefepime, metronidazole, teicoplanin) had a dose used in more than 40% of children, and most antibiotics showed up to three clear peaks in dosing strategy.

Conclusions: Dosing in IV antibiotics appears to cluster around a small number of strategies. Differences could reflect true differences in dosing strategy (e.g. reflecting different recommendations for meningitis) or equipoise towards dosing. Guidance and trials should aim to differentiate between commonly used doses and their relationship to clinical outcomes.

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Abstract 980

The Danish nationwide surveillance of azole-resistance in *Aspergillus fumigatus*: data from the first nine months

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Background: Azole resistant (azole-R) *Aspergillus fumigatus* has been increasingly reported worldwide and associated with human and environmental azole use. The environmental resistance mechanisms TR_{34}/L98H or TR_{46}/Y121F/T289A were first found in Denmark in 2007 and 2012, respectively. A nationwide surveillance was established in October-2018. We report results from the first 9-month's surveillance.

Materials/methods: Inclusion criteria were: a) isolates regarded clinically significant and b) isolates detected on a Monday to represent background prevalence. Isolates from same patients were defined as unique if found >30 days apart or with a different susceptibility pattern. The EUCAST E.Def 10.1 method using VIPcheck azole agar plates (Mediaproducts BV, Groningen NL) was used for screening, EUCAST E.Def 9.3.1 for susceptibility testing, and *cyp51A* sequencing for characterisation of target gene mutations. An isolate was deemed non-susceptible if intermediate or resistant according to EUCAST breakpoints v9.0.

Results: At the time of writing, susceptibility testing was performed for 703 *A. fumigatus* isolates from 508 patients. Fifty-three (7.5%) isolates were marked "Monday samples." Thirty-two patients harboured a non-susceptible *A. fumigatus* isolate (6.3%), incl. 29 resistant (5.7%). A target gene mutation was found in 27 isolates (all resistant), including 20 with tandem repeats from airway samples suggesting environmental origin (3.9% of all patients, 69% of resistant isolates, Table). Among the patients with non-susceptible isolates underlying diseases were: cystic fibrosis (CF, 15/32), other pulmonary disorders (12/32), solid organ transplantation and trauma (one each) and unknown (three patients). Nine out of 20 (45%) with a tandem repeat originated from CF patients. Among the Monday samples TR_{34}/L98H was detected in 3/51 (5.9%) at patient level. The TR_{34}/L98H isolates originated from all parts of Denmark except the north-Jutland, where it has previously been found. All isolates, except one, with other Cyp51A alterations originated from Zealand.

Conclusions: We report a nationwide azole non-susceptibility and resistance rate of 6.3% and 5.7%, respectively, in *A. fumigatus* at the patient level. The underlying resistance mechanisms were target gene mutations in all but two resistant cases and notably, the vast majority (69%) were of environmental origin. This implicates that the use of azole fungicides has an impact on human health.

Table. Susceptibility interpretation based on EUCAST breakpoints

Cyp51A Profile	n	Patient age range (years)	ITR	PRC	VRC	ISA	non-S	R	Geographic location
TR_{34}/L98H	19	0-70	1 I*, 18 R	19 R	2 I*, 17 R	19 R	19	19	RH, Funen, AUH, West-Jutland, Zealand
TR_{34}^{3}/L98H	1	22	1 R	1 R	1 R	1 R	1	1	RH
G54R	4	20-85	4 R	4 R	3 S, 1 R	1 S, 2 I, 1 R	4	4	RH, Funen, Zealand
M220K	1	58	1 R	1 R	1 I	1 R	1	1	RH
M220R	1	25	1 R	1 R	1 S	1 I	1	1	RH
G432S	1	68	1 R	1 R	1 R	1 R	1	1	Zealand
Wildtype	5	16-53	2 S, 2 I, 1 R	3 I, 2 R	1 S, 2 I, 2 R	2 I, 3 R	5	2	RH, AUH

*One isolate with an MIC 2 for itraconazole and voriconazole was contaminated with an isolate harbouring a *cyp51A wildtype*
RH: Rigshospitalet in Copenhagen, Zealand, AUH: Aarhus University Hospital, Central-Jutland.
R: Resistant
S: Susceptible
I: Intermediate
ITR: Itraconazole, PRC: posaconazole, VRC: voriconazole, ISA: Isavuconazole.

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Abstract 983

New raw materials for serology immunoassay quality controls

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Background: Reliable antibody-detection in patient samples requires high quality reference materials to determine cut-off values and test assay integrity. Immunoassay quality controls are mainly based on human disease state plasma which is a critical component for the development and manufacturing of diagnostic tests. However, for most indications, plasma sourcing is difficult (availability, expected features, time consuming).

ArkAb and SERION Immunologics collaborated to develop a range of substitutes to disease state plasma for immunoassay quality controls based on human chimeric monoclonal antibodies (mAbs). This study shows performance obtained for anti-*Toxoplasma gondii IgM* mAbs tested with several diagnostic kits.

Materials/methods: InEps™ transgenic mice expressing human/mouse chimeric IgM were immunized to obtain specific mAbs through classic hybridoma development technique (immunization, B Cells immortalization, IgM specific secreting hybridomas screening and stabilization, pre-industrial IgM mAb production).

First, after production using a standardized and controlled bioprocess, performance of two mAb clones was tested on different diagnostic kits from three various manufacturers. Anti-*Toxoplasma gondii* IgM were titrated in several dilution rates following manufacturer's instruction and results were compared.

Second, mAb IgM batches reproducibility was tested. In this regard, three independent batches from one clone were produced and tested on a VIDAS® Toxo IgM assay from bioMérieux.

Results:

mAb IgM candidate performance: Two clones of human chimeric monoclonal anti-*Toxoplasma gondii* IgM were titrated with different diagnostic kits. Results showed that the batches reacted in each assay until a pre-dilution of 1/16. Linearity was checked and the coefficient of determination was very good (R^2=0.99).

mAb IgM reproducibility: Three independent batches of one clone were produced and tested. The standard deviation was calculated and showed that batches have reproducible reactivity in the VIDAS® Toxo IgM assay from bioMérieux.

Conclusions: Human chimeric monoclonal anti-*Toxoplasma gondii* IgM products were tested and validated in various diagnostic assays. Results showed excellent performance and reproducibility obtained with this synthetic product. Human/mouse chimeric mAb can be easily and efficiently used as an alternative to disease state plasma for immunoassay quality controls.

A full range of products is available for infectious disease diagnostics and show equivalent performances.

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Abstract 984

Genomic and proteomic analysis of 42 bacteriophages located in the genomes of 17 clinical strains of *Klebsiella pneumoniae* resistant to carbapenems

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Abstract third-party references: Spanish Network for the Research in Infectious Diseases (REIPI), GEMARA-Spanish Society of Infectious Diseases and Clinical Microbiology (SEIMC)

Background: *Klebsiella pneumoniae* is responsible for severe nosocomial infections due to the continuous emergence of multi-drug resistant (MDR) pathogens. The decline in the effectiveness of antimicrobial treatments against MDR bacteria has generated a special interest in the study of bacteriophages. In this study, we identified a total of 42 Caudoviral bacteriophages present in 17 clinical strains of *K. pneumoniae* that produce carbapenemases belonging to 14 different STs corresponding to a total of 1.66 Mbp of sequence information (genomic/proteomic features). We determined their evolutionary relationship using comparative bioinformatic tools and microscopy techniques.

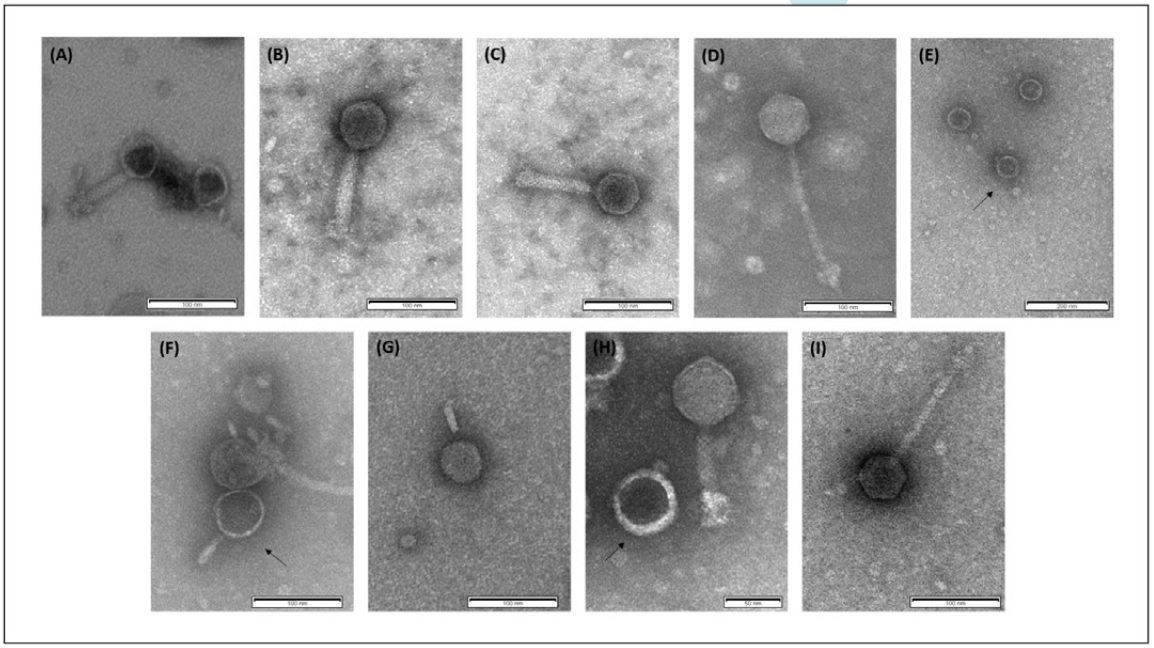
Materials/methods:

- 17 genomes of clinical strains of *K. pneumoniae* were sequenced and assembled *de novo* using the illumina-Miseq system and Velvet V1.2.10, respectively.
- Bioinformatic tools: PHASTER (bacteriophage identification), RAST PSI-BLAST and HHpred (protein annotation), ClustalW (evolutionary relationship), MVP (study interaction between bacteriophage and bacterial host) and GEPARD (dot plot alignment of nucleotide sequence).
- Microscopy studies were carried out by TEM assays.

Results: The study of the genomes resulted in the identification of 42 bacteriophages (Figure 1A), highlighting four of them with 33.3, 36.1, 39.9 and 42.2 kb genome sizes and similar genomic features present in several clinical strains and included in clusters (A, B and D) by phylogenetic analysis. Moreover, these bacteriophages showed high homology with international 4762, 4901,3499 and 4280 clusters of MVP. Bioinformatic analysis revealed the presence of 2363 proteins belonging to viral structure, transcription/replication and regulation. Although the majority of proteins had unknown functions, some of them showed an association with virulence (compounds of secretion systems-T3SS/T4SS or regulators-Mar like), antibiotic resistance (terB protein), and viral defense (Toxin-antitoxin modules, CRISPR-Cas and methyltransferase proteins) in bacteriophage genomes (Figure1B).

Conclusions: The presence of 42 caudoviral bacteriophages in the 17 clinical strains of *K. pneumoniae* showed relation with international 4762,4901,3499 and 4280 clusters of MVP database. Moreover, these bacteriophages harbored virulence, resistance and defense viral proteins that could determine the bacterial behavior. Future lines of research should focus on obtaining more information about genes of unknown function to achieve a better understanding of viral genomes for possible therapeutic application.

1A)



1B)

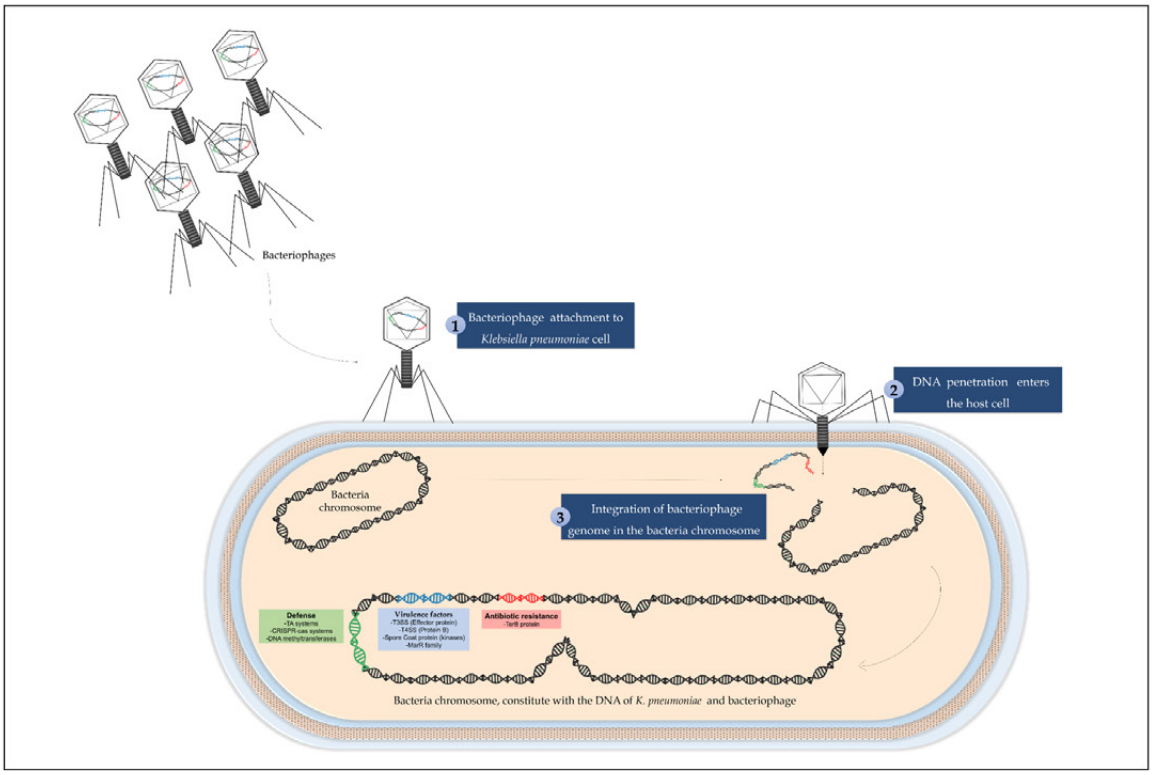


Figure 1A) Transmission electron microscopy (TEM) images showing the different families of bacteriophages present in the different clusters. (A,B,C,F,G) Myoviridae family obtained from bacteriophages ST11-OXA245phi3.1, ST13-OXA48phi12.1, ST405-OXA48phi1.2, ST101-KPC2phi6.3 and ST846-OXA48phi9.2 of cluster A1, A2, B, D and E, respectively. (D,I) Siphoviridae family obtained from bacteriophages ST13-OXA48PHI12.2 and ST974-OXA48phi18 of cluster C and E, respectively. (E,G) Podoviridae family obtained from bacteriophages ST147-VIM1phi7.2 and ST11-VIM1phi8.2 of cluster D and E, respectively. **Figure 1B)** Illustration representative of transmission of virulence, resistance and viral defense genes by bacteriophages in the bacterial chromosome of *Klebsiella pneumoniae* clinical isolates from this study.

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Abstract 985

Efficacy and safety of ceftazidime-avibactam in adults with Gram-negative bacteraemia from five phase III randomised clinical trials

John E. Mazuski[1], Florian Wagenlehner[2], Antoni Torres[3], Yehuda Carmeli[4], Joseph Chow[5], Dalia Wajsbrot[6], Greg Stone[7], Paurus Irani[8], Veronica Mascasullo[9], Karen Cheng[10], Margaret Tawadrous*[7]

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Background: An exploratory analysis was conducted in a subset of patients with Gram-negative bacteraemia from five randomised, controlled, multicentre Phase III trials in adults with complicated intra-abdominal infection (cIAI), complicated urinary tract infection (cUTI), hospital-acquired pneumonia (HAP) and ventilator-associated pneumonia (VAP), including infections caused by ceftazidime non-susceptible and multidrug-resistant Gram-negative bacteria.

Materials/methods: In each trial, RECLAIM and RECLAIM 3 (cIAI; NCT01499290/NCT01726023), REPRISE (cIAI/cUTI; NCT01644643), RECAPTURE (cUTI; NCT01595438/NCT01599806) and REPROVE (HAP/VAP; NCT01808092), patients were randomised 1:1 to intravenous ceftazidime-avibactam (plus metronidazole for those with cIAI) or comparators (carbapenems in >97% patients) for 5–21 days (treatment durations were defined by protocol for each study). Efficacy assessments included clinical and microbiological responses at a test-of-cure (TOC) visit (timed according to study protocol) in the Gram-negative extended microbiologically evaluable (GNeME) population bacteraemia subset. Safety outcomes (including adverse events [AEs] and clinical laboratory assessments up to the last visit) were summarised for patients with any positive bacterial blood culture at baseline who received ≥1 dose of study treatment.

Results: The overall Phase III pool included 3172 patients (ceftazidime-avibactam treated patients, n=1855; comparator group, n=1857), of whom 101 (ceftazidime-avibactam, n=54; comparator, n=47) comprised the GNeME bacteraemia subset. The most common primary diagnoses among these patients (acute pyelonephritis [47%] and VAP [15%]) and the most frequently isolated pathogens (*Escherichia coli* [69%], *Klebsiella pneumoniae* [21%] and *Pseudomonas aeruginosa* [17%]) were consistent with the overall Phase III pool. Considering the low denominators in the bacteraemia subset, favourable clinical and microbiological response rates at TOC were generally similar for ceftazidime-avibactam and comparators within each indication and combined across indications (Table). For 30 bacteraemia patients with ceftazidime non-susceptible isolates, overall favourable microbiological response rates were 6/11 (54.5%) for ceftazidime-avibactam ± metronidazole and 9/19 (47.4%) for comparator (difference 7.2%; 95% CI −28.72, 41.08). The pattern of AEs in patients with bacteraemia was similar between treatment groups and consistent with the known safety profile of ceftazidime-avibactam.

Conclusions: This analysis provides supportive evidence of the efficacy and safety of ceftazidime-avibactam in patients with Gram-negative bacteraemia associated with cIAI, cUTI or HAP/VAP.

Study sponsored by Pfizer.

Table. Clinical cure and favourable microbiological response rates at TOC for patients with Gram-negative bacteraemia associated with cIAI, cUTI or HAP/VAP treated with ceftazidime-avibactam and comparators (GNeME population)

	Clinical cure			Favourable microbiological response		
Indication	CAZ-AVI ± MTZ, n/N (%)	Comparator, n/N (%)	Difference, % (95% CI)	CAZ-AVI ± MTZ, n/N (%)	Comparator, n/N (%)	Difference, % (95% CI)
cIAI	9/11 (81.8)	9/10 (90.0)	−8.2 (−41.16, 27.12)	9/11 (81.8)	9/10 (90.0)	−8.2 (−41.16, 27.12)
cUTI, including acute pyelonephritis	28/28 (100)	25/29 (86.2)	13.8 (0.71, 30.74)	26/28 (92.9)	20/29 (69.0)	23.9 (3.58, 43.73)
HAP, including VAP	10/15 (66.7)	5/8 (62.5)	4.2 (−33.32, 43.99)	8/15 (53.3)	3/8 (37.5)	15.8 (−26.35, 51.79)
Overall	47/54 (87.0)	39/47 (83.0)	4.1 (−10.21, 19.09)	43/54 (79.6)	32/47 (68.1)	11.5 (−5.65, 28.72)

Data pooled from RECLAIM (NCT01499290), RECLAIM 3 (NCT01726023), REPRISE (NCT01644643), RECAPTURE (NCT01595438/NCT01599806) and REPROVE (NCT01808092). Clinical and microbiological responses at TOC and timing of TOC visits were as defined in each study protocol. All clinical cure definitions included resolution of signs and symptoms of the primary infection such that no additional antibiotics were required. Favourable microbiological response at TOC for patients in the bacteraemia subset required clearance of bacteraemia from post-baseline blood samples with eradication/presumed eradication (and no new infection) at the primary infection site; for patients with cUTI in RECAPTURE a urine culture demonstrating $<10^4$ CFU/mL of the original uropathogen was also required.

CAZ-AVI ± MTZ, ceftazidime-avibactam ± metronidazole; CAZ-NS, ceftazidime non-susceptible; CFU, colony-forming units; CI, confidence interval; cIAI, complicated intra-abdominal infection; cUTI, complicated urinary tract infection; HAP, hospital-acquired pneumonia; n, number of patients with outcome; N, number of patients in group; TOC, test of cure; VAP, ventilator-associated pneumonia.

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Abstract 986

Development of an antifungal stewardship programme at a London teaching hospital

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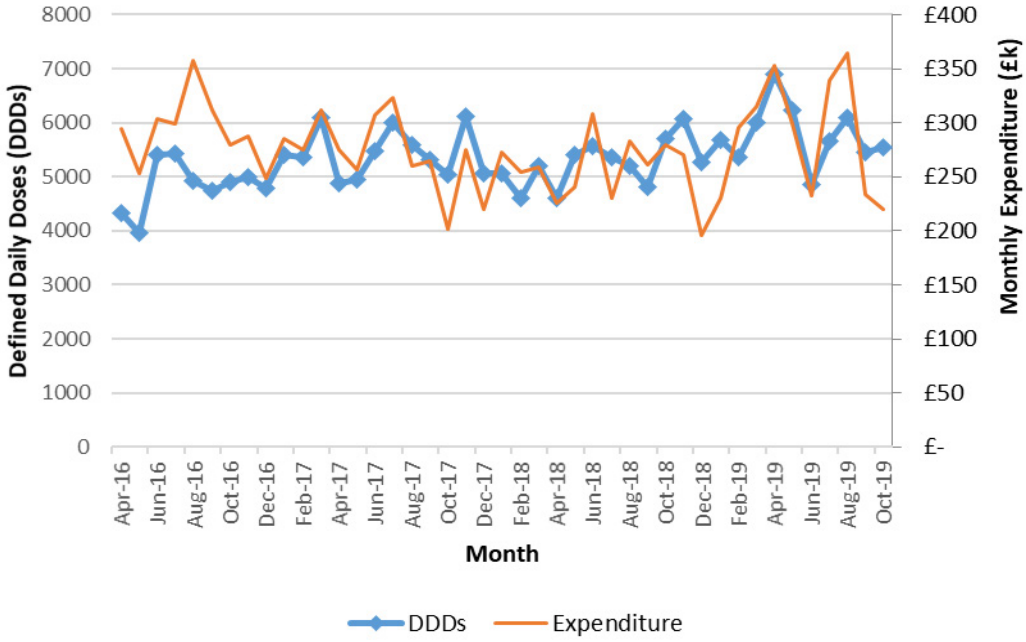
Background: The need for antifungal stewardship (AFS) is gaining recognition due to increasing incidence of invasive fungal infection and antifungal resistance. This triggered an AFS quality improvement scheme initially implemented in London hospitals (April 2018), then throughout England (April 2019). Here we describe the first 18-months of an AFS programme in a London teaching hospital.

Materials/methods: A series of interventions were implemented (April 2018-November 2019) including; establishing a multidisciplinary (MDT) AFS team, monitoring antifungal consumption and usage through regular audit, monthly fungal MDT reviews of patients on Ambisome®, guideline updates, a quality improvement project to optimise azole therapeutic drug monitoring (TDM) and weekly AFS rounds for in-patients.

Results: Antifungal consumption increased from 63,000 DDDs in 2016-17 to predicted 70,000 in 2019-20 (fig.1) with expenditure reducing in year 1 (by £30,000), but predicted to increase in year 2 (due to increasing expenditure on mold-active azoles).

Figure 1: Total Antifungal Expenditure and Consumption



An audit of 86 patients on antifungal treatment showed high compliance with Trust guidelines on treatment choice (87%) and appropriate imagining (93%). Utilisation of fungal biomarkers for suspected invasive mold infection was relatively low; galactomannan sent in 73% patients in 2018 and 65% in 2019 and beta-D-glucan in 53% and 97%, respectively. Prolonged turn-around-times (median 14d) impact the utility of these tests. MDT reviews of patients on AmBisome® (average 6/month) advise to de-escalate or stop in 39% of patients (28% and 11%, respectively), with additional diagnostics often recommended (44%). Durations of empiric therapy for invasive mold infection where a diagnosis of IFI was not established were shorter after MDT initiation (median 8d in 2019 vs. 16d in 2018).

Appropriate azole TDM increased from 20% of patients to 70-100% following the quality improvement project. Weekly AFS rounds began in November 2019. To date 11 patients have been reviewed with interventions recommended in 82%. These include stopping (n=4) or defining treatment duration (n=1), and recommending diagnostics (n=1) and TDM (n=5).

Conclusions: A multi-faceted approach with increased MDT working and central funding has optimised antifungal usage within our organization. Lessons learned from our long-standing antibiotic stewardship programme have facilitated this. Work continues to identify areas for further improvement.

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Abstract 988

Clinical experience of oral ibrexafungerp for treatment of four patients with invasive candidiasis from the FURI study

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Abstract third-party references: Synexis

Background: Ibrexafungerp is a novel glucan synthesis inhibitor and the first member of a new class of triterpenoid antifungals. Its mode of action is inhibition of 1,3-ß-D-glucan synthesis of the fungal cell wall, similar to echinocandins. However, ibrexafungerp is available orally and retains activity in candida strains resistant to echinocandins. As part of the open-label FURI trial, we report on four invasive candidiasis cases treated with oral ibrexafungerp at the Medical University of Graz.

Methods: FURI is an open-label Phase3 trial to determine the efficacy and safety of oral ibrexafungerp in patients with invasive fungal infections that are refractory to or intolerant of standard antifungal treatments or for whom long-term intravenous (IV) treatment is not feasible.

Results: Twenty-five patients were screened for study inclusion and four patients were ultimately included. The main underlying diseases were malignancy in two patients, psoriatic arthritis and kidney/pancreas transplantation in one patient each. The types of invasive candidiasis were as follows: Femoro-tibial osteomyelitis due to *C. glabrata* and *C. albicans* (N=1), candidemia due to *C. parapsilosis* (N=1), intraabdominal abscess due to *C. krusei* (N=1) and oropharyngeal candidiasis due to *C. krusei* and *C. albicans* (N=1). Two patients received oral ibrexafungerp because long-term IV treatment with an echinocandin was not feasible, one due to azole toxicity and one because of refractory disease despite standard antifungal treatment. The treatment duration with ibrexafungerp ranged from seven to 75 days.

At the end of treatment, two patients (candidemia and abscess) had a complete response, one patient (osteomyelitis) had a partial response and one (oropharyngeal candidiasis) had stable response (persisting thrush).

Most common adverse events possibly or probably related to ibrexafungerp were diarrhoea (n=3), nausea (N=1), rash (N=1) and tooth discoloration (N=1). Gastrointestinal adverse effects resolved in two out of three patients after a couple of days.

Conclusions: Oral ibrexafungerp was well tolerated, besides gastrointestinal side effects in the first days of loading dose. Ibrexafungerp was shown to be an effective treatment for invasive candidiasis infections. In addition, in-hospital stays could be significantly reduced in two patients as long-term IV treatment would be avoided with the use of oral ibrexafungerp.

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Abstract 989

The evolving landscape of group A Streptococcus in marginalised populations in England and Wales

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Background: The PHE streptococcal reference laboratory types all GAS isolates recovered from patients with invasive infections, and from superficial infections for outbreak-related cases. Increasing numbers of GAS isolates from people who inject drugs (PWID), people in prison and/or people who are homeless have been detected, and national investigation established. Surveillance data from the reference laboratory indicates an increase in the number of reported iGAS isolates from an average of 9.5 cases between 2010-2015 to 145 cases in 2017; 277 cases in 2018; 190 cases so far in 2019. We report here characterisation of strains received from January 2018 to August 2019 associated within this marginalised population.

Materials/methods: GAS isolates were characterised by *emm* gene sequence typing. PWID, prison and homeless status were updated from health protection management systems (HPZone) from 2018 onwards, leading to increased case ascertainment. Whole genome sequence data was obtained for a sample of cases to identify risk factors for transmission.

Results: 32 clusters of GAS infections were identified; 17 linked to PWID/homeless shelters and 15 to prisons with a total of 332 and 73 isolates received from these settings, respectively. The dominant *emm* types were *emm* 108.1 (29%), *emm* 66.0 (27%) and *emm* 94.0 (8%), and do not reflect those commonly found in the general population, being *emm* 1.0 (20%), *emm* 89.0 (10%) and *emm* 3 (8%). SNP analysis of WGS data of *emm* 108.1 strains suggest recent clonal expansion of single lineage within this population; data from the *emm* 66.0 strains revealed a number of geographically related clades, suggesting that this strain has been circulating for longer has become established within this population. Infections in PWID, the homeless community and prisoners were predominately found in males, and spread across England and Wales concentrating in some English cities.

Conclusions: These findings indicate increasing burden of severe, invasive GAS infections in PWID, with clusters emerging in prisons in England and Wales, dominated by lineages not commonly found in other communities. Data suggests recent clonal expansion of *emm* 108.1 strain and increased incidence of previously established *emm* 66.0 strains. Further investigations are underway to understand transmission networks.

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Abstract 990

Development of a simultaneous population pharmacokinetic model for aztreonam-avibactam

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Background: In previously reported population pharmacokinetic (PK) analyses and exposure simulations, aztreonam and avibactam were modelled separately to select the Phase IIa (completed) and Phase III (planned) aztreonam-avibactam dosage regimens (maintenance dose 1500/500 mg 3-h intravenous infusions every 6 h for adult patients with estimated creatinine clearance [CrCL] >50 mL/min), including loading doses and adjustments for renal impairment.

Materials/methods: The existing aztreonam and avibactam models were updated with additional adult (one Phase IIa trial) and paediatric (avibactam only; one Phase I and two Phase II trials) clinical PK data to develop a simultaneous aztreonam-avibactam population PK model to account for correlation in PK of the two components. Population PK analyses were conducted using nonlinear mixed-effects modelling with first-order conditional estimation method with interaction. Models were evaluated using pre-defined goodness-of-fit criteria and prediction-corrected visual predictive checks (pcVPCs).

Results: In total, 2921 aztreonam plasma concentrations from 141 adults (patients and healthy volunteers), 16,175 avibactam plasma concentrations from 2349 adults, and 510 avibactam plasma concentrations from 154 paediatric subjects (3 months to <18 years) were included in the analysis. The final aztreonam and avibactam population PK models were two-compartment disposition models with first-order elimination, with correlation in interindividual variability (IIV) on clearance (CL) and central volume (Vc). Body weight (standard allometry) and body surface area-normalised CrCL (nCrCL), or postmenstrual age for subjects <2 years, were key covariates that predicted clearance of both drugs. Estimated base and final model PK parameters for the reference typical healthy subject weighing 70 kg are shown in the Table; final estimates for aztreonam CL, and for the exponent of nCrCL on aztreonam clearance, were similar to previous analyses. In pcVPCs, model predictions of observed data were generally adequate.

Conclusions: Simultaneous modelling of aztreonam and avibactam enables estimation of the correlation of PK IIV on CL and Vc of the two drugs, facilitating efficient parametric simulation. Simulations using these models further support the adult aztreonam-avibactam dosage regimens (including renal dose adjustments) selected for Phase III evaluation and provide initial weight-based doses for evaluation in paediatric studies.

Table. Parameter estimates for the base and final simultaneous aztreonam-avibactam population PK models

Parameter	Base model (AS752744)		Final model (AS756673)	
	Estimate (%RSE)	IIV% (%RSE)	Estimate (%RSE)	IIV% (%RSE)
CL_ATM (θ_1) [L/h]	5.44 (1.65)	31 (7.21)	5.36 (2.86)	30.1 (7.97)
Vc_ATM (θ_2) [L]	7.92 (4.02)	43.4 (11.9)	7.65 (4.54)	38.1 (15.2)
Q_ATM (θ_3) [L/h]	10.8 (7.99)		10.4 (12.1)	
Vp_ATM (θ_4) [L]	6.03 (3.27)		5.79 (4.33)	
CL_AVI (θ_5) [L/h]	10.9 (1.38)	45.1 (8.35)	10.9 (1.76)	45 (11.8)
Vc_AVI (θ_6) [L]	15.3 (3.84)	49.2 (20.5)	15 (4.9)	48.8 (33.1)
Q_AVI (θ_7) [L/h]	4.62 (3.83)	35.4 (14.5)	4.6 (4.66)	35.3 (16.5)
Vp_AVI (θ_8) [L]	6.8 (1.82)	20.5 (18)	6.79 (2.09)	20.8 (18.4)
nCRCL on CL_ATM (θ_{15})	0.478 (5.05)		0.485 (5.14)	
cIAI on Vc_ATM (θ_{20})			0.33 (35.7)	
nCRCL on CL_AVI (θ_{11})	0.632 (4.48)		0.63 (4.47)	
ESRD on CL_AVI (θ_{16})	–0.918 (2.04)		–0.919 (2)	
CL_AVI_DIAL (θ_{18}) [L/h]	20.3 (12.5)		20 (12.5)	
Study 2002 on CL_AVI (θ_{17})	0.965 (15.5)		0.962 (15.6)	
APACHE II score on CL_AVI (θ_{19})	–0.168 (13.2)		–0.166 (13.7)	
Infection on Vc_AVI (θ19)	0.234 (33.6)		0.218 (35.4)	
cUTI in Phase2/3 on Vc_AVI (θ_{20})	0.889 (14.1)		0.931 (17.3)	
Study2002 on Vc_AVI (θ_{21})	3.37 (17.5)		3.44 (17.8)	
cIAI/NP Phase 2/3 on Vc_AVI (θ_{22})	0.705 (13.6)		0.766 (15.6)	
cov CL_ATM-Vc_ATM	0.0728 (0.153)		0.0555 (0.2)	
cov CL_ATM-CL_AVI	0.135 (0.0703)		0.129 (0.0607)	
cov CL_AVI-Vc_ATM	0.102 (0.168)		0.0968 (0.149)	
cov CL_ATM-Vc_AVI	0.108 (0.154)		0.0899 (0.14)	
cov Vc_ATM-Vc_AVI	0.193 (0.148)		0.171 (0.13)	
cov CL_AVI-Vc_AVI	0.17 (0.17)		0.168 (0.259)	
cov Q_AVI-Vp_AVI	0.0495 (0.232)		0.0505 (0.244)	
Additive RSV_ATM (mg/L) (θ_9)	1.32 (58.5)		1.5 (31.4)	
Prop RSV_ATM (θ_{10})	0.122 (13.3)		0.104 (13.4)	
Prop RSV_ATM Phase 2 (θ_{26})			0.205 (9.39)	
Additive RSV_AVI Phase 1 (mg/L) (θ_{11})	0.00712 (16.1)		0.00719 (17)	
Prop RSV_AVI Phase 1 (θ_{12})	0.203 (5.99)		0.203 (5.98)	
Prop RSV_AVI Phase 2 (θ_{23})	0.648 (6.92)		0.643 (8.65)	
Prop RSV_AVI Phase 3 (θ_{24})	0.567 (5.25)		0.567 (7.16)	

APACHE, acute physiologic assessment and chronic health evaluation; ATM, aztreonam; AVI, avibactam; cIAI, complicated intra-abdominal infection; CL, clearance; cov, covariance; cUTI, complicated urinary tract infection; DIAL, dialysis; ESRD, end-stage renal disease; IIV, inter-individual variability; nCRCL, body surface area-normalised creatinine clearance; NP, nosocomial pneumonia; Prop, proportion; Q, inter-compartmental clearance; RSE, relative standard error; RSV, residual variability; Vc, central volume of distribution; Vp, peripheral volume of distribution.

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Abstract 994

Prospective surveillance of health-care associated infections in residents in long term care facilities in Graz, Austria

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Background: Residents in long term care facilities (LTCF) are at increased risk for healthcare-associated infections (HCAI). Incidence rates in the literature range from 1.8 -13.5 infections per 1,000 resident days. However, data on HCAIs in residents of LTCFs in Austria are scarce. Therefore, the aims of our study were (1) to evaluate the incidence rate of HCAIs per 1,000 resident days in four LTCFs in Graz, Austria (2) to characterise the spectrum of HCAIs and (3) to study the use of antimicrobial substances.

Materials/methods: We conducted a prospective surveillance study from January 1 to December 31, 2018 in four LTCFs of the Geriatric Health Centre of the City of Graz with a total of 388 beds. HCAIs were defined based on ECDC HALT project.

Results: During the 12-month surveillance period, 306 infections of 182 residents (130/182 female) were recorded (136,988 resident days). The mean age of the residents was 85.8 ± 9.2 years (range 51-102 years). 56% (103/ 182) of residents were older than 85 years. The overall incidence rate of HCAIs was 2.2 per 1,000 resident days. Urinary tract infections occurred most frequently (160/306, 52%, 1.17 per 1,000 resident days), followed by skin, soft tissue and mucosal infections (85/306, 27%, 0.62 per 1,000 resident days), table 1. Only 7/306 (2.2%) HCAIs were acquired outside the LTCFs. 14.3% (23/160) of UTIs were device-associated. 262/306 (85.6%) infections were treated with oral antimicrobial substances. For UTIs (n=160) the most commonly used substances were quinolones (25%), folate antagonists (23%) and pivmecillinam (21%).

Conclusions: The overall incidence rate for HCAI was relatively low at 2.2 per 1,000 resident days. To our knowledge this is the first study on prospective surveillance of HCAIs in LTCFs in Austria.

Table 1:

Type of infection	Number of infections	Rate per 1000 resident days
Urinary tract infections	160 (52%)	1.17
Skin, soft tissue & mucosal infections	85 (27%)	0.62
Lower respiratory tract infections Influenza	49 (16%) 1 (0.3%)	0.36 0.01
Gastroenteritis Clostridium difficile	6 (2%) 3 (1%)	0.04 0.02
Unexplained febrile illness	6 (2%)	0.04
Total	306	2.2

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Abstract 995

Melioidosis in French Guiana? Cases with a clinical isolate of Burkholderia sp., Cayenne, 2012 – 2018

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Background: Melioidosis is an infectious disease caused by *Burkolderia pseudomallei*, a Gram-negative bacterium found in tropical soil and water. It is frequently diagnosed in South-East Asia and Northern Australia. The variety of its clinical presentations complicates the diagnosis of melioidosis, especially in low-incidence areas where it is often little known. For the past few years, cases have been regularly reported in Amazonian countries such as Colombia, Venezuela and Brazil. The disease has never been identified in French Guiana.

Materials/methods: Microbial identification of bacterial species at Cayenne Hospital has been relying on VITEK 2 since 2012 and MALDI-TOF since 2014. These two automated techniques have been known to regularly confuse *B. pseudomallei* with other species of the *Burkholderia* genus, in particular that of the *B. cepacia* complex. Cases associated with a *Burkholderia sp.* isolate between 2012 and 2018 were identified from the databases of the bacteriology laboratory of Cayenne Hospital. The clinical history of each case was then documented from their medical record.

Results: 63 cases were identified. 51 cases, of which 15 premature neonates, were diagnosed with a nosocomial *B. cepacia* infection or colonization associated with a stay in an intensive care unit. For nine cases the nosocomial origin of the *Burkholderia* isolate cannot be ruled out. Three cases have a clinical history and risk factors compatible with melioidosis; two of them are associated with a clinical isolate of either *B. pseudomallei* or *B. thailandensis*.

Conclusions: We hypothesize that melioidosis is encountered in French Guiana sporadically, in consistence with other Amazonian territories. Three observations suggest an endemic potential of melioidosis in French Guiana. Firstly, the possible soil contamination from the regular importation of vegetal species from South-East Asia. Secondly, the high prevalence in French Guiana of known risk factors for melioidosis, diabetes in particular. Thirdly, the population of clandestine gold miners, potentially at risk for transmission through their high mobility in the Region of the Guyana Shield and their repeated exposure to muddy and anthropized soils.

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Abstract 996

Antibacterial prescribing in the outpatient setting: results from a longitudinal surveillance programme and a sentinel network of physicians: Switzerland, 2018

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Background: Inappropriate or unnecessary use of antibacterials may foster the development of antibiotic resistance. Our goals were to assess the global antibacterial use, the number of antibacterial prescriptions and the proportion of antibacterial classes per clinical indications in the outpatient setting in Switzerland.

Materials/methods: We analyzed two sources of data: (i) IQVIA®, a private provider of manufacturers' sales, delivered aggregated data which were then converted in the ANRESIS database into defined daily doses (DDD) using the 2019 WHO DDD definition and (ii) all consultations with antibacterial prescriptions reported from 146 practitioners from general and internal medicine during 2018 using the representative Swiss Sentinel Surveillance Network "Sentinella". The network covers all regions of Switzerland. Extrapolation on population level was done by attributing the estimated covered population to each Sentinella physician. Data from pediatricians were excluded.

Results: In 2018, the total consumption of antibacterials for systemic use in outpatients was 9.0 DDD per 1000 inhabitants per day, corresponding to a reduction of 9% since 2015 ($p<0.05$). A total of 14'092 antibacterial prescriptions were issued by participating physicians in 2018, corresponding to 110.3 antibacterial prescriptions per 1000 inhabitants. Bladder infections (26%), upper respiratory tract infections (26%) and lower respiratory tract infections (20%) were the main clinical indications for prescribing antibacterials. Acute bronchitis and streptococcal pharyngitis accounted resp. for 9% and 7%of total antibacterial prescriptions. Fosfomycin (31%), fluoroquinolones (24%), co-trimoxazol (21%), and nitrofurantoin (15%) were the most prescribed antibacterials for bladder infections. For lower respiratory infections, amoxicillin (33%), macrolides (29%) and penicillins with beta-lactamase inhibitors (9%) were the most prescribed antibacterial classes. Fluoroquinolones accounted for 7% of antibacterials for this indication.

Conclusions: Even if antibiotic consumption in Switzerland is low in comparison with other European countries, the quality of antibacterial prescriptions can be optimized, particularly in reducing (i) the use of antibacterials in acute bronchitis, a viral infection in more than 90% of cases and (ii) the use of fluoroquinolones for bladder infections. Resources for antibiotic stewardship programs in the outpatient setting are also needed in countries with low antibacterial consumption.

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Abstract 997

Genomic epidemiology and resistome analysis of *Helicobacter pylori*

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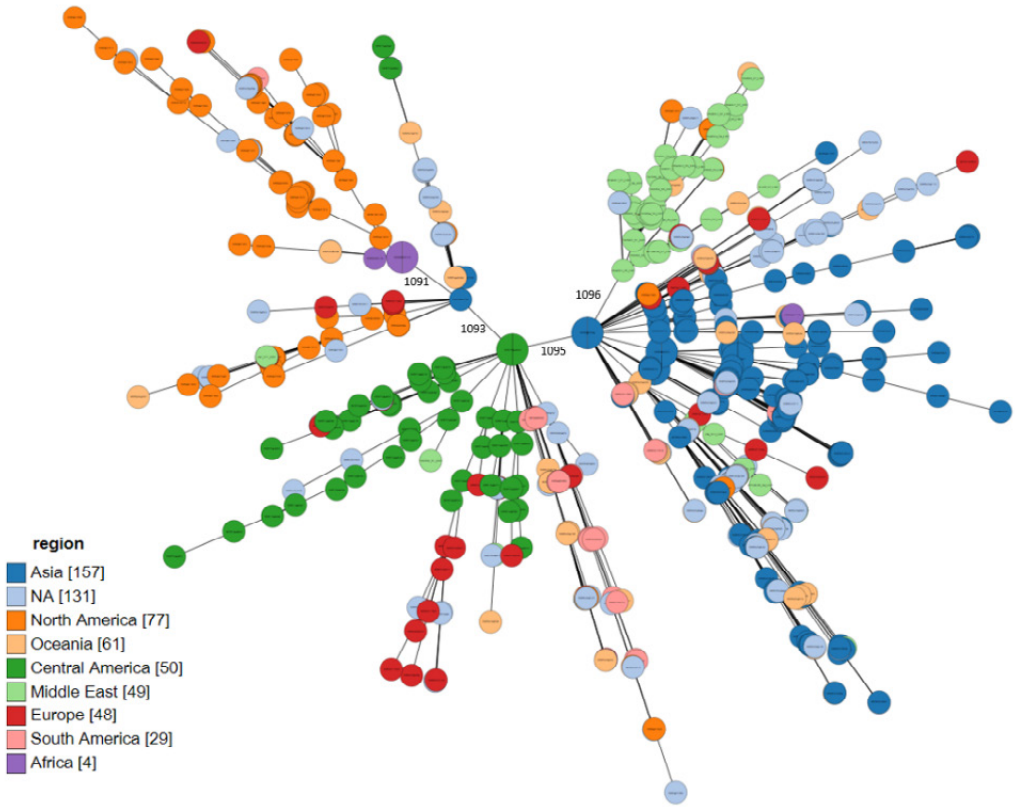
Background: Antimicrobial resistance (AMR) in *Helicobacter pylori* (HP) is increasing globally and can result in treatment failure and inappropriate antibiotic usage. Whole genome sequencing (WGS) allows a comprehensive analysis of the resistome as well as typing and can thus be used to explore the phylogeny of HP in relation to underlying mechanisms of AMR.

Materials/methods: HP isolates (n=48) recovered from routine clinical samples in northern Israel underwent phenotypic antimicrobial susceptibility testing (AST) against five antimicrobials using an E-test as per BSAC guidelines. Literature review identified 114 point mutations reported to correlate with phenotypic resistance against those antibiotics. WGS was performed on an Illumina platform following library preparation using Nextera FLEX. Publicly-available HP genomes (n=992) were assembled (total isolate n=1,040). Analysis was conducted via our *in-house* bioinformatics pipeline for resistome analysis targeting point mutations in the relevant genes (*bpb1A*, 23s rRNA, *gyrA, rdxA, frxA*, and *rpoB*) and phylogenomic analyses using multilocus sequence typing (MLST) and core genome (cg)MLST methods (chewBBACA and GrapeTree).

Results: Phylogenomic analysis revealed a notable geographical clustering of HP genomes across world regions. The majority of Israeli isolates clustered together, closely with the Asian branch (Figure 1). Resistance to at least one antibiotic was observed in 79% of Israeli isolates. Resistance rates were as follows: 54% for clarithromycin, 31% for metronidazole, 10% for amoxicillin, 4% for rifampicin, and 2% for levofloxacin. Genotype-to-phenotype correlation was inconsistent; for every analysed gene at least one phenotypically susceptible isolate was found to have a mutation previously associated with resistance. This was also observed regarding mutations used in commercial kits to diagnose AMR in HP cases; for example, our study observed that 10/17 isolates with the A2143G/23s rRNA mutation are phenotypically susceptible. Furthermore, 13 novel point mutations were identified which were associated with a resistant phenotype in some but not all studied isolates.

Conclusions: This is the largest study to date featuring the global phylogeny of HP based on >1K genomes in conjunction with a global snapshot of the HP resistome. Analysis of a unique set of Israeli isolates demonstrates that inconsistencies and limitations in inferring a genotype-to-phenotype correlation in HP remains challenging.



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Abstract 998

Carrier prevalence of vancomycin-resistant *Enterococcus faecium* (VREfm) among patients admitted to emergency departments in Copenhagen (Denmark) compared with VREfm prevalence of the background population

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Background: The aim of our study was to describe the prevalence of VREfm-carriers admitted to two of the hospitals in the Capital Region of Denmark during a 3-week screening period. The main outcome was to examine the prevalence of unknown VREfm-carriers. The secondary outcome was to compare this with the VREfm prevalence in the background population.

Materials/methods: We obtained a rectal swab from all adult patients willing to participate, who were admitted to either the Emergency Department at Bispebjerg Hospital or Frederiksberg Hospital during a 3-week period in June and July 2019. All patients were screened for age, hospital admissions in the last 6 months and antibiotic consumption within the last 6 months. The swabs were analyzed for VREfm by culture and PCR for the *vanA* gene at the Department of Clinical Microbiology, Hvidovre Hospital. We also obtained 100 fecal samples sent to our department by General Practitioners in the Capital Region of Denmark. The following exclusion criteria were set up: age below 50, VREfm and *Clostridium difficile* positive within 6 months, hospital admission within 6 months and travel abroad. They were subsequently screened for VREfm as mentioned above.

Results: We included 172 patients who were admitted during the 3-week period. The median age was 72 years. In total, 11 (6,3%) were colonized with VREfm. 6 (3,4%) were known VREfm-carriers and 5 (2,9%) were unknown VRE-carriers. Of these unknown carriers, all had been hospitalized and received antibiotics within the last month.

Of the 100 fecal swabs sent by the General Practitioners, 1 out of 100 (1%) had a positive *vanA* pcr and none were culture positive.

Conclusions: Hospital admission and antibiotic use within the last month predispose to colonization with VREfm. We found a prevalence of 2,9 % of unknown VRE-carriers. In comparison, we found that 1% of the patients without prior hospitalization or antibiotic use, were VREfm positive.

Admission VRE screening could help relieve the burden of VREfm transmission within our hospitals. From this study our recommendation is to screen all patients admitted to the ER who have been hospitalized within the last month.

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Abstract 999

Modulation of the microbiota by oral intake of a synbiotic mixture in healthy volunteers: a single-centre one-armed pilot study

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Background: A synbiotic product combines one or more probiotic microorganisms with a prebiotic fibre. Synbiotics have been demonstrated to change the microbiota composition in different patient populations.

Prebiotics, which are carbohydrates that are only metabolized by the gut bacteria, have gained much attention in recent years for their health benefits through stimulating growth of specifically the anaerobic bacteria from the *Bacteroides* family that produce short chain fatty acids.

Whether the microbiota in a steady state in healthy individuals will change by the addition of synbiotics is unexplored. Our aims were to monitor the GI-function and explore the modulation of the healthy microbiota by synbiotics in a pilot trial of healthy volunteers.

Materials/methods: We recruited 15 healthy volunteers who consumed a synbiotic mixture consisting of *Lactobacillus rhamnosus* (LGG®), *Lactobacillus acidophilus* (LA-5®), *Lactobacillus paracasei* (L. casei 431®), *Bifidobacterium lactis* (BB-12®) and the plant carbohydrate inulin (15g) for four weeks. Faecal samples were collected at visit 1 (baseline) as well as at completion of the intervention. All participants completed a faecal diary based on the Bristol Stool Scale and recorded their gastrointestinal (GI) well-being. We used shotgun metagenomic sequencing for the microbiome studies on an Illumina NextSeq, and performed taxonomic profiling using MetaPhlAn2.

Results: 14 out of 15 volunteers successfully completed the four-week synbiotic intervention. One participant was not compliant with the intervention and was therefore excluded from the analyses. At the end of the intervention, 36% experienced a better GI-function in the self-reported diary. 43% reported an unchanged GI-function, while 21% reported a worse GI-function. For our microbiome analyses, the α-diversity was unchanged before and after the intervention. We found a higher relative abundance of *Bifidobacterium* and *Lactobacillus* spp. after the intervention.

Conclusions: The intervention with synbiotics leads to higher relative abundance of the potentially beneficial species of *Bifidobacterium* and *Lactobacillus* but it did not affect the α-diversity. Most participants (79%) reported an unchanged or better GI-function at the end of the intervention.

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Abstract 1003

Rapid, sensitive diagnosis of bloodstream infection using clinical metagenomics

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Background: In the UK, approximately 250,000 cases of sepsis are reported annually, of which ff20% result in death. The estimated economic impact of sepsis is £2 billion/annum. Patients with sepsis need rapid treatment with effective antibiotics, otherwise mortality rates increase dramatically. Rapid and accurate diagnostics are needed to identify the infecting pathogen to determine the appropriate therapy. However, current diagnostic methods rely on blood culture which has low sensitivity and takes 2-5 days before results are available. Here we describe a novel clinical metagenomics-based method for the diagnosis of bloodstream infection in patients suspected of sepsis, combining highly sensitive microbial cell capture with efficient host depletion and nanopore sequencing.

Materials/methods: Whole human blood was diluted (1:1) in liquid transfer medium (Momentum Bioscience Ltd., UK). *Escherichia coli* was incubated at 37°C for 2 hours in the blood-transfer medium, and subsequently tested at 10^4 to 10^2 CFU/mL. Samples were subjected to simultaneous blood lysis and magnetic bead-based microbial capture (Momentum Bioscience Ltd.), saponin-based host DNA depletion, whole genome amplification (REPLI-g Single Cell kit, Qiagen) and MinION sequencing (RPB004 kit, Oxford Nanopore Technologies Ltd., UK). Sequence data was analysed using EPI2ME software (Oxford Nanopore Technologies Ltd.). Samples were classified as positive for a pathogen if present at >1% of the total classified reads.

Results: *E. coli* was detected in all samples tested after 1.5 hours sequencing demonstrating a limit of detection <100 CFU/mL (Table 1). Antimicrobial resistance genes were detected in all samples but transferrable resistance prediction was unreliable at low genome coverage (<5x).

Table 1: MinION sequence data for spiked blood

Sample (CFU/mL blood)	Total reads	Classified	Human	*E. coli* (genome coverage x)
10^4 E. coli	93,559	53,827	5,264	35,087 (9.4)
10^3 E. coli	93,060	32,189	4,790	6,909 (2.1)
10^2 E. coli	111,638	33,235	7,945	1,779 (0.8)

Conclusions: This proof-of-principle study demonstrates sensitive pathogen and antibiotic resistance profiling directly from blood in <8 hours using nanopore sequencing-based clinical metagenomics. This approach combined with ETGA® (Enzyme Template Generation & Amplification) technology (Momentum Bioscience Ltd.), enables the detection of viable micro-organisms from whole blood for the rapid diagnosis and management of bloodstream infections.

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Abstract 1004

A surface-engineered scaffold implant with direct antibacterial activity against *Staphylococcus aureus*

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Abstract third-party references: Part of this research was supported by Fondazione CRT 2019 (P.I. Prof. Valeria Allizond)

Background: Biomedical implants and devices, an essential part of the medical treatments for improving therapeutic efficiency, still suffer from bacterial infections that hamper patients' recovery and even threaten patients' lives. Although antibiotics are widely used to treat those infections, it has brought serious problems of antibiotic resistance. Metal ions, such as silver, are believed to be promising additives in developing antibacterial biomaterials, owing to possessing favorable bactericidal effects against antibiotic-resistant bacteria. Furthermore, the incorporation of bioactive, stiff inorganic materials (e.g. hydroxyapatite, HA, and β-tricalcium phosphate, β-TCP) into synthetic biodegradable polymers, such as poly (ε-caprolactone) (PCL) polymer can lead to significant enhancements in mechanical properties, bioactivity, and bone regeneration ability *in vivo*. The present research purpose is the development of novel PCL-based scaffolds, modified with both silver, to supply antibacterial behavior, and biphasic calcium phosphates (BCP; the mixture of HA and β-TCP) denoted as to impart bioactive/bioresorbable properties.

Materials/methods: PCL and BCP/PCL porous pellets, functionalized with silver ions (Ag+) were developed by salt-leaching method and both sodium chloride, NaCl, and sodium nitrate, $NaNO_3$ were used as pore formers. Samples were further characterized from the morphological and chemical point of view. *Staphylococcus aureus* ATCC 29213 adhesion on PCL-based biomaterials was assayed through a sonication protocol to dislodge adherent microorganisms without altering their viability. The planktonic bacteria number was also determined.

Results: Field Emission Scanning Electron Microscopy showed that the samples were characterized by square-shaped macropores (Figure 1), whose average dimension was in agreement with that of the starting salt. The presence of PCL and BCP phases and of Ag, in the correct amount, were confirmed by X-Ray Diffraction and Energy Dispersive X-ray Spectroscopy analysis, respectively. The antibacterial tests revealed a significant ($p<0.001$) decrease either of adherent staphylococci on the Ag-functionalized surfaces (Figure 2) or planktonic bacteria, thus proving the Ag release from the enriched PCL-based samples.

Conclusions: Due to the combined antimicrobial and biodegradable properties, the PCL-based scaffolds enriched with silver showed good potential for bone tissue engineering and offer a promising strategy, as an ideal microbial anti-adhesive tool for the reduction in BAIs and antimicrobial molecules-targeted delivery

Figure 1: FESEM micrographs of PCL scaffolds obtained by using NaCl (a) and $NaNO_3$ (b) salts as templates (analysis carried out on the materials sections); (c): higher magnification FESEM micrograph of PLC/BCP sample, showing the fine and homogeneous distribution of the calcium phosphate particles inside the polymer matrix (see the black arrows); Ag-functionalized PCL scaffolds obtained by using NaCl (d) and $NaNO_3$ (e) salts as templates (analysis carried out on the materials sections); (f): Typical microporous surface of the scaffolds.

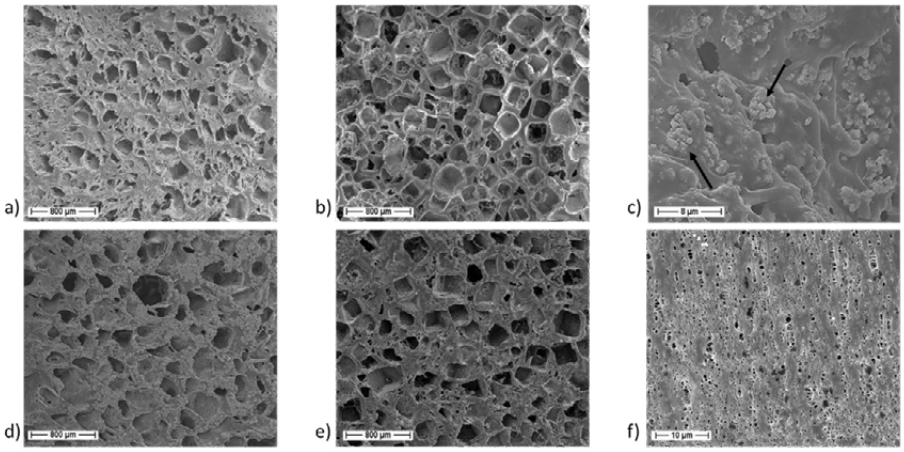
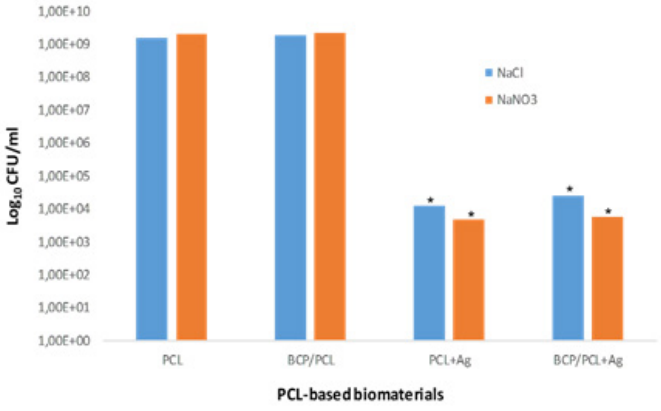


Figure 2: Adhered *S. aureus* ATCC 29213 (log_{10}CFU/ml) on different PCL-based biomaterial pellets: PCL (polycaprolactone), BCP/PLC (polycaprolactone functionalized with biphasic calcium phosphates), PCL+Ag (polycaprolactone enriched with silver ions), BCP/PLC +Ag (polycaprolactone functionalized with biphasic calcium phosphates and enriched with silver ions).



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Abstract 1006

In vitro evaluation of the influence of immunosuppressive agents on human polyomavirus BK replication

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Background: Human Polyomavirus BK (BKPyV) infection is common, ranging from 60% to 100% in the general population. After primary infection, which occurs asymptomatically during childhood, BKPyVs establishes a life-long latency in tubular kidney epithelial cells. The immunosuppressive therapy, typical of transplant recipients, is a risk factor for BKPyV reactivation, that causes Polyomavirus Associated Nephropathy (PVAN), and organ rejection in 1 to 10% of patients. Immunosuppression treatment is a complex therapy, constituted by a combination of mTOR and calcineurin inhibitors (FK506, Rapamycin and Everolimus) and antiproliferative agents, such as mycophenolic acid (MPA). In the case of post-transplant BKPyV reactivation, the reduction of the immunosuppressive regimen and the administration of Leflunomide, a nonspecific antiviral treatment, are used as effective actions.

Materials/methods: HEK293T cell line was infected with BKPyV virions. Infected cells were treated with FK506, Rapamycin, Everolimus, and MPA, as single or coupled drug treatments, after the evaluation of the IC_{50} for each drug. Leflunomide treatment was used as control of viral replication inhibition. The viral replication, in presence or absence of drugs, was tested by means of BKPyV specific quantitative real time PCR (qPCR) on cell medium. BKPyV mean replication level in treated cells was expressed as percentage of replication and normalized using the BKPyV replication level of not treated infected cells.

Results: BKPyV mean replication level were 87,03%, 70,29%, 68,41% and 44,38% after treatment with FK506, MPA, Rapamycin and Everolimus respectively. The treatment composed by FK506 and Everolimus, or MPA or Rapamycin was associated with mean replication level of 69,27%, 79,75% and 90,72% respectively. Additionally, the BKPyV mean replication level was 79,71% and 58,27% after the treatment with MPA and Sirlimus and with MPA and Everolimus, respectively.

Conclusions: Immunosuppressive therapy based on FK506 administration represents an important risk factor for the reactivation of BKPyV and the development of PVAN**.** However, FK506 post-transplant treatment is fundamental to maintain an adequate level of immunosuppression. For this reason, the administration of FK506 in association with Everolimus, instead of MPA, could represent an alternative therapeutic strategy, able to guarantee a good immunosuppressive regimen and a limited reactivation of BKPyV.

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Abstract 1007

Impact of lung transplantation on the phylogenetic diversity of *Pseudomonas aeruginosa* isolates from end-stage cystic fibrosis patients

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Background: Impaired lung function and chronic infections due to colonization and infection by complex microbiota elevates the health risk of patients with cystic fibrosis (CF) which can untimately lead to full respiratory insufficiency and death. For patients with end-stage CF lung disease, lung transplantation (LTx) is the only remaining therapeutic option. In this context, *Pseudomonas aeruginosa* is a principal cause of chronic lung infections and such strains display different phenotypic and genomic characteristics compared to their wild-type ancestors.

The aim of this study was to analyze the epidemiology and evolution of *P. aeruginosa* strains serially obtained from CF patients, and a non-CF bronchiectasis patient, who underwent LTx (Newcastle upon Tyne, UK).

Materials/methods: A panel of 708 *P. aeruginosa* strains from different niches and 4 different strain collections were analyzed for genomic relatedness. These comprised the bioMérieux collection (n = 219), Kos collection (n = 390), Pirnay collection (n = 63) and sequential strains from six LTx patients (n = 36). For each LTx patient, samples were collected before, during and after the LTx at different time points. Multi-locus sequence typing (MLST) and construction of a core genome based phylogenetic tree using bioinformatics tools was employed to define the genomic relatedness among the different *P. aeruginosa* strains.

Results: The genome wide assessment showed clustering with respect to the origin of the isolates i.e from patients from whom they were isolated implying intra-individual variability. The MLST profiles showed the *P. aeruginosa* strains from the Newcastle CF patients, but not the bronchiectasis one, had previously unidentified sequence types. Strains from Newcastle were scattered among the phylogenetic tree, indicating that the patients were neither cross-colonized nor cross-infected.

Conclusions: *P. aeruginosa* isolates from CF patients disclose very specific traits, but they could be phylogenetically distant between patients. On the other hand, LTx and associated treatment had no impact on the phylogenetic type of the *P. aeruginosa* strain harbored by each studied patient. Studying the presence of SNPs may aid our understanding of elevated resistance to the drugs used for treatment.

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Abstract 1008

Impact of underlying comorbidities on outcomes of patients treated with ceftaroline fosamil for complicated skin and soft-tissue infections: pooled results from three phase III clinical trials

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Background: In three Phase III studies, ceftaroline fosamil was shown to be non-inferior to vancomycin plus aztreonam for the treatment of complicated skin and soft tissue infections (cSSTI). This exploratory analysis evaluated the impact of underlying comorbidities on clinical outcomes in patients with cSSTI pooled from these three studies.

Materials/methods: CANVAS 1 (NCT00424190), CANVAS 2 (NCT00423657) and COVERS (NCT01499277) were Phase III, multicentre, randomised double-blind studies of ceftaroline fosamil (600 mg every 12 hours [q12h; CANVAS 1 and 2]; 600mg every 8 hours [q8h; COVERS]) vs vancomycin plus aztreonam (1 g q12h each [CANVAS 1 and 2]; vancomycin 15 mg/kg q12h and aztreonam 1 g q8h [COVERS]) in hospitalised adults with cSSTI. The primary efficacy variable in each trial was clinical response at the test-of-cure (TOC) visit in the modified intent-to-treat and clinically evaluable (CE) populations. Subgroup analyses exploring the impact of age and various baseline comorbidities were performed on the pooled CE population.

Results: In total, 1808 patients were included in the CE population (1005 ceftaroline fosamil; 803 vancomycin plus aztreonam). Baseline patient characteristics were generally balanced across treatment groups. Overall clinical cure rate at TOC in the CE population was 89.7% for ceftaroline and 90.8% for vancomycin plus aztreonam (difference [95% confidence interval]: −1.13 [−3.87, 1.67]). Clinical response rates at TOC by comorbidity are shown in the Table; results were generally consistent with those of the overall cSSTI population.

Conclusions: This analysis provides supportive evidence of the efficacy of ceftaroline fosamil in patients with cSSTI with underlying comorbidities.

Study sponsored by Pfizer.

Table. Clinical cure rates at TOC by baseline age and comorbidity subgroups in patients with cSSTI (CE population)

Subgroup	Number (%) of patients: Ceftaroline fosamil (N=1005)	Vancomycin + aztreonam (N=803)	Difference, % (95% CI)
Age (years)			
≤65	733/817 (89.7)	582/641 (90.8)	−1.08 (−4.12, 2.05)
>65	168/188 (89.4)	147/162 (90.7)	−1.38 (−7.77, 5.20)
Diabetes mellitus			
No	749/832 (90.0)	606/664 (91.3)	−1.24 (−4.19, 1.78)
Yes	152/173 (87.9)	123/139 (88.5)	−0.63 (−7.85, 6.96)
Peripheral vascular disease			
No	802/892 (89.9)	645/709 (91.0)	−1.06 (−3.94, 1.89)
Yes	99/113 (87.6)	84/94 (89.4)	−1.75 (−10.64, 7.54)
Cancer/malignancy			
No	877/978 (89.7)	714/784 (91.1)	−1.40 (−4.15, 1.41)
Yes	24/27 (88.9)	15/19 (78.9)	9.94 (−11.66, 34.41)
Renal status (CrCL, mL/min)[a]			
Severe impairment (>20 to ≤30)	3/4 (75.0)	0/1 (0.0)	75.00 (−31.08, 96.13)
Moderate impairment (>30 to ≤50)	39/46 (84.8)	29/37 (78.4)	6.40 (−10.43, 24.29)
Mild impairment or normal (>50)	851/946 (90.0)	695/759 (91.6)	−1.61 (−4.36, 1.20)
Body mass index (kg/m²)[b]			
<18.5	18/26 (69.2)	10/11 (90.9)	−21.68 (−44.09, 10.98)
≥18.5 to <25	312/343 (91.0)	232/258 (89.9)	1.04 (−3.66, 6.06)
≥25 to <30	569/632 (90.0)	486/533 (91.2)	−1.15 (−4.51, 2.28)

[a]Data not collected for 9 patients in the ceftaroline group and 6 patients in the vancomycin plus aztreonam group. [b]Data not collected for 4 patients in the ceftaroline group and 1 patient in the vancomycin plus aztreonam group.
CE, clinically evaluable; CI, confidence interval; CrCL, creatinine clearance; cSSTI, complicated skin and soft tissue infection; TOC, test of cure.

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Abstract 1015

Association of single nucleotide polymorphisms in IL1B and IL28B genes with the outcome of congenital *cytomegalovirus* infection

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Background: Cytomegalovirus (CMV) is the most common viral cause of congenital infections, which can result in a spectrum of neurodevelopmental disorders. The factors that render developing foetus prone to CMV are not well defined. The aim of this study was to evaluate polymorphisms in genes involved in human viral defence mechanisms in relation to risk and clinical outcome in newborns with congenital CMV infection (cCMV).

Materials/methods: This prospective study comprised 236 newborns, including 92 with cCMV infection confirmed by CMV-DNA detection in urine samples collected during the first 2–3 weeks of life (case group). A healthy control group consisted of 144 CMV-uninfected newborns. All children with cCMV infection underwent complete physical examination, ophthalmologic and hearing evaluation, and cranial ultrasound and/or magnetic resonance imaging. Using hypothesis-driven candidate genes and their function in viral infections, a panel of 8 single-nucleotide polymorphisms (SNPs, including: IL1B rs16944, IL12B rs3212227, IL28B rs12979860, CCL2 rs1024611, DC-SIGN rs735240, TLR2 rs5743708, TLR4 rs4986791, TLR9 rs352140) was genotyped in all newborns by TaqMan SNP Genotyping Assays (Applied Biosystems) and related to the outcome. The association between SNP genotype and cCMV infection or clinical outcome was analysed by co-dominant, dominant, recessive and over-dominant models.

Results: SNP in IL1B gene was associated with increased risk of cCMV under the over-dominant model [OR = 1.74 (95%CI: 1.03 – 2.95); p = 0.039]. On the other hand, analysis in the cCMV subgroup revealed that the same SNP had protective effect by reducing the risk of ventriculomegaly, under the dominant model [OR = 0.40 (95% CI 0.17 - 0.97); p = 0.039]. In addition, SNP in IL28 gene was associated with ventriculomegaly and thrombocytopenia, under over-dominant model [OR = 2.46 (95%CI 1.03-5.90); p = 0.04 and OR = 2.55 (95%CI 1.03-6.32); p = 0,042, respectively]. Genotype distribution of the remaining SNPs investigated did not show any significant differences.

Conclusions: SNP in IL1B gene may influence both the susceptibility and the clinical course of congenital CMV infection. SNP in IL28B may be associated with increased risk of ventriculomegaly and thrombocytopenia in cCMV newborns. Further, large prospective and genome-wide studies are needed to confirm these finding.

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Abstract 1018

Analytical performance evaluation of the BIOFIRE Blood Culture Identification 2 (BCID2) panel

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Abstract third-party references: BioMérieux, Biofire Diagnostics, LLC

Background: The BioFire Blood Culture Identification 2 (BCID2) Panel is the next-generation BioFire system for rapid detection of bacteria, yeast and select antimicrobial resistance (AMR) genes in positive blood cultures. Analytical studies evaluated compatibility of the panel with different bottle types and culture systems, established the limit of detection (LoD), reactivity, and specificity of the assays, and assessed the robustness of results from samples containing potentially interfering substances.

Materials/methods: Blood culture system compatibility was evaluated by determining organism titers and panel test results from seeded positive blood cultures grown to positivity (and 24 hours post-positivity) in 13 different bottle types incubated in 2 continuously monitoring blood culture systems. Limits of detection were estimated by serial dilution of contrived samples, and LoD was subsequently confirmed by detection in a minimum of 95% of 20 or more replicates. Analytical reactivity and specificity were evaluated by testing over 450 on-panel isolates and 200 off-panel species, and panel robustness was assessed by testing low-level analytes in the presence of over 50 substances. All testing used Investigational Use Only kits.

Results: Titers in positive blood cultures from different systems (0-24 hour post-positivity) ranged from ff3.0E+05 – 4.5E+07 CFU/mL for yeast and ff3.0E+06 – 3.0E+09 CFU/mL for bacteria, which are ≥30-fold higher than the detection capability of the assays (LoD of 5.0E+02 – 1.0E+04 CFU/mL for yeast and 1.0E+03 – 1.0E+06 CFU/mL for bacteria). Testing near LoD demonstrated assay reactivity with a diverse collection of species and AMR genes in isolates from around the globe, and the panel provided reliable results in the presence of potentially interfering substances. Testing at high concentration (>1.0E+08 CFU/mL) demonstrated few instances of cross-reactivity with unrelated off-panel species.

Conclusions: The BioFire BCID2 Panel assays are robust, specific, and reactive with expected diversity of bacterial and yeast causes of bloodstream infection. Rapid identification of organisms in blood culture, along with information about antimicrobial resistance gene status for select microorganisms, may aid in timely diagnosis and appropriate treatment decisions for bloodstream infections.

The panel has not been cleared for diagnostic use by the FDA or other regulatory entities.

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Abstract 1019

Activity of omadacycline and comparator agents against bacterial pathogens from the United States by infection type (2019)

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Abstract third-party references: This study was performed by JMI Laboratories and supported by Paratek Pharma, LLC, which included funding for services related to preparing this abstract.

Background: Omadacycline (OMC) is a novel aminomethylcycline approved by the FDA in 2018 to treat acute bacterial skin and skin structure infection (ABSSSI) and community-acquired bacterial pneumonia (CABP) for indicated organisms. OMC phase 2 clinical trials for the treatment of uncomplicated urinary tract infection (uUTI; NCT03425396) and acute pyelonephritis (NCT03757234) have completed. OMC has activity against bacterial isolates expressing common tetracycline (TET), penicillin, macrolide and/or fluoroquinolone resistance mechanisms.

Materials/methods: A total of 7,000 clinical isolates were collected from 31 medical centers in the United States in 2019 as part of the SENTRY Surveillance Program. Isolates were collected from bloodstream infection (25.5%), skin and skin structure infection (SSSI; 21.5%), pneumonia in hospitalized patients (21.6%), urinary tract infection (UTI; 14.8%), intraabdominal infection (5.4%), community acquired respiratory tract infection (8.9%) and other infection types (2.3%). Only 1 isolate/patient/infection episode was included. Identifications were confirmed by MALDI-TOF. Broth microdilution susceptibility testing of OMC and comparators was conducted according to CLSI M07 (2018) and M100 (2019) guidelines. Results were interpreted using FDA, CLSI (2019) and/or EUCAST (v9.0) breakpoints.

Results: OMC was highly active against Staphylococcus aureus isolates (MIC90, 0.12 mg/L; 99.0% susceptible [S]) from SSSI including 97.8% of MRSA and 97.7% of MSSA from (RTI) (Table). All (100%) Staphylococcus lugdunensis, Enterococcus faecalis (including vancomycin-resistant [R]) and Streptococcus pyogenes (including macrolide-R) isolates from SSSI were S to OMC. Similarly, 100% of Streptococcus anginosus isolates (MIC90, 0.06 mg/L; multiple infection types) were S to OMC (ABSSSI breakpoints). 99.7% of Streptococcus pneumoniae (CABP) isolates were S to OMC as were 100% of penicillin-R and tetracycline-R S. pneumoniae and all Haemophilus influenzae isolates (MIC90, 1 mg/L; CABP). OMC was active against Enterobacter cloacae (91.5%S) and Klebsiella pneumoniae (88.0%S) isolates from SSSI and K. pneumoniae isolates from RTI (91.7%S, CABP breakpoints). OMC inhibited 99.5% of Escherichia coli (MIC90, 2 mg/L) and 96.2% of K. pneumoniae (MIC90, 4 mg/L) UTI isolates at ≤4 mg/L.

Conclusions: OMC demonstrated potent *in vitro* activity against staphylococci, streptococci, *E. faecalis*, *H. influenzae*, *E. cloacae*, *K. pneumoniae*, and *E. coli* from ABSSSI, CABP, and UTI including drug-resistant isolates.

Organism (no. of isolates)	Infection Type[a]	MIC$_{90}$ (%S) OMC[b]	TET[c]	TGC[b]
Staphylococcus aureus (779)	SSSI	0.12 (99.0[d])	≤0.5 (94.7 / 92.6)	0.25 (100.0)
MRSA (314)	SSSI	0.25 (97.8[d])	≤0.5 (94.6 / 92.7)	0.25 (100.0)
MSSA (259)	RTI	0.25 (97.7[e])	≤0.5 (94.2 / 92.3)	0.25 (100.0)
Staphylococcus lugdunensis (22)	SSSI	0.06 (100.0)	≤0.5 (90.9 / 90.9)	0.06 (–)
Enterococcus faecalis (50)	SSSI	0.12 (100.0)	>16 (22.0 / -)	0.12 (100.0)
Vancomycin-R enterococci[f] (64)	All	0.12 (100.0[g])	>16 (17.2 / -)	0.12 (100.0)
Streptococcus anginosus group (12)	All	0.06 (100.0[h])	>4 (66.7 / -)	0.03 (100.0)
S. pyogenes (55)	SSSI	0.12 (100.0)	>4 (76.4 / 76.4)	0.06 (100.0)
S. pyogenes (19) Macrolide-R	All	0.12 (100.0[h])	>4 (21.1 / 21.1)	0.06 (100.0)
S. pneumoniae (323)	CABP	0.06 (99.7)	>4 (79.9 / 79.9)	0.06 (98.8)
S. pneumoniae (28) Penicillin-R (MIC≥2)	CABP	0.06 (100.0)	>4 (71.4 / 71.4)	0.06 (100.0)
S. pneumoniae (67) Tetracycline-R	CABP	0.12 (100.0)	>4 (0.0 / 0.0)	0.06 (100.0)
H. influenzae (204)	CABP	1 (100.0)	0.5 (99.5 / 99.0)	0.5 (84.7)
E. cloacae (48)	SSSI	4 (91.5[d])	>16 (83.3 / -)	1 (95.8)
Klebsiella pneumoniae (25)	SSSI	8 (88.0[d])	>16 (80.0 / -)	1 (92.0)
K. pneumoniae (120)	RTI	4 (91.7)	>16 (78.3 / -)	1 (96.7)
K. pneumoniae (105)	UTI	4 / (96.2[i])	>16 (76.0 / -)	1 (99.0)
E. coli (566)	UTI	2 / (99.5[i])	>16 (72.8 / -)	0.25 (99.8)

[a] All, all infection types; CABP, community acquired bacterial pneumonia; SSSI, skin and skin-structure infections; RTI, respiratory tract infection; UTI, urinary tract infection.
[b] FDA breakpoint interpretive criteria were used for OMC and tigecycline (TGC).
[c] CLSI/EUCAST breakpoint interpretive criteria applied.
[d] Using FDA ABSSSI breakpoint criteria for OMC.
[e] Using FDA CABP breakpoint criteria for OMC
[f] Contains 4 *E. faecalis* and 60 *E. faecium* isolates.
[g] ABSSSI breakpoints for *E. faecalis* applied for comparison purposes.
[h] ABSSSI breakpoints applied for comparison purposes.
[i] Percent inhibited at ≤4 mg/L.

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Abstract 1020

Gene expression analysis of transport channels in *Enterococcus faecium*

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Background: An important aspect of the bacterial response towards stress and environmental stimuli is alteration of gene expression levels[1]. A combination of carvacrol, cuminaldehyde, and vancomycin has previously been shown to re-sensitise vancomycin-resistant *E. faecium* (VRE) to vancomycin [2]. The effect of treatment with the novel antimicrobial combination for 60minutes on gene expression in VRE was analysed by microarray analysis. Microarray data showed that 15 genes were differentially regulated and five genes associated with transport channels were chosen for further analysis; *bcr*, *ecfa_1*, *ecsa1*, *ylob*, and *nhac_2*. A time course study using qPCR was conducted to further understand the antimicrobial mechanism of action of the novel formula.

Materials/methods: qPCR was carried out to validate the microarray data at 60mins. In addition, alterations in the expression levels of the five genes were assessed at 10mins, 30mins, 2hrs and 6hrs, in response to cuminaldehyde and carvacrol alone, in combination, and in combination with the vancomycin.

Results: VRE responds to the novel formula in the initial stages of exposure; at 10mins significant changes ($p \leq 0.05$) were demonstrated in the expression of the five genes, *bcr*, *ecfa_1*, *ecsa_1*, *ylob*, *nhac_2* with fold changes of -13.5, -1.41, -3.95, -5.67, and -6.31 respectively. At 60mins only *nhac_2* showed a significant fold change of -3.09. At 2hrs there were significant fold changes for *bcr* at 15.03, *ecfa-1* at 2.85 and *nhac_2* at 4.7, whereas at 6hrs there were no significant changes for any of the five genes tested.

Conclusions: This study has demonstrated that treating VRE with EOs alone and in combination with vancomycin has resulted in fold changes in the expression levels of the transport genes of interest. A new EO-vancomycin formulation to combat VRE could be developed through exploiting transport channels in *Enterococcus* sp.

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Abstract 1032

Prospective evaluation of serological and virological response in chronic hepatitis B genotype E treated with tenofovir or entecavir

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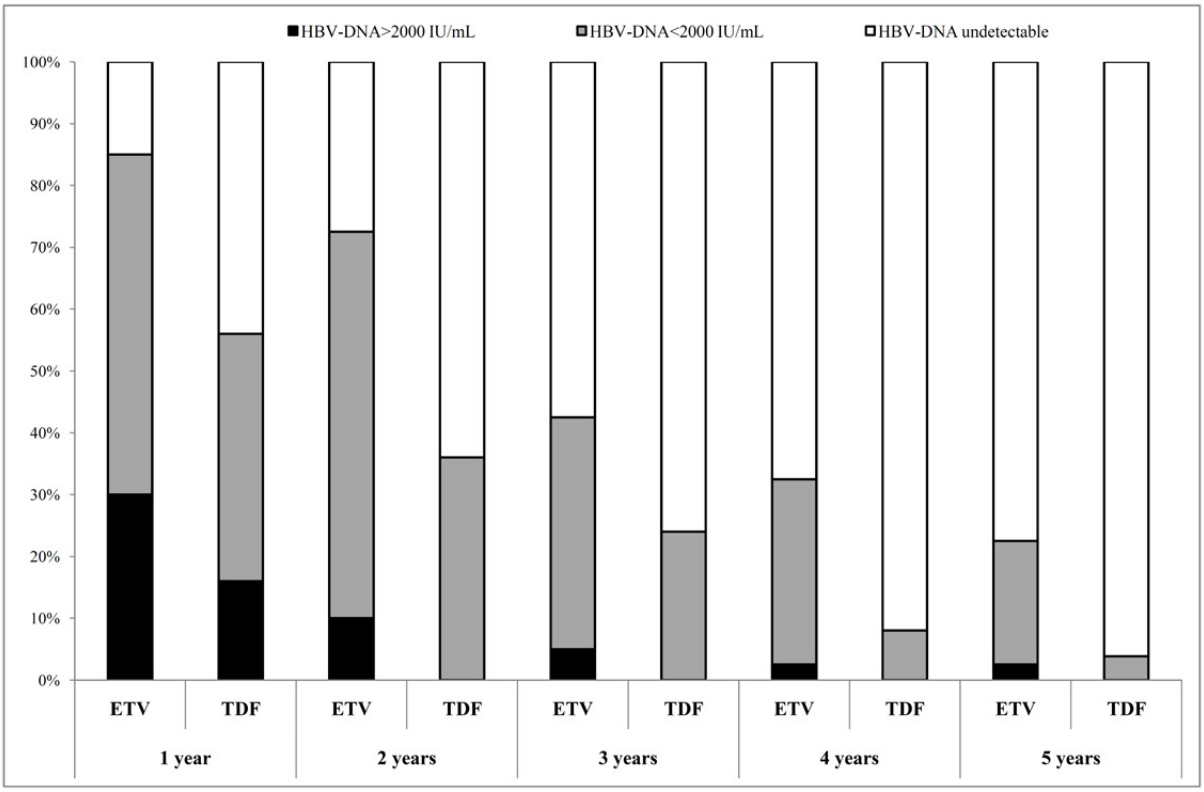
Background: European clinical practice guidelines (EASL) on chronic hepatitis B recently recognized the importance of migration flows in changing the prevalence and incidence of hepatitis B infection in low endemic European countries such as Italy and Germany. Even though differences among genotypes are reported for geographical distribution, virological and serological outcomes and response to IFN therapy, less is known about the role of different genotypes in treatment with nucleos(t)ide analogues. Phylogenetic analyses have shown that genotype E, which is mainly diffused in West Africa, is relatively recent. Decline in qHBsAg during the treatment with entecavir predict longer time to achieve HBsAg loss compared to A and D genotype.

Materials/methods: We prospectively evaluated qHBsAg decline in chronic hepatitis B, HBeAg-negative, E genotype, treated with tenofovir 245 mg (TDF) or entecavir 0.5 mg (ETV) from 2008 to 2014. Inclusion criteria were naïve patients with active chronic hepatitis B with no co-infection HCV, HDV, HIV. qHBsAg test was performed with ARCHITECT HBsAg (Abbott Diagnostics, Ireland)

Results: Sixty-five west-african patients (58; 89.2% males) were enrolled. Median age was 29 years-old [IQR 22-36] and the most prevalent route of transmission was familiar (25; 38.5%). Median liver stiffness was 7.4 kPa [IQR 4.5-9.3], ALT 65 U/L [IQR 31-122], HBV-DNA 3.4 Log IU/ml [IQR 2.8-4.5], qHBsAg 3.4 Log UI/ml [IQR 2.8-4.5]. According to clinical evaluation, 40 patients (61.5%) started ETV whereas 25 patients (38.5%) TDF. The decline in qHBsAg in ETV-patients showed a statistically significative difference compared to TDF-patients at 2 ($p<0.001$), 3 ($p< 0.001$), 4 ($p<0.001$) and 5 years ($p<0.001$). At the same time-points higher response rate in HBV-DNA suppression were observed in patients receiving TDF. In the absence of resistance-associated mutations, in 20% of ETV-patients HBV-DNA persisted detectable at 5 years. This might be explained by a lower affinity of ETV to polymerase binding site, resulting in an incomplete saturation and consequently in residual viremia.

Conclusions: In E genotype TDF-treated patients had a significantly higher decline in qHBsAg and HBV-DNA over time achieving higher rates of HBV-DNA suppression with no failure after 5 years. TDF could represent the optimal choice in this setting of patients.



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Abstract 1034

Prevalence and antimicrobial susceptibility of *Campylobacter* species isolated from Greek diarrhoeal patients (2010-2018)

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Background: *Campylobacter* species are the leading cause of bacterial foodborne illness throughout the world. In humans, most enteric infections caused by *Campylobacter* spp. are considered self-limited and generally do not require antimicrobial treatment. However, in severe or prolonged disease treatment can shorten illness duration. Aim of the present study was to determine the antimicrobial susceptibility of *Campylobacter* species isolated from stool samples of symptomatic patients in a university hospital in Crete, Greece, through a 9-year period.

Materials/methods: A total of 365 *Campylobacter* spp. were isolated from stool samples from 2010 to 2018. Identification of the isolates was performed by conventional methods and antimicrobial susceptibilities to ciprofloxacin, erythromycin, and tetracycline were assessed by the disk diffusion method. The results were interpreted by using EUCAST breakpoints.

Results: Considering a single *Campylobacter* isolate per patient, 274 *C. jejuni* subsp. *jejuni* (76.1%) and 91 *C. coli* (24.9%) isolates were identified from stool samples of patients with age ranging from 2 days to 91 years and median age 21 years. Among *C. jejuni* isolates, 74.8% (205/274) were resistant to ciprofloxacin, 1.5% (4/274) to erythromycin, and 50.7% (139/274) were resistant to tetracycline. Among *C. coli* isolates, 74.7% (68/91) were resistant to ciprofloxacin, 5.5% (5/91) to erythromycin, and 52.7% (48/91) were resistant to tetracycline. Among ciprofloxacin resistant *C. jejuni*, 1% (2/205) of isolates were found to be resistant to erythromycin, and 59% (121/205) were also resistant to tetracycline. Furthermore, 0.7% (2/274) of isolates were resistant to all three antibiotics. Similarly, among ciprofloxacin resistant *C. coli,* 7.4% were resistant to erythromycin, and 57.4% were also resistant to tetracycline. Among all *C. coli,* 4.4% (4/91) were resistant to all three antibiotics.

Conclusions: In our area, high prevalence rates of resistance to ciprofloxacin and tetracycline were observed among *Campylobacter* spp. Erythromycin remains the preferred treatment option for *Campylobacter* infections.

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Abstract 1036

Accuracy and clinical impact of fungal cell-free DNA PCR panel on plasma for diagnosis of invasive fungal infection

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Background: Invasive fungal infection (IFI) is an important cause of morbidity and mortality in oncology and transplant patients. Diagnosis of IFI is often delayed due to need for invasive biopsy and low sensitivity of conventional diagnostics. We evaluated the performance and clinical impact of a fungal cell-free DNA (cfDNA) PCR panel to noninvasively diagnose the 12 most common IFI organisms.

Materials/methods: A probe-based PCR panel targeting *Aspergillus* spp., Mucorales agents, *Candida* spp., *Fusarium* spp., *Scedosporium* spp., *Pneumocystis jirovecii* and several pathogenic dimorphic fungi was created using previously published primers and primers designed with a novel bioinformatic pipeline. Plasma cfDNA was extracted on a Promega Maxwell RSC instrument. Assay sensitivity and specificity were assessed using plasma samples from 104 patients with 115 known IFIs consisting of *Aspergillus* spp. (n = 26), Mucorales agents (n = 23), *Candida* spp. (n = 33), *Fusarium* spp. (n = 3), *Scedosporium/Pseudallescheria boydii* complex (n = 6), *Coccidioides immitis/posadasii* (n = 14), *Histoplasma capsulatum* (n = 6), *Blastomyces dermatitidis* (n = 1), and *Pneumocystis jirovecii* (n = 4); and 65 non-IFI patients. Plasma volumes ranging from 1mL to 4mL were tested. Prospective testing was carried out on high-risk patients to determine clinical impact on antifungal therapy and patient management.

Results: Sensitivity and specificity of fungal cfDNA PCR on banked plasma samples from patients with proven IFI and non-IFI controls was 56.5% (65/115) overall, and 69.6% (48/69) in cases tested with higher (optimal) plasma volume. In optimal volume samples, sensitivity was 91.7%, 57.9%, and 77.3% for Mucorales, *Aspergillus* spp., and *Candida* spp., respectively. Overall specificity was 99.4%. In a prospective evaluation of 155 patients with suspected IFI, fungal cfDNA testing was positive in 19.4%, leading to positive clinical impact in 40.0% of patients. Clinical impact was highest in patients with a diagnosis of Mucorales infection, with 81.8% (9/11) of results leading to therapeutic optimization or avoidance of surgical biopsy.

Conclusions: Fungal cfDNA detection with a PCR panel offers a rapid and accurate non-invasive approach for early diagnosis of IFI, providing actionable results for personalized treatment.

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Abstract 1038

High prevalence of multi-stress tolerant *Campylobacter* species causing human infection

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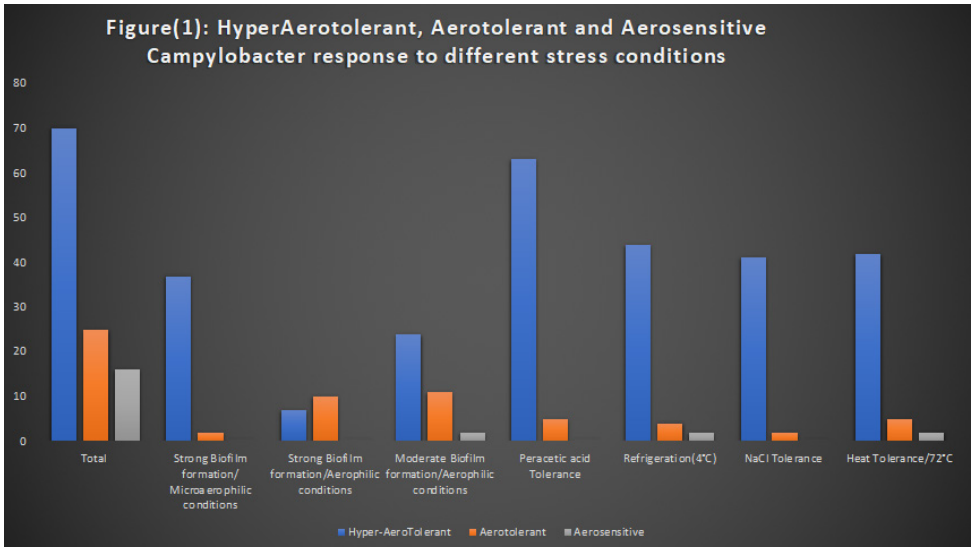
Background: *Campylobacter jejuni* and *Campylobacter coli* are zoonotic pathogens commonly associated with human gastroenteritis. The main cause of human campylobacteriosis is consumption of contaminated poultry meat and other sources as raw milk. *Campylobacter*s encounter variety of stress conditions that potentially affect bacterial survival during food processing, preservation, and cooking; thus, impacting their transmission to humans through the food chain. To survive under harsh conditions, biofilm formation is suggested to be another mechanism for bacterial adaptation in the food environment, thus switching its physiological state to promote survival under stress conditions. The aim of this study is to access the resistance of *Campylobacter* isolates to adverse stress conditions encountered throughout the food chain and compare the biofilm-forming ability of these strains under both microaerobiosis and aerobiosis.

Materials/methods: Phenotypic stress tolerance of (n=111) *C. jejuni* and *C. coli* isolates recovered from three different sources including patients suffering from gastroenteritis (n=57), broiler carcass (n=30), and dairy products (n=24) was investigated. To assess the capabilities of hyper-aerotolerant (HAT) and aerotolerant (AT) strains to survive under harsh conditions in foodborne transmission and infection, the survival rate of these isolates under different stress conditions (aerotolerance, temperature variations, freezing and thawing, peracetic acid treatment and osmotic stress) that can be encountered during food processing was investigated. Moreover, the capability of isolates to form biofilm under microaerophilic and aerophilic conditions was examined using crystal violet biofilm assay.

Results: HAT strains were highly dominant presenting 63% of the tested isolates, 22% were AT whereas 11% were aero-sensitive (AS). HAT strains exhibited a significant tolerance to stress conditions compared to AS and AT strains (Figure (1)). Analyzing the tendency of biofilm formation, it was found that half of HAT strains formed biofilm under microaerophilic/normal conditions while 44% and 85% of HAT and AT strains successfully formed biofilms under aerophilic conditions, respectively.

Conclusions: The enhanced ability of HAT strains to cope to numerous stressors (cross protection), and to form biofilm, would potentially impact human infection by increasing the potentials of the foodborne transmission of *Campylobacter* under aerobic conditions. Thus, HAT strains would potentially be of higher transmission risk than AS ones.



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Abstract 1040

Trends in resistance of bloodstream infection pathogens in Northwest Russia from 2015 to 2018

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Abstract third-party references: This abstract was produced and data collected as part of the Nordic Council of Ministers' Programme "Nordic-Russian Cooperation on Antimicrobial Resistance (AMR) Containment, 2019-2020.

Background: The Nordic Council of Ministers launched in 2019 a Nordic-Russian Cooperation Programme on Antimicrobial Resistance, and this study was proposed as part of the baseline mapping in five Russian partner-regions of the cooperation programme.

Materials/methods: Results of blood cultures and their antimicrobial susceptibility from 5 laboratories of the Northwest Russia (Karelia Republic, Arkhangelsk Oblast, Murmansk Oblast, Pskov Oblast and St. Petersburg City) between 2015 and 2018 were analysed. Antimicrobial resistance was determined by EUCAST or CLSI criteria.

Results: A total of 55,839 blood samples were investigated and 3,026 microorganisms detected (average level at 5.4%). *Staphylococcus aureus* (1055/34.9%) and *Klebsiella pneumoniae* (695/23.0%) were the most frequently identified bacteria followed by *Escherichia coli* (476/15.7%), *Enterococcus faecium* (474/15.7%), *Acinetobacter baumannii* (235/7.8%) and *Pseudomonas aeruginosa* (91/3.0%). A considerable increase in the proportion of positive cultures was observed: 3.7% (2015) – 4.1% (2016) – 5.9% (2017) – 9.4% (2018). An increase in *K. pneumoniae* detection was seen: 14.1% (2015) –18.4% (2016) – 25.8% (2017) – 28.8% (2018). In contrast, a decrease was noted in the frequency of *S. aureus* (38.0% vs 32.3%) and *E. coli* (18.2% vs 13.7%). The levels of *E. faecium*, *A. baumannii* and *P. aeruginosa* remained stable.

The average proportion of MRSA through the study period was 17.1% (180/1055). The proportion of ESBL-producing *K.pneumoniae* decreased from 70.2% in 2015 to 34.8% in 2018, with average at 49.2%. On average, carbapenem-resistant *K. pneumoniae* was registered in 32.9% cases (229 samples). Over the study period, the proportion of carbapenem-resistant *K. pneumoniae* increased: 16.7% (2015) – 20.3% (2016) – 47.4% (2017) – 46.3% (2018). The level ESBL-producing *E. coli* varied from 30.6% to 51.0%, showing an increasing tendency (average resistance proportion at 40.5%). A total of 10 carbapenem-resistant *E. coli* cultures were identified (average 2.1%). The detection of vancomycin-resistant *E. faecium* remained low (average 1.3%).

Conclusions: The increased pathogen detection, mainly due to *K. pneumoniae*, and an enhancement in the level of resistant Enterobacteriaceae shows the importance of further systematic harmonized surveillance and regional cooperation in the Northwest Russia to build adequate response. In the participating regions, microbiology results are stored based on the number of tests, therefore methodology requires standardization.

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Abstract 1041

Healthcare-associated infections reporting in developing countries: challenges and corrective measures

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Background: Health-care associated infections (HAIs) are the most frequent types of adverse events for providing health care. HAIs surveillance system is a critical part of their prevention and control. The accuracy of HAIs reporting in Iran appears to be questionable. This paper seeks to address challenges of HAIs reporting in national Iranian Nosocomial Infection Surveillance System (INIS) and discusses how to solve them.

Materials/methods: The study has been conducted with qualitative approach in two phases. In order to explore effective factors on HAIs case finding and reporting in INIS six related documents and opinions of sixteen experts were analyzed using Walt and Gillson's policy analysis framework. The experts were selected from hospitals affiliated with Tehran University of Medical Sciences (TUMS) and Ministry of Health (MOH). Consequently an expert panel session was hold due to provide the best strategies to deal with each of reported issues.

Results: Inappropriate organization structure, poor documentation, lack of participation of stakeholders, inadequate educational programs, health planning without scientific evidences, deficits in executive and evaluation infection prevention and control, individual conflicts of interest lead to poor case finding and reporting of HAIs in INIS. Identifying the lead organization for infection prevention and control programs (IPCs), managerial supports from IPCs, advocacy in order to enhancing health staffs knowledge and participation, developing and implementation a comprehensive HAIs information management system, and provide appropriate job motivation for infection prevention and control team in hospitals are suggested strategies to improve HAIs case finding and reporting in INIS.

Conclusions: Our findings indicate that a number of organizational and individual factors lead to inaccurate HAIs reporting in INIS. Accurate case-finding and reporting needs the implementation of some strategies to enhance staffs capabilities and motivation, updating guidelines and software and changing in organizational structure.

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Abstract 1042

Survey of attitudes, beliefs, and knowledge of community pharmacists in the United States on antimicrobial stewardship

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Background: Approximately 50% of antibiotics are either inappropriate or unnecessary; a problem that antimicrobial stewardship (AMS) programs seek to address. Even though the majority of antibiotic prescribing occurs in the outpatient community setting, most AMS programs are focused on inpatient training and services. In order to address the feasibility of community AMS programs, we performed a cross-sectional survey of community pharmacists investigating their attitudes, beliefs and knowledge towards community-based AMS services.

Materials/methods: The electronic survey was distributed over 6 weeks from June 12, 2019 through July 24, 2019 to pharmacists licensed in the state of Washington, U.S.A. The 40 item survey instrument was developed based on a review of the published literature. We ensured all questions and answer choices were pertinent to community pharmacy respondents. The survey included the following domains: perceptions towards AMS, current pharmacy practices, perceived barriers and facilitators to community AMS services. The questionnaire was pilot tested for readability, length and relevance of specific items. Survey participants were included if they had experience in a community pharmacy setting and completed at least one category of AMS questions.

Results: A total of 204 participants met inclusion criteria. Respondents were mostly female (63.2%), aged 30 – 39 years old (38.7%) and between 1 – 10 years of experience (38.7%). A majority of pharmacists agreed that AMS is important to improve patient care (90.1%), reduce inappropriate antimicrobial use (85.7%),and reduce antimicrobial resistance (89.7%). However, 40.3% of pharmacists disagreed that they have the necessary training to participate in AMS. Most pharmacists actively participate in AMS activities such as contacting the prescriber for appropriateness (73.9%), antimicrobial prescription checking for adverse drug reactions or allergies (92.1%) and effectively counseling on appropriate use of antimicrobials (92.1%). Some potential perceived barriers identified were time (39.0%) and financial compensation (68.7%). Lastly, facilitators for community AMS identified were education to patients (82.4%) and healthcare providers (90.2%) and increased access to patient electronic health record (92.3%).

Conclusions: Our results suggest that AMS is important to patient outcomes in the community setting and could be implemented when identified barriers are addressed.

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Abstract 1043

In vitro surveillance of eravacycline against Gram-positive pathogens, including resistant isolates, collected from European hospitals in 2018

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Background: Eravacycline (ERV) is a fully-synthetic, fluorocycline antibacterial approved for the treatment of complicated intra-abdominal infections (cIAI) in patients ≥18 years of age in both Europe and the US. Previous surveillance studies of ERV have demonstrated potent *in vitro* activity against specific Gram-positive pathogens. The purpose of this study was to further monitor the *in vitro* activity of ERV against *Staphylococcus aureus* (including methicillin-resistant *S. aureus*, MRSA), *Enterococcus* spp. (including vancomycin-resistant *Enterococcus*, VRE) and *Streptococcus* spp.

Materials/methods: Clinical isolates were collected from European hospitals during 2018 from multiple infection sources, including bodily fluids, gastrointestinal, genitourinary and respiratory. Minimum inhibitory concentrations (MICs) were determined by CLSI broth microdilution. Antibiotic susceptibility was determined with EUCAST version 9.0 breakpoints.

Results: Summary MIC data for ERV and select comparators are shown in the Table. The MIC_{90} values of ERV for *S. aureus, Enterococcus* spp. and *Streptococcus* spp. were 0.12 mg/L, 0.12 mg/L and 0.03 mg/L, respectively. ERV MICs were 2- to 8-fold lower than tigecycline. ERV susceptibilities ranged from 94.7–100%, including for resistant organisms.

Conclusions: ERV demonstrated high susceptibility rates against clinically important Gram-positive pathogens, including resistant isolates. Furthermore, ERV MIC values were up to 8-fold lower than for tigecycline. This activity suggests ERV play a role in empiric treatment choice for cIAI where Gram-positive pathogens are suscepted as part of causative infection flora.

Organism (N)	Eravacycline $MIC_{50/90}$ %S	Tigecycline $MIC_{50/90}$ %S	Vancomycin $MIC_{50/90}$ %S	Daptomycin $MIC_{50/90}$ %S
Staphylococcus aureus (220)	0.06/0.12 98.6%	0.25/0.25 99.6%	1/1 100%	0.25/0.5 100%
MSSA (163)	0.06/0.12 100%	0.12/0.25 100%	1/1 100%	0.25/0.5 100%
MRSA (57)	0.06/0.25 94.7%	0.25/0.25 98.3%	1/1 100%	0.25/0.5 100%
Enterococcus spp. (410)	0.06/0.12 99.3%	0.12/0.5 89.0%	1/2 90.7%	2/4 --
Enterococcus faecalis (197)	0.06/0.12 100%	0.12/0.5 86.3%	1/2 99.0%	1/2 --
Enterococcus faecium (213)	0.06/0.06 98.6%	0.06/0.25 91.6%	1/>16 83.1%	2/4 --
VRE (37)	0.06/0.06 97.4%	0.06/0.5 89.5%	>16/>16 0%	2/4 --
Streptococcus anginosus group[a] (23)	0.015/0.03 100%	0.03/0.06 100%	0.5/1 100%	0.25/0.5 --

Units in mg/L; $MIC_{50/90}$ - minimum inhibitory concentration required to inhibit growth of 50/90% of isolates; %S - percent susceptible; [a]*S. anginosus, S. constellatus, S. intermedius*

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Abstract 1044

No benefit with empiric aminoglycosides in paediatric febrile neutropenia: analysis of a nationwide cohort study

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Background: Antibiotics are used to reduce morbidity and mortality in children with febrile neutropenia (FN) undergoing treatment for malignancy, but variation exists among guidelines for prescribing, especially with regard to aminoglycoside therapy.

Materials/methods: We aimed to review antibiotic prescribing and guideline compliance in children with febrile neutropenia. We analyzed data from the prospective PICNICC cohort study, collected from children <18 years admitted to tertiary centers in Australia with FN between November 2016 and January 2018.

Results: Among 858 episodes of febrile neutropenia, children were prescribed up to 4 concurrent antibiotics in the first 12 hours. Piperacillin-tazobactam was the most commonly prescribed antibiotic (n=519, 60.5%) and aminoglycosides were prescribed in 255 episodes (29.7%). Of 1380 antibiotics prescribed in total, 1285 (93.1%) were marked by site research assistant as compliant with local hospital guidelines. Composite unfavorable outcome of death, ICU admission, relapse of infection or late-onset sepsis occurred in 54 episodes (6.3%). In FN episodes with receipt of aminoglycosides in the 1st 12 hours, the adjusted hazard ratio for unfavorable outcome was 3.1 (95% CI 1.7-5.7). On independent assessment of state guideline criteria, 46% (n=184) of guideline-eligible patients did not receive an aminoglycoside but there was no increased risk of unfavorable outcome in this group.

Conclusions: We found substantial variation in antibiotic prescribing for febrile neutropenia in this cohort. We found no evidence for improved outcome with aminoglycosides, even in those who met local guideline criteria for this therapy. Aminoglycosides appear to be associated with unfavorable outcome when given empirically for FN in children and their inclusion in guidelines should be reviewed.

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Abstract 1045

In vitro surveillance of eravacycline against Gram-negative pathogens, including multidrug-resistant isolates, collected from European hospitals in 2018

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Background: Eravacycline (ERV) is a fully-synthetic, fluorocycline antibiotic approved for the treatment of complicated intra-abdominal infections (cIAI) in patients ≥18 years of age in Europe and the US. The purpose of this study was to monitor the *in vitro* activity of ERV against European Gram-negative isolates, including multidrug-resistant (MDR) isolates, collected in 2018.

Materials/methods: Isolates were collected during 2018 from various body sites. Minimum inhibitory concentrations (MICs) were determined by CLSI broth microdilution. Antibiotic susceptibility was determined with EUCAST version 9.0 breakpoints. MDR was defined as resistance to ≥3 antibiotics from aztreonam, a carbapenem (meropenem or ertapenem [ETP]), cefepime/cefotaxime/ceftazidime/ceftriaxone (any one), gentamicin, levofloxacin, piperacillin-tazobactam, tetracycline or tigecycline (TIG).

Results: Summary MIC data for ERV and select comparators are shown in the Table. ERV MIC_{90} values for all-*Enterobacteriaceae* and MDR-*Enterobacteriaceae* were 0.5 mg/L and 1 mg/L, respectively. ERV MIC_{90} for MDR-*Enterobacteriaceae* was within one dilution as compared for all-*Enterobacteriaceae* isolates. ERV susceptibilities ranged from 81.6–99.5% for *Enterobacteriaceae* and were greater than ETP for all- and MDR-*Enterobacteriaceae.* ERV $MIC_{50/90}$ against carbapenem-resistant *Acinetobacter baumannii* (CRAB) were 4-fold lower than TIG.

Conclusions: ERV exhibited potent *in vitro* activity and higher susceptibility rates than TIG against clinically important Gram-negative pathogens, including resistant isolates. This ongoing surveillance further demonstrates the benefit of ERV in the treatment of cIAI, particularly where *Enterobacteriaceae* are suspected as the causative agent.

Organism (N)	ERV $MIC_{50/90}$ %S	TIG $MIC_{50/90}$ %S	ETP $MIC_{50/90}$ %S
Enterobacteriaceae (1044)	0.25/0.5 92.2%	0.5/2 68.2%	0.015/0.5 92.0%
Citrobacter freundii (200)	0.25/0.5 95.0%	0.5/2 75.5%	0.015/0.25 96.0%
Enterobacter cloacae (205)	0.25/1 89.3%	0.5/2 64.9%	0.06/1 81.5%
Escherichia coli (210)	0.25/0.25 99.5%	0.25/1 81.9%	0.015/0.06 99.1%
Klebsiella oxytoca (206)	0.25/0.25 96.6%	0.25/2 73.3%	0.015/0.03 99.0%
Klebsiella pneumoniae (223)	0.25/1 81.6%	1/4 47.1%	0.03/>8 84.8%
MDR-*Enterobacteriaceae* (248)	0.25/1 81.6%	0.5/2 52.9%	0.25/>8 68.6%
Stenotrophomonas maltophilia (40)	0.5/2 --	1/2 --	NT
CRAB (201)	0.5/1 --	2/4 --	NT

Units in mg/L; $MIC_{50/90}$ - minimum inhibitory concentration required to inhibit growth of 50/90% of isolates; %S - percent susceptible; NT - not tested

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Abstract 1054

Establishment and clinical application of a multiple touchdown PCR for detection of carbapenemase genes

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Background: Carbapenem-resistant *Enterobacteriaceae* (CRE) is rising rapidly all over the world. Early detection and identification of carbapenem resistant bacteria are important to control the spread and outbreak of infection. In the present study, we established a multiple touchdown PCR (MT-PCR) assay for detection of five carbapenemase genes.

Materials/methods: CRE resistant genes, including *bla*OXA-48 *bla*IMP *bla*VIM *bla*NDM and *bla*KPC were selected as target genes. The bla_{IMP} carried *P. aeruginosa* bla_{VIM} carried *P. putida* bla_{NDM-1} carried *K. pneumoniae* bla_{KPC-2} carried *K. Pneumonia bla*OXA-48 carried *E. Coli* (DH5α) were applied as positive controls, and the bacteria carried no target genes as negative control. The MT-PCR assay was developed and subsequently analyzed the specificity, sensitivity, and clinical application performance.

Results: The MT-PCR assay was successfully established for the detection of five carbapenemase genes, with limits of detection of 2×10^2 cfu/mL for *bla*OXA-48, *bla*VIM and *bla*KPC, and 2.0×10^3 cfu/mL for *bla*IMP and *bla*NDM. The results obtained from MT-PCR were completely consistent with single PCR in the detection of 42 carbapenem-resistant clinical isolates. Compared to antimicrobial susceptibility testing (AST) as the reference method, there was no significant difference between the results from MT-PCR (genotype) and the results from AST (phenotype) in the detection of 67 clinical sterile body fluid samples, and the clinical sensitivity and specificity was 80% and 100%, respectively.

Conclusions: The MT-PCR assay can be effectively used to detect five carbapenemase genes in clinical isolates and sterile body fluid samples.

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Abstract 1057

Impact of an antimicrobial stewardship team on the de-escalation of carbapenem use in a tertiary hospital

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Background: Carbapenems have a broad spectrum of activity and are used for empirical therapy against life-threatening infections. When inappropriate carbapenem use, such as prolonged therapy, is observed, a de-escalation (DE) strategy would change to a narrower spectrum antibiotic when susceptible bacteria were identified. However, the DE strategy has not been considered in clinical settings. We aimed to determine whether an antimicrobial stewardship team (AST) intervention could promote DE of carbapenem therapy.

Materials/methods: The AST intervention, launched in July 2017, consisted of a daily post-prescription review and feedback (PPRF) strategy. We evaluated the rate of switching to other antimicrobials or discontinuing carbapenems within 7 days during the pre-intervention (from July 2016 to June 2017) and post-intervention (from July 2017 to June 2018) period. DE was defined as changing to a narrower spectrum beta-lactam antimicrobial or by discontinuation of the carbapenem.

Results: A total of 2,685 patients were prescribed carbapenems. Confirming the use with prescribers by face-to-face or telephone contact was the primary intervention by AST (976/1,350), followed by a recommendation for discontinuation or change to another antibiotic (720/1,350). The rate of change to narrower spectrum beta-lactams significantly increased during the post-intervention period (7.0% vs. 13.0%; P < 0.001; Table). In a multivariate analysis, AST intervention was significantly associated with DE therapy (odds ratio: 1.30; 95% confidence interval: 1.10–1.54; P = 0.002).

Conclusions: Daily PPRF by AST could enhance the carbapenem antimicrobial stewardship by accelerating DE of carbapenem.

Table

Category	Pre-intervention (n=1,335)	Post-intervention (n=1,350)	P-value
Discontinuing ≤ 7 days	29.0%	28.8%	0.921
Continuing > 7 days	54.1%	51.2%	0.133
Change to narrower spectrum beta-lactams	7.0%	13.0%	<0.001
Change to other class antibiotics (other than beta-lactams)	4.9%	2.7%	0.004
Parenteral to oral conversion	5.0%	4.3%	0.374

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Abstract 1058

Essential human resources for antimicrobial stewardship teams in Japan: estimates from a nation-wide survey

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Background: Antimicrobial stewardship requires structural prerequisites for implementation of antimicrobial stewardship programs (ASPs), such as the presence of a multidisciplinary antimicrobial stewardship team (AST). In 2018, we reported data of a nationwide survey on the implementation of ASPs and staff resources in Japan. The survey revealed a shortage in manpower at most Japanese hospitals. The study aimed to describe the potential staffing structures for ASTs proposed based on a nationwide survey conducted by the Japanese Society of Chemotherapy (JSC).

Materials/methods: Data on implemented ASPs and staff full-time equivalents (FTEs) at 1358 healthcare facilities, which were collected by the nationwide ASP survey of JSC in 2018, were analyzed. Multivariate analysis was performed to evaluate whether physician and pharmacist FTEs were associated with the number of implemented ASPs in each facility, defined as the number of responses in the previous survey.

Results: Table 1 presents independent factors related to the number of implemented ASPs. Middle-to-large hospitals, additional reimbursement for infection prevention, presence of an on-site microbiology laboratory, AST organization, physician FTE, and pharmacist FTE were significantly associated with the increased number of implemented ASPs. Additional reimbursement was the strongest contributor for the implementation of ASPs. Among factors regarding staff resources, the contribution of pharmacist FTE to the implementation of ASPs was stronger than that of physician FTE.

Conclusions: Our nationwide survey analysis revealed that pharmacist and physician FTEs were significantly associated with the implementation of ASPs after adjustment for several confounders. The current findings reveal the human resources for core members of ASTs that are required for the implementation of functional and sustainable ASPs at Japanese hospitals. This study provides a directive for structural and financial support of ASTs and should aid in planning for the enhancement of AST practices.

Table 1

factors	β (95%CI)	Standardized β
Number of beds (≥301)	2.5 (1.8–3.3)	0.16
Additional reimbursement	6.3 (5.5–7.1)	0.33
Microbiology laboratory	3.0 (2.2–3.7)	0.19
AST organization	4.2(3.4–5.1)	0.22
Physician FTE, 0.5 increase	1.3 (0.7–1.9)	0.09
Pharmacist FTE, 0.5 increase	2.1 (1.4–2.7)	0.14

β, partial regression coefficient; CI confidence interval; AST, antimicrobial stewardship team; FTE, full-time equivalent

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Abstract 1063

Diagnostics value of Epstein-Barr virus DNA load in whole blood and plasma from paediatric transplant recipients

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Background: High and/or rising EBV viral loads pose a risk for development of EBV-related post-transplant lymphoproliferative disorder (PTLD), hence quantitative EBV DNA testing was incorporated into routine medical practice to assist in diagnosis and monitoring of transplant recipients. However, there is no consensus regarding the threshold of EBV DNA that warrants preemptive therapy or further diagnostic workup as well as there is no consensus on optimal component of peripheral blood for measuring viral loads. The aim of the study was to assess the utility of EBV DNA monitoring in whole blood (WB) and plasma in paediatric liver transplant recipients (LTx).

Materials/methods: This prospective study included 1262 matched WB and plasma samples from 296 LTx patients. To evaluate the diagnostic performance of an EBV DNA*emia* in whole blood and plasma, a receiver operating characteristics (ROC) curve analysis were conducted. Apart from 2 patients with PTLD confirmed within the study period, data of EBV DNA*emia* in additional 9 samples (including 5 WB and 4 plasma samples) of 4 patients included in the study but with PTLD diagnosed before (2 patients) and after (2 patients) the study period, were included in the ROC analysis.

Results: Higher EBV DNA*emia* in both whole blood and plasma was detected in patients with PTLD compared to non-PTLD patients (median 4.23 vs 3.48 $\log_{10}$copies/mL; p = 0.044 and median 3.97 vs 1.7 $\log_{10}$copies/mL; p < 0.0001, respectively for WB and plasma samples). The value of the area under the ROC curve was 0.96 (95% CI 0.94 - 0.99; p = 1.2×10^{-24}) and 0.83 (95% CI 0.76 - 0.90; p = 7.0×10^{-5}) for EBV DNA load in plasma and WB, respectively (Figure). The optimal cut-off value of EBV DNA*emia* in plasma was 2.4 $\log_{10}$copies/mL with sensitivity of 100%, specificity of 92.8%, positive predictive value (PPV) of 8.2% and negative predictive value (NPV) of 100%, whereas optimal cut-off value for EBV DNA*emia* in WB was 3.4 $\log_{10}$copies/mL, with sensitivity of 100%, specificity of 70.3%, PPV of 2.4% and NPV of 100%.

Conclusions: Monitoring of EBV DNA in plasma samples had better diagnostics performance compared to WB.

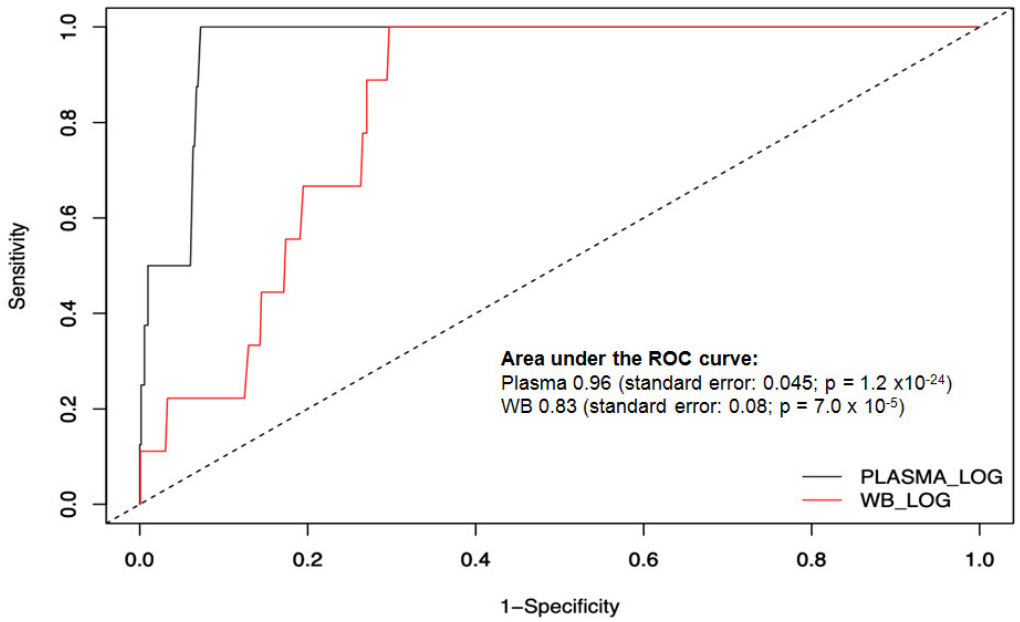

Figure. A receiver operating characteristic (ROC) curve of EBV DNA*emia* in whole blood (WB) and plasma for identification PTLD.
The ROC curve analysis, included samples obtained from 290 non-PTLD patients and 6 PTLD patients. Only samples collected up to one month prior to and at the PTLD diagnosis were considered (samples of PTLD patients collected after treatment was initiated, were excluded).
The true positive rate (sensitivity) is plotted in function of the false positive rate (1- specificity) for different cut-off points.

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Abstract 1065

HLA-DPB1*05:01 is associated with adverse drug reactions to rifampin and isoniazid for treatment of latent tuberculosis infection in South Korea

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Background: Healthcare-workers (HCWs) with latent tuberculosis infection (LTBI) are a potential risk group for tuberculosis leading to its transmission to other HCWs and patients. Therefore, screening and treatment for LTBI are recommended in HCWs. However, adverse drug reactions (ADRs) for rifampicin (RFP) and isoniazid (INH) is often challenging in initiating and completing LTBI treatment. Previous pharmacogenetics studies have reported the association of variants in the human leukocyte antigen (HLA) region with a drug-associated hypersensitivity reaction. The purpose of this study is to evaluate the association between HLA polymorphism and RFP- and INH-associated ADRs.

Materials/methods: The present analysis included HCWs who have begun treating LTBI with 3 month-regimen of RFP and INH between February and September 2017 and agreed to perform the HLA genotyping. Participants were questioned about and examined for adverse events during treatment. Association analysis for HLA alleles were conducted with PyHLA for ADRs to RFP and INH.

Results: A total of 66 subjects were enrolled; 13 (19.7%) of them met the criteria for hypersensitivity reaction while on RFP and INH treatment. Among 53 treatment tolerant group, 15 participants showed mildly elevated liver enzymes during the follow-up monitoring. In association analyses for HLA alleles with hypersensitivity reaction, we observed the HLA-DPB1*05:01 allele was associated with an increased risk of hypersensitivity reaction (OR, 4.13; 95% CI, 1.47-11.59; $p = 0.0539$). In a subgroup-analysis for moderate hypersensitivity reaction, strong associations were identified in DPB1*05:01 (OR, 9.0; 95% CI, 2.37-41.34; $p = 0.0009$) and DQA1*01:02 (OR, 7.44; 95% CI, 1.80-30.85; $p = 0.0354$). We also found an additional effect of the DPB1*05:01 for mild hepatotoxicity (OR, 5.78; 95% CI, 2.17-15.36; $p = 0.0026$).

Conclusions: The majority of participants with HLA-DPB1*05:01 allele had higher hypersensitivity reaction on RFP and INH therapy than participants without. The presence of HLA-DPB1*05:01 was also associated with an increased risk for mild hepatotoxicity during RFP and INH treatment. Our results indicated patients carrying the HLA- DPB1*05:01 allele were correlated with a considerable higher risk of ADRs to RFP and INH in the Korean population.

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Abstract 1066

Triple site versus urine only N. gonorrhoea/C. trachomatis testing among Israeli MSM in the condom fatigue era: a prospective study

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Background: *Chlamydia trachomatis* (CT) and *Neisseria gonorrhoea* (NG) are the most common sexual transmitted infections (STIs) especially among men who have sex with men (MSM). Three site testing is the recommended test for asymptomatic sexually active MSM, especially for those who are using pre exposure prophylaxis or living with HIV, practicing condom less sex. STIs such as *C. trachomatis* and *N. gonorrhoea* are site specific and are detectable mostly at the infection site. We prospectively compared triple site and urine only *C. trachomatis* and *N. gonorrhoea* testing among asymptomatic Israeli MSM.

Materials/methods: Asymptomatic MSM > 18 years of age were eligible to participate if they had not received any relevant antibiotic treatment in the previous 3 months. Participants provided informed consent, received verbal and written instructions on specimen collection and then self-collected a urine specimen, pharyngeal and rectal swabs. All samples were tested on site using the Xpert CT/NG assay (Cepheid, Sunnyvale, California, USA), according to manufacturer's instructions.

Results: The study cohort included 218 male participants. 34.5% were using PrEP, 24.3% were HIV carriers. 64 participants (29%) were positive to *C. trachomatis* or *N. gonorrhoea* in one of the tested sites or more. N. gonorrhoea was detected among 56% (47 samples) of the positive samples while in 44% (37 samples) of them *C. trachomatis* was detected**.** Most of detected samples were obtained from rectal swabs (61%), additional 35% were obtained from oral swabs, only 2.2 % were obtained from urine samples.

Conclusions: High infection rates (29%) were detected among asymptomatic Israeli MSM tested for *C. trachomatis* and *N. gonorrhoea*, in one or more of the tested sites, mostly rectal. Urine testing had a very low sensitivity raising the question of necessity to screen urine in asymptomatic MSM. The current study underscores the importance of triple site testing for a highly at-risk population.

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Abstract 1070

Performance evaluation of the Xpert HBV Viral Load assay for the quantification of hepatitis B virus DNA in plasma samples

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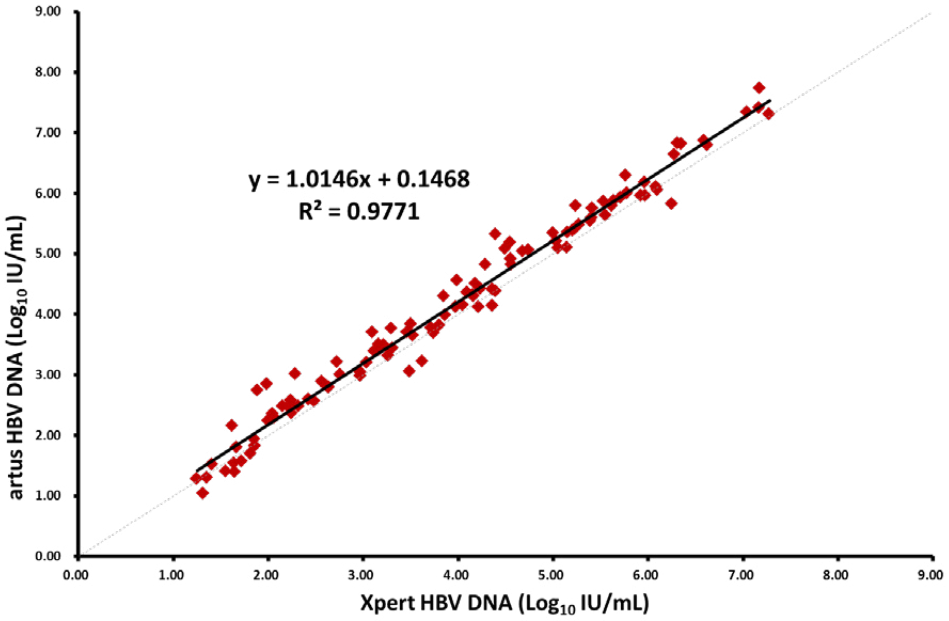
Background: Accurate quantification of Hepatitis B virus (HBV) DNA in the patients with chronic HBV infection is important for providing treatment indication and monitoring treatment efficacy. In this study, we would like to evaluate the performance of the new Cepheid Xpert HBV Viral load assay (Xpert-HBV) in comparison to the QIAGEN artus HBV QA-RGQ kit (artus-HBV) for the quantification of HBV DNA in plasma sample. Also, the analytical characteristics of Xpert-HBV were studied.

Materials/methods: A total of 137 archived plasma samples that submitted to our laboratory for HBV DNA quantification between January and October 2016 were used for performance evaluation. All plasma specimens were processed and quantified for HBV DNA using Xpert-HBV and artus-HBV. To access the analytical sensitivity and the precision of Xpert-HBV, a standard panel of HBV containing plasma sample (AcroMetrix HBV Panel 1.2 mL, Thermo Scientific) was serially diluted to 7 HBV concentrations (5, 10, 25, 50, 100, 250 and 500 IU/mL), in which 5 replicates of each HBV DNA concentration were tested.

Results: Of the 137 samples tested, 133 (97.1%) had the qualitative results that agreed on the two platforms. All 4 samples with the discordant qualitative result (detected by artus-HBV but not by Xpert-HBV) had the HBV viral load below the limit of detection of artus-HBV (<10.22 IU/mL). Further analysis of 107 samples quantified by both assays showed an excellent correlation (R^2=0.9771) across the dynamic range of quantification. Average bias between two assays, as determined in Bland-Altman analysis, was 0.20 Log_{10} IU/mL (Xpert minus artus-HBV; ±1.96 S.D: -0.29 to 0.70 Log_{10} IU/mL). All the replicates in 7 different HBV DNA concentrations of the standard panel tested positive by Xpert, except a replicate of 5 IU/mL. The precision of Xpert over the 5 HBV DNA concentrations (25, 50, 100, 250 and 500 IU/mL) ranged from 2.3% to 8.5%.

Conclusions: An excellent correlation between Xpert and artus-HBV could be demonstrated in this study. The good clinical and analytical performance, random access capability and rapid turnaround (ff60 minutes per samples) make the assay becomes a valuable tool for HBV DNA quantification in hospital-based laboratories.



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Abstract 1071

Performance evaluation of the Alinity m HBV assay for the quantification of hepatitis B virus DNA in plasma samples

Hoyin Lam*[1], Man Kin Ng[1], Bone Tang[1]

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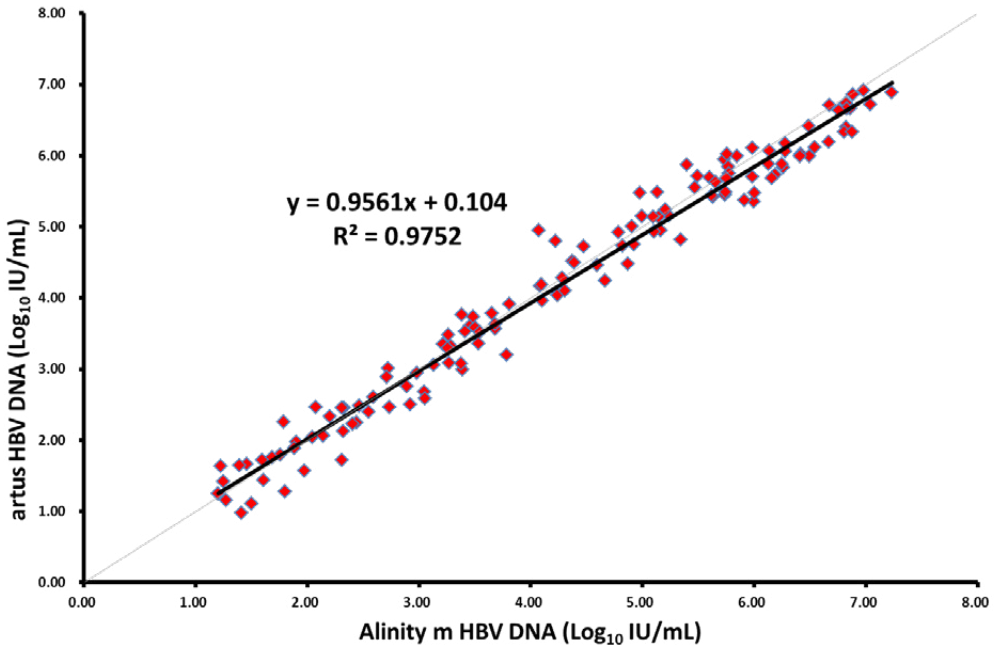
Background: Quantification of Hepatitis B virus (HBV) DNA plays an important role in monitoring HBV infection and in assessing the treatment efficacy. In this study, we evaluate the performance of the new Abbott Alinity m HBV assay (Alinity-HBV) in comparison to the QIAGEN artus HBV QA-RGQ kit (artus-HBV) for the quantification of HBV DNA in plasma sample. Also, the analytical characteristics of Alinity-HBV were studied.

Materials/methods: A total of 195 archived plasma specimens that submitted to our laboratory for HBV DNA quantification between January and December 2017 were used for performance evaluation. Linearity of the Alinity-HBV was evaluated on dilutions series of a clinical sample ranging from 8.60 to 1.60 Log_{10} IU/mL. To assess the assay precision, a standard panel comprising 8 different HBV concentration levels (5, 10, 25, 50, 75, 100, 250 and 500 IU/mL) was prepared, of which 8 replicates of each HBV DNA concentration were tested twice a day for four consecutive days.

Results: Of the 195 samples tested, 193 (99.0%) had the qualitative results that agreed on the two platforms. Among the two samples with discordant qualitative result (positive by Alinity-HBV but negative by artus-HBV), both of them had the result below the limit of detection of Alinity-HBV (<10 IU/mL). Further analysis of 138 samples quantified by both assays showed an excellent correlation (R^2=0.9752) across the dynamic range of quantification. Average bias between two assays, as determined in Bland-Altman analysis, was -0.08 Log_{10} IU/mL (Alinity minus artus; ±1.96 S.D: -0.64 to 0.47 Log_{10} IU/mL). The slope of the regression line for the linearity analysis was 0.9998. All the replicates in 8 different HBV DNA concentrations of the standard panel tested positive by Alinity-HBV, except 2 replicate of 5 IU/mL. The precision of Alinity-HBV over 6 HBV DNA concentrations (25, 50, 75, 100, 250 and 500 IU/mL) ranged from 2.7% to 8.5%.

Conclusions: An excellent correlation between Alinity-HBV and artus-HBV could be demonstrated in this study. The good clinical and analytical performance, random access capability and the extended linear range of quantification make the assay becomes a valuable tool for high-throughput HBV DNA quantification in hospital-based laboratories.



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Abstract 1073

Predicting *Pseudomonas aeruginosa* susceptibility phenotypes from whole genome sequence resistome analysis

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Background: Frequent *Pseudomonas aeruginosa* antimicrobial resistance is driven by a complex repertoire of resistance phenotypes, resulting from both, mutation-driven and horizontally-acquired mechanisms. The objective of this work was to develop and validate a resistance genotype score, based on the analysis of the whole genome sequence resistome, to predict *P. aeruginosa* antimicrobial susceptibility phenotype.

Materials/methods: Published data on clinical strains and *in vitro* resistance evolution experiments, were used to define the genes potentially involved in mutation-driven and horizontally-acquired resistance for ceftazidime, ceftolozane/tazobactam, meropenem, ciprofloxacin and tobramycin. Resistance genes/mutations were scored from 0 (no effect) to 1 (clinical resistance, EUCAST breakpoints); the negative effect of mutations known to increase susceptibility was also considered. Resfinder was used to detect horizontally-acquired determinants. The first step for the analysis of mutational mechanisms was to determine the natural polymorphisms existing in the genes involved in mutation-driven resistance. For this purpose, 50 wildtype strains obtained from 51 different hospitals during a 2017 multicenter study were fully sequenced and analyzed. Once the resistance genotype score was developed, its capacity to predict the susceptibility phenotype was tested in 204 isolates randomly selected from the 51 hospitals (4 from each hospital). Phenotypic and genetic assays for the characterization of resistance mechanisms were performed as needed.

Results: The analysis of the 50 wildtype strains allowed to develop a catalogue of natural polymorphisms in genes involved in mutation-driven resistance. None of the wildtype strains showed horizontally-acquired determinants and the scores were always <1; however a few wildtype isolates showed mutations clearly involved in resistance (for example 2 isolates showed OprD inactivating mutations). The capacity of the score to predict susceptibility (<0.5) or resistance (≥1) in the 204 clinical isolates is shown in the Table.

Conclusions: Although a margin for improvement is evidenced, an overall good correlation between the resistance genotype score and the susceptibility profile was documented. Further refining of the score system, automatization and testing of large international cohorts should follow.

Antibiotic	%S/I/R score <0.5	%S/I/R score 0.5-<1	%S/I/R score ≥1
Ceftazidime	99.2/0.8	86/14	35.5/64.5
Ceftolozane/tazobactam	100/0	100/0	0/100
Meropenem	90.2/8.9/0.9	59.6/36.5/3.9	13.2/36.8/50
Ciprofloxacin	96.2/3.8	75/25	5.9/94.1
Tobramycin	100/0	100/0	18.2/81.8

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Abstract 1074

Mortality outcome in critically ill CRO infection patients treated with polymyxin-B and its prediction based on morbidity and mortality scores

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Abstract third-party references: Glenmark Pharmaceuticals Ltd.

Background: We intent to observe the 28-day mortality in critically ill CRO infected patients treated with polymyxin-B and to analyze the impact of variables along with morbidity and mortality scores on prediction of mortality.

Materials/methods: Retrospective cohort study was planned in all consecutive polymyxin-B treated patients suffering from CRO infections at 5 centers. Patient's demographics, clinical history, and polymyxin-B therapy details were captured. CCI, Pitts score, INCREMENT scores were computed. Along with 28-day mortality, impact of variables was analyzed using Chi-square and Mann-Whitney test amongst survivors and non-survivors.

Results: 51 patients received polymyxin-B during study period, 49 considered suitable for further analysis. Pneumonia (47%) and BSI (18.3%) were the main infections with underlying bacteremia in 85.7% patients. K. pneumoniae (N=23) was the most common pathogen followed by A. baumannii complex. Mean CCI, Pitts and ICS (N=23) scores were 3.16(±2.46), 6.32(±2.51) and 9.86(±5.17) respectively. Mean dose of Polymyxin-B was 11.8 Lakh U/day (±2.73, Range: 10-19.5 LU/d) administered for mean duration of 7.5 days (±4.02, Range: 3-16 days). All-cause 28-day mortality was 30.6%. No significant association between sepsis severity (p = 0.35), neutropenia (p = 1), polymyxin-B dose ≥ 15LU/d (p = 1) and treatment duration > 7d (p = 0.13) with mortality was observed. However, near significant association of 28-mortality was noticed only with CCI ≥ 2. (Table 1)

Conclusions: Polymyxin-B therapy was associated with good (69.4%) overall survival in critically ill patients with CRO infections. We couldn't find significant association of important variables or morbidity or mortality scores with 28-day mortality. Further validation is required in larger cohort to predict the mortality of CRO infection in Indian setting.

Table 1: Mortality association of variables in critically ill patients with CRO infection. (N=49)

Variables	Non-survivors (15) Mean(±SD)	Survivors (34) Mean(±SD)	p value
Age	54.9 (±11.6)	49.9 (±13.3)	0.43
Sex (M)	10 (66.6%)	25 (73.5%)	0.73
CCI	4.06 (±2.57)	2.76 (±2.33)	0.094
Pitts score (Overall)	6.8 (±3.07)	6.11 (±2.24)	0.36
Pitts score (Bacteremia pts) (N=42)	6.76 (±3.2)	6.37 (±2.2)	0.57
INCREMENT score (N=23)	11.55 (±4.55)	8.78 (±5.4)	0.15
CCI ≥ 2	14 (93%)	23 (67%)	0.075
Pitts ≥ 6	9 (60%)	17 (50%)	0.55
INCREMENT score ≥ 8 (N=23)	7 (46.6%)	8 (23.5%)	0.39

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Abstract 1075

Evaluation of simultaneous detection of pathogens associated with sexual transmitted infection and vaginal disorders on a real-time qPCR microfluidics platform in an asymptomatic female college student's cohort

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Background: This study aimed to characterize the performance of a customized microfluidics platform – the Taqman® Array Card (TAC) on vaginal samples in comparison to conventional tests for the diagnosis of sexual transmitted infections (STI), bacterial vaginosis (BV) and vulvovaginal candidiasis (VC).

Materials/methods: This study, carried out prospectively from November 2017 to April 2019, included 211 asymptomatic female college students recruited for STI screening. Sera were collected and screened for HIV, HBV, HCV and syphilis on the Liaison XL platform, while vaginal samples were tested by TAC targeting 29 bacteria, 6 yeasts, 3 viruses and 1 parasite involved in STI, BV and VC. *Chlamydia trachomatis* (CT) and *Neisseria gonorrhoeae* (NG) targets were compared with the Abbott Real-time CT/NG assay. *Candida* spp. and *T. vaginalis* (TV) targets were compared to culture. Targets involved in BV were compared with Nugent's score (NS) in all samples and to NS and AmpliSens Florocenosis/Bacterial vaginosis-FRT PCR in 132 samples.

Results: CT was detected in 9 samples (4%) by TAC and Abbott PCR. No NG or TV was detected by either of the tests. Poor sensitivity (68%) was observed for *C. albicans* by TAC compared to culture. NS identified 99 (75%) students with normal flora, 33 (25%) with intermediate or BV compatible flora. Applying different interpretative algorithms, TAC's best sensitivity, specificity, PPV and NPV scores to detect disturbed flora were 67%, 94%, 79% and 89%, respectively. Applying the manufacturer's interpretation algorithm, AmpliSens PCR's sensitivity, specificity, PPV and NPV were: 85%, 90%, 74% and 95% respectively. All sera were negative for HIV, HCV and syphilis; one was compatible with recovered HBV.

Conclusions: TAC is a customized panel-based molecular platform that allows simultaneous detection of STI and vaginal disorders pathogens, simplifying laboratory workflow and reducing turnaround time. CT was the only STI pathogen detected, present in a low percentage in this asymptomatic female cohort. TAC needs to be improved regarding *Candida spp* detection. AmpliSens PCR showed better performances and ease of interpretation than TAC to identify disturbed flora in this asymptomatic cohort. Samples from BV symptomatic patients are needed to optimize an accurate algorithm for BV diagnosis by TAC.

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Abstract 1078

Rapid detection of methicillin-resistant *Staphylococcus aureus* in patients with late hospital-acquired/ventilator-associated pneumonia

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Background: New syndromic rapid diagnostic tests seem to be promising for antimicrobial stewardship purposes. We have tested one of them, the FilmArray Pneumonia Panel plus (FA-PPP), in patients diagnosed with hospital-acquired pneumonia (HAP), including ventilator-associated pneumonia (VAP) episodes, with the aim to describe its potential impact on the management of anti-methicillin resistant *Staphylococcus aureus* (MRSA) therapy.

Materials/methods: Single-center observational study of consecutive adult patients diagnosed with HAP, hospitalized from June 2018 to October 2018. We performed FA-PPP on residual samples of endotracheal aspirate (ETA) or bronchoalveolar lavage (BAL) obtained for the etiological diagnosis of pneumonia. The gold standard was culture method. The cut-off of bacterial growth considered as positive was ≥10ffi4 and ≥10ffi3 colony forming unit/ml for ETA and BAL, respectively. The performance of the test did not interfere in the decision-making process, so that patients were managed according to the standard of care.

Results: 58 patients were diagnosed with late-onset (≥5 days after admission) HAP, 74% was on mechanical ventilation at diagnosis. Collected samples included 43 ETA and 15 BAL. FA-PPP resulted positive for MRSA in 7 cases, but in only one of them standard culture showed the growth of MRSA. On the contrary, none of the 51 samples with a negative FA-PPP result showed bacterial growth on standard culture (Table 1). According to the observed prevalence of MRSA (1.7%), FA-PPP sensitivity, specificity, positive predictive value (PPV) and negative predictive value (NPV) for MRSA detection were 100%, 89%, 14% and 100%, respectively. According to the data of our Microbiology laboratory showing a pre-test probability (overall prevalence of MRSA among isolates from lower respiratory tract samples) of 5%, positive and negative likelihood ratio were 9.5 and <0.1 respectively.

Conclusions: Our findings suggest that FA-PPP could be useful in reducing exposure to anti-MRSA drugs in patients with late HAP/VAP. However, further studies assessing the impact of such test on therapeutic management and patient outcome are needed.

Table 1: FilmArray Pneumonia test Operating Characteristics for methicillin-resistant Staphylococcus aureus (MRSA)

MRSA	Growth in culture		
FA Pneumonia positive	Yes	No	Total
Yes	1	6	7
No	0	51	51
Total	1	57	58

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Abstract 1079

ETEST Eravacycline for antimicrobial susceptibility testing of *Enterobacteriaceae* and Enterococcus spp.: performance results from a multi-centre study

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Background: Eravacycline (XERAVA™), a fluorocycline antibiotic developed by Tetraphase Pharmaceuticals Inc. for the treatment of complicated intra-abdominal infections. This study evaluated the performance of ETEST® Eravacycline (ERV), a new gradient diffusion strip, for determining the minimum inhibitory concentration (MIC) of *Enterobacteriaceae, Enterococcus faecalis* and *Enterococcus faecium* as compared to CLSI/ISO-20776-2 broth microdilution reference method (BMD).

Materials/methods: A set of 679 isolates including 542 *Enterobacteriaceae*, 137 *Enterococci* was tested at 4 clinical trial sites using ETEST® ERV and BMD. Results were analyzed for essential (EA) and category (CA) agreements, major (ME) and very major (VME) error rates using EUCAST breakpoints [*E. coli*: ≤ 0.5 (S), > 0.5 (R) mg/L, *Enterococcus* spp.: ≤ 0.125 (S), > 0.125 (R) mg/L) as well as FDA breakpoints (*Enterobacteriaceae*: ≤ 0.5 mg/L (S), *Enterococcus faecium* and *Enterococcus faecalis*: ≤ 0.064 mg/L (S)]. Results for *Klebsiella pneumoniae* were analyzed for EA only for EU claim as EUCAST breakpoints have not been established.

Results: Results are summarized in the table below. ETEST® ERV performance for *Enterobacteriaceae* and *Enterococcus spp*. met FDA and ISO acceptance criteria for EA (≥ 90%), CA (≥ 90%), ME (≤ 3%) and VME (≤ 2 or ≤ 3% respectively) A trend to overestimate *E. coli*, *C. freundii* and *K. aerogenes* MICs was observed.

Conclusions: Results of this study support the accuracy of ETEST® ERV for determining MICs of *Enterobacteriaceae*, and *Enterococcus* spp. As such, the ETEST® ERV is considered as substantially equivalent to BMD.

Claim	Pathogens	EA	CA	ME	Adjusted ME*	VME	Adjusted VME*
US (FDA breakpoints)	*Enterobacteriaceae*	99.4%	98.0%	1.3%	NA	5.4%	1.1%
	Enterococcus faecium & E. faecalis	100.0%	94.9%	3.1%	0.0%	33.3%	0.0%
EU (EUCAST breakpoints)	*E. coli*	99.0%	100.0%	0.0%	NA	0.0%	NA
	K. pneumoniae	99.0%	NA	NA	NA	NA	NA
	Enterococcus spp.	100.0%	100.0%	0.0%	NA	0.0%	NA

* In accordance with the FDA response to Susceptibility Testing Manufacturers Association (STMA) letter dated November 3, 2015, for drugs for which there is no intermediate breakpoint, the VME rate and/or the ME rate may be adjusted to exclude the VME results and/or the ME results that were within essential agreement (EA).

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Abstract 1080

Metagenomic sequencing of urine to differentiate infected from contaminated samples

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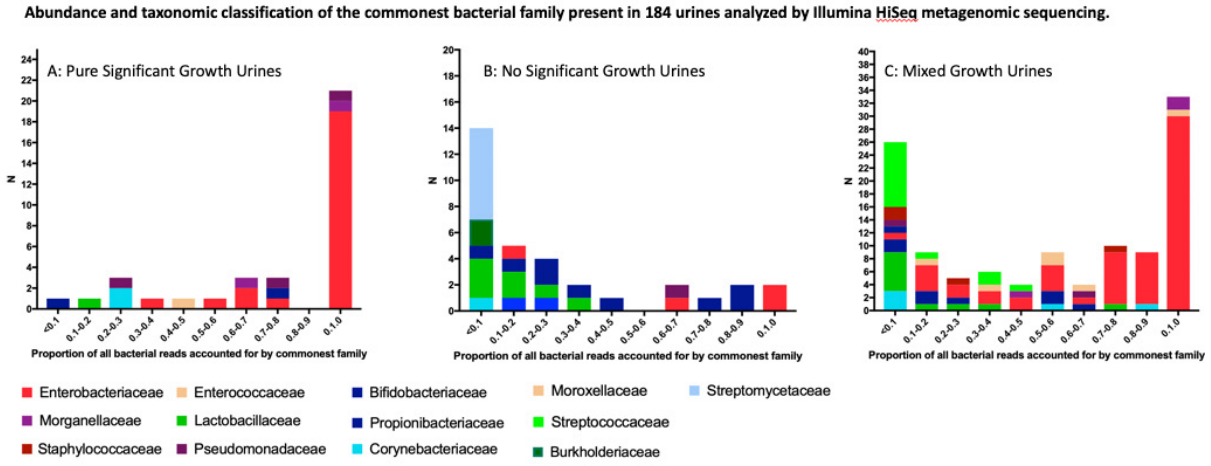
Background: Culture-based diagnostics for urinary tract infection are neither sensitive nor specific. Currently, bacterial growth in urine is semi-quantified and interpreted using thresholds defined over fifty years ago. In reality culture yield depends on patient characteristics and sample handling, and is biased towards easily culturable organisms. Culture is slow, yielding results after treatment decisions. Contamination of urine by perineal flora results in both false-negative and false-positive results. Up to 50% of urines yield 'mixed growth of uncertain significance' (MGUS). Metagenomic DNA sequencing could potentially give rapid and unbiased assessment of bacterial DNA in urine.

Materials/methods: The CONDUCT trial collected samples from >1000 women with UTI symptoms. We selected 184 urines yielding pure growth (PG) in culture (>10^5 organisms/ml) (n=34), no significant growth (NSG) (n=34) or MGUS (n=116) and compared culture findings with analysis of Illumina HiSeq metagenomic sequencing data and Centrifuge taxonomic classification.

Results: The taxonomic profiles of PG and NSG urines were strikingly different (figure). In all 25 PG urines with cultures containing coliforms or *Proteus*, reads mapping to Enterobacteriaceae or Morganellaceae families respectively predominated, and accounted for >90% of bacterial reads in 20/25. Among nine PG urines yielding Gram-positive organisms, reads mapping to the corresponding family only predominated in four. Among NSG urines, bacterial reads mostly mapped to common perineal commensals; the commonest family usually accounted for a minority of total reads. A single family predominated in 7/34 NSG urines: Enterobacteriaceae (3), Bifidobacteriaceae (3) and Pseudomonadaceae (1). Bifidiobacteriaceae reads represented *Gardnerella* spp. which is not identified by urine culture**.** Among MGUS urines, both profiles were apparent. In 33/116, >90% of reads mapped to Enterobacteriaceae, Staphylococcaceae or Enterococcaceae. In 26/116, the commonest family accounted for only 10% of reads; these were typically common perineal commensal families.

Conclusions: Our data provide proof-of-principle that the diversity and identity of bacteria present in urine revealed by metagenomic sequencing can differentiate infected from contaminated samples. Our findings highlight how this approach can now be developed through optimizing sample processing and taxonomic classification.

Figure



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Abstract 1089

In vitro activity of ceftazidime/avibactam against ceftazidime-resistant *Enterobacter*ales and *Pseudomonas aeruginosa* from hospitalised patients in Germany: 2016-17

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Abstract third-party references: On behalf of the Working Party "Antimicrobial Resistance" of the Paul-Ehrlich-Society for Chemotherapy

Background: The combination of ceftazidime plus avibactam (CTV) possesses potent activity against Gram-negative bacteria (GNB) including multi-drug resistant pathogens producing class A (ESBLs, KPCs and others), class C (AmpC), and various class D (including OXA-48) β-lactamases. CTV, however, is not active against Metallo-β-lactamase (MBL)-producing GNB. The purpose of this study was to evaluate the *in vitro* activity of CTV against ceftazidime (CTZ)-resistant *Enterobacterales* (CTZ-R-ENT) and CTZ-resistant *Pseudomonas aeruginosa* (CTZ-R-PAE), including carbapenem-resistant isolates.

Materials/methods: Susceptibility testing was performed with the broth microdilution method according to the standard ISO 20776-1. EUCAST clinical breakpoints (v.9.0) were applied for interpretation of MICs: S-susceptible, standard dosing regimen; I-susceptible, increased exposure; R-resistant). Phenotypic detection of ESBLs in ENT was performed according to the EUCAST algorithm. Genetic testing on carbapenemases was performed at the German National Reference Centre for Multidrug-Resistant Gram-negative Bacteria.

Results: 1621 ENT and 575 PAE collected at 22 laboratories were tested. There were 232 (14.3%) CTZ-R-ENT (MIC>4 mg/l) and 72 (12.5%) CTZ-R-PAE (MIC>8 mg/l). 119/304 (39.1%) isolates were obtained from intensive care patients. Of the CTZ-R-ENT, 117 group 1 isolates and seven group 2 isolates with an inducible chromosomal AmpC showed an ESBL-phenotype. 23/232 (9.9%) CTZ-R-ENT had meropenem MICs >0.125 mg/l. A carbapenemase was detected in six CTZ-R-ENT, namely in *Citrobacter freundii* (VIM-1), *Enterobacter cloacae* (OXA-48), *Escherichia coli* (NDM-5), *Klebsiella oxytoca* (VIM-4), and *Klebsiella pneumoniae* (n=2, VIM-like). Of the 72 CTZ-R-PAE, 24 were carbapenem-susceptible (imipenem MIC≤4 mg/l; meropenem MIC≤8 mg/l), 17 were additionally resistant to one carbapenem, and 31 were additionally resistant to both imipenem and meropenem. Carbapenemases were detected in 12 CTZ-R-PAE: VIM-like (n=6), IMP-like (n=3), GIM-1 (n=2) and NDM-like (n=1). Susceptibility to CTV (MIC≤8 mg/l) was observed in 226/232 (97.4%) CTZ-R-ENT, 226/227 (99.6%) non-MBL-producing CTZ-R-ENT, 55/72 (76.4%) CTZ-R-PAE, and 55/60 (91.7) non-MBL-producing CTZ-R-PAE. Number and percent CTV-susceptible and CTV-resistant isolates for various subgroups of CTZ-R-ENT and CTZ-R-PAE are presented in the Table.

Conclusions: Overall, >99% and about 92% of the non-MBL-producing CTZ-R-ENT and CTZ-R-PAE, respectively, from hospitalized patients in Germany were CTV-susceptible. Based on these findings, CTV represents a valuable option for targeted treatment of infections caused by these pathogens.

Table: Number and percent ceftazidime/avibactam susceptible (CTV-S) and resistant (CTV-R) isolates for various subgroups of ceftazidime-resistant *Enterobacterales* (CTZ-R-ENT) and *P. aeruginosa* (CTZ-R-PAE)

Group / subgroup	N	CTV-S		CTV-R	
		n	%	n	%
CTZ-R-*Enterobacterales**					
All	232	226	97.4	6	2.6
Meropenem MIC ≤ 0.125 mg/l	209	209	100	0	0
Meropenem MIC > 0.125 mg/l	23	17	73.9	6	26.1
Carbapenemase-producing	6	1	16.7	5	83.3
Non-MBL-producing	227	226	99.6	1	0.4
CTZ-R-*P. aeruginosa*					
All	72	55	76.4	17	23.6
Susceptible to imipenem/meropenem	24	22	91.7	2	8.3
Resistant to one carbapenem	17	16	94.1	1	5.9
Resistant to both carbapenems	31	14	54.8	14	45.2
Carbapenemase-producing	12	0	0	12	100
Non-MBL-producing	60	55	5	91.7	8.3

**C. braakii* (n=1), *C. farmeri* (n=1), *C. freundii* (n=10), *C. koseri* (n=2), *E. cloacae* complex (n=56), *E. coli* (n=74), *H. alvei* (n=9), *K. aerogenes* (n=19), *K. oxytoca* (n=1), *K. pneumoniae* (n=43), *K. quasipneumoniae* (n=2), *K. variicola* (n=1), *M. morganii* (n=8), *P. mirabilis* (n=1), *P. stuartii* (n=1), *Salmonella* sp. (n=1), *S. fonticola* (n=1), *S. marcescens* (n=1)

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Abstract 1093

Effectiveness of IV fosfomycin in critically ill patients with CRE infection and analysing the impact of variables on mortality in Indian setting

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Background: Though clinical evidence on usage of fosfomycin in CRE infections is promising its limited. We intent to observe the clinical outcome with fosfomycin and also to check the impact of variables amongst survivors and non survivors.

Materials/methods: Multicentric retrospective study conducted among critically ill patients with CRE infection treated with IV fosfomycin. Patient's medical records analyzed and important variables like mechanical ventilation, mental status, fosfomycin dose and duration, along with CCI, Pitts and INCREMENT score were compared between survivors and non-survivors.

Results: Among 51 critically ill CRE infection patients, successful clinical outcome was observed in 47% patients. Klebsiella was the most common (74.5%) organism and septic shock (41.2%) was the most common clinical diagnosis. Underlying bacteremia was present in 88.2% of the patients. Mean dose of fosfomycin was 13.2 g/d (±3.12, Range: 8-24 g/d) administered for mean duration of 6.7 days (±5.93, Range: 3-39 days). Pitt score was significantly higher among non-survivors (5.44 ± 2.33 vs. 4.36 ± 2.16, p=0.04), however no significant difference was seen in CCI (p=0.22) and INCREMENT score (p=0.1) among survivors and non-survivors. Septic shock was the only factor associated with significant (0.008) impact on the survival. Overall mortality was 35.2%.

Conclusions: IV Fosfomycin therapy was associated with good (64.7%) overall survival in CRE infections in critically ill patients. Presence of septic shock significantly impacted the mortality. Such association was lacking for other variables in our study.

Table 1: Comparison of variables among survivor and non-survivor

Variables	Survivor (n=33)	Non-survivor (n=18)	P value
Age	56.39 ± 18.86	54.55 ± 11.06	0.66
Male	25 (75.7%)	16 (88.9%)	0.46
Septic shock	9 (27.3%)	12 (66.7%)	0.008
Mental status (Other than alert)	26 (78%)	15 (83%)	1
Mechanical Ventilation	27 (81%)	14 (77%)	1
CCI ≥ 2	23 (69.7%)	11 (61.1%)	0.55
Pitts score ≥ 4 (Overall)	25 (75.7%)	15 (83.3%)	0.72
INCREMENT score ≥ 8 (N=45)	14 (60.9%)	9 (39.1%)	0.75
Fosfomycin dose ≥ 16 g/d	12 (36.4%)	8 (44.4%)	0.76

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Abstract 1095

Methicillin-resistant *Staphylococcus aureus* USA300 persister cells show chaperone upregulation in contrast to planktonic cells and the biofilm phenotype

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Background: Bacteria produce biofilms – bacterial communities embedded in an extracellular matrix that protects the organisms from antibiotics and the host immune response – and persisters (PS) – cells that neither grow nor die in the presence of bactericidal agents, thus exhibiting multidrug tolerance. We developed distinct models to isolate PS and biofilms formed by methicillin-resistant *Staphylococcus aureus* USA300 (MRSA-USA300), a highly virulent clone that causes fulminant infections. Here, we compared the transcriptomic profiles of MRSA-USA300 biofilms and PS against planktonic (PL) cells.

Materials/methods: MRSA-USA300 biofilm was grown in brain heart infusion (BHI) medium with 0.1% glucose under static conditions for 24h, 48h and 72h. PS were isolated by treating a 16h stationary phase culture with 5 µg/ml ciprofloxacin for 24h. Samples were taken at 0h, 0.5h, 1h, 2h, 4h, 6h, 8h and 24h, washed and plated for viable cell count. As a comparator, PL cultures were generated in parallel in both cases. Total RNA-extraction (MasterPure™Complete DNA/RNA Purification Kit, Lucigen), rRNA depletion (Ribo-Zero rRNA Removal Kit (Gram-Positive Bacteria), and RNA-seq (NextSeq, Illumina) were performed on all samples. Differential-gene-expression analysis was performed using DESeq2 with $\log_2$ fold change (FC) > 1 or < -1 and p≤0.05 considered significant.

Results: MRSA-USA300-PS were successfully generated after 24h ciprofloxacin treatment, typified by a biphasic killing curve (Figure A). Components of chaperone-complex *dnaK-dnaJ-grpE* and complementary genes *clpB* and *tig* showed significant upregulation ($\log_2$ FC: 2.47, 2.08, 3.15, 2.14 and 1.32 respectively) in PS compared to PL (p≤0.001). In contrast, significant downregulation of said genes, except *tip* (p>0.05), was observed in biofilm ($\log_2$ FC: -2.72, -1.13, -1.95 and -3.10 respectively) compared to PL (p≤0.024) (Figure B). In addition, chaperone-complex *groEL-groES* gene showed significant upregulation in PS ($\log_2$ FC: 1.70 and 2.70 respectively; p≤0.001) and again contrasting significant downregulation in biofilm ($\log_2$ FC: -2.01 and -1.98 respectively; p≤0.004) compared to PL (Figure C).

Conclusions: Our data shows that MRSA-USA300-PS upregulate chaperone-complexes, in contrast to the biofilm phenotype, as was previously suggested for *E. coli* PS. Upregulated chaperone expression aids in preventing protein misfolding and aggregation under stress conditions. Increased activity would also lead to ATP-depletion, a known feature of PS.

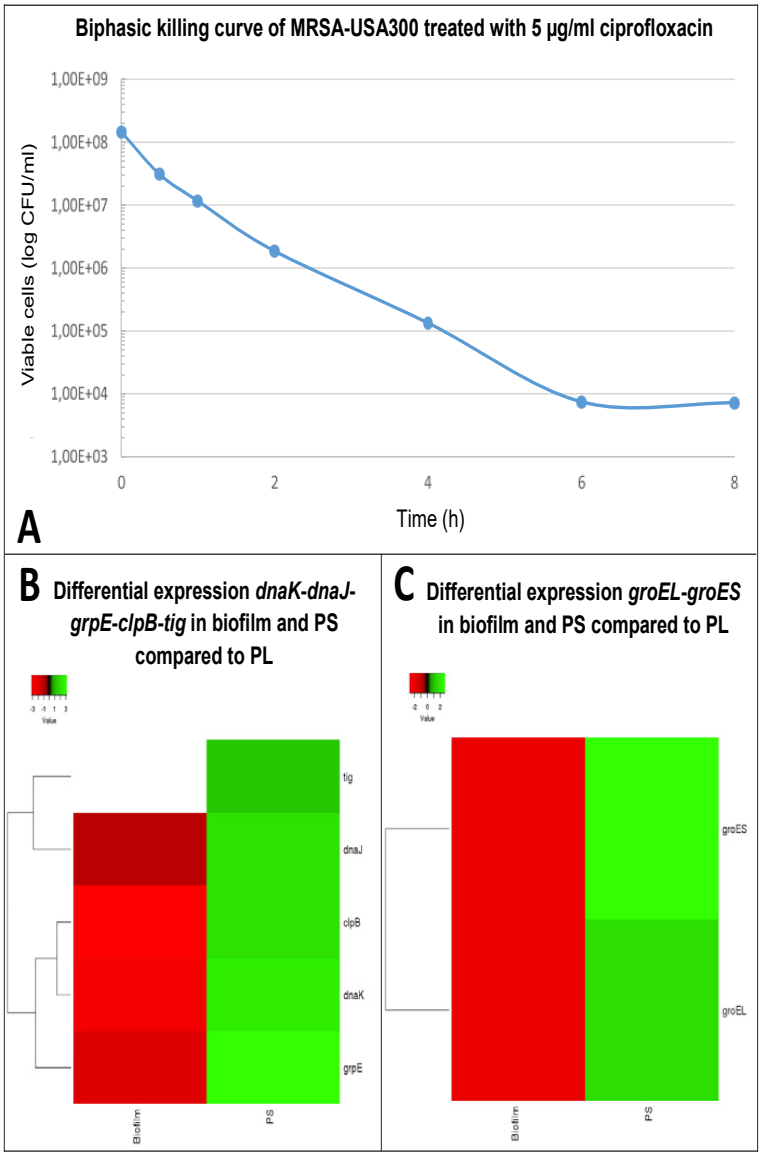

Figure: A) When treating MRSA-USA300 with 5µg/ml ciprofloxacin, the killing curve has a biphasic nature. The susceptible cells die faster in the earlier stages of antibiotic treatment whilst the killing plateaus at 6-8h indicating that, at this stage, only PS form a major part of the bacterial population. 0h equals start of antibiotic treatment of a 16h stationary culture. **B)** Differential expression analysis of *dnaK-dnaJ-grpE-clpB-tig* shows significant upregulation (log_2 FC > 1; green) in PS compared to PL but contrasting downregulation (log_2 FC < -1; red) in biofilm compared to PL. *tig* did not show significant differential expression in biofilm (white). (*dnaK*: Chaperone protein DnaK – *dnaJ*: Chaperone protein DnaJ – *grpE*: Nucleotide exchange factor GrpE – *clpB*: Chaperone protein ClpB – *tig*: Trigger factor Tig) **C)** Additionally, differential expression analysis of *groEL-groES* shows significant upregulation (log_2 FC > 1; green) in PS compared to PL but contrasting downregulation (log_2 FC < -1; red) in biofilm compared to PL.

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Abstract 1096

Antimicrobial prophylaxis administration after umbilical cord clamping in caesarean section does not increase risk for surgical site infection: a prospective analytic study with 55,901 patients

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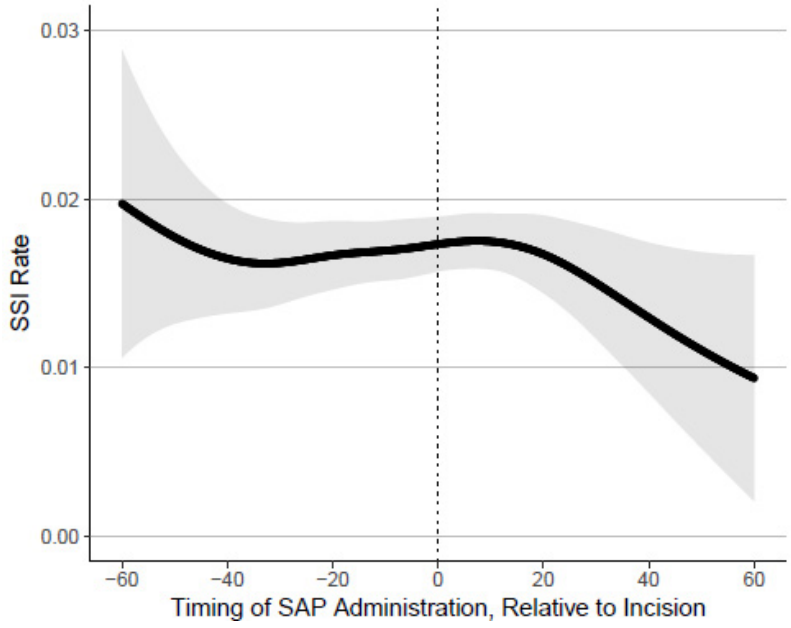
Background: The World Health Organization (WHO) recommends administration of surgical antimicrobial prophylaxis (SAP) in cesarean section prior to incision to prevent surgical site infections (SSIs), including endometritis. However, SAP may disrupt the developing neonate's gastrointestinal microbiome if given before umbilical cord clamping.

Materials/methods: Analytic study within the Swiss national SSI surveillance system, from 2009 to 2018. Multicenter study including patients from 178 hospitals. We included all cesarean section patients that were given the SAP agents cefuroxime, cefazolin, amoxicillin/clavulanate or ceftriaxone, either within 60 minutes before incision or after clamping. Data of the 30 day post-discharge follow-up was available in 89%. We assessed the association between SAP administration relative to incision and clamping and the SSI rate, using generalized linear multilevel models, adjusted for patient characteristics, procedural variables, and health-care system factors.

Results: A total of 55,901 patients met the criteria: SAP was administered before incision in 26'405 patients (47.2%) and after clamping in 29,496 patients (52.8%). Overall 846 SSIs were documented, of which 379 (1.6% [95 % CI, 1.4-1.8%]) occurred before incision and 449 (1.7% [1.5-1.9%]) after clamping (p=0.759). The adjusted odds ratio (OR) for SAP administration after clamping was not significantly associated with an increased SSI rate (1.14, 95% CI 0.96-1.36; p=0.144) when compared to before incision. Supplementary and subgroup analyses supported these main results.

Conclusions: The results of this large prospective study provide strong evidence that the risk of SSI for the mother in cesarean section is not increased if SAP is given after umbilical cord clamping compared to before incision. Given the latest research on the potentially detrimental effects of early-life antimicrobial exposure, guidance from WHO and other national organisations should reflect this.

Figure: Unadjusted generalized additive model with surgical site infection as the dependent variable and timing relative to incision as the predicting variable



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Abstract 1098

Laser light scattering technology in the diagnosis of infections in children on dialysis

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Background: to assess the possibility of using laser light scattering technology for the diagnosis of infections in children on dialysis.

Materials/methods: From January to September 2019, 148 samples, 106 urine and 42 dialysates, were examined from 115 children from the nephrological Department with a chronic renal failure diagnosis.

Dialysate samples were analyzed both by classical culture method on blood-serum agar, thioglycol and two-phase medium and by ALIFAX HB&L LIGHT analyzer (Alifax, Italy) based on laser light scattering technology inoculating 500 µl of the sample into specific enriched broth vials.

Native urine samples, detected positive by ALIFAX HB&L LIGHT analyzer with cutoff of 10E3 CFU/ml, were cultured on blood agar by the Eisenberg method

Results: A complete agreement within the 2 methods was found in 42 dialysate samples: 38 negative (90.5%) and 4 positive (9.5%) results.

A pyogenic coccus *Staphylococcus aureus* with a count of 10E4 CFU/ml was detected in two different specimens and in a wound drainage sample cultured along with peritoneal catheter outlet, where *S. aureus* was isolated in moderate growth.

Corynebacterium sp. was one of the dialyzates isolated, it belongs to the skin biota and represents a potential contaminant during sample collection.

Polymicrobial culture was detected from one patient, including *E. coli*, *Candida sp., S. haemolyticus*. The latter two are skin and mucous normobiota that could contaminate the sample or colonized the peritoneal catheter.

After three hours' incubation using alternative technology, a negative result was obtained for 81 urine samples (76.4%), and a positive result for 25 samples (23.5%). Enterobacterales were identified in 39.3% (*E. coli, M. morganii, C. amalonaticus, E. cloaceae*), non – fermenting gram-negative bacteria in 14.3% (*P. aeruginosa, R. picketii, Oligella sp.*), *Enterococcus sp.* in 21.4%, coagulase-negative staphylococci in 10.7% (*S. haemolyticus, S. epidermidis*), *S. viridians* in 7.1%, *C. albicans* and *Corynebacterium sp.* in 3.6%.

Conclusions: In our workflow, the data on the absence bacteriuria in urine is received by the physician within 3-4 h allowing a better management of young patients and avoiding unnecessary use of antibiotics in 2/3 cases. Moreover, the system is highly sensitive detecting minimum bacterial concentration in small amount of sample.

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Abstract 1103

Improved molecular diagnosis of dermatomycosis

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Background: PCR is more sensitive than culture and microscopy for the detection of dermatophytes in clinical specimens. However, most assays focus on the detection of the entire group and few important species. We have evaluated the EuroAssay Dermatomycosis, a commercially available test permitting detection and identification of a large number of dermatophyte species and a few other fungi relevant in dermatomycosis.

Materials/methods: A total of 206 clinical specimens (124 nail, 78 skin and 4 hair specimens) from patients with suspected dermatomycosis were included in the study. Specimens were analyzed by microscopy, culture and PCR (EuroAssay Dermatomycosis; Euroimmun). For molecular detection, DNA was extracted with the EZ1Tissue Kit (Qiagen) after overnight incubation in ATL buffer (Qiagen) containing proteinase K. Amplification, hybridization and read-out was according to the instructions of the manufacturer. Fungal species were categorized in three groups A to C based on their clinical significance (true pathogen, possible pathogen, no pathogen). Specimens were grouped accordingly considering the fungal species with the highest significance only.

Results: Group A and group B organisms were found by culture and PCR in 42 and 9, by PCR only in 43 and 22, and by culture only in 4 and 1 specimens, respectively. Thus, PCR detected significantly more group A (85 versus 46) and group B organisms (31 versus 10) than culture. The concordance of species identification by culture and PCR was 100% for the 51 specimens categorized into the same group (A or B) by both methods. Additional organisms of equal or lower significance were found by culture (N=2), PCR (N=6) or both (N=4). Microscopy was positive in 35/42 (83.3%) of specimens with group A organisms detected by culture and PCR and was negative in 82/85 (96.5%) specimens without clinically significant organism (group C).

Conclusions: The Euroimmun assay is significantly more sensitive than culture and microscopy and provides accurate species identification. Microscopy may be especially helpful when PCR detects possibly pathogenic organisms.

Number of specimens per group (thereof number with positive microscopy)		Culture		
		A	**B**	**C**
PCR	**A**	42 (35)	1 (1)	42 (26)
	B	0	9 (7)	22 (4)
	C	4 (2)	1 (1)	85 (3)

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Abstract 1106

Human papilloma virus-testing in extragenital samples: usefulness and importance of complete genotyping

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Background: Human papillomavirus (HPV) infection outcomes range from benign to malignant processes. The correlation between cervical cancer and HPV infection is almost complete, but the impact of HPV infection in the development of tumours in other human anatomical sites (such as anal or head-neck) appears to be slighty lower. There is a growing interest to evaluate the relationship between the presence of HPV in extragenital sites and the developement of cancerous processes. However, routin systems for cervical cancer screening are not usefull for detection of all HPV-types, especially in extragenital samples.

Materials/methods: All extragenital samples tested for HPV from September 2017 to October 2019 in a tertiary hospital in Madrid (Spain) were reviewed. DNA extraction from biopsies was performed using Wizard® SV Genomic DNA Purification System (Promega) and HPV-typing using HPV Direct Flow Chip Kit (Master Diagnóstica). This assay detects 18 high-risk or putative high-risk genotypes (hrHPV) and 17 low-risk genotypes (lrHPV). Demographics and clinical information of the patients were also reviewed.

Results: 39 extragenital samples from 35 patients (median age 56.5 years, interquartile range: 37.5-67.5 years; 63.6% males) were analyzed. Most common type of samples were laryngeal biopsy (n=18, 46.2%), pleural biopsy (n=7, 17.9%) and mediastinal adenopathy (n=5, 12.8%). Other 9 samples were recovered from very diverse sites (including 5 oral cavity and 2 skin biopsies). Seventeen samples yielded a positive result (43.6%), but only in 6 of them, hrHPV were detected: HPV-16 in five cases (29.4%) and HPV-58 in one (5.9%). Among them, five cases corresponded to five distant metastases (one pulmonar and four mediastinal adenopathies) from cervical cancer (HPV-16 in four cases and HPV-58 in one). Besides, HPV-16 was detected in a pleural biopsy, being the same HPV-type previously detected in the primary amygdala epidermoid carcinoma. The remaining positive results were lrHPV: 8 HPV-6 (47.1%) and 3 HPV-11 (17.6%), all detected in laryngeal samples.

Conclusions: The hrHPV detected in extragenital samples corresponded to distant metastases, suggesting viral dissemination from primary cervical or head-neck carcinoma. The implementation of the nonavalent vaccine could avoid these cases, because all HPV-genotypes detected are included in this vaccine.

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Abstract 1108

Reduced *in vitro* killing of methicillin-resistant *Staphylococcus aureus* blood culture isolates by vancomycin as the bacterial inocula increases

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Background: MRSA blood stream infections (with or without endocarditis) and other serious life threatening infections require prompt and adequate therapy. Vancomycin remains a drug of choice for treating MRSA infections including bacteremia, however, failures necessitating different drugs (i.e. ceftaroline/ceftobiprole, linezolid, daptomycin) are becoming more common. We had previously reported mutant prevention concentration (MPC) values for vancomycin against MRSA strains of $\geq$32 µg/ml. In an attempt to determine if higher MPC values could impact bacterial activity, we compared killing of MRSA by vancomycin at 4 different drug concentrations and against increasing bacterial densities.

Materials/methods: Four unselected MRSA strains were exposed to 4 different vancomycin drug concentrations (minimum inhibitory concentration (MIC), MPC, maximum serum concentration (C_{max}; 20 µg/ml), maximum tissue concentration ($Tissue_{max}$; 10 µg/ml) and the $\log_{10}$ reduction and percent kill of viable cells recorded at 0.5, 1, 2 4, 6, 12 and 24 hours after drug exposure against bacterial densities ranging from 10^6-10^9 colony forming units per milliliter (cfu/ml). Measurements at each time point were in triplicate and results averaged.

Results: The MIC/MPC values for the 4 strains were 1/$\geq$32, 0.5/16, 0.5/4 and 1/2. MIC and MPC drug concentrations were poor at killing over all inocula tested. At the 10^6 cfu/ml density a 1.9 and 3.7 $\log_{10}$ reduction was seen at 12 and 24 hours respectively for the C_{max} drug concentration which decreased to a 0.7 and 2.4 $\log_{10}$ reduction at the 10^7 inocula and growth at the 10^8 and 10^9 cfu/ml inocula. For the $Tissue_{max}$ drug concentration, a 2.1 and 3.3 $\log_{10}$ reduction was seen following 12 and 24 hours of drug exposure at the 10^6 cfu/ml inocula, a 0.5 and 1.8 $\log_{10}$ reduction at the 10^7 cfu/ml inocula and growth or a 0.09 $\log_{10}$ reduction at the 10^8 and 10^9 cfu/ml.

Conclusions: Patients are infected with higher bacterial densities than used in MIC susceptibility testing. Determining antimicrobial activity against higher bacterial densities is essential. As bacterial densities increased, the bacterial activity of vancomycin decreased. Such a finding is a concern for vancomycin therapy where higher bacterial burdens may be present and could explain vancomycin failures.

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Abstract 1113

Added value of throat and perineal *Staphylococcus aureus* screening, in addition to nasal screening, for identifying patients at risk of S. aureus surgical site infection

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Abstract third-party references: This research project receives support from the Innovative Medicines Initiative Joint Undertaking under grant agreement n° 115523, 115620, 115737 resources of which are composed of financial contribution from the European Union Seventh Framework Programme (FP7/2007-2013) and EFPIA companies in kind contribution.

Background: Nasal carriage of *Staphylococcus aureus* (SA) increases the risk of surgical site infection (SSI). In centres with pre-operative SA decolonization protocols, it is a common practice to screen the nose only. The aim of this analysis was to estimate the added value of screening the throat and the perineum, in addition to the nose, for identifying patients at risk of SA SSI.

Materials/methods: We analysed preliminary data from a prospective observational cohort study conducted at 33 European hospitals (ASPIRE-SSI). Adult patients undergoing surgical procedures were screened pre-operatively in the nose, throat and perineum. All SA colonized (at any of three body sites) and a sample of non-colonized subjects were enrolled into the study cohort in a 2:1 ratio, and followed for 90 days after surgery. Two weighted multivariate mixed-effect logistic regression models, including common risk factors for SSI and a random intercept for hospital, were developed: nasal-only colonization (n-model) or any of the three body sites (ntp-model). The predictive performance of the two models was compared by estimating the area under the receiver operating characteristic curve (AUC), adjusted for the sampling design.

Results: We included 3039 SA carriers of whom 72 (2.4%) developed SA-SSI. 2360 SA carriers were positive in the nose (of whom 62 [2.6%] developed SA-SSI) and 679 were negative in the nose and positive in the throat and/or perineum (of whom 10 [1.5%] developed SA-SSI). Out of 6205 non-carriers from the source population, we included 1470 (23.7%) who served as controls (of whom 12 [0.8%] developed SA-SSI). Taking into account the sampling of controls, the sensitivity of the screening increased from 51.7% in the n-model to 60.0% in the ntp-model, while the specificity decreased from 73.9% to 66.3%. The prediction models yielded an AUC of 0.74 (95%CI: 0.67-0.81) in the n-model and 0.74 (95%CI: 0.677-0.81) in the ntp-model.

Conclusions: Extending SA pre-operative screening to throat and/or perineum led to identification of 679 additional at-risk subjects (29% increase) and 10 additional SA-SSI episodes in this at-risk group (14% increase), suggesting a potential benefit when implemented in clinical practice.

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Abstract 1115

Incidence of hospitalisation for respiratory syncytial virus in children aged 0-5 years in Ontario, Canada

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Background: In high-income countries, respiratory syncytial virus (RSV) contributes significantly to morbidity in children, placing a substantial burden on the health system. The development of an RSV vaccine has been identified as a public health priority. More data are needed by policy-makers to understand the burden of RSV throughout the lifespan, but particularly among children in order to help identify priority populations as vaccines are developed and licensed.

Materials/methods: We used population-based health administrative data to calculate rates of RSV hospitalizations in children born between May 2009 and June 2015 in Ontario, Canada. Children were followed until their first RSV-hospitalization, death, 5th birthday, or the end of the study period (June 2016). RSV hospitalizations across the province were identified with a validated algorithm using international classification of diseases 10th revision (ICD-10) codes and/or laboratory-confirmed outcomes collected from a subset of hospitals. We calculated hospitalization rates by various characteristics of interest, including finely-stratified age groups, sex, and comorbidities, overall and by gestational age. We also examined RSV hospitalizations by calendar month in order to understand temporal trends, including for individual age groups.

Results: The overall hospitalization rate for children <5 years was 4.2 per 1,000 person-years (PY) with a wide range across age groups (from 0.52 per 1,000PY in children aged 36-59 months to 29.6 per 1,000PY in children aged 1 month). Rates of RSV hospitalization were higher in males compared to females (4.7 and 3.7 per 1,000PY, respectively) and in children who were born at a younger gestational age (ranging from 3.9 in those born at ≥37 weeks to 23.2 per 1,000PY in those <28 weeks). For all age groups, rates were highest between December and March; however, there was substantial variation within age groups by calendar month, with the highest risk of RSV-hospitalization in those who were 1 month of age in February (Figure 1).

Conclusions: Our results reiterate the high burden of RSV hospitalization and highlight young infants at increased risk, including with respect to seasonality. These results may help inform current and future prevention efforts.

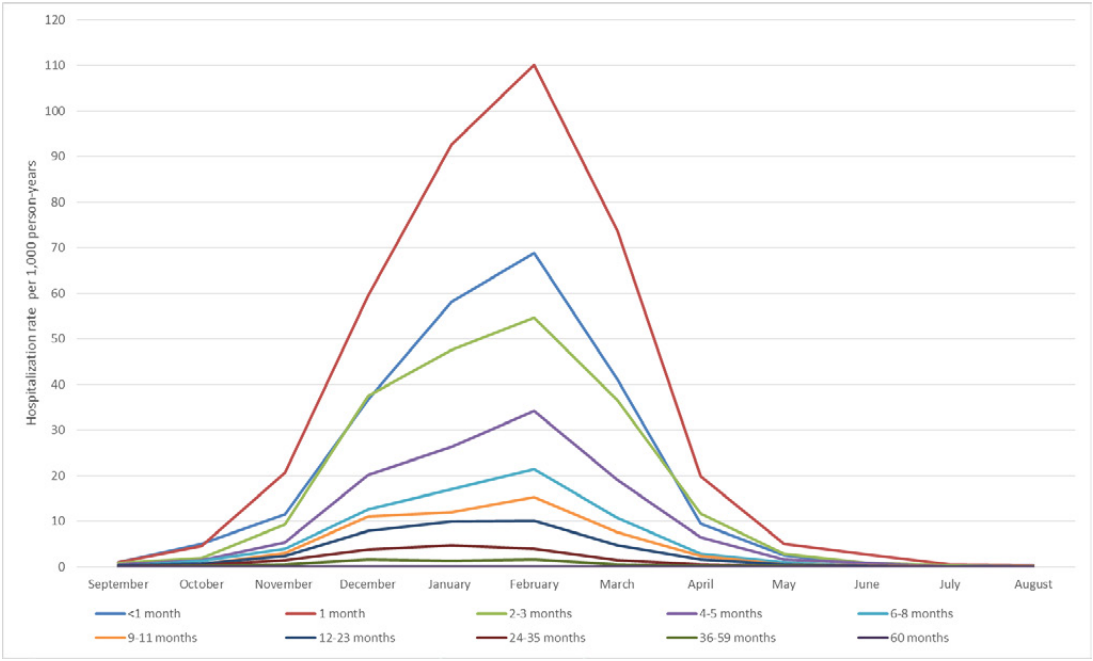

Figure 1. Rate of RSV hospitalization by age group and calendar month

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Abstract 1116

Fitness cost of mgrB alterations in carbapenem-resistant *Klebsiella pneumoniae* isolates from Moscow

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Background: Several mechanisms of resistance to colistin have been described in *Klebsiella pneumoniae*. One of them includes chromosomally encoded alterations in MgrB, which lead to lipopolysaccharide modification. To assess the impact of this colistin resistance mechanism on the bacterial fitness, we analyzed growth capacity among colistin-susceptible (Col-S) and colistin-resistant (Col-R) *K. pneumoniae* and performed competitive growth experiments.

Materials/methods: Colistin susceptibility among carbapenem-resistant (Carba-R) *K. pneumoniae* collected from patients at ICUs in Moscow was determined using the broth microdilution method. In Col-R (MIC >2 mg/L) isolates, the structure of *mgrB* was detected using the Sanger sequencing. Growth rates were determined by OD_{600} measuring for 15 hours every 30 minutes. The fitness of Col-R isolates was assessed against a Col-S strain using a competitive growth assay. Exponentially growing cells of Col-R and Col-S strains were mixed in a 1:1 proportion and grown in Luria-Bertani (LB) broth for 18 h. After incubation, the mixture was directly plated onto LB agar plates with or without 10 mg/L of colistin. The competitive index (CI) was calculated as a ratio between the number of Col-R and Col-S colonies.

Results: Among 22 Carba-R *K. pneumoniae*, 16 and 6 isolates were Col-R and Col-S, respectively. Colistin MICs of Col-R strains ranged from 16 to 1024 mg/L. In 8 Col-R isolates, the following *mgrB* alterations were detected: (1) IS*Kpn14*, IS*1A*, and IS*1R* (n=2, n=1 and n=1, respectively; IS1 family); (2) IS*Kpn26* and MITE*Kpn1* (n=1 and n= 2, respectively; IS5 family); (3) *mgrB* deletion (n=1). Eight Col-R carried a wild-type *mgrB*. Growth rates of Col-S and Col-R isolates did not differ significantly. Competitive co-culturing experiments demonstrated that 15 of 16 (94%) isolates carrying disrupted or wild-type *mgrB* displayed similar CIs, which were below 1 ranging from 0.01 to 0.3. One Col-R isolate with wild-type *mgrB* exhibited the equal fitness with the Col-S isolate (CI=1). Thus, 15 of 16 Col-R *K. pneumoniae* demonstrated a reduced fitness (CI<1) comparing to the Col-S strain.

Conclusions: Although colistin resistance did not affect the growth rates, the vast majority of Col-R *K. pneumoniae* demonstrated a reduced fitness (irrespective of the *mgrB* status) in competitive experiments.

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Abstract 1119

Inhibitory effect of whole blood on the antiseptic action of E-101 solution, a myeloperoxidase-mediated formulation, compared to conventional wound cleansers

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Background: Background: E-101 Solution (E-101) is a myeloperoxidase-mediated antimicrobial wound wash for physical irrigation, cleansing, and moisturizing of open wounds. It is composed of porcine myeloperoxidase (pMPO), glucose oxidase (GO), in an aqueous vehicle and activated by the addition of glucose. Once activated, hydrogen peroxide (H_2O_2) is produced *in situ* by GO dehydrogenation of glucose and reduction of oxygen. The MPO-catalysed oxidation of chloride ion by H_2O_2 generates hypochlorous acid (HOCl). Once generated, HOCl reacts in a diffusion-controlled reaction with a second H_2O_2 molecule to yield singlet oxygen. We evaluated the effect of blood on the performance of E-101 and three commercially available wound cleansers comprised of stabilized organic derivatives of HOCl.

Materials/methods: Antiseptics were tested against *Escherichia coli* ATCC 8739, *Pseudomonas aeruginosa* ATCC 9027, *Staphylococcus aureus* ATCC 6538, *Candida albicans* ATCC 10231, and *Aspergillus braziliensis* ATCC 16404 in accordance with the antimicrobial effectiveness test USP-51. Comparative antiseptics included Vashe (SteadMed), Microcyn (Oculus Innovative Sciences), and NeutroPhase (NovaBay Pharmaceuticals, Inc.). All antiseptics were tested in the absence and presence of 1, 2, and 5% whole human blood. Time kill studies were also performed with E-101 solution against *P. aeruginosa* ATCC 27853, *S. aureus* ATCC 43300, *E. coli* ATCC 25922, and *Candida auris* CDC B11903 in absence and presence of 2, 5, 10, and 20% blood.

Results: In the USP-51 test, E-101 demonstrated >2-$\log_{10}$ reduction against bacterial and fungal isolates in the presence of 5% blood at day 14 and day 28. With the exception of NeutroPhase vs *S. aureus*, all comparative antiseptics demonstrated <2-$\log_{10}$ reduction in the presence of 5% blood at days 14 and 28. Time-kill results for E-101 against *E. coli* and *P. aeruginosa* showed a >5-$\log_{10}$ reduction in the presence of 2, 5, 10 and 20% blood; for *S. aureus* a >5-$\log_{10}$ reduction in the presence of 2% and 5% blood; for *C. auris* a >5-$\log_{10}$ reduction in the presence of 2% blood.

Conclusions: E-101 remains active in the presence of blood containing catalase and other competitive substances. In contrast, comparative antiseptics with the active component HOCl were easily inactivated by the presence of blood.

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Abstract 1122

Evaluation of the BIOFIRE FILMARRAY Bone and Joint Infection (BJI) panel for the detection of microorganisms and resistance markers in synovial fluid specimens

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Background: Bone and Joint Infections (BJIs) present with non-specific symptoms that may include pain, swelling, and fever and are associated with high morbidity and significant risk of mortality. BJIs can be caused by a variety of bacteria and fungi, including anaerobes and microorganisms that can be challenging to culture or identify by traditional microbiological methods. Clinicians currently rely primarily on culture to identify the pathogen(s) responsible for infection. The BioFire® FilmArray® Bone and Joint Infection (BJI) Panel (BioFire Diagnostics, Salt Lake City, UT) was designed to detect 15 gram-positive (seven anaerobes) and 14 gram-negative bacteria (one anaerobe), two yeast, and eight antimicrobial resistance (AMR) genes from synovial fluid specimens in about an hour. The objective of this study is to evaluate the performance of an Investigational Use Only (IUO) version of the BioFire BJI Panel compared to various reference methods.

Materials/methods: Remnant synovial fluid specimens, which had been collected for routine clinical care at 13 study sites in the US and Europe, are undergoing testing using an IUO version of the BioFire BJI Panel. Performance is determined by comparison to Standard of Care (SoC) testing consisting of bacterial culture at each study site (performed according to each site's routine procedures).

Results: To date, 336 specimens (out of an anticipated 1,500) have been collected and tested with the panel. The majority are from knee joints (71.7%) and arthrocentesis (86.6%) is the most common collection method. Compared to SoC culture, overall sensitivity is 90% and specificity is 99.8%. Testing is ongoing.

Conclusions: The BioFire® BJI Panel is a sensitive, specific, and robust test for rapid detection of a wide range of analytes in synovial fluid specimens. The number of microorganisms and resistance markers included in the BioFire BJI Panel, together with a reduced time-to-result and increased diagnostic yield compared to culture, is expected to aid in the timely diagnosis and appropriate management of BJIs.

Data presented are from assays that have not been cleared or approved for diagnostic use.

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Abstract 1129

National ambulatory care prescribing of oral antibiotics and prevalence of inappropriate prescribing in the United States, 2009 to 2016

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Background: Antibiotic resistance is a global public health issue. A significant proportion of antibiotic use occurs in the outpatient setting for conditions not commonly caused by bacterial pathogens. Despite initiatives to decrease inappropriate antibiotic use, it is unclear how national prescribing rates have changed in recent years. This study aimed to describe outpatient antibiotic prescription trends and evaluate changes in inappropriate prescribing in the United States (U.S.) over an eight-year period.

Materials/methods: This was a cross-sectional study using the Centers for Disease Control and Prevention's National Ambulatory Medical Care Survey (NAMCS) from 2009 to 2016. All patient visits were eligible for inclusion. Antibiotic use was defined by at least one oral antibiotic prescription during the visit as identified by Multum code(s). Patient visits were categorized by health care provider, geographic regions within the U.S., and season. International Classification of Diseases, 9th Revision, Clinical Modification (ICD-9-CM) codes were used for survey years 2009 to 2015 and ICD-10 codes were used for 2016. Appropriate, possibly appropriate, and inappropriate antibiotic use were defined by the patient's ICD codes during their visit. Lastly, baseline characteristics were compared between visits involving receipt of an antibiotic and those that did not utilizing chi-square or Wilcoxon rank-sum tests where appropriate.

Results: A total of 7 million visits were included for analysis, of which 793,415,182 (11.3%) included an antibiotic. Prescribing rates were relatively stable over the study period, ranging from 102.9 to 124.9 prescriptions per 1000 visits; however, 2016 had one of the lowest prescribing rates (107.7 prescriptions per 1000 patient visits). The most commonly prescribed antibiotic class was macrolides (25 prescriptions per 1000 visits). The South region and winter season had the highest antibiotic prescription rates (118.2 and 129.7 prescriptions per 1000 visits, respectively). Of patients that received an antibiotic, 55.9% were classified as inappropriate use, 8.4% had an appropriate indication, and 35.7% had a possibly appropriate indication.

Conclusions: There was no significant reduction in outpatient antibiotic prescribing rates among outpatients in the U.S. from 2009 to 2016 and inappropriate antibiotic prescribing was common. Further public health campaigns are warranted to promote outpatient antimicrobial stewardship programs.

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Abstract 1131

Comparison of multidrug-resistant *Salmonella enterica* serovar I 4,[5],12:i:- and *Salmonella enterica* serovar Typhimurium isolated from swine in the USA

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Background: The Centers for Disease Control and Prevention has reported an rise in multi-drug resistant (MDR) *Salmonella enterica* serovar I 4,[5],12:i:-, which has been increasingly isolated from swine and pork products. *Salmonella* I 4,[5],12:i:- is antigenically similar to *Salmonella* enterica serovar Typhimurium yet lacks the phase 2 flagellar antigen; thus, is referred to as monophasic *Salmonella* Typhimurium. The overall objective of this study is to determine and compare phenotypic and genotypic traits of monophasic and biphasic *Salmonella* Typhimurium isolated from swine head trim and cheek meat collected from a pork processing plant in the United States.

Materials/methods: Phenotypic antimicrobial susceptibility patterns were identified by broth microdilution on a Sensititre® system. Bacterial growth curves were determined using a BioScreen C under different concentrations of enrofloxacin, tetracycline, ceftiofur, and ciprofloxacin; growth curves were analyzed using a 4-parameter Gompertz-model in Stata® to evaluate bacterial fitness. Motility and biofilm assays were used to assess swimming and swarming and biofilm production capabilities between monophasic and biphasic Typhimurium strains. Whole genome sequencing was performed on an Illumina MiSeq and Oxford Nanopore MinION to detect resistance genes, plasmids, and point mutations. Whole-genome alignment was performed to detect differences in the phase 2 flagellar antigen region using Geneious Software.

Results: Phenotypic and genotypic analyses confirmed all 47 *Salmonella* I 4,[5],12:i:- isolates were MDR, 45 displaying the common ASSuT phenotype and 2 the SSuT phenotype, while 44 displayed the ASSuT genotype. Thirty-seven also harbored the plasmid-mediated quinolone resistance gene, *qnr*B. There was no fitness cost to *Salmonella* I 4,[5],12:i:- harboring the *qnr*B, bla_{CMY} and *tet* genes. There were no significant differences between *Salmonella* I 4,[5],12:i:- and *Salmonella* Typhimurium swarming motility. However, the swimming motility *Salmonella* Typhimurium was greater over a period of 18 hours. Further analyses of bacterial growth curves, motility and biofilm assays, whole-genome alignment, and hybrid assembly between MinION and Illumina reads are ongoing.

Conclusions: This study is important to determining the pathogeniciy traits of MDR *Salmonella* I 4,[5],12:i:- in order to develop mitigation strategies and prevent this serovar from dissemination into the food chain and ultimiately aid in preventing salmonellosis linked to swine and pork products.

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Abstract 1136

Effectiveness and safety of aminoglycosides for the empirical treatment of patients with upper urinary tract infection

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Background: Aminoglycosides have favorable urinary tract pharmacokinetics and in vitro activity against uropathogens, but their use is limited by concerns over nephrotoxicity. We implemented an institutional program to promote aminoglycosides as initial empirical treatment of patients with upper urinary tract infection (UTI).

Materials/methods: We reviewed the records of patients with upper UTI at the Tel Aviv Medical Center from January 2017 to April 2018. The primary outcome was death within 30 days of index culture. Initial treatment with an aminoglycoside was compared to non-aminoglycoside antibiotics. Propensity score matching was performed to adjust for between-group differences in baseline covariates.

Results: The study cohort included 2,026 patients, 715 treated with aminoglycosides and 1,311 treated with non-aminoglycoside drugs; 589 patients (29%) were bacteremic. Treatment with aminoglycosides was associated with a higher likelihood of *in vitro* activity against clinical isolates (odds ratio, 2.0; P <0.001). Death at 30 days occurred in 55 (7.6%) versus 145 (11%) of patients treated with aminoglycosides and non-aminoglycoside drugs, respectively (adjusted hazard ratio, 0.78; P =0.013). Aminoglycosides were non-inferior to comparator drugs in all patient subgroups, stratified according to age, glomerular filtration rate, bacteremia, hemodynamic shock and infection with 3rd generation cephalosporin-resistant Enterobacterales. Aminoglycosides were associated with significantly shorter hospital stay, fewer days of antibiotic treatment, and lower rates of readmission within 90 days. The rate of acute kidney injury was similar for aminoglycosides and comparators (2.5% versus 2.9%, respectively; P =0.6).

Conclusions: Within the context of an institutional program, initial empirical treatment of upper UTI with aminoglycosides was associated with higher rates of appropriateness and lower overall mortality compared to non-aminoglycoside drugs, without excess nephrotoxicity.

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Abstract 1137

Prospective survey of mucormycosis in Israel

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Background: Mucormycosis is a clinically heterogenous invasive mycosis that can affect a broad population of human hosts. Incidence and associated patient risk factors vary significantly across geographical locations. IsraMOLD is an ongoing prospective multicenter laboratory-based survey of invasive mold disease in Israel. We report on the microbiological and clinical characteristics of mucormycoses identified in IsraMOLD.

Materials/methods: Clinical filamentous fungal isolates were collected at 10 medical centers throughout Israel (7 tertiary and 3 community hospitals). Clinical data were collected prospectively by researchers at each center. Isolate identification and drug-susceptibility testing were performed at a central reference laboratory. Mucorales species were identified by sequencing the internal transcribed spacer (ITS) and large subunit (LSU) ribosomal DNA segments.

Results: 363 mold isolates were collected from 1/2015 to 9/2019. Of these, 63 isolates (17%) were Mucorales, second only to *Aspergillus* species (236 isolates, 65%). 46 isolates (73%) represented invasive infection; neutropenia, stem cell transplantation and high-dose corticosteroid treatment were associated with invasive mucormycosis, whereas structural lung disease was associated with colonization. Median patient age was 49 years (range 1-87 years); 8 (17%) were aged under 18 years. Predominant risk factors were hematologic malignancy (15 patients, 32%), stem cell transplantation (24%), corticosteroids (24%), diabetes mellitus (21%), and trauma (8.7%). The frequent species were *Rhizopus* (n=26), *Lichtheimia* (n=12) and *Mucor* (n=6). Pulmonary mucormycosis was associated with hematologic malignancy and corticosteroid treatment, rhino-orbital mucormycosis was associated with hematologic malignancy and *Rhizopus* species, and soft tissue mucormycosis with trauma, *Lichtheimia* and *Mucor* species. Sixteen patients (34%) died within 30 days, similar to other invasive molds (logrank P=0.34). Death was associated with pulmonary disease, stem cell transplantation, GVH and corticosteroids. Surgery, performed in 28 patients (60%), was not associated with increased survival rate.

Conclusions: The annual incidence of mucormycosis in Israel was 1.5 per million population, high compared to other surveys. Hematologic malignancy emerged as the predominant risk factor. Mortality rate was similar to that of other invasive mycoses, possibly reflecting improvements in the diagnosis and pharmacotherapy of mucormycosis.

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Abstract 1138

Evaluation of the accuracy of the panel for antimicrobial susceptibility testing of *Enterobacteriaceae* and carbapenemase detection

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Background: The recent spread of carbapenemase-producing organisms (CPO) is a global threat. Carbapenem resistance in Enterobacteriaceae can be mediated by extended-spectrum beta-lactamase (ESBL) or AmpC beta-lactamase production in combination with decreased permeability or by carbapenemase production. In 2017, the Phoenix™NMIC-500 panel was launched. In this study, we evaluated the accuracy of antimicrobial susceptibility testing (AST) of Phoenix™NMIC-500 against Enterobacteriaceae.

Materials/methods: A total of 239 isolates were tested. They consisted of 47 CPO, 45 non-carbapenemase-producing carbapenem-resistant Enterobacteriaceae (non-CP-CRE), 47 ESBL-producing Enterobacteriaceae with ciprofloxacin MIC ≤1mg/L, 49 ESBL-producing Enterobacteriaceae with ciprofloxacin MIC ≥2mg/L, and 51 non-ESBL-producing Enterobacteriaceae. Bacterial isolates were subcultured on sheep blood plate and were tested for imipenem, meropenem, ertapenem, amikacin, gentamicin, ciprofloxacin, fosfomycin, cefazolin, ceftriaxone, nitrofurantoin with Phoenix™NMIC-500. As a reference method, broth microdilution was performed for all antibiotics tested except fosfomycin, for which agar dilution method was performed according to CLSI M07. The rate of category agreement (CA), very major error (VME), major error (ME), minor error (MinE) were calculated. We also evaluated the detection of ESBL and carbapenemase of the panel compared with the PCR results for ESBL and carbapenemase genes.

Results: The CA and error rates are described in the Table. In general, CA was >90% for all antibiotics tested. The ciprofloxacin CA of ESBL-producing Enterobacteriaceae with ciprofloxacin MIC ≤1mg/L and ≥2mg/L are 66.0%, 100%, respectively. The sensitivity and specificity of ESBL detection are 71.1% (69/97), 98.0% (50/51), respectively, and those of carbapenemase detection are 97.9% (46/47), 82.9% (160/193), respectively. Most (30/35) of isolates giving false-positive CPO results were non-CP-CRE. The rate of correct classification of CPO was 85.1% (40/47).

	CA (%)	VME (%)	ME (%)	MinE (%)
Imipenem	90.4	0	2.5	8.0
Meropenem	95.8	1.4	0.6	3.3
Ertapenem	96.2	0	1.5	2.9
Amikacin/Gentamicin	98.3/97.5	3.6/1.1	0/1.3	1.3/0.8
Ciprofloxacin	90.4	0.7	2.3	8.4
Fosfomycin	96.7	3.5	0	2.9
Cefazolin	97.9	0	0	2.1
Ceftriaxone	99.2	0	3.3	0
Nitrofurantoin	94.6	0	1.5	4.6

Conclusions: The Phoenix™NMIC-500 panel could provide alternative AST result to the reference method, except ciprofloxacin, especially in Enterobacteriaceae with low MICs. The detection of ESBL showed low sensitivity and CPO showed low specificity.

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Abstract 1142

Comparative variant analysis of *Aspergillus fumigatus* genomes for identification of novel mutations in candidate genes possibly be involved in mediation of azole resistance

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Background: Invasive pulmonary aspergillosis (IPA) is a life-threatening infectious disease in immunocompromised patients. In view of characterization of azole resistance whole genome sequencing (WGS) of *Aspergillus fumigatus* specimens was performed with the aim to identify novel genetic alterations leading to resistant phenotypes.

Materials/methods: In total, twenty-four *A. fumigatus* isolates from immunocompromised patients were investigated composed of 20 azole resistant and four susceptible samples. WGS was performed using the Illumina next generation sequencing (NGS) system. Results were mapped against the *A. fumigatus* AF293 genome followed by Burrows-Wheeler-Aligner (BWA) based sequence alignment. After variant calling by the use of GATK Haplotype caller, the annotation of variants was performed by implementation of SnpEff and programs based on annotation information provided by the *Aspergillus* genome database.

Results: Inspection of the small variant annotation revealed known mutations in the *cyp51A* gene for 11 out of the 20 resistant isolates. The TR46/Y121F/T289A variant was detected in five, the TR34/L98H alteration in two samples. With focus on further members of the ergosterol biosynthetic pathway, mutations in the genes *Hmg1* and *Erg6* were identified. Concerning *Hmg1*, two different mutations located in the sterol sensing domain were detected in two samples. In one sample a mutation in the HMG-CoA reductase domain was found. Three *Erg6* missense variants have been identified in five samples all negative for *cyp51A* mutations. Twenty-seven mutations have been found in the transmembrane transporter *abcA* gene, one missense mutation in the *mdr1* gene was detected in one sample. Missense mutations in the putative ABC multidrug transporter sitT have been found in 12 of the resistant strains.

Conclusions: Pending further validation in a larger cohort, on protein level and *in vivo*, the WGS of the genomes of azole resistant *A. fumigatus* strains identified several candidate genomic alterations that might pinpoint alternative pathways to acquisition of resistance, independent of the previously described *cyp51A* mutations. The discovery of previously undescribed resistance pathways in fungal strains might aid in identifying suitable biomarkers for effective clinical and epidemiological surveillance.
The study was supported by a scientific grant from Gilead Sciences, Germany.

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Abstract 1143

Phylogenetic analysis of complete genomes reveals the circulation of multiple lineages of rabies lyssavirus in India

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Background: Rabies is fatal zoonotic encephalitis caused by viruses of the Lyssavirus genus, in the family Rhabdoviridae. About 60,000 people die of rabies world-wide every year; India accounts for almost a third of this global burden. Most studies on the phylogenetic analysis/molecular epidemiology of RABV reported from India are based on partial gene sequencing, with only a single report of a complete RABV genome. Further molecular epidemiological and phylogenetic analysis of full-length genomes provide more accurate and precise information compared to partial gene sequences. It is in this context that metagenomic sequencing of rabies infected human and canine brains was carried out by MinION Oxford Nanopore (ONT), Oxford, UK.

Materials/methods: Extracted RNA from post-mortem human brain tissues from confirmed cases of rabies infection (n = 5) and brain tissue from laboratory confirmed canine rabies cases (n = 9) were subjected to metagenomics by protocol supplied by ONT. Fast5 files generated by MinION sequencing were base called, demultiplexed, trimmed, filtered and aligned to human and canine reference genomes. Unaligned reads were analysed further using Geneious Prime software. Mapping based assembly was done with rabies sequences and consensus sequences were submitted to Genbank. Phylogenetic analysis was done with using the maximum likelihood method. Model selection and tree building were carried out using iqtree and visualized in Figtree software.

Results: Full length genome of RABV was obtained in three canine and one human sample. Phylogenetic analysis revealed that RABV sequences from canine samples belonged to the Arctic like lineages and that from human brain sample clustered into the Cosmopolitan lineage.

Conclusions: Phylogenetic analysis of RABV whole genome sequences revealed circulation of two different lineages of RABV in India. Therefore extensive molecular epidemiological survey using full genome sequences of ample number of samples would be useful to study the epidemiology and heterogenecity of circulating Rabies lyssa virus in India.

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Abstract 1152

Efficacy of ceftazidime-avibactam for multidrug-resistant Gram-negative bacteria infections: a retrospective evaluation in a Belgian teaching hospital

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Background: Ceftazidime/avibactam (CAZ/AVI) demonstrates *in vitro* activity against multidrug-resistant (MDR) Gram-negative bacteria, including KPC-producing *Klebsiella pneumoniae* (KPC-Kp) and extended-spectrum beta-lactamases (ESBL)-producing *Enterobacteriaceae*, but clinical data remain limited.

Materials/methods: We aimed to evaluate the CAZ/AVI use in our Belgian tertiary hospital, from December 2016 to October 2019. Patients with confirmed infections and local laboratory *in vitro* confirmed sensitive strains to CAZ/AVI (≤ 8mg/L) who received CAZ/AVI for ≥ 48h, either as intermittent infusion of 2,5g every 8 hours or as a 24-hour continuous infusion (CI), were included in our retrospective study. Dosage adjustments for renal impairment were taken into account as per manufacturer prescription. Each initiation of treatment was supervised by an infectious disease (ID) specialist.

Results: Thirty-three episodes of infections (EI) occurred in twenty-seven patients and were predominantly caused by KPC-Kp and *Pseudomonas aeruginosa* (62% and 23,5%, respectively) (Table 1). Complicated intra-abdominal infections (24%), ventilator-associated pneumonia and tracheobronchitis (30%) and complicated urinary tract infections (24%) were the most frequent sites of infection. Bacteremia occurred in 36% of cases. Sepsis and septic shock were present in 36 % and 9 % of cases, respectively. CAZ/AVI was initiated as a first antibiotic therapy in 14 EI (42%). Other antibiotics were prescribed in 58% of the remaining cases with a median duration of 5,5 days before initiation of CAZ/AVI. CAZ/AVI was used as monotherapy in 76 %. Clinical cure or improvement was achieved in 84 % and microbiological cure was observed in 69 % of EI respectively. Median duration of therapy was 11,5 days. Thirty days after the CAZ/AVI treatment onset, eight patients (30%) had died. Except for one patient, no death was directly attributed to infection. Emergence of CAZ/AVI resistance occurred in one patient but was deemed not clinically relevant. Interestingly, 10/33 EI (30%) were treated with CI and reached 70% and 86% of clinical and microbiological cure respectively.

Conclusions: In our cohort of difficult-to-treat infections due to multidrug-resistant Gram-negative bacteria with limited therapeutic options, CAZ/AVI was used predominantly as monotherapy, under ID supervision and allowed good clinical and microbiological outcome with relatively low short-term mortality including when administered as a CI.

Table 1. Characteristics of the patients treated with CAZ/AVI

Characteristics [a]	
Patient variables (n = 27)	
Age, years, median (IQR)	59 (54,5-69,5)
Male sex (%)	11 (40,7)
At the onset of infection (n= 33) [b] (%)	
- Sepsis	12 (36,4)
- Septic shock	3 (9,1)
- Bacteremia	12 (36,4)
- Febrile neutropenia	4 (12,1)
- Ward	
- Medical	23 (69,7)
- ICU	10 (30,3)
Type of infection (n = 33)	
- cIAI	8 (24,2)
- cUTI	8 (24,2)
- VAP	8 (24,2)
- Bone and joint infection	3 (9,1)
- Bacteremia	2 (6,1)
- VAT	2 (6,1)
- Complicated skin and soft tissue infection	1 (3,0)
- Prothesis joint infection	1 (3,0)
Type of organisms (n = 34) [c]	
- KPC-producing *Klebsiella pneumoniae*	21 (61,8)
- *Pseudomonas aeruginosa*	8 (23,5)
- ESBL-producing *Klebsiella pneumoniae*	3 (8,8)
- *Enterobacter aerogenes*	2 (5,9)

Abbreviations: CAZ/AVI, ceftazidime-avibactam; cUTI, complicated urinary tract infection; cIAI, complicated intra-abdominal infection; VAP, ventilator-associated pneumonia; VAT, ventilator-associated tracheobronchitis; IQR: interquartile range.
[a] Values are number (%) unless indicated otherwise.
[b] Including 4 patients with relapsing infection, one patient with distinct episode of infection and one patient with concomitant cIAI and ventilator-associated pneumoniae due to the same pathogen.
- A relapse has been defined as a recurrence of infection due to the same pathogen at the same site of infection within a period of time less than or equal to one month (except for bone and joint infection where the period of time is less than or equal to 12 months).
- A distinct episode of infection has been defined as a recurrence of infection at the same site of infection within a period of time longer than one month (except for bone and joint infection where the period of time is longer than 12 months).
[c] For one patient, nosocomial pneumoniae was due to concomitant ESBL-producing *Klebsiella pneumoniae* and *Pseudomonas aeruginosa*, with both confirmed sensitive strains to CAZ/AVI.
[d] For one patient, duration of therapy with temocillin was unknown.
[e] For five of the eleven cases with empirical therapy, CAZ/AVI was switched to another antibiotic(s) after a mean of 3 days, including one case with sepsis attributed definitely to *Escherichia coli* bacteremia.
[f] After reviewing, it appeared that one case was not considered as an active pneumonia (unnecessary treatment).
[g] No death was directly attributed to MDR-infection in 7 patients: one patient died after seven days of therapy for a relapsing pneumonia which was clinically improved, death being related to others underlying diseases; six patients died of unrelated reasons a few days after the end of therapy. Partially under controlled MDR-infection cannot be ruled out as a cause of death in a single patient.

Table 2. CAZ/AVI treatment results.

Antibiotic regimens prior to CAZ/AVI (n = 33)	
- Meropenem	4 (12,1)
- Meropenem plus tigecycline	3 (9,1)
- Fosfomycin plus meropenem	2 (6,1)
- Piperacilline/tazobactam	2 (6,1)
- Tigecycline	2 (6,1)
- Amikacin plus meropenem	1 (3,0)
- Ceftriaxone	1 (3,0)
- Ciprofloxacine followed by meropenem	1 (3,0)
- Gentamicin plus co-trimoxazole	1 (3,0)
- Temocillin	1 (3,0)
- Temocillin plus tigecycline (plus gentamicin in loco)	1 (3,0)
- None	14 (42,4)
Duration of therapy before CAZ/AVI, days, median (IQR)	
- all infections (n = 32) [d]	1 (0-7,5)
- infections with antibiotic regimen prior to CAZ/AVI (n = 18)	5,5 (1,25-13,75)
Use of CAZ/AVI	
- Empirical therapy	11 (33,3)
- Documented therapy	22 (66,7)
- Monotherapy	25 (75,7)
- Combination therapy	8 (24,2)
- Continuous infusion	10 (30,3)
- Outpatient Parenteral Antimicrobial Therapy	3 (9,1)
Duration of CAZ/AVI, days, median (IQR)	
- all infections (n = 33)	10 (5-14)
- infections with definite therapy with CAZ/AVI (n = 28) [e]	11,5 (7-15,5)
Outcomes	
Clinical response (n = 32) [f]	
- Cured	18 (56,2)
- Improved	9 (28,1)
- Relapsed	4 (12,5)
- Failed	1 (3,1)
Microbiological response (culture proven eradication at the site of infection and/or in blood)	22/32 (68,7)
30-day mortality after the onset of CAZ/AVI treatment [g] (n = 27)	8 (29,6)

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Abstract 1153

Continuous infusion and outpatient parenteral antimicrobial therapy with ceftazidime-avibactam: evaluation of efficacy based on therapeutic drug monitoring

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Background: Based on recent PK/PD evidence, continuous infusion (CI) of beta-lactam administration is increasingly recommended for serious infections. Since 2016, the combination of ceftazidime and avibactam (CAZ/AVI) is administered per manufacturer prescription as an intermittent infusion of 2,5g every 8 hours thus CI has not yet been evaluated in clinical trials.

Materials/methods: We aimed to evaluate the use of CI of CAZ/AVI in a retrospective case series, from December 2016 to October 2019. All isolates displayed *in vitro* susceptibility to CAZ/AVI in agreement with EUCAST breakpoint. Patients were initially given CAZ/AVI as CI of 5g q12h. CAZ/AVI dosages were adjusted according to therapeutic drug monitoring (TDM) of ceftazidime with a therapeutic goal of 4-5xT> MIC in the plasma and/or at the site of infection. The latter was extrapolated from plasma concentrations and literature data

Results: CAZ/AVI was administered as CI in ten of thirty-three infectious episodes in twenty-seven patients treated with CAZ/AVI in our hospital. These infections were mainly caused by *Pseudomonas aeruginosa* (54,5%). Bacteremia occurred in 30% of cases and septic shock was only present in one patient. CAZ/AVI was used as monotherapy in 60% of cases. Clinical cure or improvement was achieved in 70 % of cases and microbiological cure was achieved in 6/7 (86%) evaluable cases (Table 1). Thirty days after the CAZ/AVI treatment onset, two patients (20%) had died, with death possibly related to uncontrolled infection in one case. Three patients were discharged home with an outpatient parenteral antimicrobial therapy (OPAT). Based on repeated TDM (3,5 samples/patient), therapeutic goals were achieved in 100% of cases in plasma and 88% of cases at the site of infection (8/10 evaluable), CAZ/AVI looked stable for 12-hour infusions and no drug-related adverse events were noted.

Conclusions: Although the sample size was limited, our case series shows promising clinical results for CI of CAZ/AVI, including for OPAT. Based on repeated TDM, therapeutic goals were achieved in 100% of cases in plasma. CAZ/AVI looked stable for 12-hour infusions and no drug-related adverse events were noted.

Table 1 - Ceftazidime-avibactam administered as continuous infusion

Patient	Type of infection	Type of organisms	CAZ/AVI MIC (mg/L)	Daily dose of CAZ/AVI (g)	Therapeutic goals 4-5xT > MIC (mg/L)		TDM of ceftazidime, mean (mg/L)	Sample of ceftazidime TDM /patient (n)	Duration of CAZ/AVI as CI (days)	OPAT	Clinical response	Microbiological response
					Plasma	Site of infection						
1	Bone and joint infection	KPC-producing *Klebsiella pneumoniae*	2	10	8 - 10	24 - 30	35,1	5	25	Yes	Cured	Cured
2	cUTI and bacteremia	KPC-producing *Klebsiella pneumoniae*	8	7,5 for 18 days 5 for 5 days	32 - 40	32 - 40	47,6 (7,5g daily) 44,6 (5g daily)	4	23	Yes	Cured	NE
3	VAP	*Pseudomonas aeruginosa*	8	10	32 - 40	96 - 120	84,3	5	24	No	Improved	Cured
4	VAT	*Pseudomonas aeruginosa*	8	5	32 - 40	NA	82,0	2	5	No	Cured	NE
5	VAT	*Pseudomonas aeruginosa*	0,5	10	2 - 2,5	NA	124,0	1	3	No	Improved	Cured
6	cIAI	*Enterobacter aerogenes*	6	5	24 - 30	48 - 60	>80	2	7	No	Relapse	Cured
7	VAP	ESBL-producing *Klebsiella pneumoniae* and *Pseudomonas aeruginosa*	1 (ESBL-producing *Klebsiella pneumoniae*) 2 (*Pseudomonas aeruginosa*)	10	8 - 10	24 - 30	76,2	2	7	No	Cured	Cured
8	cUTI	ESBL-producing *Klebsiella pneumoniae*	0,25	5	1 - 1,25	7 - 8,75	17,6	7	37	Yes	Cured	NE
9	prothesis joint infection and bacteremia	*Pseudomonas aeruginosa*	4	7,5	16 - 20	48 - 60	56,7	4	12	No	Failure	Failure
10	cIAI and bacteremia	*Pseudomonas aeruginosa*	2	10	8 - 10	16 - 20	67,4	3	12	No	Relapse	Cured

Abbreviations: CAZ/AVI, ceftazidime-avibactam; MIC, minimum inhibitory concentration ; TDM, therapeutic drug monitoring ; CI, continuous infusion; OPAT, outpatient parenteral antimicrobial therapy; cUTI, complicated urinary tract infection; cIAI, complicated intra-abdominal infection; VAP, ventilator-associated pneumonia; VAT, ventilator-associated tracheobronchitis; ESBL, extended-spectrum beta-lactamases; NA, not applicable; NE, not evaluable.

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Abstract 1159

Transmission dynamics of multidrug-resistant *Escherichia coli* sequence type 131 in the community

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Background: *E. coli* sequence type (ST) 131 is a predominant cause of community-onset extended-spectrum beta-lactamase-producing Enterobacteriaceae bloodstream infections globally.

Materials/methods: We performed a prospective study from February 2017 to November 2018 to investigate *E. coli* ST131 transmission dynamics in Singaporean households. We enrolled hospitalized patients with *E. coli* infections and screened their clinical isolates with qPCR. Families of index participants with *E. coli* ST131 infections and non-ST131 infections were further consented for a household transmission study. We modelled the transmission dynamics using a multistate model.

Results: One-hundred and thirty participants were enrolled. They contributed 635 stool samples at 2- to 6- week intervals, 200 food and environmental samples. The specimens yielded 6571 isolates (up to 12 *E. coli* isolates per sample), 7.9% (516/6571) of which were tested positive for *E. coli* ST131 via qPCR. All but two ST131 positive samples were human stools (one raw chicken and one toilet swab). During the year of follow-up, 52% (67/130) participants carried *E. coli* ST131 on at least once occasion and 85% (29/34) of families had at least one family member carrying ST131. The estimated probability for any individual to become colonized with *E. coli* ST131 in one year was 81% (95% CI 76-85%). The estimated duration of carriage in individuals is 68 days per year. Carriage of *E. coli* ST131 was strongly associated with the presence of a high-density carrier in the same family (an individual with any stool sample containing ST131 in >20% of all *E coli* isolates). Comorbidities and prior hospital admissions were not associated with carriage. Index patients infected with ST131 had significantly longer mean duration of carriage (137 days vs 21 days) and at higher densities (20% vs 6%) compared to those infected with non-ST131 *E. coli*. Whole genome sequencing of the ST131 isolates suggest high within-host diversity with multiple lineages of ST131 and repeated acquisition/ decolonization episodes within host across time points and between family members.

Conclusions: There is a high prevalence of *E. coli* ST131 in the Singapore community where transmission is largely through human-to-human contact particularly in families with high density carriers as 'reservoirs'.

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Abstract 1160

Streptococcal and *Staphylococcus aureus* prosthetic joint infections: are they really different?

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Background: Streptococci are the second most frequent bacteria isolated in prosthetic joint infections (PJIs) after staphylococci. Only few studies, including a small number of patients, compared streptococcal and staphylococcal PJIs. The objective of our study was to compare characteristics and outcomes of streptococcal and methicillin-susceptible *S. aureus* (MSSA) PJIs.

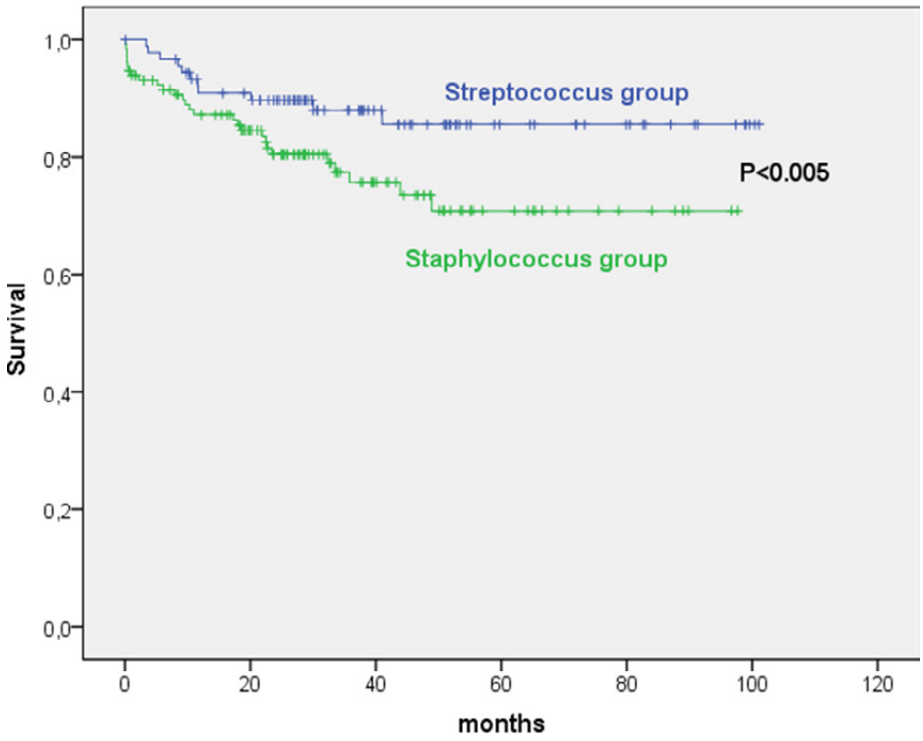
Materials/methods: Monocentric cohort study including all monomicrobial streptococcal and MSSA prosthetic knee (KPJIs) and hip (HPJIs) infections managed in our reference center from 01/2010 to 07/2017. We compared epidemiological data of the population, PJI type and outcome according to the medico-surgical strategy. The following events were noted: reinfection including relapse with the same and new infection with different bacteria, PJI-related and non-related death. Patients were followed for at least 2 years.

Results: Two hundred twenty-three PJIs, 91 streptococcal and 132 MSSA, developing on 92 knees and 131 hips, in 209 patients, were included. Comparison between the 2 groups (streptococci vs MSSA) showed that streptococcal PJI patients were older (77 vs 74 years, p=0.031), had more frequently cancer (10% vs 2%, p=0.016) and developed more frequently hematogenous acquired PJIs (88% vs 48%, p=0.0001). Surgical strategies did not differ between groups: debridement and implant retention (DAIR) (17/91 vs 29/132 p=NS), exchange arthroplasty (50/91 vs 84/132, p=NS).

At 2 years, all medico-surgical strategies taken together, reinfection rates were higher in the MSSA group (figure). Reinfection rates after DAIR (n=44) were higher in the MSSA group (2/15 vs 13/29, p= 0.032), but not different after exchange arthroplasty (n=129) (5/50 vs 6/79, p=NS).

Prolonged suppressive antibiotic therapy (n=33) was more commonly used in the streptococcal group (21/86 vs 12/123, p=0.002). Relapses were higher in the MSSA group (1/21 vs 4/13, p= 0.004).

Conclusions: Streptococcal compared to MSSA PJIs showed different characteristics and outcomes. Patients were older, had more frequently cancer, and PJI spread more frequently via the hematogenous way. Outcome after DAIR or suppressive antibiotic therapy was better, but no difference was observed after prosthesis exchange.



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Abstract 1161

ESBL-producing *Escherichia coli* causing community-onset bloodstream infection and the association of bacterial clones and virulence genes with septic shock

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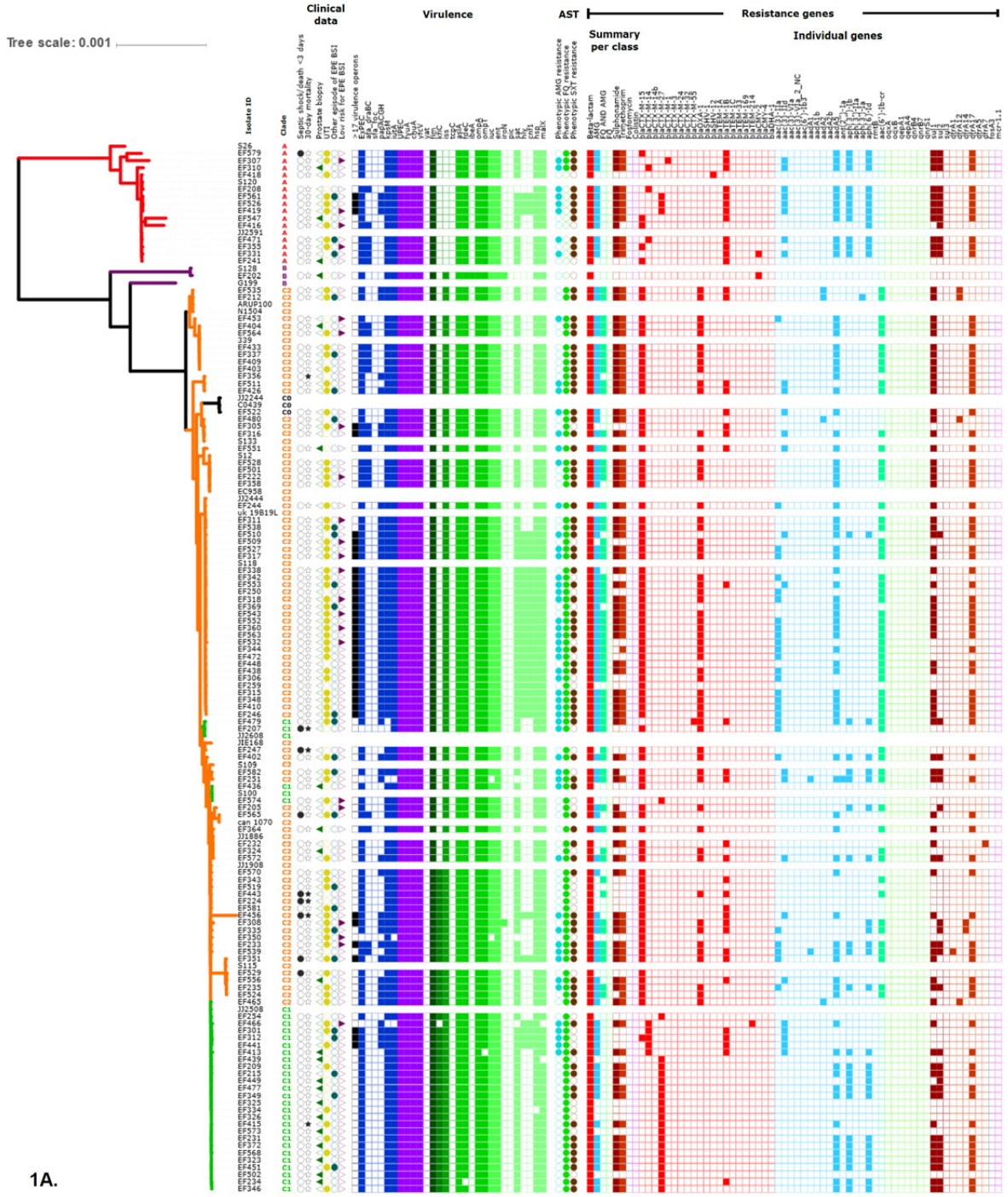
Background: Bloodstream infections (BSI) due to extended-spectrum β-lactamase-producing *Escherichia coli* (ESBL-EC) are an important cause of morbidity and mortality. The relative influence of host immunocompetence versus microbiological virulence factors (VF) in the acquisition and outcome of BSI is poorly understood.

Materials/methods: Whole genome sequencing was used on 278 blood culture isolates of ESBL-EC from 260 patients with community-onset infection collected during 2012-2015 in Stockholm, Sweden. Patient data was collected from medical records. The association of 108 virulence genes (26 operons), sequence types and antimicrobial resistance (ResFinder v2.1) to severity of disease and source of infection was assessed with multivariable logistic regression. SNP-phylograms were obtained with Enterobase.

Results: Results are shown in Figure 1. The fluoroquinolone-resistant high-risk clone ST131 subclade C2 comprised 30% and the emerging clone ST1193, 2%. Risk factors remaining in the final multivariable model for association with septic shock/short-term mortality had the following odds ratios (95% confidence intervals) and p-values: patient history of hematologic cancer/transplantation: 10.8 (95%CI 3.2-36.6), p<0.001, reduced daily living activity: 3.8 (1.4-9.9), p=0.007, infection source urinary tract infection (UTI)/prostate biopsy: 0.3 (0.1-0.9) p=0.026, presence of the *E. coli* VF *iss* (increased serum survival) 5.5 (1.3-22.8), p=0.019, multidrug-resistance 0.3 (0.1-0.7), p=0.010 and *pap* 0.2 (0.1-0.6), p=0.004. Adhesins, particularly *pap*, were associated with UTI-derived BSI, while isolates from post-prostate biopsy BSI had low overall virulence, low adhesin occurrence and commonly belonged to ST131 subclade C1, ST131 subclade A/B, ST1193 and ST648. ST131 was associated with recurrent episodes and repeated isolates from the same patient were often closely related.

Conclusions: ST131 subclade C2 was the dominating clone in community-onset ESBL-EC BSI in Stockholm. Detection of *iss* in the *E. coli*-isolate was associated with septic shock in immunocompetent patients and ISS could be a potential target for anti-virulence treatment.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Clinical data
Virulence
AST
Resistance genes
Summary per class
Individual genes
Isolate ID
Clade
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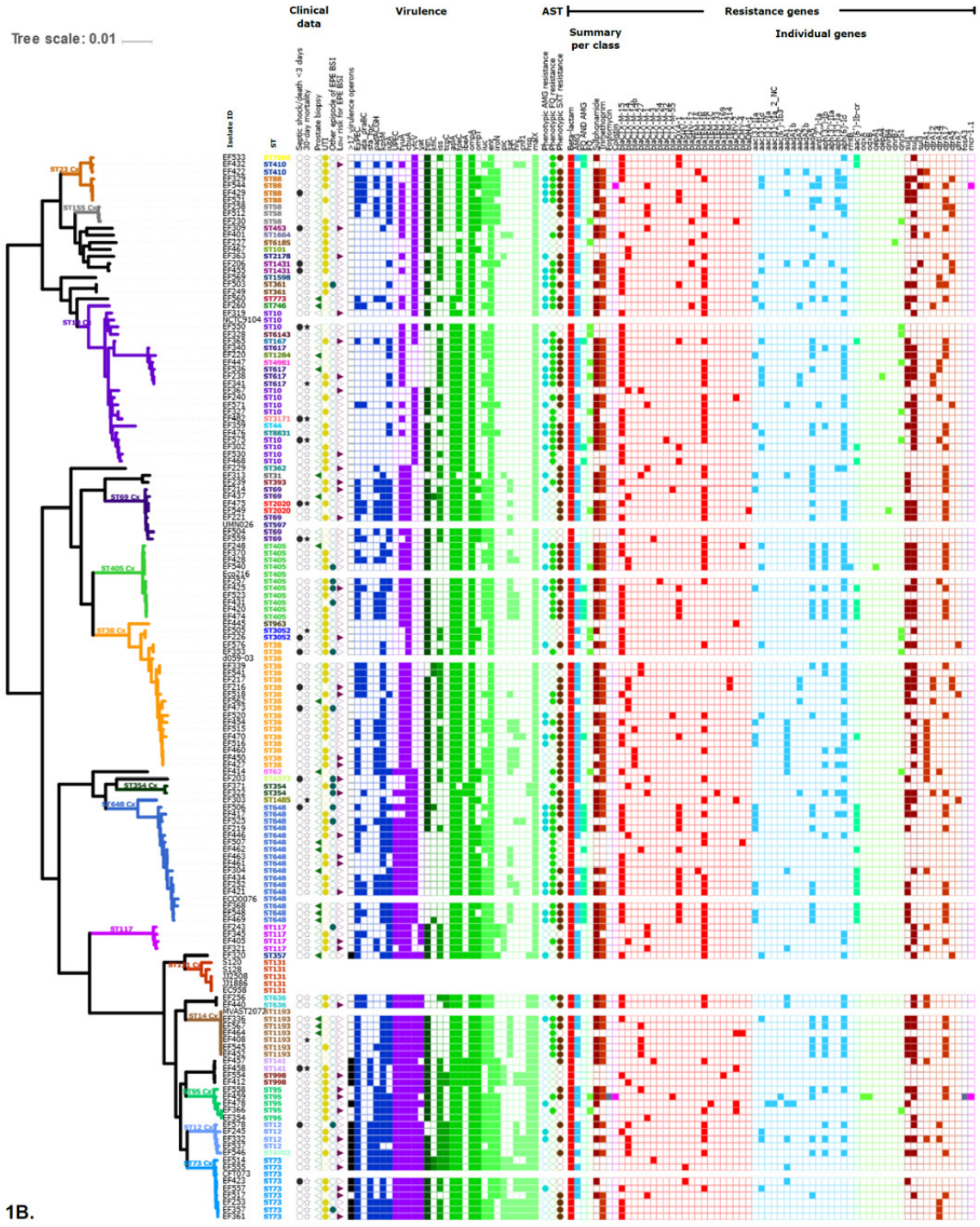

Figure 1. Maximum likelihood SNP-phylograms with data on patient history, outcome, virulence operons, phenotypic AST and resistance genes. Reference genome EC958 was used for SNP-mapping. The tree scale is number of substitutions per site. Patient isolates and reference genomes shown A) ST131 (n=121) B) Other STs (n=139). SNP: Single nucleotide polymorphism. AST: Antimicrobial susceptibility testing. Cx: Clonal complex.

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Abstract 1164

Persistent human papilloma virus type 16 infections in an established cohort of Slovenian women

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Background: Human papillomavirus (HPV) variants are associated with viral persistence and development of cervical cancer. The objective of our study was to determine and evaluate viral variants in paired HPV16-positive cervical smear samples, obtained at two sampling points (initial and after three years) from women aged 20-64, who were included in the previously described cohort of Slovenian women, attending the routine organized cervical cancer screening program.

Materials/methods: The presence of high-risk HPV infections in baseline and follow-up cervical samples was evaluated using the RealTime High Risk HPV test (Abbott, Wiesbaden, Germany), which allows concurrent partial genotyping for HPV16 and HPV18. In paired samples of women, in whom the presence of HPV16 was found in both samples, the complete long control genomic region (LCR) was amplified using the previously described conventional in-house PCR with g16f-7122/g16r-913 primers, and subsequently Sanger sequenced on the ABI3500 Genetic Analyzer (Thermo Fischer Scientific, Waltham, MA, USA). The obtained nucleotide sequences were edited and compared to HPV16 reference isolates using the Vector NTI Advance v11 software (Invitrogen, Carlsbad, CA) and phylogenetic relationships were inferred from the maximum likelihood tree, obtained based on the MAFFT alignment of eligible nucleotide sequences.

Results: At baseline, 160/4,432 (3,6%) women were HPV16 DNA positive. Of these 160 samples, 104 follow-up samples were available, of which 36 (34.6%) were HPV16-positive. Due to degradation of extracted DNA, further three samples were excluded from subsequent analyses. In available 33 paired cervical samples, identical HPV16 LCR viral variants were identified, suggesting the presence of persistent HPV16 infections. Using phylogenetic analyses, all HPV16 viral variants, obtained from samples of Slovenian women, clustered to the European HPV16 lineage (A).

Conclusions: Identical HPV16 LCR viral variants were found in all 33 paired cervical smears and all identified viral variants clustered to the European HPV16 lineage (A), confirming a significant burden of persistent HPV16 infections in our cohort of Slovenian women.

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Abstract 1166

Comparison of the Accelerate Pheno rapid diagnostic system with standard of care for diagnosing Gram-negative bloodstream infections: bacterial identification, antimicrobial sensitivity and turnaround time

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Abstract third-party references: Accelerate Diagnostics Inc., AZ, USA

Background: The Accelerate Pheno system (AXDX) is a diagnostic assay providing rapid identification (ID) of bacteria and yeast from blood cultures, as well as phenotypic antimicrobial susceptibility testing (AST). This multicentre study evaluated the accuracy and rapidity of AXDX in characterising Gram-negative bloodstream infections (BSI) in comparison with standard of care (SOC).

Materials/methods: Positive blood cultures with Gram-negative bacteria from three hospital sites were processed in parallel using AXDX and SOC (MALDI-TOF for identification, VITEK2 for AST). ID discrepancies between AXDX and SOC were classified as either false positive or false negative. Categorical agreement (CA) occurred when AXDX and SOC had the same interpretation of susceptibility of the isolate/antibiotic combination. 'Very major errors' (VME) occur when AXDX reported susceptibility but SOC resistance.

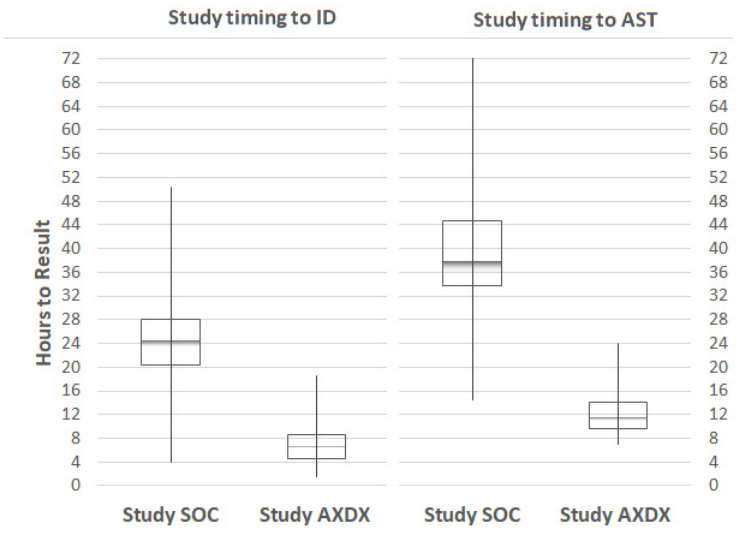
Multidrug-resistant organisms of interest (MOI) are those resistant to co-amoxiclav and gentamicin. Time difference to AST between AXDX and SOC was calculated for these MOI if patients were on inactive therapy as identified on chart review.

Results: 148 blood cultures were included. Of these, 141/148 (95.2%) had valid, reportable results on AXDX. 148 organisms were identified. 133/148 organisms were 'on-panel' Gram-negatives. AXDX identified 126/133 organisms correctly (sensitivity 93.3%). 1,128 Gram-negative probes were deployed with 4 false positive results giving a specificity of 1124/1128 (99.6%). From AST, CA was 94.9% (1,270/1,338). There were only 4 VME out of 262 resistant AST results. Turnaround time (TAT) for both ID and AST were calculated for AXDX and SOC. Timing data was available for 111/141 (79%) of blood cultures. Compared with SOC, AXDX gave an average reduction in ID TAT of 16.8 hours (CI 15.1-18.4 hours, $p<0.0001$) and an average reduction in AST TAT of 31.2 hours (CI 29.9-32.5hrs, $p<0.0001$).

There were 15 MOI. 9 of these patients were on inactive therapy, for whom AXDX gave an average time saving to AST results of 12hrs 04min.

Conclusions: AXDX provides accurate ID and AST for Gram-negative BSI, and has a significantly improved TAT that may optimise antimicrobial therapy.

Figure: Box plot of TAT for ID and AST from time of blood culture positivity (AXDX vs SOC)



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Abstract 1171

Rapid identification of pathogens, antibiotic resistance genes and plasmids in blood cultures by nanopore sequencing

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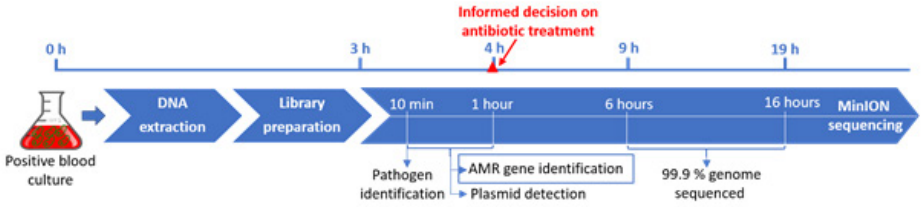
Background: Bloodstream infections (BSIs) and sepsis are major causes of morbidity and mortality worldwide. Blood-culture-based diagnostics usually requires 1-2 days for identification of bacterial agent and an additional 2-3 days for phenotypic determination of antibiotic susceptibility pattern. With the escalating burden of antimicrobial resistance (AMR) rapid diagnostics becomes increasingly important to secure adequate antibiotic therapy. Whole genome sequencing approaches offer a way to reduce clinical test turnaround times compared to conventional culture-based methods.

Materials/methods: We spiked eight blood cultures with bla_{CTX-M} positive *Escherichia coli* and *Klebsiella pneumoniae*, *mecA* positive *Staphylococcus aureus*, or a combination of these, and incubated them until they were flagged as positive. We measured the DNA concentrations and extracted bacterial DNA for sequencing with nanopore. For real-time analyses we used (a) What´s In My Pot, Centrifuge and BLAST against the NCBI Prokaryotic RefSeq for identification of bacterial species; (b) BLAST search against CARD and ResFinder databases for identification of resistance genes; and (c) PlasmidFinder and BLAST searches against plasmid database for identification of plasmids. We verified our results through whole genome sequencing with short-read Illumina sequencing and hybrid assembly using nanopore and Illumina sequences.

Results: Identification of pathogens was possible after 10 minutes of real-time sequencing, and all predefined AMR-encoding genes and plasmids from the different culture experiments were detected within one hour. Furthermore, we demonstrate correct identification of plasmids and bla_{CTX-M} subtypes using *de novo* assembled nanopore contigs. This proof-of-concept study represents a molecular approach to diagnosis of BSIs which can provide clinicians with detailed information on etiologic agent and AMR within four hours of a blood culture becoming positive. To our knowledge this is the first study applying nanopore sequencing to blood cultures for a rapid and comprehensive analysis of pathogens, plasmids and AMR-encoding genes.

Conclusions: We have shown that with a sequence-based approach to diagnostics it is possible to identify pathogens and specific AMR-encoding genes using raw nanopore sequencing data, obtained within four hours after a blood culture is flagged as positive by the incubation system. Results from this study hold great promise for future applications in clinical microbiology and for healthcare surveillance purposes.



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Abstract 1172

Influenza vaccine effectiveness against laboratory-confirmed influenza in Europe: results from DRIVE network 2018/19

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Abstract third-party references: Funding: Innovative Medicines Initiative 2 Joint Undertaking under grant agreement No 777363. This Joint Undertaking receives support from the European Union's Horizon 2020 research and innovation programme and EFPIA.

Background: DRIVE (Development of Robust and Innovative Vaccine Effectiveness) aims to establish a public-private platform to annually estimate brand-specific influenza vaccine effectiveness (IVE), in accordance with revised EMA guidance on influenza vaccines. IVE analyses and interpretation are conducted by public partners in the consortium.

Materials/methods: In 2018/19, four test-negative design (TND) studies in primary care (Austria, Italy, England), five TND studies in hospitals (Finland, Italy, Romania, Spain), and one register-based cohort study (Finland) were conducted. Case definitions were ILI, SARI and laboratory-confirmed influenza (LCI), respectively. Site-specific IVE estimates were centrally calculated and pooled through meta-analysis. Data cut-off was the end of influenza circulation at the study site level, or April 30, whichever occurred first.

Results: For the TND studies, 1897 LCI cases and 2570 controls from primary care and 1444 LCI cases and 3440 controls from hospitals were retained for analysis. Confounder-adjusted pooled IVE estimates against LCI for any vaccine were 48% (95%CI 0-78) and 38% (-65-81) in those <17 years (y) in primary care and hospital respectively, 45% (18-63) and 40% (2-63) in those 18-64y, and 18% (-85-71) and 27% (6-44) in those ≥65y. Sample size was still insufficient for reliable brand-specific estimates.

The register-based cohort study included 274,079 vaccinated person-years and 494,337 unvaccinated person-years, obtaining brand-specific IVE. Confounder-adjusted IVE estimates against LCI A, from out- and inpatients combined, were 36% (24-45) for Fluenz Tetra and 54% (47-62) for Vaxigrip Tetra in those <7y and 30% (25-36) for Vaxigrip Tetra in those ≥65y.

Conclusions: DRIVE is a growing new platform, that will expand to thirteen TND sites in 2019/20 and 2 register-based cohort sites. Sample size in future seasons is expected to increase, enabling the calculation of more brand-specific IVE estimates.

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Abstract 1177

Mechanisms of linezolid resistance in Belgian Enterococcus isolates (2013-2019)

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Background: Vancomycin-resistant enterococci (VRE) are a major cause of nosocomial infections for which a only a few treatment options, like linezolid, remain. Linezolid-resistant enterococci (LRE) are still rare but require strict surveillance to identify emerging resistance mechanisms and clones Linezolid resistance can result from mutational mechanisms (23S rRNA and/or ribosomal protein mutations) or resistance gene acquisition (*cfr*, *cfr(B)*, *optrA* and *poxtA* genes). The aim of this study was to investigate the mechanisms of linezolid resistance in Belgian LRE.

Materials/methods: Enterococci (n=2,836), including 2087 VRE, were submitted voluntarily to the Belgian Reference Centre for enterococci between 2013 and 2019. Susceptibility to linezolid was determined by MIC gradient testing according to EUCAST. Conventional PCR was applied for detection of *cfr* and *optrA*. WGS was performed on *cfr/optrA* negative LRE strains using Nextera XT (2 x250bp), MiSeq (Illumina Inc.). Spades v3.10 was used for genome assembly and LRE-finder 1.0 for detection of linezolid resistance mutations or genes. Susceptibility to tigecycline and daptomycin was tested by MIC gradient test for LRE that were also resistant to vancomycin (LVRE).

Results: 38 strains (31 clinical and 7 screening isolates) were identified as LRE (29 *E. faecalis* and 9 *E. faecium*) with linezolid MIC levels between 8 and 64 µg/ml (median 16µg/ml). 28/29 *E. faecalis* LRE were positive for *optrA* and 5/8 *E. faecium* LRE carried the G2576T 23S rRNA mutation (Table 1). *cfr* positive strains were not detected. Of the 8 LVRE (6 *vanA* and 2 *vanB E. faecium* strains), 2 were tigecycline resistant (MIC 0.5 µg/ml) and none were daptomycin resistant.

Conclusions: The majority of Belgian LRE are *E. faecalis*, in contrast to other countries where *E. faecium* LRE predominate. The linezolid resistance mechanisms in *E. faecium* LRE consisted of both chromosomal mutations and gene acquisition while *E. faecalis* LRE contained only transferable resistance determinants, predominantly *optrA*, which corroborates earlier findings on emerging *optrA*-mediated resistance.

Table 1. Characteristics Belgian LRE

	E. faecalis (n=29)	*E. faecium* (n=9)
optrA	28	2
poxtA	1	1
G2576T mutation	0	5
cfr(B) and G2576T-mutation	0	1

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Abstract 1178

A global point prevalence study of antimicrobial use in the neonatal intensive care unit: the NO-More-AntibioticS and Resistance study (NO-MAS-R)

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Abstract third-party references: On behalf of the NO-MAS-R Study Group, Nationwide Children's Hospital, The Ohio State University, Merck & Co. Inc

Background: Antimicrobial agents are the most prescribed medications in the NICU. Global assessment of all antimicrobial use provided to infants in the NICU and reasons for their use may inform future antimicrobial stewardship efforts.

Materials/methods: We conducted a prospective one-day (7/1/2019) global NICU point prevalence study of all antimicrobial use and obtained the following: NICU level, census, birth weight, gestational/postnatal age, diagnoses, culture results, antimicrobial therapy (reason for use; duration of therapy), antimicrobial stewardship program (ASP), and 30-day in-hospital mortality.

Results: 528 (27%; range, 0 to 100%) of 1927 infants in 71 NICUs (67, Level 3/4) from 26 countries (1, low; 12, middle; 13, high income; 5 continents) received at least one antimicrobial agent (91%, antibacterial; 19%, antifungal; 4%, antiviral). Of the 483 infants on antibiotics at a median postnatal age of 12 days (IQR, 4-33), their mean gestational age and birth weight were 32.6 ± 6 weeks and 1980 ±1017 grams, respectively. The most common reasons for receiving antibiotic therapy were rule-out sepsis (26%), "culture-negative" sepsis (16%), prophylaxis (15%), culture-positive infection (15%), and pneumonia (13%). The most frequently used antibiotics were ampicillin (40%), gentamicin (35%), amikacin (21%), vancomycin (15%), and meropenem (10%). For definitive treatment of presumed/confirmed infection, vancomycin (15%), amikacin (13%), and meropenem (10%) were the most prescribed agents. Planned duration of therapy was shorter (3 or 7 days) than actual treatment duration (7 to 14 days). Specifically, duration of antibiotic treatment for "culture-negative sepsis" was 7 days (IQR, 5-10 days) and for culture-positive sepsis was 11 days (IQR, 10-14 days; p-value=0.07). Mortality was 4.7%. 63% of the hospitals had an ASP, but among the 55% that had a NICU-specific ASP, antibiotic utilization rate was significantly lower than among those centers without an NICU-ASP (21% vs. 33%; p<0.01).

Conclusions: Ascertainment of overall antimicrobial use among NICU infants showed marked variability by NICU and country, with a single day prevalence of 27%. The majority of antibiotic use was in infants without a culture-confirmed infection. Duration of therapy was prolonged in most instances, and NICU-specific ASPs were associated with lower antibiotic utilization rates, suggesting the need for their implementation worldwide.

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Abstract 1179

Non-lethal concentrations of ceftazidime and ceftazidime-avibactam select for multiple-resistant genotypes

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Background: Drug concentrations below the minimum inhibitory concentration (sub-MIC) resulting from environmental pollution or found in body compartments during therapy can select for antibiotic resistance. OXA-48, unlike other carbapenemases, exhibits neglectable hydrolysis towards the cephalosporin ceftazidime (CAZ). Consequently, CAZ and the combination ceftazidime-avibactam (CAZ-AVI) are possible treatment options for infections caused by OXA-48-producers. Here, we show that exposure to sub-MIC concentrations of CAZ and CAZ-AVI selects for clinical resistance and variants of OXA-48.

Materials/methods: *E. coli* MG1655, harbouring a clinical bla_{OXA-48}-carrying plasmid, was evolved (n=3) for 300 generations in the absence and presence of sub-MIC (0.25xMIC) concentrations of CAZ and CAZ-AVI. At every 50th generation, we determined the proportion of clones exhibiting lower susceptibility towards CAZ/ CAZ-AVI and their MICs (broth microdilution). The allele frequencies of bla_{OXA-48} were identified at 50 and 300 generations using Sanger sequencing.

Results: Sub-MIC evolution using CAZ and CAZ-AVI selected for clones with decreased susceptibility already after 50 generations. No such clones were detectable without selective pressure during the whole evolution experiment, revealing at least a 10,000-fold difference in clones with reduced susceptibly between treatments. We determined the MICs of 50 clones every 50th generation. For CAZ, we found that at all times more than 50% of the tested clones (n=900) exhibited MICs above the clinical breakpoint, but did not show cross-resistance towards CAZ-AVI. For CAZ-AVI, one out of three populations displayed clones (n=18) at 50 generations with an up to 16-fold increase in the CAZ-AVI MICs. Sequencing of bla_{OXA-48} showed that resistance development towards CAZ-AVI was not due to mutations in bla_{OXA-48}. However, all populations evolved in the presence of CAZ carried clones expressing variants of OXA-48. In total, we identified seven different alleles of bla_{OXA-48} over the course of the experiment.

Conclusions: Non-lethal concentrations of CAZ and CAZ-AVI select for clinical resistance in *E. coli*. While the exposure to CAZ-AVI did not select for variants of OXA-48, seven mutants of OXA-48 were identified during the evolution with CAZ. Worryingly, two of the mutants have been described in environmental samples, underlining the importance of antibiotic pollution as a contributor to resistance development.

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Abstract 1180

Costs and benefits of OXA-48 variants selected under sub-lethal concentrations of ceftazidime

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Background: OXA-48 hydrolyses the 3rd generation cephalosporin ceftazidime (CAZ) inefficiently. Therefore CAZ is a relevant treatment alternative against infections caused by OXA-48-producing *Enterobacterales*. Antibiotic concentrations below the minimum inhibitory concentration (sub-MIC) can select for high-level resistance. Indeed, we previously found seven different variants of OXA-48 while evolving bla_{OXA-48}-encoding *E. coli* at sub-MIC levels of CAZ. These displayed single amino acid substitutions within the active site of OXA-48. Here, we characterise these mutants and show that their expression is beneficial, increasing MIC and bacterial fitness due to enhanced hydrolysis activity.

Materials/methods: bla_{OXA-48} alleles (wild-type and mutants) were sub-cloned into a pCR-blunt II vector, expressed in *E. coli* TOP10 and subsequently subjected to MIC testing (broth microdilution). All alleles were expressed from a pDest17 vector in *E. coli* AI for protein isolation and purification using His-trap columns. Purified enzymes were used to determine the catalytic efficiencies (k_{cat}/k_M) and thermostabilities. *E. coli* MG1655 carrying a pACYC184 vector encoding the bla_{OXA-48} alleles was used in head-to-head competitions against the wild-type allele at sub-MIC concentrations of CAZ to measure fitness.

Results: Expression of mutant bla_{OXA-48} alleles decreased CAZ susceptibility by 2 to 32-fold, compared to *E. coli* carrying wild-type bla_{OXA-48}. However, they displayed significantly increased susceptibilities towards carbapenems and penicillins with MICs decreased up to 32-fold. While the catalytic efficiencies of OXA-48 mutants increased by 2 to 44-fold towards CAZ, activity towards imipenem, meropenem and piperacillin decreased significantly. Additionally, all mutants exhibited thermostabilities 4°C to 8°C lower than wild-type OXA-48. While the expression of the OXA-48 variants did not negatively affect fitness in the absence of drug, at sub-MIC concentrations of CAZ (0.25xMIC wild-type OXA-48) all tested mutants displayed an up to 60% increase in relative fitness.

Conclusions: OXA-48 mutants selected under sub-lethal conditions of CAZ exhibited increased MICs and/or catalytic efficiencies towards CAZ. Resistance development imposed functional trade-offs towards other β-lactams, likely due to increased enzyme flexibility. We found these alleles to be beneficial under sub-MIC conditions, and some have been already described in environmental samples, supporting the idea that β-lactam contamination may facilitate the selection of resistance.

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Abstract 1184

Does C Diff Quik Chek display the same sensitivity than C Diff Quik Chek Complete for GDH detection?

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Background: One option for the diagnosis of *C. difficile* infection is to use an EIA (enzyme immunoassay) for GDH detection (glutamate dehydrogenase) (C Diff Quik Chek (Abbott)) followed, if positive, by an EIA for toxins. Alternatively, a combined test detecting both targets at the same time on the same device (C Diff Quik Chek Complete (Abbott)) can also be used. Based on biologists' feedback, some discrepancies between GDH detection by a stand-alone test for GDH and the combined test GDH+-toxin have been reported. The objective of this study was to compare the performances of the C Diff Quik Chek and C Diff Quik Chek Complete for detecting GDH compared to culture.

Materials/methods: From November 2018 to March 2019, 88 stool samples positive by culture for *C. difficile* (58 fresh stools and 30 frozen stools stored at -80°C) and 220 fresh stool samples negative by culture were tested simultaneously by both assays: C Diff Quik Chek and C Diff Quik Chek Complete. Discrepant results were defined as results that do not match with results of culture. In cases of negative-GDH assay and culture-positive, stool samples were tested again by another technician with both assays. In cases of positive-GDH assay from stool samples that were negative by culture, enriched culture was performed. In addition, serial dilution experiments were conducted on 5 culture-positive stool samples. Stool samples were diluted with the diluent from 1/10 to 1/10000 and each dilution was tested by 2 assays.

Results: Among the 88 culture-positive samples, 27 (30.7%) were non toxigenic strains and 61 (69.3%) isolates were toxigenic strains. After resolving discrepant results, both tests displayed a sensitivity and specificity for GDH detection of 97.9% [CI 95% 92.7-99.7] and 97.2% [CI 95% 93.9-98.9], respectively. Using serial dilution experiments, the results of each assays were similar in terms of detection threshold for GDH detection.

Conclusions: The C Diff Quik Chek and C Diff Quik Chek complete display a similar sensitivity and specificity for GDH detection.

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Abstract 1185

Epstein-Barr virus biomarkers in HIV-related non-Hodgkin lymphoma in the modern cART era

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Abstract third-party references: ANRS

Background: The usefulness of Epstein-Barr virus (EBV) biomarkers in HIV-related non-Hodgkin's lymphomas (NHL) is poorly explored in the context of improvement of the prognosis of these patients in the recent combined antiretroviral therapy (cART) era.

Materials/methods: We evaluated EBV DNA load and a panel of EBV antibodies in HIV-NHL patients prospectively enrolled in the French ANRS-CO16 Lymphovir cohort between 2008 and 2015. Pretreatment whole blood (WB), plasma EBV DNA load and serological profiles were analyzed in 76 HIV-infected patients. Moreover, for the 53 patients with available data, comparisons were performed between values at diagnosis and 6 months after the initiation of chemotherapy.

Results: Pretreatment WB and plasma EBV DNA loads were positive in 80% and 45% of HIV-NHL patients, respectively. Eighteen out of 43 (42%) tested cases for in situ EBV were positive. The detection of the EBV-encoded small RNA (EBER) was associated with plasma EBV DNA positivity (p = 0.002) but not with WB EBV DNA positivity (p =0.14). Two-year progression-free survival (PFS) estimates did not differ between the patients with pretreatment WB (n=61) or plasma (n=34) EBV DNA(+) and the patients with pretreatment WB (n=15) or plasma (n=42) EBV DNA(−) (82% vs 67% or 62% vs 69%, p=0.15 and 0.52, respectively). At diagnosis, 62% of patients harbored an EBV reactivation serological profile defined by high anti-EBV IgG antibody levels or high anti-VCA IgG antibody titers combined with high anti-EA IgG antibody titers. Two-year PFS estimates did not differ between the patients with a normal profile or those with a reactivation profile. Following chemotherapy, WB and plasma EBV DNA levels significantly declined from medians of 3970 (interquartile range, 268–14400) and 0 (0–342) copies/mL to 0 (0–0) and 0 (0–0) copies/mL, respectively (p<0.0001 and p<0.0001, respectively). Anti-EA IgG, anti-EBNA-1 IgG, anti-EBV IgA antibodies significantly dropped at 6 month follow-up (p<0.0001, p=0.01 and p<000.1, respectively). No significant decrease was observed with the anti-VCA or the anti-EBV IgG antibody titers/levels (p=0.10 and 0.07, respectively).

Conclusions: WB and plasma EBV DNA loads at NHL diagnosis do not constitute prognostic markers in HIV-NHL patients in the modern cART era.

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Abstract 1186

Needles in a haystack: ultra-orphan invasive fungal infections reported in FungiScope: global registry for emerging fungal infections

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Abstract third-party references: On behalf of FungiScope® Team

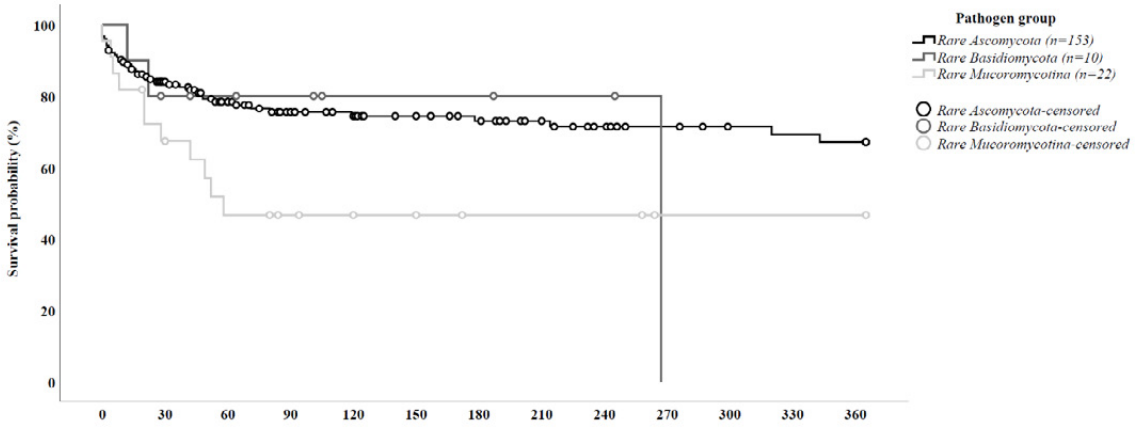
Background: Emerging invasive fungal infections (IFIs) have become a major challenge in patient management, as effective therapies have not been evaluated due to low number of patients affected. Apart from the more frequently described fusariosis, lomentosporiosis, mucormycosis, scedosporiosis, and certain dematiaceous fungi or yeasts, little is known about ultra-orphan IFIs. Our aim is to present an overview of ultra-orphan IFIs collected in the FungiScope® registry

Materials/methods: Ultra-orphan IFIs were collected in FungiScope® registry. Cases were grouped in Rare Ascomycota (subgroups *Rare Dematiaceae*, *Rare Hypocreales*, *Rare Saccharomycetales*, *Rare Eurotiales*, and *Invasive Dermatomycetes*), *Rare Basidiomycota*, *Rare Entomophthorales*, and *Rare Mucorales*.

Results: Between 2003 and June 2019, 187 ultra-orphan IFIs were documented in FungiScope®. *Rare Dematiaceae* (35.3%), *Rare Hypocreales* (22.5%), *Rare Mucorales* (11.8%) or *Rare Saccharomycetales* (10.7%) caused most IFIs. The majority of the patients had an underlying malignancy (38.0%). Disseminated infection was observed in 48 patients. Complete or partial responses were observed in 67.9% overall, ranging from 50.0% in *Rare Entomophthorales* to 83.3% in *Rare Eurotiales* related cases. Overall mortality rate was 28.9%, ranging from 11.1% in *Rare Eurotiales* to 50.0% in *Rare Mucorales*.

Conclusions: Physicians are confronted with a complex variety of fungal pathogens, for which treatment recommendations are lacking and successful outcome might be incidental. Only through an international joint effort of physicians and scientists, an adequate number of cases of ultra-orphan IFIs can be collected to further investigate the epidemiology and eventually identify effective therapy regimens.

Figure: Kaplan-Meier survival plots of ultra-orphan invasive infections reported in FungiScope®



Number of patients at risk

Rare Ascomycota	153	113	89	73	65	59	53	47	41	36	33	31	30
Rare Basidiomycota	10	7	6	5	3	3	3	2	2	0	0	0	0
Rare Mucoromycotina	22	14	9	7	6	5	3	3	3	1	1	1	1

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Abstract 1187

Effect of antiretroviral therapy on resistant *Escherichia coli*

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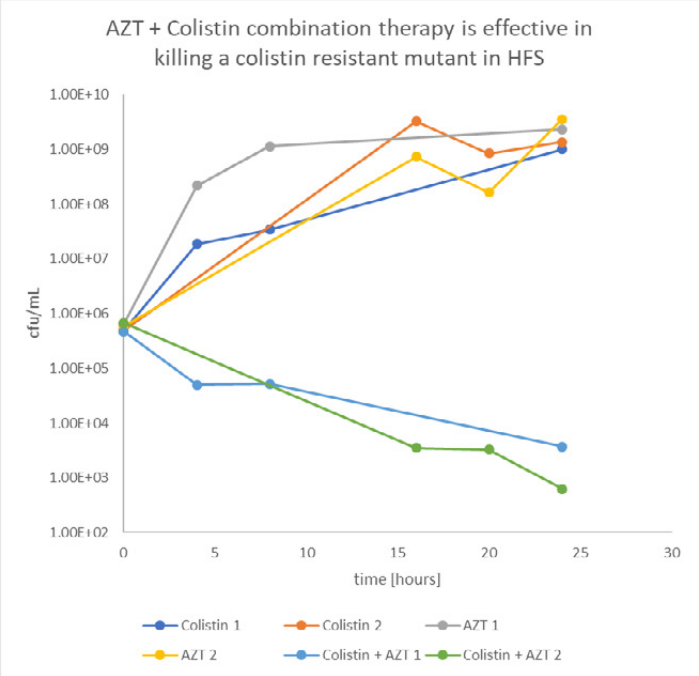
Dr Robert J H Hammond, University of St Andrews

Background: Colistin is one of the last line antibiotics we have in our toolkit against the rising tide of antimicrobial resistance (AMR). When bacteria become resistant to colistin they are classified as untreatable. Zidovudine (AZT) is an antiretroviral that prevents mother-to-child spread of HIV and works by inhibiting DNA reverse transcriptase. Combination therapy is an exciting branch of potential chemotherapy for resistant bacteria. The use of combinations of drugs can overcome resistance mechanism and render untreatable organisms susceptible.

Materials/methods: In this work we created a colistin resistant mutant *E. coli* 25922 and subjected it to colistin + zidovudine therapy. We used a Hollow Fiber Bioreactor (HFS) to growth our mutated strain of *E. coli* to ff1x10^5 cfu/mL in Mueller Hinton cation adjusted broth and then began drug infusion with a syringe driver. We ran four sets of experiments; a dug free trail as a control followed by a colistin only, AZT only and a colistin + AZT run.

Results:



Data indicates that the colistin only arm as well as the AZT arm had no effect however when the combination therapy was applied bacterial killing began within 4 hours and continued for 24 hours resulting in a nearly 3-log reduction in viable cells.

Conclusions: We hypothesise that AZT is unable to cross the bacterial membrane therefore has no effect on the resistant mutant. However, in the combination therapy the colistin is able to form pores in the bacterial membrane and this facilitates the AZT entry to the cell.

These data imply that combinations of seemingly unrelated antimicrobials could be used as novel treatment options in the cases of extreme drug resistance

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Abstract 1188

UV-C light application after terminal disinfection for vancomycin-resistant enterococci: an additional safety?

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Background: Surfaces may be contaminated by patients colonized or infected with multidrug resistant microorganisms. The environment of patients colonized/infected with Vancomycin-resistant Enterococci (VRE) are commonly contaminated with VRE. Several studies indicate that VRE may survive in these rooms even after terminal disinfection (TD) after discharge of the patient, an established risk factor for the next patient hospitalized in the same room acquiring VRE. Our aim was to see whether UV-C disinfection of rooms occupied by patients colonized or infected with VRE leads to a measurable decrease in VRE compared to standard TD procedures.

Materials/methods: Between 10/2018-10/2019, 29 rooms from 19 different patients colonized with VRE were examined after discharge (5 VanA (26.3%)/14 Van B (73.7%)). Eight samples per site have been checked: Toilet seat, toilet button flush, toilet paper cover, tap, floor, patient bed bell, bedside drawer and folding table. Standard TD was performed by a commercially licensed product – a mix of quaternary ammonium compound with aldehyde (Deconex® 50 FF, 0.5%) by in-house trained cleaning staff. The microbiological samples were taken using RODAC contact plates and eSwab™ at three time points: a) before TD, b) after TD and before UV-C disinfection, c) after TD and UV-C disinfection. When growth was detected, isolates were subcultured on Columbia blood agar and CNA plates, and microorganisms were identified by MALDI-TOF massspectrometry, and strains of patients as well as positive environmental samples were typed by whole genome sequencing.

Results: Overall, 688 samples were analyzed. At time point a) 16% (37/232), b) 2% (5/224) and c) 0% (0/232) samples were positive for VRE. In one patient room, 8 samples could not be taken after TD and before UV-C. Significant reductions were achieved before TD as well as after UV-C disinfection ($p<0.0001$). The addition of UV-C after TD did significantly reduced the environmental burden with VRE, even after TD ($p = 0.028$).

Conclusions: The applied TD failed to completely eliminate VRE. The additional exposure with UV-C succeeded to eliminate VRE from the analyzed sites, and may be needed to safely provide a clean room to the next patient.

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Abstract 1190

Systematic evaluation of development pathways of centrally-approved antibiotics in Europe including an innovative graphical illustration method

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Background: Development of new antibacterial agents is necessary as drug-resistant bacteria are a threat to global health. In Europe, the European Medicines Agency (EMA) has been guiding this development process for more than two decades. We investigated preclinical and clinical studies to illuminate the various phases within the authorization process.

Methods: All centrally authorized systemic antibacterial and antimycobacterial drugs were included without any time restriction. Additionally, Food & Drug Administration (FDA)-approved antibiotics of the last three years, which were not yet approved by the EMA, were included. We focused on the preclinical pharmacokinetic/pharmacodynamic (PK/PD) studies and phase II and phase III clinical trials. Furthermore, we investigated the recommended dosing regimens and correlation between preclinical studies and finally approved indications. Tree diagrams as a novel way of illustrating the development process of antibiotics were developed.

Results: We included 23 (EMA 18, FDA 5) antimicrobials. Tetracyclines, carbapenems and cephalosporins were the leading classes with 13% each. The recommended dosing interval was significantly shorter in time-dependent versus exposure-dependent drugs (median 8 versus 12, Mann-Whitney U test: $p = 0.006$). The majority of approved indications used non-inferiority trials (i.e. acute bacterial skin and soft tissue infection, community-acquired pneumonia, complicated intra-abdominal infection, complicated urinary tract infection, and complicated skin and soft tissue infection). Phase II and phase III clinical trials investigating community-acquired pneumonia involved the fewest patients (mean 85 and 494 patients, respectively) while complicated urinary tract infections phase III trials included the largest number (mean 688 patients). The Figure depicts the way to approval of ceftazidime-avibactam as one example. The branches of the development process demonstrate the increasing evidence for clinical efficacy.

Conclusions: Some promising drugs were marketed in the last years. The individual steps to their authorization were illuminated. We confirmed the relevance of PK/PD studies in dosing optimization and decision making in modern antimicrobial development and identified important differences in pathways according to antimicrobial class and target indication.

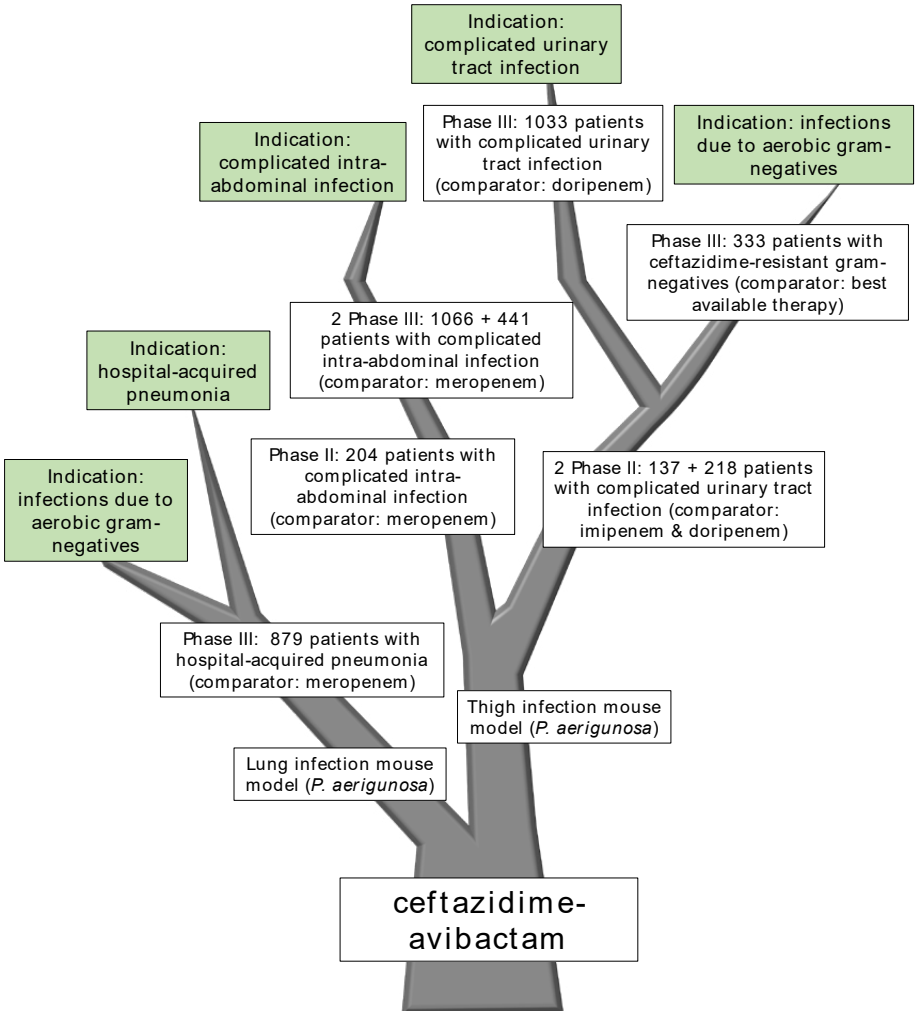

Figure. Pathway towards approved indications of ceftazidime-avibactam.

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Abstract 1191

An open-label, phase I, multi-centre study to evaluate the pharmacokinetic, safety and tolerability profile of oral isavuconazonium sulfate in paediatric patients

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Abstract third-party references: This abstract was submitted by Cello Health MedErgy, on behalf of the authors. Editorial assistance was provided by Cello Health MedErgy, funded by Astellas Pharma Global Development, Inc., Northbrook, IL, USA.

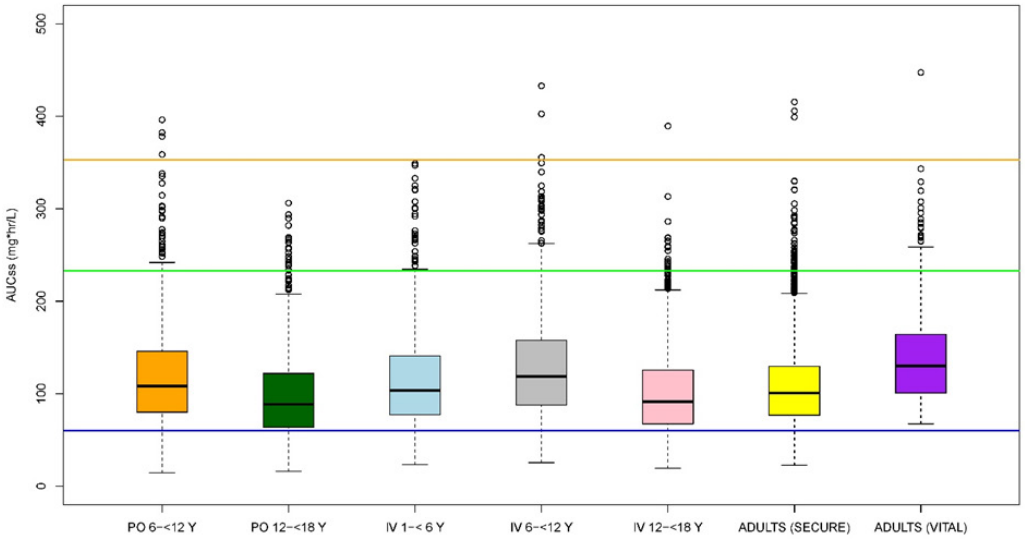
Background: Isavuconazonium sulfate (ISAVUSULF) is the prodrug of isavuconazole (ISAV), a broad-spectrum mould-active triazole with proven efficacy in treating invasive aspergillosis and mucormycosis in adults. The purpose of this study (NCT03241550) was to evaluate the pharmacokinetics (PK), safety and tolerability of multiple-dose oral ISAV in paediatric subjects at risk for invasive mycoses.

Materials/methods: Subjects were grouped into two age cohorts (6–<12 years and 12–<18 years). The ISAVUSULF formulation was a novel 74.5 mg oral capsule equivalent to 40 mg ISAV. Subjects received a target dose of 10 mg/kg (to a maximum of 372 mg), q8h on days 1 and 2, then once daily on days 3–28. Plasma ISAV concentrations were used to update a population PK model previously built using intravenous (IV) data from paediatric subjects (1–<18 years) in this study, plus IV data from a phase I study in adults (NCT01555866). Monte Carlo simulations were performed and area under the concentration–time curve at steady state (AUC_{ss}) was calculated. The target exposure range was based on efficacious ranges from adults in the phase III SECURE (NCT00412893) and VITAL (NCT00634049) studies; an upper safety threshold was derived from an adult study (NCT01565720) that used a supratherapeutic dose (1116 mg) with increased adverse events (AEs).

Results: Of 20 enrolled subjects, 19 were evaluable for PK and safety. Using modelling and simulation, paediatric ISAV exposures at the studied oral dosage were similar to paediatric exposures following IV administration and to exposures shown to be efficacious in adults, and were significantly below the safety threshold reported previously following supratherapeutic dosing in adults (Figure). AEs were reported in 18 subjects, with drug-related AEs in 10. Six drug-related AEs (nausea, vomiting, pyrexia, elevated alanine aminotransferase, elevated aspartate aminotransferase, abdominal pain) led to treatment withdrawal in 3 subjects. No deaths were reported.

Conclusions: Oral ISAVUSULF administered to paediatric subjects (10 mg/kg, q8h on days 1 and 2 and once daily thereafter) resulted in steady-state ISAV exposures similar to those observed with IV administration and comparable to the efficacious range observed in adults. The safety profile was similar to that of adults.

Figure. Paediatric and adult exposures to isavuconazole



Box-and-whisker plots of simulated drug exposure (AUC_{SS}) for paediatric age cohorts (1–<6 [IV only], 6–<12, 12–<18 years; oral or IV ISAVUSULF 10 mg/kg to a maximum of 372 mg, q8h on days 1 and 2 and once daily thereafter) and predicted drug exposure (AUC_{SS}) for adult populations (data from the SECURE [NCT00412893] and VITAL [NCT00634049] studies; oral or IV ISAVUSULF 372 mg once daily). Boxes represent the medians (thick black lines) and interquartile ranges, whiskers represent the range of maximum and minimum values within 1.5 × the interquartile range, and outliers are shown as circles. The blue line is the AUC_{SS} from the SECURE study (25th percentile; 60 mg*h/L) that represents the lowest targeted value. The green and orange lines are the minimum (233 mg*h/L) and mean (353 mg*h/L) AUC_{SS} values, respectively, in a high-dose adult study (1116 mg; NCT01565720) with increased adverse events.

AUC_{SS}, area under the concentration–time curve at steady state; ISAVUSULF, isavuconazonium sulfate; IV, intravenous; PO, oral; q8h, every 8 hours; Y, years.

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Abstract 1192

Meropenem-Vaborbactam (VABOREM) in treatment of patients with hospital- and ventilator-acquired pneumonia (HABP/VABP) and bacteraemia due to carbapenem-resistant *Enterobacteriaceae*

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Abstract third-party references: Menarini, Melinta

Background: Meropenem-vaborbactam (M-V) is a beta-lactamase inhibitor combination active against carbapenemase-producing *Klebsiella pneumoniae*. We report outcomes in patients with HABP/VABP and bacteremia due to CRE who were treated with M-V monotherapy vs best available therapy (BAT).

Materials/methods: TANGO 2 was a randomized, Phase 3, open-label trial in patients with confirmed or suspected CRE infections, including cUTI, HABP/VABP, bacteremia, or cIAI. Patients were randomized 2:1 to M-V monotherapy or BAT for 7-14 days. BAT could include (alone or in combination): carbapenem, aminoglycoside, polymyxin B, colistin, tigecycline or ceftazidime-avibactam (monotherapy only). Enrollment was stratified by infection type and geographic region. For the patients with HABP/VABP and with primary bacteremia, the primary efficacy endpoint was all-cause mortality at Day 28. The secondary endpoint was the proportion of patients with clinical cure at test of cure (TOC, 7±2 days following end of treatment). This study was not powered for inferential statistical testing; results are presented descriptively.

Results: Of the 75 patients treated in this study, 34 patients had HABP/VABP or bacteremia; 27 (79%) had baseline CRE, comprising the microbiologic CRE modified intent-to-treat primary population (mCRE-MITT). Patients with HABP/VABP or bacteremia were white (82.4%), with mean age 61.2 y (30-84 y). Most patients were from Europe (52.9%) or North America (29.4%) and had a CrCl ≥50 mL/min (76.5%). Charlson comorbidity score of ≥5 was present in 73.5%. Half of patients had SIRS at baseline; 47.1% of patients were immunocompromised.

In HABP/VABP/bacteremia patients with CRE infection, the all-cause mortality at day 28 was 22.2% (4/18) M-V vs 44.4% (4/9) BAT. Clinical Cure at TOC was seen in 66.7% (12/18) M-V vs 22.2% (2/9) BAT. In the study, incidence of AEs was similar between groups (84 % M-V vs 92% BAT). M-V was associated with fewer drug-related AEs (24% vs. 44%), severe AEs (14% vs. 28%), serious AEs (34% vs. 44%) and less nephrotoxicity vs BAT.

Conclusions: In this prospective comparative trial of M-V monotherapy in CRE infections, M-V showed consistent reduction in mortality and improvement in clinical cure and safety/tolerability over BAT. M-V appears to be an effective treatment option for HABP/VABP/bacteremia due to CRE.

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Abstract 1194

Mutant prevention concentration values of linezolid, moxifloxacin and vancomycin against *Staphylococcus pseudintermedius* strains recovered from humans

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Background: SP is a commensal and opportunistic pathogen of dogs and cats. SP recovered from human specimens seems to be increasing and multidrug resistant strains from humans are being reported. Two particular cases from our hospital were a 4 month old pediatric oncology patient with SP bacteremia and the second a middle aged female oncology patient with persistent wound infection and catheter tip colonization. SP strains were recovered from family pets of both patients. We tested the SP strains from humans to determine minimum inhibitory concentration (MIC) and MPC values to L, M and V.

Materials/methods: A total of 24 isolates from humans were tested. MIC testing was as per the recommended procedure of the Clinical and Laboratory Standards Institute (CLSI) utilizing a 10^5 colony forming unit/milliliter (cfu/ml) inoculum and incubation under ambient conditions for 18 to 24 hours. For MPC testing $\geq 10^9$ CFU were applied to the surface of drug containing agar plates. Inoculated plates were incubated under ambient conditions and screened for growth after 24 and 48 hours of incubation. The lowest drug concentration blocking growth was recorded as the MIC or MPC depending on the method.

Results: MIC range values for L, M and V were 1-2, ≤0.016-0.63 and 0.25-0.5 µg/ml respectively. The $MIC_{50/90}$ values were 1/2, ≤0.016/0.031 and 0.25/0.5 µg/ml. MPC range values were 1-2, 0.125-0.25 and 4-≥8 µg/ml with $MPC_{50/90}$ values of 2/2, 0.125/0.25 and ≥8/≥8 µg/ml. Considering CLSI breakpoints (BP) and MPC values, all isolates would be susceptible to linezolid (MIC BP ≤4 µg/ml) and moxifloxacin (MIC BP ≤0.5 µg/ml). In contrast all strains would be considered non-susceptible to vancomycin (MIC BP ≥4 µg/ml).

Conclusions: SP is being recovered more frequently from human infections including invasive disease (i.e. bacteremia). The high vancomycin MPC values reported here are consistent with similar results for *Staphylococcus aureus* and suggest concern with potential therapeutic failure in patients where vancomycin may be used for treat SP infections.

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Abstract 1203

Real-world experience of dalbavancin use for the treatment of Gram-positive infections

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Background: Dalbavancin is a lipoglycopeptide antibiotic with prolonged half-life approved for the treatment of acute bacterial skin and skin structure infections (ABSSSIs). However, in real life it can be used for several gram-positive infections, when protracted treatment is required. We examined the effectiveness and safety of dalbavancin in the treatment of various gram-positive infections other than ABSSSIs.

Materials/methods: This retrospective study was performed in the University Hospital of Heraklion in Greece from September 2017 through August 2019. All adult patients who received at least one dose of dalbavancin with a minimum follow-up of three months post-treatment were included.

Results: Twelve patients were identified, 7 (58.3%) were female. Mean age was 65.5 (SD, 13.1) years. Dalbavancin was used for treatment of osteomyelitis, prosthetic joint infection, epidural abscess, and permanent pacemaker lead infection (Table). Nine patients (75%) received dalbavancin as targeted therapy, whereas 3 (25%) were treated empirically. The isolated pathogens were methicillin-resistant *Staphylococcus aureus*, methicillin-resistant *Staphylococcus epidermidis* and *Enterococcus* spp. All patients received dalbavancin as sequential therapy after the administration of vancomycin or daptomycin for a median duration of 14 (range, 10-28) days due to the feasibility for early discharge and treatment on outpatient basis. Dalbavancin was administered as 1000 mg i.v. on Day 1 followed by 500 mg i.v. weekly. The median duration of dalbavancin therapy was 21 (range, 7-42) days. Eleven patients (91.7%) had favourable outcome, while 1 (8.3%) patient with spinal epidural abscess who refused surgical intervention experienced clinical failure. Regarding safety, only the patient with treatment failure experienced a non-clostridial transient diarrhea.

Conclusions: The use of dalbavancin for sequential treatment of gram-positive infections other than ABSSSIs seems to be safe and effective. Prospective trials are needed to validate novel indications for this new compound.

Infection type	Overall, n	Causative pathogen, n				Culture-negative	Cure, n (%)
		MRSA	MRSE	*E.faecium*	*E.faecalis*		
Osteomyelitis	7	2	2	0	0	3	7 (100)
Prosthetic joint infection	2	1	1	0	0	0	2 (100)
Epidural abscess	2	1	0	1	0	0	1 (50)
Pacemaker lead infection	1	0	0	0	1	0	1 (100)

MRSA: *Staphylococcus aureus*, MRSE: methicillin-resistant *Staphylococcus epidermidis*

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Abstract 1204

A multi-modal intervention to improve hand hygiene compliance in peripheral wards of a tertiary care university centre: a cluster randomised controlled trial

Seven Johannes Sam Aghdassi*[1], Petra Gastmeier[1], Christin Schröder[1], Michael Behnke[1], Patricia Manuela Fliß[2], Janina Wenk[2], Carolin Plotzki[2], Tobias Kramer[1]

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Background: Compliance to hand hygiene is a key factor in preventing healthcare-associated infections. It was our objective to assess the effect of a multimodal intervention on hand hygiene compliance at a tertiary care university hospital. As a secondary objective, we investigated the effect of the intervention on the occurrence of device-associated bloodstream infections.

Materials/methods: We performed a single centre cluster randomised controlled trial at a university hospital in Germany. Twenty peripheral wards were invited to participate and randomly assigned to either the intervention (n=10) or control group (n=10). Quarterly, trained observers conducted direct compliance observations on all twenty wards. The intervention entailed dissemination of teaching materials on aseptic procedures, equipment with flexibly mountable alcoholic hand rub dispensers, and quarterly feedback on hand hygiene compliance rates. The duration of the intervention was twelve months in the year 2018. Prospective surveillance was conducted for device-associated infections during the intervention. A multivariable logistic regression analysis was performed to identify factors significantly influencing the likelihood of compliant performance of hand hygiene.

Results: In total, 21424 hand hygiene opportunities were observed. Overall, compliance rates did not change significantly in either group (59% vs. 60% in the control group; 59% vs. 61% in the intervention group). Compliance prior to aseptic procedures improved significantly from 44% to 53% (p=0.03) in the intervention group, while no significant increase was noted in the control group. Multivariable logistic regression analysis revealed that non-nursing, non-physician staff ("others") were significantly less likely to perform compliant hand hygiene than nurses and physicians (p<0.01). In the intervention group, rates of device-associated bloodstream infections were significant lower than in the control group (p<0.01).

Conclusions: A significant effect of the intervention was observed with regard to hand hygiene compliance prior to aseptic procedures. The lack of a significant overall improvement of hand hygiene compliance shows that comprehensive implementation of hand hygiene interventions and creation of a sense of ownership of the intervention among healthcare workers on multiple wards simultaneously is difficult. Observed differences between professional groups suggest that education of healthcare workers other than nurses and physicians should be a target of future hand hygiene interventions.

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Abstract 1205

Lyme disease spirochete variants and human endothelial cells determinants for transendothelial migration: development of an *in vitro* system using primary human microvascular endothelial cells

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Background: Lyme disease is a tick born infection caused mainly by *B. burdorferi* in North America. Hematogenous dissemination is an important pathogenic strategy for Lyme spirochetes. Since *B. burgdorferi* does not produce any toxins or classical virulence factors, it likely uses a mechanism distinct from what has been observed with other pathogens. In spite of the importance of vascular transmigration in Lyme disease pathogenesis there has been little research into this area and there are only a few conflicting reports on whether *B. burgdorferi* endothelial transmigration is transcellular or paracellular. In addition, cellular features are crucial and no published studies have used primary microvascular endothelial cells, which accurately reflect the site of *B. burdorferi* transmigration.

Materials/methods: We aimed to develop an efficient *in vitro* system to study *B. burdorferi* migration through human primary microvascular endothelial cells. We are using two types of primary human microvascular endothelial cells: dermal and synovial. Co-culture conditions were optimized based on spirochete growth, viability and length in the new media. Cell viability was assessed using trypan blue stain, as well as immuno-staining for junction (VE-cadherin) and cytoskeleton (F-actin). Transmigration assays are performed using Transwells chambers. Relative percentages of transmigrated spirochetes were estimated by counting the lower transwell chamber.

Results: Using wild type *B. burgdorferi* compared to a non-adherent high passage strain, we showed that our system reflects the *in vivo* conditions, with a 8 fold higher transmigration of the low passage strain after 4 hours of co-incubation in both synovial and dermal endothelial cells. Studies are now in progress to assess *B. burgdorferi* strains deficient for various adhesins as well as to define the major pathway (paracellular or transcellular) involved in the process and to characterize the required cellular signaling pathways.

Conclusions: The potential of our proposed study is the use of resulting information to eventually block hematogenous dissemination of *B. burdorferi* shortly after tick-bite exposure and cripple the ability of the spirochetes to invade host organ systems.

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Abstract 1207

Probability of target attainment analyses inform ceftolozane/tazobactam dosing regimens in hospital-acquired pneumonia/ventilator-associated pneumonia patients with end-stage renal disease on intermittent haemodialysis

Hwa-Ping Feng*[1], Yogesh Patel[2], Zufei Zhang[1], Jill Fiedler-Kelly[2], Christopher J. Bruno[1], Elizabeth G. Rhee[1], Carisa De Anda[1], Wei Gao[1]

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Abstract third-party references: This work was supported by Merck Sharp & Dohme Corp., a subsidiary of Merck & Co., Inc., Kenilworth, New Jersey, USA (MSD)

Background: Ceftolozane/tazobactam (C/T) combines a potent anti-pseudomonal cephalosporin with a beta-lactamase inhibitor. The 2g/1g C/T high dose by 1-hour infusion every 8 hours (Q8H) was evaluated in participants with hospital-acquired pneumonia/ventilator-associated pneumonia (HAP/VAP) in the Phase 3 study ASPECT-NP, demonstrating safety and efficacy in this population. Both compounds are eliminated renally, and dose adjustment is necessary based on renal function. HAP/VAP patients with end-stage renal disease (ESRD) on intermittent hemodialysis (HD) were not eligible for ASPECT-NP. This study utilized probability of target attainment (PTA) analyses to inform the C/T recommended dosing regimen in this population.

Materials/methods: Population PK models for C and T in HAP/VAP patients were developed to describe C and T concentration data in plasma collected in 16 clinical studies, including ASPECT-NP and in ESRD subjects without infection, and in pulmonary epithelial lining fluid (ELF) collected in 2 Phase 1 studies. The final population PK models were used to simulate C and T concentration-time profiles in plasma and ELF of ESRD patients at three different dose levels by 1-hour infusion Q8H over a 14-day treatment duration, with HD on every other weekday:

- 1g/0.5g C/T loading+200mg/100mg C/T maintenance (2X cIAI/cUTI)
- 1.5g/0.75g C/T loading+300mg/150mg C/T maintenance (3X cIAI/cUTI)
- 3g/1.5g C/T loading+400mg/200mg C/T maintenance (4X cIAI/cUTI)

Daily C and T exposures and PTA in ELF and plasma were estimated.

Results: For the 14-day treatment duration, daily plasma PTA for all 3 regimens was 100% for C at 30% fT>MIC=4mg/L and >99% for T at 20% fT> C_T=1mg/L. Daily ELF PTA was ≥95% for C at 30% fT>MIC=4mg/L for all 3 regimens and was >90% for T at 20% fT>C_T=1mg/L for the 3X and 4X cIAI/cUTI regimens. ELF PTA for T at the 2X cIAI/cUTI regimen was <80% at 20% fT>C_T=1mg/L on HD days. Plasma AUC distribution for T at the 4X cIAI/cUTI regimen extended above the clinical experience of ASPECT-NP.

Conclusions: Based on the results of the analyses, the 1.5g/0.75g C/T loading+300mg/150mg C/T maintenance by 1-hour IV infusion Q8H is considered to balance efficacy and safety considerations and is recommended for ESRD patients with HAP/VAP.

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Abstract 1211

Candida spp. in the respiratory tract secretions of critically ill patients and the impact of antifungal treatment

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Background: In critically ill patients *Candida* is often isolated from bronchial secretion (BS) or bronchoalveolar lavage (BAL) samples. The significance of this finding is undetermined. We examined the impact of antifungal treatment in previously immunocompetent patients with intensive care unit (ICU)-acquired respiratory tract infection (RTI) and *Candida* spp. isolation from their BS or BAL.

Materials/methods: All adult patients admitted to the ICU of the University Hospital of Heraklion, Greece, from January 2014 through December 2016, with ICU-acquired RTI and *Candida* spp. isolation in their BS were evaluated. Demographics, clinical characteristics, antifungal treatment for any reason ±10 days around *Candida* spp. isolation, and 28-day and in-hospital mortality were recorded. Associations of antifungal treatment and mortality were tested with univariate (chi-square test) and multivariate logistic regression analysis.

Results: Seventy-nine patients were evaluated and 58 (73.4%) of them were male. Mean [standard deviation, (SD)] age was 66.1 (16.6) years. Thirty-nine (49.4%) received antifungals and 33 (41.8%) had more than two comorbidities. The mean body mass index (SD) was 28.4 (6.6) and the mean APACHE II score (SD) was 21.6 (7.8). The 28-day and in-hospital mortality rate were 22.8% and 30.4%, respectively. There were no differences in 28-day and in-hospital mortality when patients receiving antifungal treatment were compared to those that did not, even after adjustment for selected confounders (Table).

Conclusions: Antifungal treatment in previously immunocompetent patients with ICU-acquired RTI and *Candida* spp. isolation in their secretions did not influence survival. Larger prospective or interventional studies are needed to elucidate the exact importance of *Candida*'s presence in the respiratory tract of ICU-patients.

Table. Multivariate logistic regression analysis

Variable	*28-day in-hospital mortality, OR (95% CI)*	*In-hospital mortality, OR (95% CI)*
Antifungal administration	1.68 (0.54-5.36)	1.88 (0.66-5.39)
Age	1.01 (0.97-1.05)	1.01 (0.96-1.04)
Gender	1.29 (0.36-4.65)	1.47 (0.45-4.81)
>2 comorbidities	1.08 (0.32-3.65)	1.65 (0.53-5.10)
APACHE II	1.04 (0.96-1.12)	1.03 (0.96-1.10)
Body mass index	1.06 (0.97-1.15)	1.04 (0.96-1.13)

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Abstract 1213

Ceftolozane/tazobactam probability of target attainment in patients with hospital-acquired pneumonia/ventilator-associated pneumonia

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Abstract third-party references: This work was supported by Merck Sharp & Dohme Corp., a subsidiary of Merck & Co., Inc., Kenilworth, New Jersey, USA (MSD)

Background: Ceftolozane/tazobactam (C/T) combines a potent anti-pseudomonal cephalosporin with a beta-lactamase inhibitor. The 2g/1g C/T high dose or equivalent dose adjusted based on renal function administered by 1-hour infusion every 8 hours was evaluated in mechanically ventilated participants with hospital-acquired pneumonia/ventilator-associated pneumonia (HAP/VAP) in the Phase 3 study ASPECT-NP, demonstrating safety and efficacy in this population. Probability of target attainment (PTA) analyses were conducted to support the recommended C/T dosing regimens in HAP/VAP patients.

Materials/methods: Population PK models for C and T in HAP/VAP patients were developed to describe C and T concentration data in plasma from 16 clinical studies, including ASPECT-NP, and in pulmonary epithelial lining fluid (ELF) from 2 Phase 1 studies. The final population PK models were used to simulate C and T concentration time profiles in plasma and ELF in HAP/VAP patients at various dosing regimens over a 14-day treatment duration. PTA in plasma and ELF was calculated using the PK/PD targets of 30% $fT>MIC$ for C and 20% $fT>C_T$=1mg/L for T.

Results: Based on projected PTA in plasma and ELF, the C/T dosing regimens in HAP/VAP patients evaluated in ASPECT-NP were:

- 2g/1g C/T (CrCL>50mL/min)
- 1g/0.5g C/T (30mL/min≤CrCL≤50mL/min)
- 500mg /250mg C/T (15mL/min≤CrCL≤29mL/min)

At these C/T dosing regimens, steady-state plasma PTA was 100% for C at 30% $fT>MIC$=4mg/L and >99% for T at 20% $fT> C_T$=1mg/L across renal categories at CrCL up to 150mL/min. Steady-state ELF PTA was >99% for C at 30% $fT>MIC$=4mg/L and >87% for T at 20% $fT> C_T$=1mg/L across renal categories at CrCL up to 150mL/min.

Conclusions: At the dosing regimens evaluated in ASPECT-NP, high plasma and ELF PTA were achieved in HAP/VAP patients across renal function categories. Together with demonstrated safety and efficacy in the study, the PTA results support the appropriateness of these dosing regimens for the treatment of HAP/VAP.

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Abstract 1214

Exposure-efficacy analyses support optimal dosing regimens of ceftolozane/tazobactam in patients with hospital-acquired pneumonia /ventilator-associated pneumonia in ASPECT-NP

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Abstract third-party references: This work was supported by Merck Sharp & Dohme Corp., a subsidiary of Merck & Co., Inc., Kenilworth, New Jersey, USA (MSD)

Background: Ceftolozane/tazobactam (C/T) combines a potent antipseudomonal cephalosporin with a beta-lactamase inhibitor. A C/T dose of 2g/1g, or adjusted based on renal function, was evaluated in patients with HAP/VAP in the phase 3 ASPECT-NP study, demonstrating safety and efficacy in this population. Exposure–response (E–R) analyses were conducted to assess the potential relationship between plasma pharmacokinetics and the clinical efficacy endpoints to support the optimal C/T dose regimens in adult patients with HAP/VAP.

Materials/methods: Plasma C/T exposure metrics (%*f*T>MIC or %*f*T>C_T) for each patient at the end of treatment were derived from the population pharmacokinetic models. Actual dosing records and the highest MIC value for relevant baseline lower respiratory tract (LRT) pathogens identified for each patient were used. The primary efficacy endpoints were all-cause mortality (ACM) at day 28 and clinical response at test of cure. The relationship between %*f*T>MIC for ceftolozane or %*f*T>C_T for tazobactam and efficacy endpoints was explored.

Results: In the analysis set (N=231), the ACM rate was 16% (36 died on/before day 28) and clinical cure rate 65% (151 achieved cure). No E–R relationship for ceftolozane %*f*T>MIC was observed for both clinical endpoints.

Additionally, among 177 patients with a baseline LRT pathogen MIC ≤4μg/mL, a low ACM rate (13%) and high clinical cure rate (71%) were observed versus those with MIC >4μg/mL (24% and 48%, respectively). No E–R relationship for ceftolozane was observed in these 177 patients; 173 patients had 99%*f*T>MIC, with ACM and clinical cure rates of 13% and 70%, respectively, and the remaining 4 patients had ≥73%*f*T>MIC, with ACM and clinical cure rates of 0% and 100%, respectively. Tazobactam exposure was not considered related to efficacy, as ACM rates increased and clinical cure rates decreased with increasing tazobactam PK measure %*f*T>C_T.

Conclusions: There was no E–R trend with C/T, and among those with a baseline LRT pathogen MIC below the breakpoint, all patients achieved exposures above the pharmacokinetic/pharmacodynamic targets. These results support the appropriateness of a C/T 2g/1g dose, or adjusted dose for renal function, in adult patients with HAP/VAP.

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Abstract 1215

Emergence of non-susceptibility among Gram-negative respiratory pathogens from a phase III clinical trial for treatment of nosocomial pneumonia (ASPECT-NP)

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Background: The phase 3, randomized, double-blind, multicenter ASPECT-NP trial evaluated ceftolozane/tazobactam 3g every 8 hours (q8h) versus meropenem 1g q8h for 8–14 days in adults for treatment of ventilated nosocomial pneumonia. Genetic typing was performed to assess relatedness of baseline and post-baseline *Pseudomonas aeruginosa* (PsA) and Enterobacterales (ENT) isolates.

Materials/methods: Pairs of isolates were selected for molecular typing among patients in the microbiological intention-to-treat population when a susceptible baseline organism and a non-susceptible post-baseline organism of the same genus and species were identified. Applied interpretive criteria to determine non-susceptibility were provisional ASPECT-NP breakpoints (susceptible breakpoints: PsA, ≤8 mg/L; ENT, ≤4 mg/L) for ceftolozane/tazobactam and CLSI breakpoints for meropenem. Multilocus sequence typing was performed among baseline and post-baseline pairs; pulsed-field gel electrophoresis was used for *Serratia marcescens* and *Proteus mirabilis* isolates. Emergence of non-susceptibility (EoNS) was defined as the isolation of a non-susceptible post-baseline organism with the same sequence type (ST) as the susceptible baseline organism; in contrast, a non-susceptible post-baseline isolate with a different ST was considered to represent the acquisition of a different strain of the same species (ie, new infection, not EoNS). EoNS was compared between ceftolozane/tazobactam and meropenem treatment arms.

Results: Among susceptible PsA isolates at baseline, EoNS was noted in 1 of 61 (1.6%) isolates in the ceftolozane/tazobactam arm versus 13 of 58 (22.4%) in the meropenem arm. Two additional post-baseline PsA isolates in each of the ceftolozane/tazobactam and meropenem arms were non-susceptible but had different STs. In the meropenem arm, the predominant resistance mechanism observed among non-susceptible-PsA isolates was OprD loss/decrease; elevated MexXY-OprM expression was also noted.

Among susceptible ENT isolates at baseline, EoNS was noted in 6 of 189 (3.2%) isolates in the ceftolozane/tazobactam arm (3 *S. marcescens*, 2 *Klebsiella pneumoniae*, and 1 *Enterobacter cloacae*) versus 4 of 192 (2.1%) in the meropenem arm (4 *K. pneumoniae*). Seven and 5 additional post-baseline ENT isolates in the ceftolozane/tazobactam and meropenem arms, respectively, were non-susceptible but had different STs.

Conclusions: EoNS was more common among PsA isolates in the meropenem arm compared to the ceftolozane/tazobactam arm, but was rare among ENT isolates in both arms.

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Abstract 1216

What is the role of colonisation by carbapenem-resistant *Enterobacteriaceae* in older people who live in nursing homes? A multi-centre study

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Background: Carbapenem-resistant Enterobacteriaceae (CRE) infections are a worldwide priority. These events are more frequent in elder people. It is known the prevalence of CRE colonization at hospital environment. However, real-life data from other context as nursing homes is still unknown. The aim was to measure the CRE colonization (CREc) rate in institutionalized elders. Secondary objective was to assess linked factors with CREc and new CRE infections during follow-up.

Materials/methods: Prospective observational study which included residents from 6 geriatrics from Buenos Aires City (Argentina), between November 2018 and November 2019. Patients were screened by swab collections (rectal, axillar and inguinal) to evaluate CREc. Chromogenic agar cultures for CRE and molecular techniques for *blaKPC, blaNDM* and *blaOXA* were used. We identified possible linked variables with CREc and subsequent infections at the beginning, and after 12-month follow-up. These centers did not apply restrictive policies for admission or contact precautions. Also, these institutions did not assist patients who required mechanical ventilation. $p<0.05$ was considered significant.

Results: 205 patients were recruited. 77.1% were women, the median age was 87 years (IQR11) and the median length of stay was 26 months (IQR39.8). Median of Katz-Score was 2 (IQR2) and Charlson-Index was 5 (IQR2). At baseline, 17.1% was admitted at hospital wards the previous year and 9.8% had taken antimicrobials the previous month. The initial CREc prevalence was 1.46%. Colonized patients had not shared the same room. During follow-up 11.21% died (n=23); none of them due to CRE infections. It is remarkable that none of colonized patients died. Among survivors, CREc rate was 2.19% (OR 0.66, $p=0.60$ vs. the initial cohort). No CRE infections were detected. In multivariate analysis, using of antibiotics the previous month was the only linked factor (OR 2.9, CI95% 1.3-273.7, $p=0.03$). Surprisingly, living with previously colonized residents did not lead to the acquisition of new CREc.

Conclusions: A relatively low CREc rate was observed. Also, prior antibiotic use was associated with this condition. These findings are unprecedented in our continent. Our data suggest that not applying contact precautions for CRE in this scenario could be a safe practice.

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Abstract 1217

Genotyping, phylogenetic analysis and *in vitro* antifungal susceptibility profile of clinical isolates of Neoscytalidium species

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Background: The genus Neoscytalidium is mainly distributed in (sub) tropical areas which principally have been described as phytopathogens. However, there are several reports of human infection caused by Neoscytalidium through direct or indirect contact with contaminated plants or soil. The pathogenicity of Neoscytalidium species is not well-known. On the other hand, because of the rarity and emergence of this organism, and no effective treatment approaches, the accurate diagnosis would be critical for therapeutic strategies.

Materials/methods: During two years (from October 2016 to September 2018), all patients with critical underlying conditions referred to the Reference Center for Tuberculosis and Pulmonary Diseases of Iran, Tehran, Iran were included in the study. The isolates of Neoscytalidium species obtained from deep clinical specimens of patients were collected. Partial sequences of five loci (the ITS region, D1/D2 domains of 28S rRNA gene, beta tubulin, elongation factor 1α and chitin synthase genes) of these isolates were analyzed. Phylogenetic analysis of the isolates was also evaluated. In-vitro antifungal susceptibility testing of the isolates against 16 antifungal agents was performed according to the Clinical & Laboratory Standards Institute (CLSI) M38-A2 guideline.

Results: In general, out of 640 clinical samples, 13 (2.0%) were positive for Neoscytalidium species growth, of which 8 isolates were characterized as N. dimidiatum and 5 isolates as N. novaehollandiae according to ITS sequencing. The sequence alignment of 1846 bp in 13 isolates identified nine polymorphic sites (0.49%), representing two sequence types (ST1 and ST2). All of eight N. dimidiatum strains and five N. novaehollandiae species were detected as ST1 and ST2, respectively. The phylogenetic analysis of ITS sequences revealed 2 clades. In addition, we observed the highest in vitro antifungal activity against both Neoscytalidium species by luliconazole, followed by micafungin, amphotericin B and anidulafungin.

Conclusions: This is the first report of N. novaehollandiae isolation from deep clinical samples. One unique genotype could be detected among the studied isolates in each of the species using the mentioned loci. LUL represented the lowest MIC against all isolates which could propose as a good topical antifungal candidate against Neoscytalidium superficial infections.

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Abstract 1218

The non-tuberculous mycobacteria experience: a single-centre study in Ireland

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Background: Recent studies suggests the increasing prevalence of non-tuberculous mycobacteria (NTM) pulmonary disease (PD). However, NTM is not a reportable disease in Ireland and national data is not available regarding the prevalence of disease. We looked at our NTM isolates from January 2013 to July 2018 and the profile of patients whose care was based in the tertiary care hospital where the study was performed.

Materials/methods: A record of NTM isolates from January 2013 to July 2018 was collected via the laboratory electronic records. Respiratory isolates belonging to patients whose care is based in the tertiary referral hospital was separated for further analysis of patient's demographics via patient's electronic record. Patients with at least 1 respiratory isolate were included in the demographic analysis. Identification of Mycobacterium isolates to species level was done by Genotype Mycobacterium CM (Hain-Lifescience). Drug susceptibility testing (DST) was done at a reference laboratory in Scotland.

Results: In the study period, we had 116 isolates in 71 patients. 12 *M.chimaera* isolates were excluded from this study. Our NTM isolates composed of: *Mycobacterium avium* complex 45.9%, *M.kansasii* 8.0%, rapid growing mycobacteria 28.3% and slow growing mycobacteria 13.3%. 49 isolates in 36 patients were included in the analysis of patient's demographics. 45 of these isolates were from respiratory samples (24 sputum and 21 bronchoalveolar lavage), 1 from a bone marrow biopsy, 1 from tonsillar tissue, 1 from a groin abscess aspirate and 1 from cerebro-spinal fluid. 75% (27/36) of patients had pre-existing pulmonary disease and 30.6% (11/36) were immunosuppressed. The ATS/IDSA diagnostic criteria for NTM lung disease was fulfilled in 27.8% of patients. The microbiologic criteria were fulfilled in 66.7% of patients. 15 patients had radiological changes consistent with nodular-bronchiectatic disease and 5 had changes consistent with fibrocavitatary disease. 23.7% (9/38) patients received treatment for NTM disease. 6 had NTM PD and 3 had disseminated disease. The median age of our patients was 61.5 years. 50% of the patients were female.

Conclusions: NTM disease is diverse with regional differences. Our study adds to the available data on NTM isolated from clinical specimens and NTM disease in Ireland.

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Abstract 1220

Cost-benefit analysis comparing trough, two-Level AUC, and Bayesian AUC dosing for vancomycin

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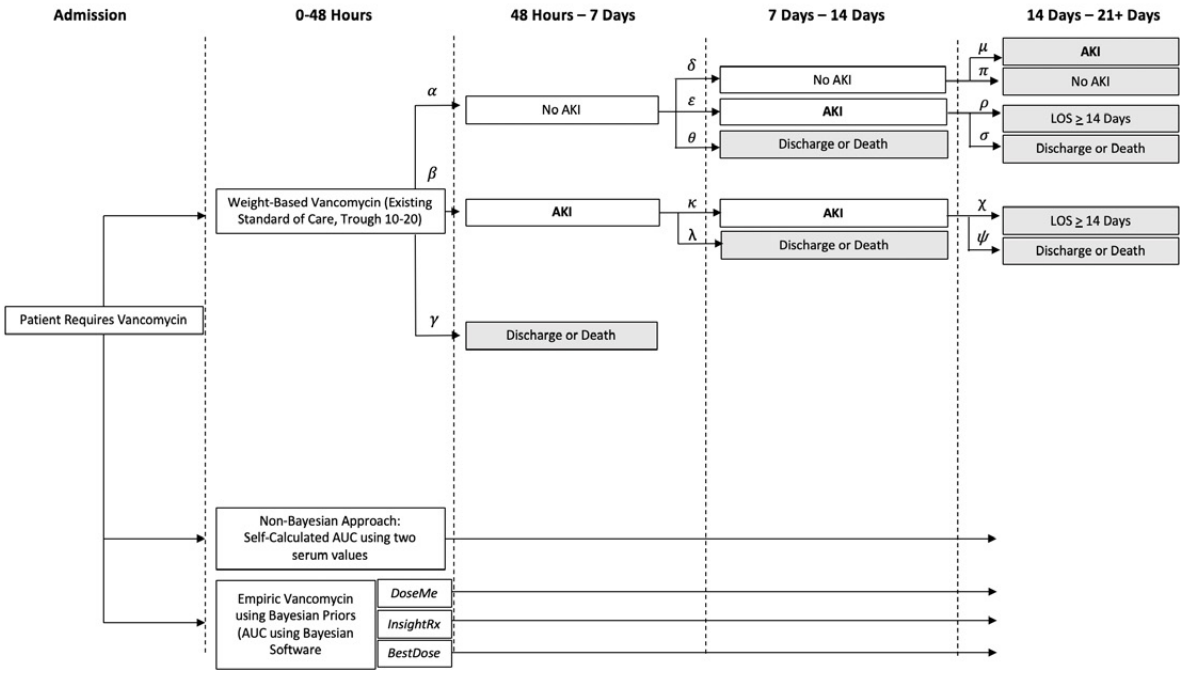
Background: Trough levels have been demonstrated to be inadequate surrogates for vancomycin exposure, with troughs of 15-20 mg/L associated with increased rates of nephrotoxicity while minimally improving outcomes. Newer dosing methods provide clinical benefit, but with uncertain costs. The objective of this study was to quantify the cost benefits of using two-point or Bayesian AUC vs. trough dosing for patients treated with vancomycin.

Materials/methods: A cost benefit analysis from the institutional perspective was conducted utilizing a decision tree to model the probabilities and costs of acute kidney injury (AKI) associated with vancomycin administered over 48 hours up to 21+ days. Costs included obtaining vancomycin levels, pharmacy time, AKI hospitalization costs, and Bayesian software costs. Probabilities and costs were obtained from primary literature, the Healthcare Cost and Utilization Project National Inpatient Sample, the US Bureau of Labor Statistics, and manufacturer-provided quotes for software costs. Incremental costs were calculated for each strategy in 2019 US Dollars. Robustness of results was assessed via one-way sensitivity analyses varying probabilities and costs in the model.

Results: In the base-case model, two-point AUC vs. trough saved an average $847 per patient encounter. Bayesian AUC vs. trough saved an average $2066 per patient encounter. This translates into annual cost-savings of $846,810 and $2,065,720 for two-point and Bayesian methods vs. trough respectively, assuming 1000 vancomycin-treated patients per year. In one-way sensitivity analyses, "Probability of AKI, 48 Hours to 7 Days" and "Probability of Discharge or Death, 48 Hours to 7 Days" were the most sensitive parameters in the model. Assuming a budget of $100,000 per year for Bayesian software, an institution would need to treat ≥41 patients with vancomycin for at least 48 hours to break even. At a budget of $20,000 per year, ≥10 patients would need to be treated with vancomycin to achieve a break-even cost.

Conclusions: There are significant institutional cost-benefits using two-point AUC or Bayesian methods over trough dosing, even after accounting for the annual costs of Bayesian programs. The potential to decrease rates of AKI, improve clinical outcomes, and reduce costs to the institution strongly warrants consideration of newer dosing methods for vancomycin.



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Abstract 1224

Exebacase resensitises methicillin-resistant *Staphylococcus aureus* to oxacillin in a rabbit model of infective endocarditis

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Background: Our recent *in vitro* data demonstrated that exposure of MRSA to exebacase results in synergy with β-lactam antibiotics and a "resensitization" to these agents; i.e., lowering the MRSA β-lactam MICs into the CLSI "susceptible range". To understand the *in vivo* impact and relevance of the resensitization, we used a rabbit model of MRSA IE to compare treatment with OXA alone vs treatment with exebacase in addition to OXA

Materials/methods: A indwelling transcarotid artery-to-left ventricle catheter-induced model of aortic valve IE in rabbits utilizing MRSA strain MW2 (USA400) was used. Animals were treated with OXA (50 mg/kg, IM tid x 4 d) alone or with one of two single-dose regimens of exebacase (0.7 or 1.4 mg/kg; IV). Vehicle controls and exebacase alone were included. At 24 h after the last dose of OXA, cardiac valve vegetations, spleens and kidneys were removed and quantitatively cultured. Vegetations were parallel-plated on media supplemented with exebacase over a range of concentrations, and resulting colonies were subcultured, and tested for exebacase and OXA MICs.

Results: Both single-dose regimens of exebacase (0.7 and 1.4 mg/kg) administered in addition to OXA significantly reduced MRSA counts by 5 $\log_{10}$ cfu/g tissue ($p<0.0001$) compared to OXA treatment alone, exebacase alone, and growth controls. This marked reduction in target tissue MRSA CFUs is consistent with resensitization in vivo (enhanced OXA-mediated killing). Bacteria recovered from vegetations following exebacase + OXA treatments did not exhibit lower OXA MICs, however the majority (>98%) of isolates demonstrated repeatedly reduced exebacase MICs (from 1 to ≤0.5 µg/mL). Bacteria recovered from vegetations exposed to exebacase alone exhibited up to >16-fold reductions in OXA MICs (from 32 µg/mL to <2 µg/mL).

Conclusions: In this rigorous model of endovascular infection, the addition of exebacase + OXA, significantly reduced MRSA counts in all target tissues. The observed efficacy may be driven by both the resensitization to OXA and the increased susceptibility to exebacase. The striking ability of exebacase to resensitize MRSA to OXA may have important therapeutic implications and is a potentially promising approach to combat and "reverse" antimicrobial resistance.

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Abstract 1225

Overuse of antibiotics in primary care: a secondary analysis of standardised patient studies across four low- and middle-income countries

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Background: Antibiotics are largely prescribed in primary care globally. However, an accurate assessment of the extent of inappropriate use is limited by the low quality of available data, especially in low- and middle-income countries (LMICs). Standardized patient (SP) studies offer more insights, since diagnoses are fixed, by design, and inappropriateness of antibiotic use is easier to determine.

Materials/methods: We performed a pooled analysis of data from 10 cross-sectional SP studies implemented between 2010 and 2019 to estimate the proportion of patients receiving antibiotics across primary care settings in China, India, Kenya and South Africa. In all studies, SPs portrayed clinical conditions that are commonly encountered in primary care and for which antibiotics should not be given (watery diarrhea, presumptive tuberculosis, angina, asthma, upper respiratory illness). The dataset included information on drug prescription/dispensing for each SP-provider interaction, along with characteristics of providers (qualified or not), facilities (urban/rural, public/private) and cases presented. We analysed overall antibiotic use as the primary outcome and performed stratified analyses to evaluate differences over important variables of interest.

Results: Of 6,083 SP-provider interactions in health facilities and 2,722 in pharmacies, 2,928 (48.1%; 95%CI: 46.9-49.4) and 374 (13.7%; 95%CI: 12.5-15.1) respectively resulted in inappropriate use of at least one antibiotic. Access-group antibiotics (mostly penicillins) were predominantly used in Kenya and South Africa (85% and 74% of total antibiotics used) but use of Watch-group antibiotics (especially quinolones and certain cephalosporins) was disproportionately high in China (33%) and India (49%). Across SP conditions in health facilities, 1293/2253 (57.4%; 95%CI: 55.3-59.4) presumptive tuberculosis patients, 490/997 (49.1%; 95%CI: 46.0-52.3) paediatric diarrhea cases, 330/718 (46%; 95%CI: 42.3-49.6) asthmatics, and 169/955 (17.7%; 95%CI: 15.4-20.3) subjects with angina received antibiotics. Factors associated with increased antibiotic use included higher provider qualification (aOR 2.46; 95%CI: 2.16-2.81), urban location (aOR: 1.34; 95%CI: 1.17-1.52) and private sector (aOR: 1.78; 95%CI: 1.38-2.28).

Conclusions: Antibiotics, including a substantial proportion of those with a high potential for selecting resistance, are frequently used without indication across primary care settings in 4 countries, and – unexpectedly - providers with higher qualifications were more likely to misuse antibiotics. Why this may be so requires further research.

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Abstract 1229

Comprehensive proteomics and active immunisation reveals that extracellular vesicles derived from Streptococcus equi subspecies equi as an effective candidate for vaccine platform

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Background: Strangles caused by Streptococcus equi subspecies equi (S. equi) is a contagious disease, which can cause economic losses to the equine industry. Therefore, vaccine-based prevention has been recommended. Extracellular vesicles (EVs) are attractive novel vaccine targets because EVs contain many surface proteins, which are antigenic and keep intact form in EV.In this study, we purified EVs from S. equi and performed proteomic analysis to identify antigenic proteins. Then, we confirmed EVs of S. equi as a potential vaccine candidate by vaccine trial.

Materials/methods: For the preparation of purified extracellular vesicles (EVs), we used a QuixStand benchtop system and differential centrifugation method. EVs were quantified using microBCA reagent. Identification and purification purity of the EVs was confirmed by transmission electron microscope (TEM). The vaccination reagents were prepared by mixing the EVs with Freund's Complete Adjuvant. The 6 weeks female blab/c mouses were divided into two groups (intraperitoneal, intranasal) and were immunized with vaccine reagents for three times on day zero, seven, and fourteen. For active immunization studies, the challenge with LD90 of S. equi occurred day seven after the last immunization (day 21).

Results: We confirmed purity of EVs by TEM and LC-MS/MS analysis. The EVs of S. equi have a circular form with a double layer and the size of EVs is around 50um to 150um. According to LC-MS/MS results, the EVs had a distinct protein profile from whole cell lysates, such as presence of a large number of membrane proteins. The mouse immunization study confirmed the effective vaccination effect in the intraperitoneal group. When challenged with LD90 of S. equi, the control group died in 24 hours, but in the IP group, 60% of mice were survived during the same time, and finally 20% of mice survived for more than 2 weeks. Immuno-proteomic analysis suggest several candidate vaccine proteins, which were originated from EVs

Conclusions: Our results elucidate the overall proteome profiles of S. equi and provide candidates for potential vaccine targets.

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Abstract 1232

Increase in potentially measles-susceptible young healthcare workers in South Korea

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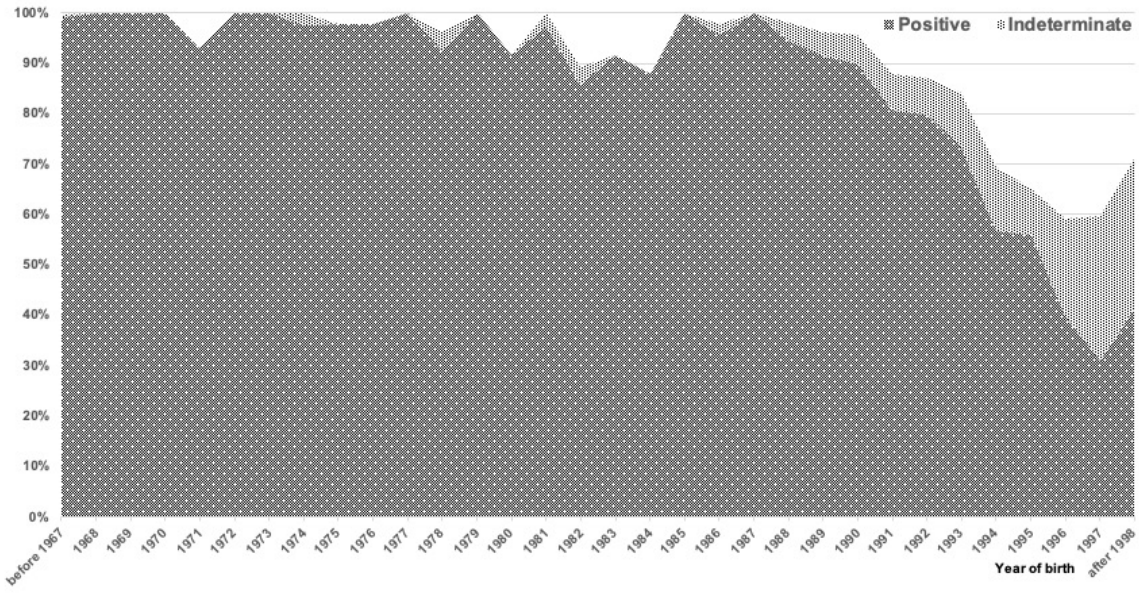
Background: Healthcare workers (HCWs) are known to be at high risk of infection and transmission of measles virus. Although measles had been eliminated in Korea, the resurgence of measles outbreaks related to imported and import-associated case occurred among HCWs. The measles immunity of HCWs was evaluated for vaccination.

Materials/methods: We evaluated the seroprevalence of measles in HCWs in a tertiary university hospital, Wonju, Korea. A total of 2,456 HCWs born from before 1967 to 2000 underwent antibody test using enzyme immunoassay. In Korea, a 2-dose of measles-containing vaccine (MCV) was implemented in the national immunization program(NIP) in 1997. The catch-up program was performed targeted 1985-1993 birth cohort in 2001. According to the policy of NIP, the birth cohort was categorized into A) before 1967, B) 1968-1984, C) 1985-1993, D) after 1994.

Results: The overall seropositivity of measles was 78.3% (95% confidence interval, 76.7 -79.9). According to birth cohort, the seropositivity as follows; A: 251 of 253 (99.2%), B: 597 of 620 (96.3%), C:731 of 867 (84.3%), D: 345 of 716 (48.2%). The seropositivity of measles is showed as figure 1.

Conclusions: Young HCWs born after 1994 showed lower seropositivity of measles although 2-dose of MCV. This trend may be related to limitation of vaccine-induced immunity without natural boosting by the wild virus.



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Abstract 1234

Factors associated with low uptake of HIV testing among middle aged 15-17 adolescent girls in Uganda

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Background: There are significant gaps in the HIV clinical cascade among young people in terms of reaching the 90–90–90 targets set by Joint United Nations Programme on HIV and AIDS. The impact of recent interventions on uptake of HIV testing among women 15-24 years is unknown. To inform efforts in the implementation of "test-and-treat', we draw on data collected by Uganda Demographic Health Survey 2016 to assess rate of HIV testing uptake and associated factors among young women aged 15–24 years in Uganda.

Materials/methods: UDHS 2016 data was analysed. Univariate analysis was used summarize rate of HIV testing uptake among women 15-25 years. Bivariate analysis to examine associations between socio-demographic factors, HIV knowledge, socio-cultural factors and outcome variable. A complete case analysis was used and missing observations for women were disregarded. All variable with p< 0.2 were included in the multivariate analysis. Using the backward elimination strategy, variables significant at p <0.05 were identified and included in the final model. Statistical analyses were be performed using the Stata version 14

Results: The overall mean age of the study participant's was19.3 ± 2.88 years. Uptake of HIV testing was observed to be associated with age group, secondary/higher education, marital status, being employed year-round, media exposure, and age at sexual debut, number of lifetime sexual partners and level of HIV knowledge. Young women with a high level of HIV knowledge were 3.65 (95% CI: 1.68, 7.96) times more likely to uptake HIV testing when compared to those with a low level of HIV knowledge. Compared to those with no lifetime sexual partners, young with one reported lifetime sexual partner were 3.76 (95%CI: 2.88, 4.90) times more likely to uptake HIV testing; those with two partners 3.89(2.86, 5.28) times more likely and 5.53(4.13, 7.39) times more likely to uptake HIV testing among those with 3 or more lifetime sexual partners

Conclusions: There was significant improvement in HIV testing uptake among women 15-24 years, uptake among middle adolescents remained very low. Local and international implementing partners should focus their efforts to promoting HIV testing uptake among middle adolescents

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Abstract 1235

Emergence of blaNDM and mcr-1 positive pan- and extremely-drug resistant bacterial infections in patients with renal diseases

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Background: Infectious diseases are second most common cause of mortality among chronic kidney disease (CKD) patients. With emergence and dissemination of resistance genes like bla_{NDM} and *mcr-1*, for β-lactam antibiotics and colistin respectively, treatment is becoming difficult. This study aimed to screen the patients with renal diseases for bacterial pathogens and perform their antimicrobial drug resistance profiling.

Materials/methods: 100 urine samples from patients with renal diseases (diabetic nephropathy and incompatible renal transplant) admitted in tertiary care hospital, SGPGIMS, India were screened between 2016-2018. The bacterial strains were isolated using standard microbiological techniques. Antibiotic sensitivity testing was done by Kirby-bauer disc diffusion method. The minimum inhibitory concentrations were determined by E-test strips and antibiotic resistance genes were screened by PCR and Sanger sequencing.

Results: Twenty of 100 urine samples were positive by culture (20%). of these, 5/20 (25%) were positive for Gram positive bacteria while 14/20 (70%) were positive for Gram negative bacteria. One sample (5%; 1/20) had both Gram positive and negative bacteria. Among Gram positive, *Enterococcus* sp. and coagulase-negative *Staphylococcus* were dominant while among Gram negative, dominant species were *Enterobacter cloacae*, *Escherichia coli*, *Klebsiella pneumoniae*, *Providencia rettgeri*, *Morganella morganii* and *Pseudomonas aeruginosa*. Antibiotic sensitivity screening revealed that all these were multidrug resistant. Two isolates (*Enterobacter cloacae and Klebsiella pneumoniae)* were pan-drug resistant, while one isolate was extremely-drug resistant (*Providencia rettgeri*). Both pan-drug resistant isolates harboured *bla*NDM-1 gene while in *Klebsiella pneumoniae* isolate *Oxa*-48 gene was co-harboured. Transmissible colistin resistant gene *mcr-1* was present in extremely drug resistant isolate.

Conclusions: Extremely-drug resistant isolate was resistant to all antibiotics and harboured the transmissible colistin resistant gene *mcr-1*. Emergence of pan-drug and extremely drug resistant bacteria in patients suffering from renal diseases is a matter of concern. There are limited or no options available for treatment of such infections.

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Abstract 1239

The clinical application of FILMARRAY respiratory panel in children with acute respiratory tract infections

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Background: The Filmarray respiratory panel (FARP) can reliably and rapidly identify viruses and bacterial pathogens. This study is to evaluate the performance and clinical significance of FARP in children with acute respiratory tract infections (ARTIS).

Materials/methods: A total of 90 nasopharyngeal secretion (NPS) samples from children with ARTIS were enrolled. The FARP assay for 17 pathogens and direct fluorescence assay (DFA) methods for 8 pathogens were performed to analyze these samples. Clinical data of all patients was also collected and evaluated.

Results: Among the 90 samples, 58 samples (64.4%) were positive for 13 pathogens by FARP and 18 positive samples were detected with multiple-virus (31.3%, 18/58). Human rhinovirus/ enterovirus (21.0%%, 17/58) were predominant pathogen, followed by adenovirus (18.5%). Higher proportions of various pathogens were identified in the infant and toddler (0–2 years) groups with human rhinovirus/enterovirus being mostly virus. Adenovirus were common in the group aged 3–5 years, but only three pathogens including M.pneumoniae, respiratory syncytial virus, and adenovirus were also found in age group (6-14 years). Among 58 FARP positive patients, there were no significant difference in length of hospitalization stay, hospitalization cost, use of anti-virus, rate of secondary infection, and clinical outcome between single organism and multiple organism group ($P>0.05$), but significant differences were in antibiotic prescription and use of hormone ($P<0.05$).

Conclusions: This study demonstrated that FARP can provide the rapid detection of respiratory virus and atypical bacteria for children, especially with severe respiratory tract infections.

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Abstract 1245

Risk factors and clinical manifestations of Group B streptococcal invasive infection in adult population

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Background: The objective of this study is to determine clinical manifestations and risk factors of adult patients who are not pregnant with invasive group B streptococcal (GBS) infection.

Materials/methods: Retrospective study was conducted from January 2014- August 2019. Patients with positive blood culture and/or sterile fluids for GBS were included. Clinical history was consulted to identify underlying diseases, clinical syndrome and focus of infection. Microbiological diagnosis was made by conventional culture of sterile liquids and/or blood culture [BACTEC FX, BD®]. The identification was made by MALDI Biotyper [Bruker®] and the sensitivity following the CLSI criteria.

Results: 72 episodes were diagnosed in 69 patients, which 2 had more than one episode in the study period. 41 (59.42%) were men, with a mean age of 70.07 years (SD ± 16.58 years). 43 (62.32%) were > 70 years old.

63 (91.30%) patients had underlying disease: 43 (68.20%) cardiovascular disease, 24 (38.10%) diabetes mellitus, 19 (30.16%) renal failure, 18 (28.57%) solid organ tumour, 11 (17.46%) respiratory disease, 5 (7.94%) hepatopathy, 5 (7.94%) onco-hematological disease and 1 (1.59%) immunosuppressive treatment.

GBS isolation occurred in: 57 (79.17%) blood, 10 (13.89%) abdominal fluid, 3 (4.17%) joint fluid and 2 (2.78%) pleural fluid. There was no cerebrospinal fluid isolation.

In the case of bacteraemia (57), 17 (29.82%) had origin in skin, 10 (17.54%) pneumonia, 4 (7.02%) abdominal focus, 3 (5.26%) urinary focus and 2 (3.51%) arthritis. In 21 (36.84%) bacteraemia was primary. Three (5.26%) of these patients had complications: 2 (3.51%) endocarditis and 1 (1.75%) spondylodiscitis and meningoencephalitis. In episodes without bacteraemia (15), 10 (13.89%) had abdominal infection, 3 (4.17%) arthritis and 2 (2.78%) respiratory infection.

The 30-day mortality was 17.39%. Nine of the 12 deaths (75%) were >70 years old, and the mortality rate was 20.93% (9/43) in this population.

All GBS isolates were sensitive to penicillin.

Conclusions:

- 79% were bloodstream infection, with the skin being the primary focus of the infection.
- The most common underlying diseases were cardiovascular disease and diabetes mellitus.
- Invasive GBS infection in non-pregnant adults mainly affects patients over 70 years of age, with mortality in this population being 20.93%.

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Abstract 1250

Comparison of three chromogenic agars for the detection of *Candida auris*

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Background: *Candida auris* is a newly emerged pathogen that spreads easily and is highly resistant. To prevent transmission and control outbreaks early and sensitive detection is necessary. According to Dutch guidelines every patient that has been hospitalized abroad recently, is cultured for highly resistant microorganisms upon hospital admission in the Netherlands. To determine which medium should be added to this screening for the detection of *C. auris*, we compared three ready-made chromogenic yeast agar plates.

Materials/methods: BD BBL Chromagar Candida Medium (BD Diagnostics), chromID Candida (bioMérieux) and Oxoid Brilliance Candida agar (Thermo Fisher) agar plates were each inoculated with standardized suspensions of *Candida albicans*, *Candida parapsilosis*, *Candida krusei*, *Candida glabrata*, *Candida tropicalis*, *Candida haemulonii*, *Candida lusitaniae*, *Trichosporon mucoides* and three strains of *C. auris*. Colony colours and sizes were evaluated after 24, 48 and 72 hours of incubation according to the manufacturers' instructions. We also cultured on each agar a mix of four *Candida* species including *C. auris*.

Results: On all three media some strains needed 48 hours of incubation to show visible growth. On all three media the colony colours matched the manufacturers' listing and were stable after 72 hours of incubation. Colonies were smaller on Brilliance Candida agar than on the other media and cream coloured or white colonies were harder to detect on this opaque plate. Different yeast species in a mix were easiest to distinguish on BBL Chromagar Candida Medium due to the different colony colours.

Conclusions: *C. auris* grew with uncoloured colonies on all tested chromogenic yeast agars. As long as a specific *C. auris* selective agar is not available, we found that of the three tested agar media BD BBL Chromagar Candida Medium is the best choice to quickly distinguish between possible *C. auris* colonies and other yeasts, especially in a mixed culture. The development of a selective and differential *C. auris* agar is urgently needed.

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Abstract 1251

Implementation of appropriate antibiotic prophylaxis in surgery: high benefit with no risk

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Background: Extended surgical prophylaxis is one of the most common problems in antimicrobial stewardship. Implementation of the shorter duration of prophylaxis is necessary but could be avoided by the fear of surgical site infections (SSIs). Therefore, we aimed to demonstrate the no harm of the shorter duration in surgical antibiotic prophylaxis on the SSIs.

Materials/methods: This study was performed in American Hospital and Koc University Hospital, which are under the umbrella of the Vehbi Koc foundation. We prepared and implemented local surgical prophylaxis guideline for thoracic surgery in January 1, 2015 to decrease inappropriate surgical prophylaxis. Infection control team followed up the process prospectively based on "surgical prophylaxis document" filled in for each case and discussed the data with surgical team, monthly. We compared pre-intervention (January 1, 2011 to December 31, 2014) and post-intervention period (January 1, 2015 to December 31, 2018) in terms of appropriate type, dose and duration of antibiotic use and healthcare associated infections.

Results: In total 1460 patients were evaluated between January 1, 2011 and December 31, 2018 that were operated by thoracic surgery team. Antibiotic prophylaxis was given in 82% of the patients. Inappropriate prophylaxis use decreased from 92% to 14% (p<0.001). The mean duration of antibiotic prophylaxis declined from 60 hours to 23.6 hours, and there was no SSIs in both periods (Table).

Conclusions: We demonstrated that by implementing local surgical prophylaxis guideline, duration of prophylaxis and inappropriate prophylactic antibiotic use decreased without increase in SSIs. Our study results provide evidence for the implementation of appropriate surgical prophylaxis.

Table. The appropriateness of surgical site prophylaxis

	2011-2014 n=547 (%)	**2015-2018 n=913 (%)**	**p**
Female	228 (42)	376 (41)	0.851
Diagnosis			
Lung cancer	149 (27)	332 (36)	<0.001
Lung nodule, tumor, cyst	123 (23)	229 (25)	0.286
Hemothorax and pneumothorax	78 (14)	79 (9)	<0.001
Duration of prophylaxis			
Mean hour (ss)	60 (33)	23.6 (23)	<0.001
Inappropriate prophylaxis	404 (92)	99 (14)	<0.001
Extended prophylaxis	312/385 (81)	47/731 (6)	<0.001
Inappropriate dose	138 (31)	28 (4)	<0.001

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Abstract 1255

Filamentous bacteriophage (Pf-8) in *Pseudomonas aeruginosa* isolates belonging to the international cystic fibrosis clone (CC274)

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Abstract third-party references: GEMARA-Spanish Society of Infectious Diseases and Clinical Microbiology (SEIMC)/Spanish Network for the Research in Infectious Diseases (REIPI)

Background: Cystic fibrosis (CF) chronic respiratory infections are mainly caused by *Pseudomonas aeruginosa*. Bacteriophages of the genus *Inovirus* are filamentous and do not lyse host cells, but they establish a persistent association with the host, producing and releasing phage particles from the growing and dividing host cells and affecting the virulence. In *P. aeruginosa* isolates a group of related filamentous bacteriophages called the "Pf-like" phages have been described (Pf1, Pf4, Pf5, Pf6, Pf7). We analysed the presence of a new "Pf-like", Pf8 phage, in 25 *P. aeruginosa* genomes belonging to the clonal complex (CC274) from CF-patients.

Materials/methods: All isolates had been previously classified within the CC274, 10 from Australian CF-patients and 15 from Spanish patients, all were CF isolates except PAMB148, which was a blood isolate. Isolates were recovered during an 18-year period(1995-2012). Whole-genome sequencing was developed by Illumina MiSeq benchtop sequencer with MiSeq reagent kit v2(Illumina Inc., USA) and "*de novo*" assembled using Velvet v1.2.10(https:// www.ebi.ac.uk/ffzerbino/velvet/). Bacteriophage genome analysis(PHAST, PHASTER, RAST, HHprep, BLAST-Nucleotide) and protein identification(Protein, CRISPR Finder tools), were performed. The results were confirmed by PCR.

Results: We found an intact filamentous bacteriophage (Pf8) in the genome from AUS411.500 isolate. Interestingly, Pf8 showed high protein identity with the Pf4 (*P. aeruginosa* PA01) and Pf5 (*P. aeruginosa* PA14) filamentous bacteriophages, which have been associated with host virulence via biofilm and dispersal mediated by host cell death (Fig-1). However, new proteins involved in the viral defense were identified in Pf8 bacteriophage such as putative toxin-antitoxin module and methyltransferase. Finally, this Pf8 filamentous bacteriophage was located in all strains belonging to CC274 clone with a query cover and percentage of identities around 51%-76% and 97.75%-99.80%, respectively. Only three strains did not have this Pf8 filamentous bacteriophage (AUS034 and AUS037 strains from CF-patients and PAMB148 blood isolate.

Conclusions: We described for the first time the Pf8 filamentous bacteriophage (Pf-likes) in the genome of *P. aeruginosa* CC274 from CF-patients. This Pf8 showed high protein identity with Pf4 (*P. aeruginosa* PA01) and Pf5 (*P. aeruginosa* PA14) filamentous bacteriophages which have been associated with the maintenance of *P. aeruginosa* producing biofilm in long-term chronic CF-infections.

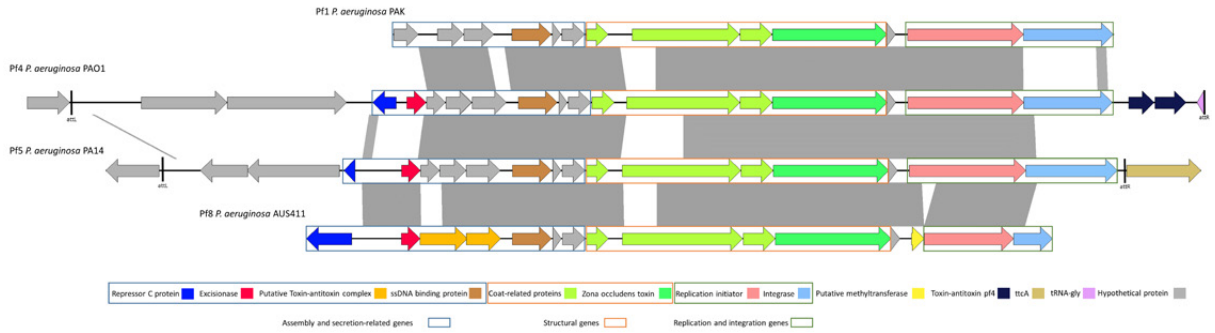

Fig 1. Schematic representation and identity of filamentous phage Pf1, Pf4, Pf5 and Pf8. Genes are classified by function into assembly and secretion, structural and replication/integration. Dark gray regions represent >90% of nucleotide sequence identity between Pf genomes.

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Abstract 1257

The role of liposome positive charge on immune response generated in BALB/c mice immunized with Leishmania homologue of receptors for Activated C Kinase (LACK) of *Leishmania major*

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Background: Leishmaniasis is a complex parasitic disease that represents a major public health problem. Despite numerous attempts over the past decades, yet there is no effective vaccine against human leishmaniasis probably due to the lack of suitable adjuvants. In this study, a first generation liposomal-based Leishmania vaccine was developed using Cloned gene of *leishmania* Homologue of receptors for Activated C Kinase (*LACK*) and IL-12. In this liposome structure, the cationic lipid 1,2-Di-oleoyl-3-Trimethylammonium propane (DOTAP) and 1,2-Dioleoyl-snGlycero-3-Phosphoethanolamine (DOPE) provides intrinsic adjuvant activity and cholesterol was added as a membrane stabilizer.

Materials/methods: BALB/c mice were subcutaneously (SC) immunized with different nanoliposomal and non-liposomal sampels. Immunization was done three times in a four week interval. The immunized mice were then challenged SC with 1×10^6 stationary phase *leishmania major* (*L. major*) promastigotes (50 µl), at 2 weeks after last booster injection.

Results: Towards this goal, we formulated LACK gene based vaccines that with entrapped within cationic liposomes. The liposomes prepared vesicles showed a diameter of about 200- 300 nm, a positive zeta potential. The serum antibody responses increased from 0 to 90 days post infection/challenge. Immunized animals showed greater IgG2a levels in comparison to the infected controls. The splenocytes from immunized mice were cultured, stimulated with LACK and analyzed for cytokine profile. The levels of IFN-γ were greater in immunized mice as compared to control mice.

Conclusions: Immunization with liposomes containing DOTAP and/or DOPE in combination with LACK indicate that liposomes might be used as a suitable immunoadjuvant for evelopment of leishmania vaccine.

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Abstract 1265

Determining the burden of infectious diseases caused by carbapenem-resistant Gram-negative bacteria in Spain

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Background: According to WHO approximately 4 million patients are affected by nosocomial infections each year in the EU. Carbapenems are reserved for difficult-to-treat Gram-negative infections, but resistance is increasing. The objective was to estimate the clinical and economic burden of nosocomial infections produced by carbapenem-resistant Gram negative (CRGN) pathogens in Spain for 2017.

Materials/methods: Total CRGN infections were estimated by multiplying the total number of hospital discharges, the incidence of nosocomial infections and the percentage of carbapenem resistant pathogens (Acinetobacter baumannii, Klebsiella pneumoniae, Pseudomonas aeruginosa). Mortality was calculated by multiplying the percentage of deaths attributed to CRGN pathogens and the total estimated number of patients with CRGN nosocomial infections.

Direct cost was estimated by multiplying the number of patients with CRGN infections by the hospital cost of CRGN infections.

Indirect costs included productivity loss (PL) due to temporary disability and premature mortality due to CRGN infections. The PL due to temporary disability was obtained by multiplying the length of stay due to CRGN infections by the average wage and adjusting with the unemployment rate. The cost of premature mortality was estimated by multiplying the total number of years of life lost in working age and the average wage, adjusting by the employment rate. Also Disability-Adjusted Life Years (DALYs) were obtained.

Results: A total of 12,090 patients were estimated to have a CRGN nosocomial infection in 2017 with P. aeruginosa producing the highest mortality.

In Spain, the direct cost of CRGN nosocomial infections was estimated to be 390M€ with P. aeruginosa accountable for 78% of the total direct cost. Indirect costs were estimated to be 82M€. Life years lost due to premature mortality caused by CRGN nosocomial infections were estimated as 192,833, of which 111,369 were years of productive life lost. Finally, CRGN nosocomial infections produced a total of 13,353 DALYs.

Conclusions: CRGN infections produce a high burden of disease. Total cost was estimated to be more than 472M€ in Spain in 2017. Direct cost accounted for 83% of total economic cost and P. aeruginosa was the pathogen that contributed the most to burden of CRGN infections.

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Abstract 1267

Mycoplasma genitalium infections in men who have sex with men: prevalence and macrolide resistance in north-east Italy

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Background: *Mycoplasma genitalium* (MG), one of the most common bacterial pathogens of sexually transmitted infections (STIs), causes non-gonococcal urethritis in man and has been proposed as a cause of proctitis in Men who have Sex with Men (MSM).

The 2016 European guideline on MG infections recommends treatment with Azithromycin or Josamycin in uncomplicated infections. Given the increasing prevalence of macrolide resistance during the last years, Moxifloxacin is recommended as second line treatment.

We aimed to determine the proportion of MSM who had MG in the rectum and the prevalence of macrolide resistance. We compared these data with the prevalence during the previous 3 years.

Materials/methods: From February to September 2019, we retrospectively evaluated the prevalence of MG infections in 358 patients from STIs-AIDS Unit. We also evaluated the prevalence of MG during 3 years before. Anal swabs were tested for MG infection using Allplex™ MG & AziR Assay (Seegene). Test simultaneously detects MG and six 23S rRNA mutations associated with macrolide resistance: A2058C, A2058G, A2058T, A2059C, A2059G, A2059T.

Results: Overall, the prevalence of MG was 6.7% (24/358). All positive-MG patients (median age 41 years) did not present symptoms. During 2014-2016 the prevalence was respectively 12.4% (14/113), 17.0% (27/159), 7.4% (23/313).

23S rRNA mutations were reported in 25.0% (6/24) of strains: A2059G substitution accounted for 66.7% (4/6), A2058C for 33.3% (2/6). Of six resistant-MG patients, five had been treated with Azithromycin for STIs before.

Conclusions: To date, there is no data about prevalence of macrolide-resistant MG in Italy. We report a high presence of MG, decreasing over the years, and resistant strains. Our selected patients may be particularly vulnerable to acquire and transmit MG due to their higher risk of STIs and previous macrolide therapy. Given the 25% of resistance, Azithromycin should not be longer considered a first choice for empirical therapy in our selected population.

Therefore, our findings support the routine use of an assay to detect MG and macrolide resistance-associated mutations, as recommended in the European guideline. This will help to limit inappropriate azithromycin treatment and to control antimicrobial resistance progression.

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Abstract 1268

Quality control of therapeutic bacteriophages: the Belgian experience

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Background: The greatest hurdle to the introduction of phage therapy in Western medicine remains the lack of an appropriate legal and regulatory framework. Since 2018, Belgium is implementing a pragmatic phage therapy framework that centers on the unlicensed ad hoc preparation of tailor-made phage medicines. Central to this approach is a two-step quality control of phage active pharmaceutical ingredients (APIs) effectuated by Sciensano.

Materials/methods: API QC consists of the construction of a genetic passport which contains information of phage's lifestyle, genome size and content, and its capacity for horizontal gene transfer. The host bacterium is checked for the presence of active prophages and phage-inducible chromosomal islands. Secondly, each production lot is checked for microbial contamination, endotoxin levels, pH and presence of the specific active component. The obtained results are condensed in a Certificate of Analysis which is returned to the manufacturer, and then transferred to the hospital pharmacy to enable preparation of the formulation upon a physician's prescription.

Results: To date, Sciensano controlled 7 seed lots and 15 production lots of phage APIs. All 7 phages, infecting either *Pseudomonas aeruginosa*, *Staphylococcus aureus* and *Mycobacterium abscessus*, were found to be strictly lytic and non-transducing. All but one propagation strain were approved; One particular *P. aeruginosa* strain was found to produce the toxin pyocyanine and contained at least two active prophages which were induced during phage production. All approved production lots were of high quality, with no microbial contamination detected so far, and endotoxin levels frequently below the detection limit of 0.5 IU/ml. However, our experience shows that certain hosts are correlated to much higher endotoxin contaminations.

Conclusions: With the implementation of a national regulatory framework, Belgium is enabling the treatment of desperate patients with phages upon prescription of a physician outside compassionate use. The relative small number of QC requests clearly reflect its current limited implementation and its use as agents of last resort. In addition the already obtained QC data, we will present our broader experience with the various aspects surrounding the implementation of phage therapy, including the political and economic context of the personalized approach pursued in our country.

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Abstract 1269

Characterisation of NDM-producing *Klebsiella pneumoniae* isolates from different Roman hospitals

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Background: Multi-drug-resistant (MDR) *Klebsiella pneumoniae* producing NDM carbapenemase is a serious nosocomial pathogen causing a variety of infections. Treatment options are particular limited, given their intrinsic and acquired resistance genes. The objective of the study was to investigate the molecular epidemiology of clinical *K. pneumoniae* isolates from different hospitals of the Latium region.

Materials/methods: Between May and September 2019, *7 K. pneumoniae* strains were isolated from clinical samples of patients treated in 4 different hospitals. Identification and antimicrobial susceptibility testing were performed using the Phoenix system (BD). Genome sequences were generated by Next Generation Sequencing (NGS) using the Ion Torrent sequencer (Life Technologies). Antimicrobial resistance genes were extracted from the NGS data identified by in silico analysis using the ResFinder webserver. Molecular typing was performed using the core genome MLST (cgMLST) approach (Ridom), which uses 2358 target genes to characterize allelic profile of *K. pneumoniae*.

Results: All isolates showed an MDR profile; the *bla*NDM-1 gene was detected in 6/*7* isolates, one isolates harboured *bla*NDM-5 gene variant. The *bla*OXA-48 was detected in two isolates, which carried additionally the ampC cephalosporinase *bla*CMY-6; 5/*7* isolates were positive for *bla*CTX-M-15. Five different Sequence Types (STs) were detected among the *7* NDM-producing *K. pneumoniae*: ST11, ST15, ST14*7*, ST383 and ST30*7*. Two strains belonging to ST11 and ST15 each. Clonal relationships within the STs using the cgMLST scheme showed the presence of 2 complex type, each composed by two isolates belonging to ST15 and ST11. The strains within each cluster showed a very high level of correlation (up to 8 allele differences) and *K. pneumoniae* strains ST11 were collected from the same hospital. No genetic correlation was observed for the remaining 3 isolates.

Conclusions: The emergence of NDM-producing *K. pneumoniae* in Italy is a real threat for the public health. There is a need for increased capacity to support surveillance and investigations with NGS to identify high-risk clones and to implement enhanced control measures in order to avoid further spread; the use of gene-by-gene analysis by cgMLST for epidemiological investigations allows an in-depth analysis, owing to its high discriminatory ability in determining clonal relatedness.

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Abstract 1271

Characterisation of KPC-50, a novel transferable KPC-3 variant conferring resistance to ceftazidime-avibactam in a colistin-resistant *Klebsiella pneumoniae* from Switzerland

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Background: The widespread of KPC-type carbapenemases in *Klebsiella pneumoniae* most often possessing additional resistance leading to multidrug resistance represent a very high clinical concern. Avibactam, a non-β-lactam inhibitor, is able to restore the efficacy of ceftazidime against KPC producers. However, resistance to the novel ceftazidime-avibactam (CAZ-AVI) association is increasingly reported among clinical strains producing KPC variants.

We described a novel KPC-3 variant, KPC-50, produced by the *K. pneumoniae* N859 clinical isolate, recovered in 2019 from an intraabdominal abscess of a patient hospitalized in Zürich, Switzerland. This isolate was resistant to carbapenems but also uncommonly resistant to CAZ-AVI.

Materials/methods: The *bla*KPC-50 and *bla*KPC-3 genes were amplified and transformed into *E. coli* TOP10. Antimicrobial susceptibility was performed by the disc diffusion method. Minimum inhibitory concentrations (MICs) were confirmed by broth microdilution and E-test. Further, KPC-X and KPC-3 enzymes were purified with a cation column and using a lab-scale chromatography system AKTA-prime. Finally, kinetic measurements were performed with a spectrophotometer.

Results: The KPC-50 ß-lactamase possessed a 3-amino-acid insertion (E-A-V) located between amino acids 276 and 277 compared to the KPC-3 amino acid sequence. Cloning and expression of this plasmid-borne *bla*KPC-50 gene in *Escherichia coli*, followed by determination of MIC values and kinetic parameters, showed that KPC-50, compared to those of KPC-3, has an increased affinity to ceftazidime and a decreased sensitivity to avibactam, leading to resistance to ceftazidime-avibactam once produced in *K. pneumoniae*. Furthermore, KPC-50 exhibited a decrease of its carbapenemase activity. In addition this strain was resistant to colistin by modification of the *pmrB* gene that governs the lipopolysaccharide biosynthesis.

Conclusions: This report highlights that (i) insertion/deletion in the KPC sequence may be an important evolution pathway for conferring ceftazidime/avibactam resistance in *K. pneumoniae,* and (ii) the diversity of KPC variants conferring resistance to ceftazidime-avibactam already circulating in Europe.

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Abstract 1272

The guideline compatibility of mucormycosis management: a retrospective review of the case reports from European quality (EQUAL) score perspective

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Background: Mucormycosis is a rare, but life-threatening disease. European QUALITY (EQUAL) score was recently developed that reflects the strongest recommendations from the international guidelines for the management of mucormycosis. Here, we investigated the compliance of the individual diagnostic and treatment approaches with the guideline recommendations in the published case reports.

Materials/methods: A Pubmed search was performed by using the keyword "mucormycosis" between 01 January 2015 and 31 December 2018. Cases with pulmonary and/or rhinocerebral involvement were included in the analysis. Only the items that were clearly described in the case report were scored.

Results: The search revealed 882 publications. A total of 165 cases were included in the study. The median age of patients was 48.5 years (Minimum 1.5, maximum of 77 years). The 96 were male. The most common underlying disease was diabetes mellitus in 82 patients, followed by hematological malignancy in 37 patients. Rhinocerebral involvement was the most common presentation in 84 patients, 68 patients had pulmonary mucormycosis, and 13 had pulmonary and rhinocerebral mucormycosis. The achievable score from the diagnostic approach was 1314, the achieved score was 631 (48.1%). Direct microscopy was performed in only 18 of 44 patients, culture was performed in 33 out of 44 patients who underwent bronchoscopy, fungal culture from biopsy specimen was performed in only 65 of 135 patients who underwent biopsy, and species identification with antifungal susceptibility test was performed in 14 out of 43 culture-positive patients. The achievable score for treatment was 1024 but achieved to 424 (47.3%). Surgical debridement was performed in 95 patients, amphotericin B deoxycholate was first choice antifungal in 30 patients, the dose was lower than 5 mg/kg/day in 15 of 87 patients who received liposomal amphotericin B, none of the patients who received posaconazole or isavucanazole had therapeutic drug level monitoring, and the control of risk factors such as neutropenia, ketoacidosis, hyperglycemia, and corticosteroids was reported in only 37 patients. The mortality rate was 38.8% (64 out of 165).

Conclusions: The case reports achieved to 50% of the achievable scores, approximately. The management of mucormycosis is an area that needs continuous improvement.

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Abstract 1277

Population pharmacokinetic modelling and simulations to support ceftazidime-avibactam dose selection for paediatric patients with nosocomial pneumonia

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Background: The ceftazidime-avibactam paediatric investigation programme includes one Phase I and two Phase II completed trials in children with complicated intra-abdominal infection or complicated urinary tract infection. A further single-dose Phase I PK trial in children with NP (NCT04040621) is underway. In this analysis, previously reported population PK models were used to guide ceftazidime-avibactam dosage selection for the paediatric NP trial.

Materials/methods: The ceftazidime and avibactam population PK models included 2130 subjects with 9628 samples and 2403 subjects with 14,223 samples, respectively, including 154 and 153 children with 509 and 488 samples, respectively. Both were two-compartment disposition models in which body weight and renal maturation (subjects ≤2 years) or body surface area-normalised creatinine clearance (nCrCL; subjects >2 years) were key covariates predicting ceftazidime and avibactam clearance. The final PK models using NP population effects were used to simulate steady-state exposures and probability of target attainment (PTA) for various ceftazidime-avibactam dosage regimens (1000 NP patients/simulation), and different age and renal impairment categories. Simulations used plasma-free fractions (85% ceftazidime; 92% avibactam) and a joint PK/pharmacodynamic target (achievement of free plasma ceftazidime ≥8 mg/L and avibactam ≥1 mg/L simultaneously for ≥50% of the dosing interval). Adult NP patients were used as reference for matching exposures and PTA.

Results: In simulated paediatric NP patients (age >3 to ≤6 months) with normal renal function, ceftazidime-avibactam 40-10 mg/kg 2-h infusions q8h achieved similar mean exposures to adult patients with normal renal function receiving 2000-500 mg q8h (Table); joint PTA was 98.0% and 95.4% respectively. In simulated paediatric patients (>6 months to <18 years) with NP and normal renal function, ceftazidime-avibactam 50-12.5 mg/kg (capped at 2000-500 mg) q8h achieved ≥91.8% joint PTA with exposures similar to adults with normal renal function. Dose adjustments for paediatric patients with renal impairment of equivalent magnitude as in adults resulted in similar exposures and PTA.

Conclusions: These analyses support evaluation of ceftazidime-avibactam 40-10 mg/kg (>3 to ≤6 months) and 50-12.5 mg/kg (>6 months to <18 years) q8h in paediatric patients with NP and normal renal function, with dose adjustments for renal impairment (nCrCL <50 mL/min/1.73 m^2).

Study sponsored by Pfizer.

Table . Predicted steady-state exposures (geometric mean) and PTA in paediatric patients with NP and normal renal function† following administration of ceftazidime-avibactam (40-10 mg/kg or 50-12.5 mg/kg q8h) and adults with NP receiving the standard ceftazidime-avibactam dose

Age group	Dose‡ (ceftazidime-avibactam)	Ceftazidime§				Avibactam§				Joint PTA (%)‖
		$C_{max,ss}$ (mg/L)	$AUC_{ss,0-24}$ (mg•h/L)	$C_{max,ss}$ Ratio to adults	$AUC_{ss,0-24}$ Ratio to adults	$C_{max,ss}$ (mg/L)	$AUC_{ss,0-24}$ (mg•h/L)	$C_{max,ss}$ Ratio to adults	$AUC_{ss,0-24}$ Ratio to adults	
>3 months to ≤6 months	40-10 mg/kg q8h	71.4 (19.4)	745 (30.2)	1.10	1.05	12.9 (53.6)	121 (43.5)	1.26	1.15	98.0
>6 months to ≤1 year	50-12.5 mg/kg q8h	80.4 (19.4)	769 (29.9)	1.24	1.08	14.9 (53.1)	132 (43.2)	1.46	1.26	96.8
>1 year to ≤2 years	50-12.5 mg/kg q8h	76.2 (19.2)	698 (29.8)	1.17	0.98	14.4 (52.8)	125 (42.8)	1.41	1.19	92.3
>2 years to <6 years	50-12.5 mg/kg q8h	76.4 (21.0)	691 (29.9)	1.17	0.97	13.8 (48.9)	118 (41.3)	1.35	1.12	91.8
≥6 years to <12 years	50-12.5 mg/kg q8h	80.8 (19.6)	785 (29.8)	1.24	1.10	15.1 (43.2)	136 (36.0)	1.48	1.30	96.6
≥12 years to <18 years	50-12.5 mg/kg q8h	71.8 (24.1)	747 (30.4)	1.10	1.05	13.0 (67.5)	121 (51.1)	1.27	1.15	98.7
Adults with NP (normal renal function)	2000-500 mg q8h	65.1 (31.0)	712 (41.8)	N/A	N/A	10.2 (77.6)	105 (71.8)	N/A	N/A	95.4

†Normal renal function defined as body-surface area normalised creatinine clearance (nCrCL) ≥80 mL/min/1.73 m^2 or renal maturation based on post-menstrual age for subjects aged <2 years. ‡All doses administered as 2-h IV infusions. Paediatric doses were capped to a maximum dose of 2000 mg ceftazidime and 500 mg avibactam. §Exposure values are geometric mean (%CV). ‖Joint target (50% $fT>8$ mg/L for ceftazidime and 1 mg/L for avibactam). $AUC_{0-24,ss}$, area under the plasma concentration–time curve over 24 h at steady-state; $C_{max,ss}$, maximum concentration at steady-state; IV, intravenous; NP, nosocomial pneumonia; PTA, probability of target attainment.

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Abstract 1278

Antimicrobial resistance and genotypic markers of trimethoprim resistance in *Escherichia coli* and *Klebsiella* spp. isolated from patients with urinary tract infections

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Background: Urinary tract infections are among the most common bacterial infections. Isolation of causative uropathogens and their resistance profiles are not routinely performed, hence antibiotic therapy is often empirical. This study aimed to determine antimicrobial susceptibility of urinary *Escherichia coli* and *Klebsiella* spp. isolates from two Health and Social Care Trusts in Northern Ireland and to assess the use of trimethoprim resistance (*dfrA*) and ESBL-encoding (bla_{TEM}) genes as biomarkers for rapid detection of trimethoprim resistance.

Materials/methods: Antimicrobial susceptibility of *E. coli* and *Klebsiella* spp. (n=124) to trimethoprim, amoxicillin, ceftazidime, ciprofloxacin, co-amoxiclav and nitrofurantoin was determined by ETEST® and interpreted according to EUCAST breakpoints. The *dfrA* and bla_{TEM} genes were detected by PCR while ESBL production was measured using the combined disc method.

Results: Trimethoprim resistance was found in 37/124 (29.8%) of the isolates with MIC_{90} >32 mg/L. Eighty-one of the 124 isolates (65.3%) were resistant to amoxicillin, while 18/124 (14.5%) were resistant to nitrofurantoin. *DfrA* and bla_{TEM} genes were detected in 29/37 (78.4%) and 30/37 (81.1%) of the trimethoprim-resistant isolates respectively. The detection of *dfrA* was highly sensitive in predicting phenotypic trimethoprim resistance (93.6%) and resistance to both trimethoprim and amoxicillin (100%). Bla_{TEM} was less sensitive in detecting phenotypic trimethoprim resistance (45.8%). ESBL production was observed in 13/124 (10.5%) isolates and there was no significant association (P>0.05) between ESBL production and trimethoprim resistance.

Conclusions: This study demonstrates that *dfrA* could be used to determine trimethoprim resistance among urinary *E. coli* and *Klebsiella* spp. and guide the timely prescription of appropriate antibiotics for treatment of UTIs.

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Abstract 1280

Multiple mutations in dihydrofolate reductase gene in cotrimoxazole-resistant *Streptococcus pneumoniae* isolated from HIV adults in a community setting, Tanzania

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Background: Cotrimoxazole, a combination of trimethoprim and sulfamethoxazole, is widely used in people living with HIV to prevent opportunistic infections, including pneumococcal infections. Resistance to trimethoprim may render pneumococci fully cotrimoxazole-resistant. This study characterizes the molecular mechanisms of trimethoprim resistance in pneumococcal isolates from newly HIV-diagnosed patients in Dar es Salaam, Tanzania.

Materials/methods: A total of 1877 nasopharyngeal swabs were collected from 537 individuals newly diagnosed with HIV at four clinic visits during one-year follow-up in 2017 - 2018. Swabs were screened for pneumococcal colonization. Isolates were identified by colonial morphology on sheep blood agar and optochin susceptibility and serotyped by latex agglutination. Antimicrobial resistance was characterized by disk diffusion, E-test, polymerase chain reaction and sequencing.

Results: The majority of the pneumococcal isolates (48/76, 63.2%) were penicillin non-susceptible (MIC 0.06 – 2 mg/ml). Isolates were frequently resistant to cotrimoxazole (80.3%), but less so to chloramphenicol (23.7%), tetracycline (21%), erythromycin (22.4%), azithromycin (18.4%) and clindamycin (10.5%). None were resistant to levofloxacin. Twenty-five percent were resistant to three or more antibiotic classes (multi-drug resistant, MDR). The majority (n=40, 59.7%) were conjugate vaccine (PCV 23) serotypes. Vaccine-type pneumococci were more frequently MDR (OR 7.5, 95CI 1.55 – 36.27, p 0.01). There was no difference in cotrimoxazole MIC-values between vaccine- and non-vaccine-types (median 4 for both groups, p=0.9). Cotrimoxazole-resistant isolates carried from 1 to 11 different trimethoprim-resistance mutations, the majority (n=52) having 6-8 mutations. The most common mutations conferring trimethoprim-resistance were Ile100Leu (100%), Glu20Asp (92%), Glu94Asp (61%), Leu135Phe (57%), His26Tyr (53%), Asp92Ala (53%) and His120Gln (53%). There was no difference in numbers of mutations between vaccine-type (median 5.5) and non-vaccine type pneumococci (median 6, p=0.3). There was no significant association between cotrimoxazole MIC-values and type or number of mutations.

Conclusions: *Streptococcus pneumoniae* isolated from newly HIV-diagnosed patients are frequently non-susceptible to penicillin and resistant to cotrimoxazole. Most isolates carried multiple mutations in the *dhfr* gene.

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Abstract 1285

Epidemiology typing and molecular analysis of vancomycin-resistant *Enterococcus faecium* in haemato-oncological patients

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Background: A long-term increased prevalence of vancomycin-resistant Enterococci (VRE) colonization has been observed in the haemato-oncological department of the University hospital Brno (CZ). The aim of this study was to describe the genetic diversity of the local VRE population and determine the nosocomial transmission rate. An additional goal was to focus on establishing a rapid VRE typing method suitable for routine practice.

Materials/methods: Between 06/2019-07/2019, all hospitalized patients in one ward were screened for VRE presence. In total, 99 patients were screened on admission, at discharge and once a week during their hospitalization using rectal swabs. All collected VRE isolates were analysed using mini-MLST and whole genome sequencing (WGS).

Results: In total, 331 samples were taken, from which 24 VRE strains and one linezolid-resistant Enterococcus faecium isolate were isolated from 16 patients (16%, n=99). Using mini-MLST, 22/24 (88%) VRE isolates were identified as MelT55 and 3/24 (12%) as MelT420. In silico MLST was performed and allocated the obtained isolates to 6 ST (ST17, ST80, ST117, ST761, ST787 and one new ST). All isolates were VanA positive, 5 isolates were both VanA and VanB positive. The single-nucleotide variant (SNV) number was determined using SeqSphere+ software and was in a range from 1 to 5,687 within the isolates belonging to the same ST.

Conclusions: The whole genome SNV analysis showed high genetic diversity in the VRE population in our haematology ward. Most patients had their unique strain, indicating a lower rate of transmission than expected considering the generally accepted assumption that hospital transmission is the main source of VRE. Thus, other factors such as ATB treatment or patient's overall health condition are likely to affect higher VRE colonization rates.

The current mini-MLST scheme does not have sufficient resolution power to distinguish VRE strains within our population. Therefore, we developed a new universal algorithm for WGS data to find variable regions that can be used to extend the existing mini-MLST scheme or to replace it with population-specific markers.

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Abstract 1290

The *in vitro* effect of azithromycin on *P. aeruginosa* biofilms

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Background: Azithromycin (AZM) is efficient for treatment of chronic *P. aeruginosa* biofilm infection in cystic fibrosis (CF) patients although conventional susceptibility testing according to EUCAST shows resistance to AZM. It has, however, been shown that planktonic *P. aeruginosa* are more susceptible to AZM when tested in RPMI 1640 medium due to increased cell-wall permeability and reduced expression of the MexAB-OprM (van Bambecke).

Materials/methods: The aim of this study was to investigate the effect of AZM on planktonic and biofilm *P. aeruginosa* in LB vs RPMI 1640 medium in wild-type (WT) *P. aeruginosa* (PA01) and two different mutants with relevant phenotypes for chronic infections: the hypermutable (Δ*mutS*) and the antibiotic resistant phenotype(Δ*nfxB*) due to the expression of the MexCD-OprJ efflux pump. The effect of AZM exposure for 24h and 72h of young (1 day-old) and mature (3 days-old) biofilms was investigated by establishing the minimal biofilm inhibitory concentration(MBIC$_{90}$) in the modified Calgary Biofilm Device.

Results: The AZM MBIC$_{90}$ in LB/RPMI1640 on young biofilms treated for 24h was 16/4 µg/ml for PA01, 32/8 µg/ml for Δ*mutS* and 256/64 *µg/ml for Δnfxb.* The effect of AZM was improved when the treatment was prolonged to 72h, the AZM MBIC$_{90}$ of young biofilm decreased to 8/4 µg/ml for PA01, 8/1 *µg/ml for Δmut*S and 32/4 *µg/ml for Δnfx*B supporting the intracellular accumulation of AZM.

The AZM MBIC$_{90}$ in LB/RPMI1640 on mature biofilms treated for 24h was 256/2 *µg/ml for PAO1 and Δmut*S and 16/1 *µg/ml for Δnfx*B. and decreased to 4/4 µg/ml for PA01 and 8/1 for *ΔmutS* and was measured to 32/4 µg/ml for *ΔnfxB* with 72h treatment.

Conclusions: Our results show that AZM has a better effect on *P. aeruginosa* biofilms in RPMI 1640 than in LB medium and AZM effect is time and concentration-dependent in biofilms, suggesting that prolonged treatment at high dosages is recommended.

We show also that the production of MexCD-OprJ efflux pump is an important resistance mechanism for the in vitro efficacy of AZM on *P. aeruginosa* biofilms. Our results may have implications for susceptibility testing and for the dosing of AZM to CF patients.

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Abstract 1291

Acinetobacter baumannii complex, the beast of the weakest

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Background: We conducted surveillance for Acinetobacter baumannii (AB) blood isolates. Our objectives were: to describe the prevalence and trends of antimicrobial resistance; to characterize of colistin resistance; to identify risk factors and to provide data for policies and guidelines.

Materials/methods: Surveillance was conducted at 12 sentinel academic sites, in South Africa from September 2018 to 2019. Isolates were identified by MALDI-TOF MS. Susceptibility testing was performed on the MicroScan Walkaway System and broth microdilution assay for colistin. Results were interpreted by the CLSI guidelines. PCR assay for mcr 1-5 genes, followed by WGS on the MiSeq Instrument was completed for colistin resistant isolates. Genome assembly and single nucleotide polymorphism analysis, for the pmrCAB operon and the lpxA, lpxC, lpxD and lpsB genes was done in CLC Genomics workbench. Resistome prediction was done with ResFinder and the Comprehensive Antibiotic Resistance Database (CARD).

Results: We have received 1823 isolates (43%) with clinical information for 1409 (33%) patients from a total number of 4269 AB isolates. AB was more prevalent in male patients (54%) and in children less than 14 year (40%). Crude mortality was 34%. During hospitalization 54% patients received meropenem and 32% received colistin treatment. The majority of the patients had medical devices (83%); long stay in hospitals (67%); 20% had treatment with carbapenems and 14% with colistin prior to AB isolation. Amongst those with known HIV status (890) 20% were positive. Susceptibility to majority of antibiotic classes was extremely low, from 1-14% except for colistin (96%). Of the 45 colistin resistant isolates none harbored the mcr 1-5 genes. A subset of 21 isolates were established with chromosomal non-synonymous mutations in various genes (pmrCAB operon, lpsB, lpxD and lpxC). Colistin resistance had no impact on patient outcome and no significant difference was noted in patients that died from susceptible versus resistant strains (p=0.689).

Conclusions: AB pathogen is a highly prevalent among children in South African hospitals. Low resistance to colistin was chromosomally mediated with no plasmid genes. Risk factors were duration of the stay in hospitals, prior antibiotic use and interventions. High crude mortality in patients with AB is of concern.

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Abstract 1293

Whole genome sequencing to detect antimicrobial resistance-associated determinants in *Staphylococcus epidermidis*

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Background: *Staphylococcus epidermidis* is a common cause of opportunistic nosocomial infections including prosthetic device-related infection. Nosocomial strains are commonly resistant to multiple antibiotics necessitating antimicrobial susceptibility testing of clinically significant isolates to guide treatment. Genotypic prediction of antimicrobial resistance from whole genome sequencing (WGS) has been successfully demonstrated in *Staphylococcus aureus*. We investigated the accuracy of this method for predicting antimicrobial resistance from WGS in *S. epidermidis*.

Materials/methods: Thirty nine isolates from orthopaedic device-related infection specimens and 48 carriage isolates (total 87) underwent disc diffusion phenotyping for 13 antibiotics routinely tested in our hospital microbiology laboratory against *S. epidermidis*. A panel of 27 resistance conferring genes and mutations in 11 housekeeping genes associated with staphylococcal antibiotic resistance was generated from previously published studies. All 87 isolates were sequenced on an Illumina HiSeq. Genomes were assembled *de novo* using Velvet 2.0 and interrogated using Basic Local Alignment Search Tool (BLASTn) for the presence of resistance conferring genes and mutations. Discrepant results were checked by repeat phenotypic testing and manual inspection of the relevant antimicrobial resistance genes

Results: A total of 1131 comparisons (13 antibiotics in 87 isolates) were performed. There were 12 (1.06%) major errors (susceptible phenotype, resistant genotype) and 1 (0.09%) very major error (resistant phenotype, susceptible genotype). Overall the sensitivity and specificity of resistance genotype detection were 100% (95% CI 97% – 100%) and 99% (95% CI 98% - 99%) respectively.

Conclusions: These data demonstrate that detection of resistance conferring genes and mutations concord well with current routine phenotyping methods. Major error and very major error rates were within the acceptable limits of <3% and <1.5% respectively stipulated by the United States Food and Drug Administration Guidance for Antimicrobial Susceptibility Test Systems. A validation study is now required to determine if antimicrobial resistance of *S. epidermidis* is accurate and clinically viable as has been demonstrated previously for *S. aureus*.

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Abstract 1295

Transjugular intrahepatic portosystemic shunt and infections: a single-centre retrospective study

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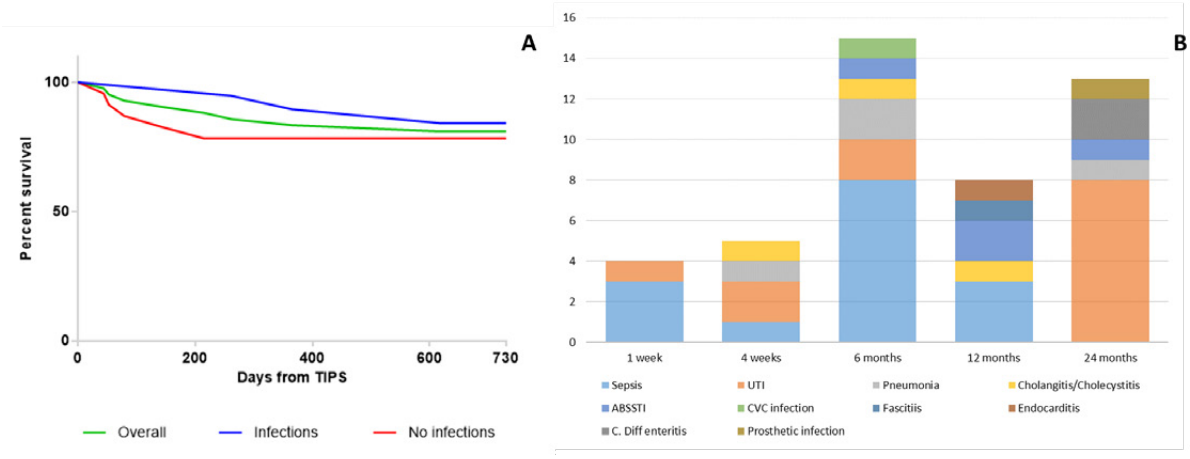
Background: Transjugular intrahepatic portosystemic shunt (TIPS) is a procedure employed in advanced liver disease to reduce portal hypertension and its complications. Few data are available on infectious complications of TIPS, the best described of which being endotipsitis. However, uncertainties remain on the real incidence of other infectious events, including their prevalence and impact on the overall survival.

Materials/methods: We retrospectively identified infections occurred during a 2-year follow-up after TIPS placement in a cohort of patients who underwent this procedure between January 2010 and October 2019 in a large referral hospital. We recorded the microorganism isolates, the antimicrobial agents administered and the mortality rate during follow-up.

Results: Overall, we identified 42 patients subjected to TIPS placement, mostly males (62%) with a mean age of 61.5 years and a median baseline MELD score of 11. The hepatic venous pressure gradient was 23 mmHg before and 10 mmHg after the procedure. Forty (95%) patients received antibiotic prophylaxis concomitantly with TIPS placement: 17 (40%) received ceftriaxone, 16 (38%) cefotaxime, 2 (5%) meropenem, 2 (5%) piperacillin/tazobactam and 1 (2.5%) each ampicillin, amoxicillin/clavulanate and ciprofloxacin. During follow-up, infections occurred in 21 (50%) patients, for a total of 45 events. The most frequently observed were sepsis (33%) followed by urinary tract infections (29%). Pneumonia and acute bacterial skin and skin structure infections accounted for 9% of the events. The most frequently identified microorganisms were *Enterobacteriales* (39%) followed by *Staphylococcus* spp., *Enterococcus* spp. and *Candida* spp., each accounting for 14% of the events. Overall mortality rate was 19%, 16% in patients who developed infection(s) during follow-up, which was not significantly different from the 22% of those who did not (p=0.5, Fig.1A). The types of infection are shown in Fig.1B.

Conclusions: Infections, particularly sepsis and those caused by *Enterobacteriales*, were common in patients during the 2-years following TIPS placement. Occurrence of infections did not modify mortality rates.

Figure: *Overall survival rates at 2-year and stratified according to the occurrence of infections. (**A**) Infections recorded during the follow-up period subdivided in 5 time periods (**B**).*



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Abstract 1296

Development of intravascular microdialysis as a tool for therapeutic drug monitoring and intensive PK studies in children

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Background: Pharmacokinetics (PK) of antibiotics in children differs considerably compared to adults. However, the limited blood volume of children and the ethical restrictions that are associated with repetitive blood sampling severely hamper PK studies and individualization of therapy by means of dense therapeutic drug monitoring (TDM) in children.

Microdialysis (MD) overcomes the aforementioned obstacles of PK sampling in children. However, MD has rarely been used in children and the currently available MD probes do not fit the common intravenous lines used on pediatric wards.

Materials/methods: We conducted this study to develop and validate a method for PK measurements in blood of children using modified MD catheters that fit small intravenous lines. For this purpose, *in-vitro* and *in-vivo* experiments with cefuroxime (CEF) were performed.

In-vitro MD experiments were performed in triplicates with three sampling time-points of 1h and with CEF concentrations of 2.5, 25 and 250µg/ml.

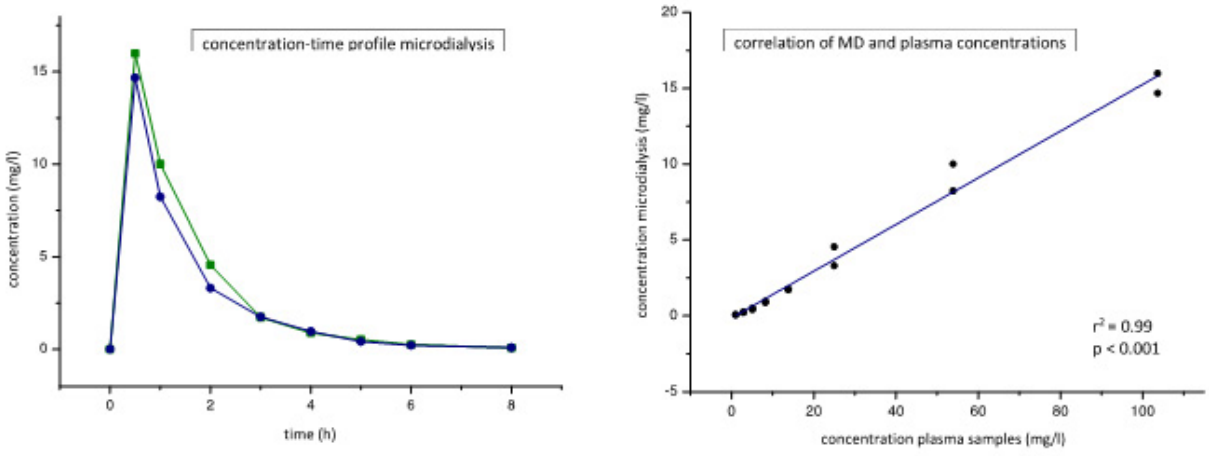
For the *in-vivo* PK study, a single intravenous dose of CEF 1500mg was administered over 30minutes to ten healthy volunteers (HV). Two modified intravascular MD catheters were inserted and serial MD and blood samples were taken. The retrodialysis technique was employed to measure the *in-vivo* recovery.

Results: Mean recovery in the *in-vitro* experiments during forward dialysis ranged from 31% to 33% and mean loss during retrodialysis ranged from 30% to 41% for all sampling time-points and CEF concentrations. Mean recovery during the *in-vivo* MD experiments was 14.4±4.6%, markedly lower than the recovery found in the *in-vitro* experiments.

Figure 1 shows the representative concentration-time profiles of CEF and a scatter plot correlating the MD and plasma concentrations for one HV, demonstrating a strong linear correlation. Preliminary PK analysis of all samples yielded a mean half-life of 1.15±0.2h for MD and 1.3±0.26h for plasma.

Conclusions: We developed an innovative MD catheter that can be inserted into small intravenous lines, allowing PK measurements of free antibiotic concentrations in children and thereby enabling individualization of therapy through TDM. In our experiments with this new MD catheter we were able to correlate MD and plasma concentrations and show reproducibility over time and for different concentrations *in-vitro* and *in-vivo.*

Figure 1



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Abstract 1297

Design and implementation of a Real-Time Carbapenem List (RTCL) using Electronic Patient Record (EPR) to enable Post Prescription Review and Feedback (PPRF) as a carbapenem stewardship strategy for resource-constrained antimicrobial stewardship team

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Background: Pre-prescription authorisation is a commonly employed carbapenem stewardship strategy however Tamma et al demonstrated that postprescription review with feedback (PPRF) had a greater impact in terms of carbapenem use. The introduction of the electronic prescribing record (EPR) to our institution enabled the development of a real time carbapenem list (RTCL) with robust identification of all carbapenem prescriptions in real-time. Our aim was to perform PPRF on all patients initiated on a carbapenem (outside of critical care) and to assess the safety, impact and efficiency of the system.

Materials/methods: A real-time carbapenem prescription list was designed using Cerner® electronic prescribing system that can be executed and updated by the antimicrobial stewardship (AMS) team. The PPRF was performed daily by the AMS team during the normal working week and consisted of a review of the patient EPR, microbiological results and a telephone consultation with patient's clinician. Carbapenem use was measured in defined daily doses (DDD) per 100 bed days used (BDU).

Results: Over an 11-week period (June to August 2019), carbapenem PPRF was carried out on 163 patients (Table 1). The time required for the activity was 30 minutes of AMS pharmacist time and 90 minutes of consultant microbiologist time per day.

Conclusions: The design and implementation of a RTCL on EPR to perform carbapenem PPRF led to a safe and effective reduction in meropenem use and allowed for the identification of several areas to target for stewardship interventions. The group would recommend this approach be adopted by institutions with resource depleted AMS teams in which EPR is available.

Table 1.

Median time to PPFR	2 Days	
Median duration of carbapenem prior to de-escalation	1.45 days	
Major Prescription Indications	Respiratory tract infection 40% Urinary tract infection 17% Intra-abdominal 11%	
Carbapenem defined daily doses (DDDs) per 100 bed days reduction	0.79 (4.29 (Quarter 1 2019) – 3.5 (Jun-Aug 2019))	
Prior infection specialist approval	63%	
History of multi-drug resistant organisms (MDRO)	39%	
Targeted therapy	30%	
De-escalation advised De-escalation advice followed (reviewed at 48 hours) Subsequent re-escalation	25.7% 76.1% 3.1%	
Crude mortality (30 day) De-escalated group Non de-escalated group	 15.6% 21%	 p=0.49

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Abstract 1298

Effect of short-term antimicrobial therapy on the tolerance and antibiotic resistance of multidrug-resistant *Staphylococcus capitis*

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Background: Bacteria undergo adaptive mutation in the host under the selective pressure of an antimicrobial agent. However, the specific effect of clinical antimicrobial use on bacterial evolution and genome mutations related to bacterial survival within a patient is unclear.

Methods: Three *S.capitis* strains were continuously isolated from cerebrospinal fluid of a clinical inpatient. Antimicrobial susceptibility was determined by using agar dilution method. The growth rate and whole blood tolerance of the three *S.capitis* strains were measured and relative fitness were calculated. Biofilm formation were measured by crystal violet Staining. The virulence of the bacteria was examined in the *Galleria mellonella* model. Whole-genome sequencing(WGS) and *in silico* analysis was performed to explore the genetic mechanisms of the apparent changes in the antimicrobial resistance phenotype. Identification of hypothetical protein was done by molecular cloning.

Results: The first isolate was susceptible to rifampin (MIC=0.25 μg/ml), resistant to gentamicin (MIC=16 μg/ml), while the later two isolates were resistant to rifampin (MIC >64 μg/ml), susceptible to gentamicin (MIC=4 μg/ml). Growth curve showed the later two isolates grew faster than the first isolate with a relative fitness cost of 19.2%, and 15.0%, accordingly. Their ability to form biofilm and *in vitro* whole blood tolerance were enhanced. No significant differences of virulence in the *G. mellonella* model were observed.Genome SNPs analysis revealed three genes(*saeR*, *moaA*, and *rpoB*) harbored missense base substitution mutations and one hypothetical protein harbored frameshift mutation. The mutation of *rpoB* gene caused rifampicin resistance. Mutations in seaR moaA and hypothetical protein are associated with changes in other biological traits. Amino acid sequence-based structure and function identification the hypothetical protein indicated that a mutation in the encoding gene might be associated with altered aminoglycoside susceptibility.

Conclusions: We report here for the first time that short-term clinical antibiotic use causes resistance mutations, collateral sensitivity, and adaptive enhancement of *S. capitis*. The impact of clinical short-term antimicrobial use on bacterial ability to survive within the host should not be underestimated, and appropriate measures should be introduced to address the adaptive evolution of bacteria to antimicrobial agents.

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Abstract 1305

Cold plasma activated liquid reduces bacterial biofilm produced by *Staphylococcus aureus* and *Escherichia coli*

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Background: Hospital surfaces are a source of infection due to contamination by bacteria. A novel potential method of hospital surface decontamination is the use of cold atmospheric pressure plasma (CAPP) systems. CAPP has antimicrobial properties that can inactivate bacterial cells on surfaces directly but also through the use of plasma activated liquid (PAL). Although the mechanisms of action are not fully understood, it is thought to be due, in part, to the production of reactive oxygen and reactive nitrogen species (RONS) in the liquid. To be an effective hospital decontamination tool, CAPP must also inactivate bacteria within biofilms. Multi-cellular, biofilm structures confer a higher resistance to disinfectants than singular, planktonic bacteria. Here we aimed to assess the microbial inactivation by CAPP and to examine the possible mechanisms of the antimicrobial action of CAPP treated phosphate buffered saline (PBS) against bacteria in bacterial biofilms.

Materials/methods: PBS was treated with CAPP for 300 seconds to generate PAL. PAL was then evaluated for levels of RONS using colorimetric assays. Planktonic *Staphylococcus aureus* (*S. aureus*) and *Escherichia coli* (*E. coli*) were incubated with PAL and viability was assessed using colony forming unit (CFU) assays. *S. aureus* and *E. coli* biofilms were grown for 48 hours and inoculated with PAL. Biofilm viability was assessed using metabolic assays. Damage throughout the biofilm structure was assessed via imaging using LIVE/DEAD staining and confocal microscopy.

Results: RONS levels were greatly increased in PAL compared to untreated PBS. A seven-log reduction in CFU was achieved in planktonic *S. aureus* and *E. coli* after incubation with PAL. *S. aureus* and *E. coli* biofilm viability decreased by 48% and 64%, respectively, after PAL treatment. Confocal microscopy showed membrane damage in treated bacterial cells throughout the biofilm structure. The bacterial inactivation in treated biofilms could be, in part, due to the RONS present in PAL.

Conclusions: CAPP treated PBS results in PAL that has antimicrobial and anti-biofilm activity, probably mediated in part by RONS. Further research is required to confirm these finding with other pathogens and under different conditions to conform the potential of PAL as an effective decontaminant.

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Abstract 1313

Aztreonam-avibactam activity against carbapenemase-producing *Enterobacter*ales collected in Europe, Asia and Latin America (2017-2019)

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Abstract third-party references: This study was performed by JMI Laboratories and supported by Pfizer, Inc., which included funding for services related to preparing this abstract.

Background: Aztreonam-avibactam (ATM-AVI) is under clinical development for treatment of serious infections caused by Gram-negative bacteria and has demonstrated potent activity against *Enterobacterales* producing all types of clinically relevant β-lactamases, including metallo-β-lactamases (MBL). We evaluated ATM-AVI activity against a worldwide collection of carbapenemase-producing *Enterobacterales* (CPE).

Materials/methods: A total of 748 clinical CPE isolates were collected in Europe (n=504; 27 centres in 15 nations), Latin America (LATAM; n=152; 7 centres in 4 nations), and Asia-Pacific region (APAC; n=92; 8 centres in 7 nations) in 2017-2019. All isolates were tested for susceptibility against ATM-AVI and comparators by reference broth microdilution method and submitted to whole genome sequencing analysis for identification of β-lactamase genes.

Results: The collection included 636 *Klebsiella pneumoniae*, 51 *Enterobacter cloacae*, 20 *Escherichia coli* and 41 isolates of other species. The most common MBL (n=219) was NDM-type (193; 88.1% of MBLs) and the most common OXA-type (n=234) was OXA-48 (188; 80.3% of OXA-type). Among KPC-producers (n=294), KPC-2 and KPC-3 represented 51.7% and 48.3%, respectively. ATM-AVI was very active against the entire collection of isolates with overall $MIC_{50/90}$ values of 0.25/0.5 mg/L and 99.3% of isolates inhibited at ≤4 mg/L (Table). Isolates with ATM-AVI MIC >4 mg/L demonstrated additional resistance mechanisms, including PBP3 alterations. Among comparators, the most active agents overall were tigecycline ($MIC_{50/90}$, 1/2 mg/L; 92.6% susceptible [S] at ≤2 mg/L) and colistin ($MIC_{50/90}$, 0.12/>8 mg/L; 77.5%S at ≤2 mg/L). ATM-AVI ($MIC_{50/90}$, 0.12/0.5 mg/L; 98.6% inhibited at ≤4 mg/L), tigecycline ($MIC_{50/90}$, 1/2 mg/L; 92.7%S at ≤2 mg/L), and colistin ($MIC_{50/90}$, 0.12/>8 mg/L; 79.4%S at ≤2 mg/L) were the most active compounds against MBL-producers. When tested against KPC-producers and OXA-producers, ATM-AVI (100.0% and 99.1% inhibited at ≤4 mg/L, respectively) and ceftazidime-avibactam ($MIC_{50/90}$, 1/2 mg/L and 100.0%S for both subsets) were the most active agents.

Conclusions: ATM-AVI displayed potent activity against MBL-, KPC-, and OXA-producing *Enterobacterales* from Europe, LATAM, and APAC, inhibiting >99% of isolates at ≤4 mg/L. Our results support further clinical development of ATM-AVI for treatment of infections caused by CPE, including MBL-producing isolates.

Carbapenemase subset (no.)	No. of isolates (cumulative %) inhibited at ATM-AVI MIC (mg/L) of:									
	≤0.03	0.06	0.12	0.25	0.5	1	2	4	8	16
MBL-producers (219)	30 (13.7)	31 (27.8)	60 (55.2)	64 (84.5)	23 (95.0)	3 (96.3)	4 (98.2)	1 (98.6)	3 (100.0)	
KPC-Producers (294)	14 (4.8)	27 (13.9)	59 (34.0)	127 (77.2)	57 (96.6)	7 (99.0)	3 (100.0)			
OXA-producers (234)	6 (2.6)	14 (8.5)	49 (29.5)	119 (80.3)	39 (97.0)	5 (99.1)	0 (99.1)	0 (99.1)	1 (99.6)	1 (100.0)
All (748)[a]	50 (6.7)	72 (16.3)	169 (38.9)	310 (80.3)	119 (96.3)	15 (98.3)	7 (99.2)	1 (99.3)	4 (99.9)	1 (100.0)

[a]. Includes an IMI-producing *E. cloacae* with ATM-AVI MIC of 0.12 mg/L.

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Abstract 1315

Resistance to extended-spectrum β-lactams, aminoglycosides and quinolones in multidrug-resistance *Enterobacter*ales isolated in patients receiving an allogeneic haematopoietic stem cell transplantation: the ENTHERE-SCT Study. PI16/01415

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Background: To analyze the mechanisms of resistance to extended-spectrum β-lactams, aminoglycosides and quinolones in MDRE isolated between June 2017 and August 2019 in 44 patients of the 127 recruited in the study, who receiving an Allo-SCT in four Spanish hospitals.

Materials/methods: Overall, 117 MDRE, (AmpC-hyperproducing and/or producers of extended-spectrum β-lactamases (ESBLs) or carbapenemases), isolated in rectal swabs (pretransplant, weekly during the first month post-transplant, biweekly up to 100 days post-transplant and monthly up to 180 days post-transplantation) and 8 MDRE isolated from different clinical samples, were studied.

The minimum inhibitory concentrations (MICs) of 24 antibiotics were determined by broth-microdilution (EUCAST breakpoints). PCR was performed for ESBLs (SHV, TEM, CTX-M), plasmid-mediated AmpC β-lactamases, carbapenemases (KPC, IMP, VIM, NDM, GES, OXA-48), plasmid-mediated quinolone-resistance (PMQR) (*qnrA, qnrB, qnrC, qnrD, qnrS, qepA, oqxAB*) and aminoglycoside-modifying-enzymes (AMEs)(*aac(3)-Ia, aac(3)-IIa, aac(6´)-Ib, ant(2")-Ia, aph(3´)-Ia, aph(3´)-IIa*). Clonal relatedness was assessed by REP-PCR and pulsed-field gel electrophoresis (PFGE).

Results: The microorganisms isolated were: *E.coli* 52 (41.6%), *Enterobacter* spp. 36 (28.8%), *K.pneumoniae* 16 (12.8%), *Citrobacter* spp. 13 (10.4%) and others species 8 (6.4%) (5 *K.oxytoca*, 1 *H.alvei*, 1 *K.intermedia*, 1 *S marcescens*). PFGE analysis identified 19 clonal patterns in *E.coli*, 9 in *E.cloacae*, 5 in *K.pneumoniae* and 3 in *C.freundii*. The antimicrobial susceptibility, corresponding 74 MDRE (one isolate per REP-PCR pattern/antibiogram and patient) are shown in Table 1.

In seven patients MDRE were detected in clinical samples, in all but one patient, the same MDRE was detected in different rectal swabs days on the follow-up. ESBLs were detected in 60.8% and CTX-M was (47.3%) the most prevalent, 29.7% isolates were AmpC-hyperproducers. Carbapenemases were detected in 8 (10.8%) isolates: VIM (2 *E.cloacae*, one *S.marcescens* and *K.intermedia*), GES (2 *K.oxytoca* and one *E.cloacae*) and IMP (*E.aerogenes*). AME-genes were detected in 45.9%, being *aac(6´)-Ib* the most prevalent (85.3%), 50.0% of strains harboured two AME-genes. PMQR-genes were detected in 35/60 (58.3%) isolates quinolone-resistant and *qnrB* was the most prevalent (51.4%).

Conclusions: In 6 of the 44 transplant patients who were colonized by MDRE, an infection by the same microorganism was documented. *E. coli* producing CTX-M was the MDRE most prevalent followed by *Enterobacter* spp. AmpC-hyperproducer.

Table 1. In vitro activity to 24 antibiotics in 74 multidrug-resistance *Enterobacterales* (MDRE) isolated from patients with Allo-SCT transplant.

Antimicrobial agent	MIC_{50}	MIC_{90}	% Resistant
Amoxicillin	> 256	> 256	100.0
Amoxicillin-Clavulanic acid	256	> 256	82.4
Piperacillin	256	> 256	89.2
Piperacillin-Tazobactam	32	> 256	54.1
Cefoxitin[a]	32	> 256	59.5
Cefotaxime	128	> 256	93.2
Ceftazidime	32	256	79.7
Cefepime	8	> 256	51.4
Aztreonam	32	256	67.6
Imipenem	≤0.125	4	5.4
Meropenem	≤0.125	0.5	1.4
Ertapenem	≤0.125	4	19.0
Gentamicin	0.5	32	17.6
Tobramycin	1	32	29.7
Amikacin	1	8	1.4
Netilmicin	0.5	16	17.6
Arbekacin	0.5	2	NA
Nalidixic acid	64	> 256	NA
Ciprofloxacin	2	> 256	60.8
Levofloxacin	2	32	55.4
Trimethoprim-Sulfamethoxazole	256	> 256	78.3
Tigecycline	0.5	4	36.5
Fosfomycin	8	256	25.7
Colistin	≤0.125	32	23.0

[a] for cefoxitin using ECOFF for EUCAST.
NA. Not available (breakpoints have not been established for EUCAST)

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Abstract 1316

Antimicrobial activity of aztreonam-avibactam and comparator agents when tested against a large collection of contemporary *Stenotrophomonas maltophilia* isolates collected from medical centres worldwide

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Abstract third-party references: This study was performed by JMI Laboratories and supported by Pfizer, Inc., which included funding for services related to preparing this abstract.

Background: *Stenotrophomonas maltophilia* represents a major cause of hospital-acquired pneumonia (HAP) and bloodstream infections (BSI). There are very limited therapeutic options to treat *S. maltophilia* infections due to intrinsic production of metallo-β-lactamases (MBL) by these organisms. Aztreonam-avibactam (ATM-AVI) is under clinical development for treatment of serious infections caused by Gram-negative bacteria, including MBL-producers.

Materials/methods: A total of 1,839 isolates were collected in Western Europe (W-EU; n=388; 24 centres in 9 nations), Eastern Europe (E-EU; n=156; 15 centres in 12 nations); North America (NA; n=1,095; 77 centres), Latin America (LATAM; n=92; 12 centres in 9 nations), and Asia-Pacific region (APAC; n=108; 17 centres in 8 nations) in 2016-2019. The isolates were mostly from HAP (70.4%) and BSI (12.6%). Susceptibility testing was performed by reference broth microdilution method at a central laboratory and CLSI breakpoints were applied when available.

Results: ATM-AVI was very active against isolates from all geographic regions and infection types ($MIC_{50/90}$, 2-4/4 mg/L), inhibiting 90.7-96.7% of isolates at ≤4 mg/L (92.1% overall) and 96.3-100.0% at ≤8 mg/L (97.8% overall), which are the current CLSI susceptible (S) and intermediate breakpoints, respectively, for ATM alone (Table). Trimethoprim-sulfamethoxazole (TMP-SMX; $MIC_{50/90}$, ≤0.5-1/1 mg/L) and minocycline ($MIC_{50/90}$, 0.5/1-2 mg/L) were active against 93.5-96.9% and 99.0-100.0% of isolates at the respective, current CLSI susceptible breakpoints. Moreover, 74.1%/84.7% of TMP-SMX-non-susceptible isolates were inhibited at ≤4/≤8 mg/L of ATM-AVI. Levofloxacin ($MIC_{50/90}$, 1/4->4 mg/L) was active against 74.0-87.0% of isolates at the current CLSI breakpoint (≤2 mg/L). Ceftazidime ($MIC_{50/90}$, >32/>32 mg/L; 16.7-30.4%S at ≤8 mg/L) and colistin ($MIC_{50/90}$, 4-8/>8 mg/L; 29.3-42.9% inhibited at ≤2 mg/L) exhibited limited activity, whereas tigecycline ($MIC_{50/90}$, 1/2-4 mg/L) inhibited 82.7-90.7% (85.0% overall) of isolates at ≤2 mg/L. Ceftolozane-tazobactam, meropenem, imipenem, amikacin, and tobramycin exhibited very limited activity against these organisms.

Conclusions: ATM-AVI demonstrated potent *in vitro* activity against a large collection of *S. maltophilia* isolated from patients with HAP, BSI, and other systemic infections. ATM-AVI may represent a valuable option to treat *S. maltophilia* infections, addressing a major unmet medical need.

Region (no. isolates)	% susceptible per CLSI criteria				
	ATM-AVI[a]	TMP-SMX	Minocycline	Levofloxacin	Ceftazidime
W-EU (388)	91.2 / 96.6	96.9	100.0	84.3	17.3
E-EU (156)	93.6 / 98.7	93.5	100.0	78.8	16.7
NA (1,095)	92.0 / 98.1	95.0	99.2	74.0	22.0
LATAM (92)	96.7 / 100.0	96.7	100.0	88.0	30.4
APAC (108)	90.7 / 96.3	95.3	99.0	87.0	21.3
All (1,839)	92.1 / 97.8	95.4	99.5	78.0	20.9
[a] % inhibited at ≤4 / ≤8 mg/L for comparison purpose.					

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Abstract 1317

Rapid detection of fungal feet infection by LED-UV light

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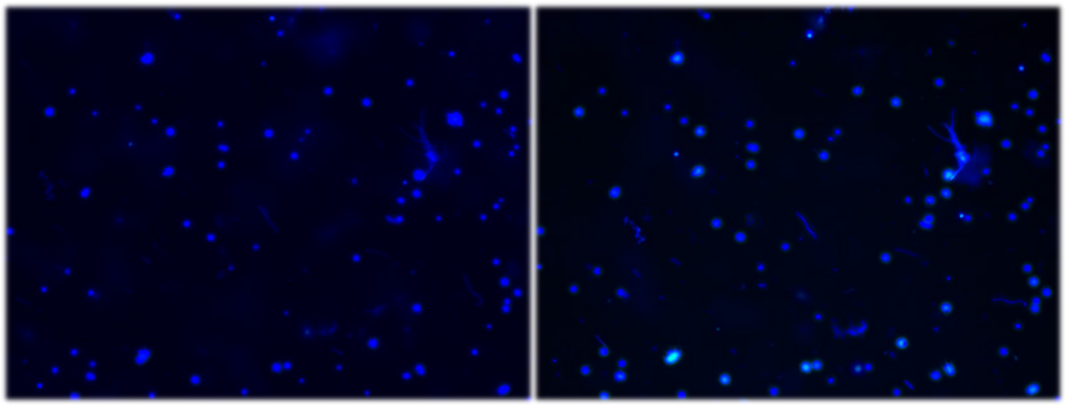
Background: Fungal feet infections are usually torpid diseases whose specific diagnostic is compulsory as similar clinical entities are treated with steroids that can worsen the mycotic infection. To avoid inaccurate therapies, a fast and accurate detection of fungi is needed. Potassium hydroxide (KOH) treatment of samples is used for clarifying specimens (rich in keratin), before examination by bright light microscopy but it requires skilled observers. Fluorescent brighteners absorbing UV light and emitting blue light, with affinities for polysaccharides with β-links, have been used to facilitate observation. Our group uses for this purpose Leucophor®, a disulphonated stilbene brightener along with KOH treatment. Based on the report of Denny G et al referent to hand held UV illumination, we aimed to evaluate an alternative easy to use, none-expensive method to fasten the time elapsed between the clinical suspicion and the confirmation of the presence of a fungal infection. We examined patients with clinical suspicion of mycotic infection as well as nail or skin samples, by means of a hand held LED UV, comparing it with the visualization by a fluorescence microscopy.

Materials/methods: 40 patients with clinical suspicion of fungal feet infection and 40 healthy individuals were analyzed *in vivo* by both methods. Their collected specimens were KOH digested, Leucophor® stained and examined in a fluorescence microscopy (Nikon E800). After switching the UV source off, they were observed under tangential illumination from a hand-held LED UV Flashlight (HAN-WY6975*4) at 395 nm. Also a 1418 90X Phone LED UV Light Magnifier 90 x and 60 X adapted to a Smart Phone Huawei with a Leica Camera was used. Culture in appropriate media was performed in all cases. Moreover, a series of 30 nails and scrapings of our collection were examined and imaged (15 positive: *Aspergillus sp.*, *Trichophyton rubrum*, *Scopulariopsis sp*.and 15 culture negative).

Results: Even that the brightness of the conidia and hyphae using the hand-held LED UV Flashlight diminished slightly, it appears still clear permitting an accurate diagnosis of the presence of fungi.



Hand held LED UV

Nikon Ellipse 800

Conclusions: The use of low cost devices seems feasible for detection of fluorescence from samples containing fungi with reasonable resolution.

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Abstract 1319

MYCOPLASMA IST3, a new *in vitro* medical device to aid the diagnosis of urogenital mycoplasma infection: performance results from an international multi-centre trial

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Background: *Mycoplasma hominis* (Mh) and *Ureaplasma* spp (Uspp) are possible pathogens associated with urogenital infections. This study assessed performance of MYCOPLASMA IST3, a new *in vitro* diagnostic test designed to detect, identify, enumerate and test the susceptibility of Mh and/or Uspp to relevant agents (Levofloxacin, Moxifloxacin, Tetracycline, Erythromycin, Telithromycin and Clindamycin).

Materials/methods: 516 vaginal/cervical or urethral swabs, semen and urines were included. For detection/identification, performance was expressed as the positive (PPA) and negative agreements (NPA) between MYCOPLASMA IST3 and sample status defined using A7 agar and PCR. For indicative enumeration, performance was expressed as the agreement between MYCOPLASMA IST3 and A7 agar results. For Antimicrobial Susceptibility Testing (AST) application, Category Agreement (CA, %) Major Error rate (ME, %) and Very Major Error counts (VME, #) were calculated comparing MYCOPLASMA IST3 category (S or R) to Broth Micro Dilution Minimum Inhibitory Concentration (MIC) results interpreted using CLSI M43-A interpretive breakpoints.

Results: 312 samples were negative, 109 grew viable Uspp, 73 grew Mh and 22 grew both, 38% of the positive samples were contrived (spiked) samples. Regarding the detection/identification application, MYCOPLASMA IST3 had a PPA of 98.5% (129/131) and 92.6% (88/95) and a NPA of 99.7% (384/385) and 99.0% (410/414) with A7 agar for Uspp and Mh, respectively. Among the 22 mixed samples, MYCOPLASMA IST3 recovered both species for 18 samples while only the Uspp was recovered for the remaining samples. Indicative enumeration results were in agreement between MYCOPLASMA IST3 and A7 agar in 84.6% (99/117) and 83.7% (72/86) of the cases for Uspp and Mh, respectively. MYCOPLASMA IST3 AST application produced CA ranging from 96.0% to 100.0% and ME rates from 0.0% to 4.2% (Table). Three VMEs were observed (1 Uspp with tetracycline, 1 Mh with tetracycline, 1 Mh with Moxifloxacin), 2 of them originated from isolates with MIC within ± 1 doubling dilution from the CLSI breakpoint value.

Conclusions: MYCOPLASMA IST3 is an accurate aid in the diagnosis of urogenital infections related to Uspp or Mh, providing clinicians with valuable information to guide treatment.

Table: MYCOPLASMA IST3 Antimicrobial Susceptibility Testing performance.

	Isolates status (BMD)			Performance index		
***Ureaplasma* spp**	Total	# S	# R	CA (%)	ME (%)	VME (#)
Levofloxacin	124	120	4	96.0% (119/124)	4.2% (5/120)	0
Moxifloxacin	124	123	1	98.4% (122/124)	1.6% (2/123)	0
Tetracycline	124	120	4	97.6% (121/124)	1.7% (2/120)	1
Erythromycin	124	120	4	99.2% (123/124)	0.8% (1/120)	0
Telithromycin	125	122	3	99.2% (124/125)	0.8% (1/122)	0
All drugs combined	621	605	16	98.1% (609/621)	1.8% (11/605)	1
Mycoplasma hominis	Total	# S	# R	CA (%)	ME (%)	VME (#)
Levofloxacin	84	82	2	98.8% (83/84)	1.2% (1/82)	0
Moxifloxacin	84	81	3	97.6% (82/84)	1.2% (1/81)	1
Tetracycline	84	65	19	97.6% (82/84)	1.5% (1/65)	1
Clindamycin	84	84	0	100.0% (84/84)	0.0% (0/84)	N/A
All drugs combined	336	312	24	98.5% (331/336)	1.0% (3/312)	2
All drugs and species combined	957	917	40	98.2% (940/957)	1.5% (14/917)	3

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Abstract 1321

Comparison of the distribution of quinolone resistance markers in *Escherichia coli* in a human-animal health interface model

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Background: Quinolone action is the inhibition of DNA gyrase and topoisomerase IV DNA enzymes. However, two types of resistance are detected for these antibiotics: chromosome (modifications in gyrases and overexpresión of efflux pumps) and PMQR (production of qnr proteins, acetylases, and efflux pumps). The aim is to know the distribution of quinolone resistance genetic markers in *E. coli* obtained from humans and porcine in a close model.

Materials/methods: Total of 1,407 *E. coli* isolates (982 from pigs and 425 from humans with diarrhoea) were obtained from a farm located in Morelos, Mexico (June 2015- April 2016). MIC was obtained for CIP and NAL. Phylogroup according to Clermont system and the genes gyrA and PMQRs were amplified by PCR. The plasmid was performed according to Kieser.

Results: Three different phenotype were identified: I (NALr/CIPr), II (NALr/CIPs), and III (NALs/CIPs); the most frequent in both population porcine (PEI) and human (HEI), was phenotype II, (PEI 56.3%); HEI 50.1%). A representative sample of isolates was selected: 47/425 PEI, and 100/982 HEI. The major phylogroup was A (PEI 56%, HEI 44.6%), follow by B1 (PEI 31%, HEI 17%), D (PEI 11%, HEI 25.5%) and B2 phylogroup (PEI 2%, HEI 12.8%). QRDR region of gyrA gene was wild type (HEI 57.4%, PEI 54%) follow by S83L (HEI 14.9%, PEI 19%) and S83L/D87N (HEI 19.1%, PEI 18%) mutations. The major PMQR was qnrB in PEI (43%) and HEI (23.4%). Additionally, 39% of PEI and 59.6% of HEI, no qnr genes were identified. OqxA/OqxB, qepA and aac(6´)-Ib-cr were detected at low frequency (<7%). The phylogenetic tree shows three clades: 1) phenotype I/S83L/D87N, 2) phenotype II/S83L, and 3) phenotype II and III/wild QRDR region and qnrB. A plasmid of 150 to 160 kb was identified in most of the isolates

Conclusions: No difference of qnrB was identified in both groups of *E. coli*. Eflux pumps and acetylation enzyme are more frequent in PEI than in HEI. A 150-160 kb plasmid was detected in most of the isolates. Further studies will be conducted to know the structure of the plasmids.

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Abstract 1322

Resistance mechanisms associated with pleuromutilins among Gram-positive clinical isolates from the worldwide surveillance programme for lefamulin in 2018

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Abstract third-party references: This study was performed by JMI Laboratories and supported by Nabriva Therapeutics, which included funding for services related to preparing this abstract.

Background: Lefamulin is a first-in-class, semi-synthetic pleuromutilin antibiotic that inhibits bacterial protein synthesis via a unique mechanism of action was approved by the United States Food and Drug Administration (FDA) in 2019 for the treatment of community-acquired bacterial pneumonia (CABP) in adults. This study characterized the resistance mechanisms associated with elevated lefamulin MICs in a global surveillance isolate collection from 2018.

Materials/methods: A total of 4,406 *S. aureus*, coagulase-negative staphylococci (CoNS), *S. pneumoniae* and β-haemolytic and viridans group streptococci were tested using reference broth microdilution. A total of 36 (0.8%) isolates met the criteria based on FDA breakpoints or MICs above the normal wildtype distribution. Bacterial genomes were sequenced (MiSeq Sequencer, Illumina) and screened *in silico* for possible lefamulin resistance genes and mutations in the 23S rRNA, L3, L4 and L22.

Results: 8 of 1,607 (0.5%) *S. aureus* harboured *vga*(A) (6/8; lefamulin MIC, 1–8 mg/L) or *lsa*(E) (2/8; lefamulin MIC, >32 mg/L). 20 of 270 (6.7%) CoNS carried either *vga* gene variants (18/20; lefamulin MIC, 2–>32 mg/L) or showed G2576T alterations in the 23S rRNA along L3 mutations at H146 and M156 or at position V154 (2/20; lefamulin MIC of 0.5 mg/L). Only 2 of 1,866 (0.1%) *S. pneumoniae* were non-susceptible to lefamulin (MIC, 1–2 mg/L); both isolates had mutations in ribosomal proteins (L4 or in L3 and L22). Among other streptococci, 3 of 522 (0.5%) β-haemolytic and 2 of 141 (1.4%) viridans group streptococci carried *lsa*(E) (lefamulin MIC, 2–32 mg/L), while one *S. oralis* (lefamulin MIC, 1 mg/L) did not show any resistance mechanisms. Other plasmid-mediated genes, such as *cfr* were not detected.

Conclusions: Gram-positive isolates from a global collection causing human infections exhibiting elevated lefamulin MICs are rare. The most common resistance mechanisms identified were *vga* and *lsa*(E); *cfr* was not detected. Longitudinal surveillance studies will monitor the stability of the *in vitro* activity of lefamulin.

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Abstract 1329

Efficacy of bacteriophage-antibiotic combinations on two different phenotypes of methicillin-resistant *Staphylococcus aureus*

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Background: The widespread use of antibiotics has generated selective pressures that have driven the emergence of multi-drug resistant strains. The antimicrobial of choice for invasive methicillin-resistant *Staphylococcus aureus* (MRSA) infections has been vancomycin; however, treatment failures have continued to be reported secondary to poor drug performance or the development of various resistant phenotypes. Bacteriophages (phages) have been suggested as a potential adjunctive/alternative therapy. These phages exhibit bactericidal activity by infecting bacterial cells, redirecting the cellular machinery to produce progeny virions and killing the bacterial cell upon lysis and release of those progeny phages. *Staphylococcus aureus* naturally releases extracellular vesicles (EVs) during growth, which are known to play important functions in bacteria-bacteria interactions and potentially transferring antibiotic resistance genes. Unfortunately, there is limited data on the use of phage-antibiotic combinations and bacterial response to these. The objective of this study was to test the in-vitro activity of various standard of care (SOC) antibiotics with phages and their effects on EVs formation.

Materials/methods: Phage-antibiotic exposure was tested on two different phenotypes of MRSA, isolates MW2 (daptomycin non-susceptible) and D712 (vancomycin intermediate resistant *S. aureus*). Phage, bacterial counts and EVs formations were performed during time-kill analysis (TKA) experiments. MRSA isolates were examined against an array of antibiotics alone (daptomycin, vancomycin, ceftaroline and cefazolin) and in combination with phages. Bacteriophage Sb-1 was used for experiments at ff10^5 PFU/ml. Bactericidal activity was defined as a $\geq$3 $\log_{10}$ CFU/ml reduction from baseline. Synergy between two agents was defined as a $\geq$2 $\log_{10}$ CFU/ml reduction at 24 hours compared to either agent alone.

Results: *In vitro* 24-hour TKA experiments demonstrated bactericidal activity with phage-antibiotic combinations. While addition of ceftaroline or cefazolin to vancomycin or daptomycin was synergistic, both daptomycin-phage and vancomycin-phage combinations resulted in bactericidal activity against the D712 strain. In addition, emergence of EVs in presence of phages was suppressed in antibiotic-phage combination regimens for both MRSA isolates.

Conclusions: The combination of antibiotic-phages showed promising results against MRSA. If shown to be reproducible *in vivo*, this phenomenon would be valuable in the treatment of clinical cases that are treatment refractory or have failed SOC antibiotics.

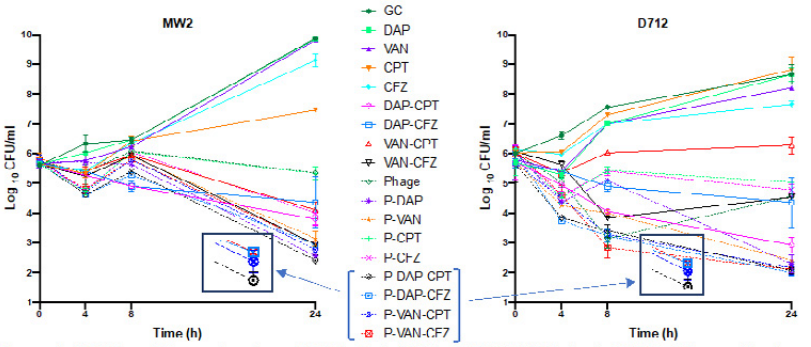

Figure 1. 24 h time kill experiments vs. MRSA strain MW2 and DNS-VISA strain D712. Triple combinations are highlighted; however, even combinations of VAN-phage or DAP-phage were synergistic. Legend: Vancomycin (VAN), Daptomycin (DAP), Ceftaroline (CPT), Cefazolin (CFZ).

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Abstract 1330

Vaccination Perception (VP) and Vaccination Coverage (VC) among healthcare students (HCS), a prospective French study : PERCEVAC Study

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Background: Vaccine hesitancy has been increasing and spreading throughout the world. However data are scarce regarding HCS. The aim of this study was to determine VC and VP among HCS

Materials/methods: A self-reporting electronic questionnaire, related to VP and VC, was prospectively sent to HCS (physicians, nurse, pharmacist, midwifes, physiotherapist students and 1st year of health sciences students (PACES)) of Normandy University (France) between 18/03/2019 and 8/04/2019. Global VC was defined as being vaccinated for french mandatory and recommended vaccines. VP was evaluated through various binary questions and numeric scales.

Results: Out of a population of 4546 HCS, 542 took part in this survey (12%, mean age 22.3 year, female 79%).

	VC All students n=542	VC physicians n=284	VC nurses n=86	VC physiotherapists n=14	VC pharmacists n=31	VC midwife n=10	VC PACES n=117	p (compared to physicians)
DTP*	94%	95%	94%	93%	97%	100%	87%	0.08
Pertussis**	88%	92%	90%	71%	90%	80%	81%	**0.03**
HBV***	89%	96%	95%	100%	87%	90%	62%	**<0.001**
HPV**	64%	66%	63%	73%	68%	50%	60%	0.85
MMR**	95%	96%	94%	79%	100%	90%	93%	0.2
Meningococcus C**	62%	61.2%	67%	50%	84%	70%	54%	**0.03**
Global VC	40%	44%	45%	36%	52%	40%	26%	**0.01**

*mandatory, **recommended, *** mandatory in HCS

On multivariate analysis only being a PACES student is associated with a lower global VC (OR 1.9 [1.2-3.3] p=0.04).

Regarding VP, 98% of HCS think that vaccine are effective. On a 0-10 scale, 91% think that vaccine safety is ≥ 7 and 80% have vaccine hesitancy < 3, the benefit/risk balance is judged as always positive in 66%. 81% of HCS follow French recommendations. Not recommended vaccines are against *Haemophilus influenza b* (69%), HPV (63%), Influenza (71%), zona (82%) and meningococcus (46.4%). 92% agree with the recent french law increasing the mandatory vaccines for infants, and 62% with a flu mandatory vaccination for healthcare workers.

Conclusions: Despite the good VP, less than half HCS are well vaccinated. Some vaccines are not considered useful nor indicated. Information regarding these vaccines should be done with a focus on PACES students.

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Abstract 1331

Comparative *in vitro* activity of cefepime-enmetazobactam and other agents against 3rd-generation cephalosporin-resistant and extended-spectrum β-lactamase-producing clinical isolates of *Enterobacterales* collected between 2016-2018

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Background: Third generation cephalosporin (3GC)-resistant *Enterobacterales* are WHO critical priority pathogens in need of development of new agents. Enmetazobactam is a novel β-lactamase inhibitor targeting extended-spectrum β-lactamases (ESBL), the main resistance determinants in 3GC-resistant *Enterobacterales*. This study examined the *in vitro* activity of enmetazobactam combined with cefepime against clinical isolates of *Enterobacterales* collected between 2016-2018, including those resistant to 3GC or producing ESBL.

Materials/methods: µµClinical isolates of *Enterobacterales* (n=7168) were collected from the US and Europe maintaining a proportion of clinically prevalent pathogens causing serious infections. Organisms were identified by MALDI-TOF mass spectrometry, and β-lactamase genotypes determined by multiplex PCR and sequencing for isolates with a ceftazidime or ceftriaxone MIC ≥ 1 mg/l. MIC and susceptibility were determined according to CLSI guidelines.

Results: Resistance to 3GC was 19.8% amongst the *Enterobacterales* collected, with 54.9% of those isolates expressing an ESBL with or without an AmpC and/or an OXA β-lactamase. The addition of enmetazobactam (fixed at 8 mg/l) to cefepime reduced the MIC_{90} >32-fold relative to cefepime alone against the *Enterobacterales* groups (table). Cefepime-enmetazobactam activity was comparable to meropenem against 3GC-resistant and ESBL-producing isolates and outperformed piperacillin-tazobactam and ceftolozane-tazobactam.

Conclusions: Cefepime-enmetazobactam may prove to be an important carbapenem-sparing therapy for serious infections caused by 3GC-resistant, ESBL-producing *Enterobacterales*.

Antibacterial agent	*Enterobacterales* group (n)							
	All (7168)		3GC-Resistant (1416)		ESBL co-producing (801)[1]		ESBL only (722)	
	MIC_{90} (mg/l)	% Susceptible	MIC_{90} (mg/l)	% Susceptible	MIC_{90} (mg/l)	% Susceptible	MIC_{90} (mg/l)	% Susceptible
Ceftazidime	32	82.9	>64	14.9	>64	19.0	>64	20.1
Cefepime[2]	16	87.0/89.9	>64	35.5/48.8	>64	12.0/26.1	>64	11.9/26.5
Cefepime-enmetazobactam[8][3]	0.25	*(98.3/98.8)*	2	*(91.7/94.1)*	0.5	*(98.9/99.9)*	0.25	*(99.2/99.9)*
Piperacillin-tazobactam	32	87.4	>256	51.3	256	71.4	128	75.1
Meropenem	0.06	97.6	4	88.4	0.12	96.0	0.06	98.8
Ceftazidime-avibactam	0.25	99.6	1	97.7	0.5	100	0.5	100
Ceftolozane-tazobactam	1	92.7	64	63.6	16	82.1	4	87.0

[1]ESBL group co-producing AmpC and/or OXA β-lactamases

[2]Cefepime susceptibility using CLSI breakpoints for susceptible (S; ≤2 mg/l)/susceptible, dose dependent (SDD; ≤8 mg/l).

[3]Breakpoints for cefepime-enmetazobactam have not been established. Values in *(italics)* represent the percent susceptibilities using cefepime CLSI breakpoints for S (≤2 mg/l)/SDD (≤8 mg/l).

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Abstract 1334

Administration of ceftazidime to patients undergoing haemodialysis: are trough levels consistently above the EUCAST breakpoints for *Enterobacter*ales and Pseudomonas ?

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Background: Patients undergoing haemodialysis should receive reduced ceftazidime doses. Based on a 6-patients study, a 1g interdialytic dose was considered sufficient to act on most frequent pathogens (Antimicrob Agents Chemother. 2013;57:5854-9). Beta-lactams serum levels, however, are highly variable (Crit Care 2011;15:R137) while optimal PK/PD targets for beta-lactams are still under discussion (Expert Rev Anti Infect Ther. 2017;15:677-688). Our aim was to measure actual ceftazidime trough serum concentrations in a larger cohort of haemodialysis patients to determine whether these would reach the current EUCAST ceftazidime R breakpoints for *P. aeruginosa* and Enterobacterales.

Materials/methods: Enrolment: 30 patients on long-term haemodialysis (3 times a week) suffering from infections justifying ceftazidime administration. Dosing: ceftazidime 1st dose: 2g, followed by 1g after each dialysis session. Sampling: serum obtained at approx. 44 or 68h after each administration, and after 1st and 4th dialysis session. Assay: validated HPLC-UV and UPLC-MS-MS. Calculations: since only trough levels were recorded, no pharmacokinetic model could be developed and data were used to fit (visual inspection and iterative optimization) a one-compartment decay model (k_e=0.032 h^{-1}; clearance 7.4 mL/min [non-renal clearance of ceftazidime]) to calculate values at two fixed standard post-administration times (44 and 68h).

Results: The Table shows the ceftazidime concentrations reached at 44 and 68h for each of the 4 successive administrations, and the number of evaluable patients for whom these concentrations were ≥ 8 or 4 mg/L. Levels were highly variable with significant correlation (simple and multivariate analysis) only demonstrable (i) with maintenance or not of a residual renal function and (ii) for 2d, 3d and 4th post-administration levels, with the 1st post-administration actual trough levels (multiple linear regression), suggesting larger inter-subject than within-subject variability. No correlation was seen with CRP, WBC, positive haemoculture, or clinical outcome of the infection. Ceftazidime concentration decrease by haemodialysis was 82.7±9.3%.

Conclusions: 2g of ceftazidime and post-administration times ≤44h are necessary to ensure > 73% of patients to have trough concentrations above the ceftazidime *Pseudomonas* R breakpoint. 1 g dosing and/or lengthening the post-administration time up to 68h will only ensure the same proportion of patients to show through concentrations up to 4 mg/L.

Time (h) [a]		Mean total ceftazidime concentration (mg/L ± SD) in evaluable patients [b]			
		administration			
		1st (2g)	2d (1g)	3d (1g)	4th (1g)
44		26.9±14.4 A,a (n=27)	16.8±10.3 B,a (n=29)	16.8±12.0 B,a (n=26)	14.8±7.86 B,a (n=25)
68		12.5±6.68 A,b (n=27)	7.81±4.76 B,b (n=29)	7.79±5.59 B,b (n=26)	6.86±3.65 B,b (n=25)
Threshold	Time (h)	Number of patients with concentration above threshold at 44h or 68h / total number of evaluable patients			
> 8 [c]	44	24/27 A,a (88.8%)	23/29 B,a (79.3%)	19/26 B,a (73.1%)	19/25 B,a (76.0%)
	68	19/27 A,a (70.3%)	13/29 B,b (44.8%)	8/26 B,b (30.7%)	10/25 B,b (40.0%)
> 4 [c]	44	25/27 A,a (92.6%)	27/29 A,a (93.1%)	24/26 A,a (92.3%)	23/25 A,a (92.0%)
	68	24/27 A,a (88.8%)	22/29 A,a (75.8%)	19/26 A,a (73.1%)	19/25 A,a (76.0%)

[a] h after the end of ceftazidime infusion (and corresponding to the time of starting the dialysis session).

[b] total concentrations (free concentrations are 83.9±20.4% (95%CI 79.2 to 86.6) of the corresponding total concentrations)

[c] R EUCAST breakpoint (mg/L) for *Pseudomonas* and Enterobacterales, respectively

Statistical analyses: entries with different letters are significantly different from each other ($p<0.05$) for (i) comparisons across each row [horizontal]: upper case letters [A or B]; (ii) for comparisons across each column [vertical]: lower case letters [a,b,...]). For concentrations: (i) comparison across each row: ANOVA with Tukey-Kramer Multiple Comparisons Test; (ii) comparison across each column: unpaired t-test. For number of patients: contingency tables (i) across each row: Chi square for all 4 entries (4x2 table) followed by Fisher exact test for successive comparisons between 2 entries (2x2 table); (ii) across each columns but limited to pairs of entries corresponding to the same threshold (44 or 68h; 2x2 table): Fisher exact test.

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Abstract 1335

Human dirofilariasis in a changing world, evolving zoonosis just under the skin

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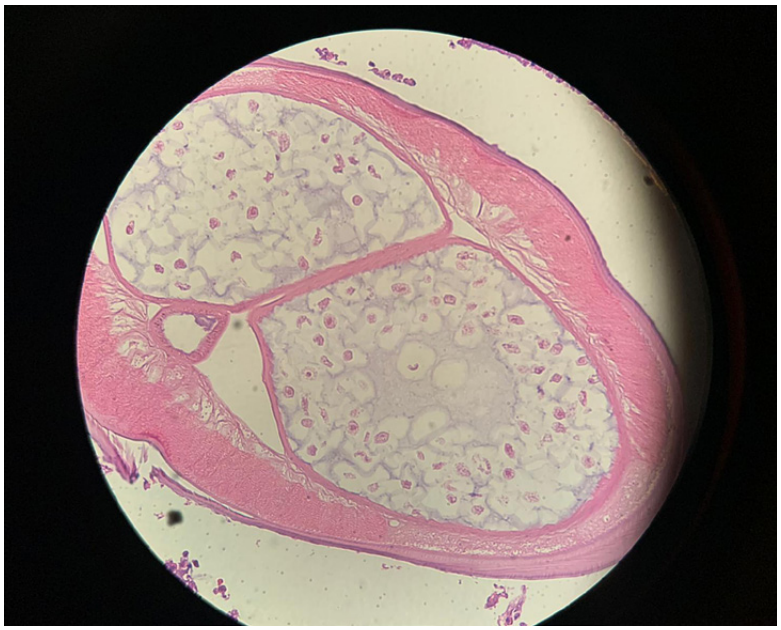
Background: Neglected tropical diseases are emerging in western countries due to migration routes, climate change and widespread access to travel for touristic or working reasons. Generally, clinicians are not aware of prevention measures linked to travel medicine outside vaccination schedules. Parasites are ubiquitous in the world and may mimic different medical conditions making diagnostic workup challenging.

Materials/methods: Case report.

Case report description: A 67-years old colleague, returning from 1-month fellowship in a rural hospital in Ethiopia, consulted our unit after three months of generalized pruritus and after the appearance of a palpable lump on his right forearm associated to intense generalized pruritus. His past medical history was unremarkable except for seasonal rhinitis well controlled by antihistamines. During his stay he remained asymptomatic except for a circumscribed arm swelling that progressed slowly in the following weeks. The lesion was evident at the time of consultation, appearing as a 20 mm swelling with intact superficial skin with no redness, warmness or pain. Baseline blood analysis showed normal leukocyte count without eosinophilia. All other laboratory parameters, including total IgE levels, tested within reference ranges. Ultrasonography found a well-circumscribed lesion, measuring 11x7x10 mm and containing anechogenic fluid with linear hyper echoic worm-like structures resting at the bottom of the cyst. Microscopic evaluation of three stool samples, blood specimens for microfilariae detection, as well as serologies for *Filaria* spp, *Strongyloides* spp, *Trichinella* spp. and *Echinococcus* spp. resulted negative. The nodule underwent excision and parasitological examination confirmed the presence of *Dirofilaria repens* (Figure attached).

Conclusions: Human dirofilariasis is currently considered a re-emerging mosquito-borne zoonosis caused by filarial worms of the genus *Dirofilaria*. Adults *D. repens*, the most significant *Dirofilaria* coupled with *D. immitis*, are commonly located in subcutaneous tissues, and the approach is primarily surgical. *D. repens* is currently found in Europe, Asia, and Africa, but has recently spread into colder regions: we are facing a continuous increase in the risk for humans to acquire dirofilariasis, because of climate changes, frequent travel and more extensive distribution of vectors outside tropical settings. The always evolving epidemiology should prompt physicians attention on neglected tropical diseases.



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Abstract 1336

Emergence of a mupirocin-resistant, methicillin-susceptible *Staphylococcus aureus* clone associated with skin and soft tissue infections in Greece

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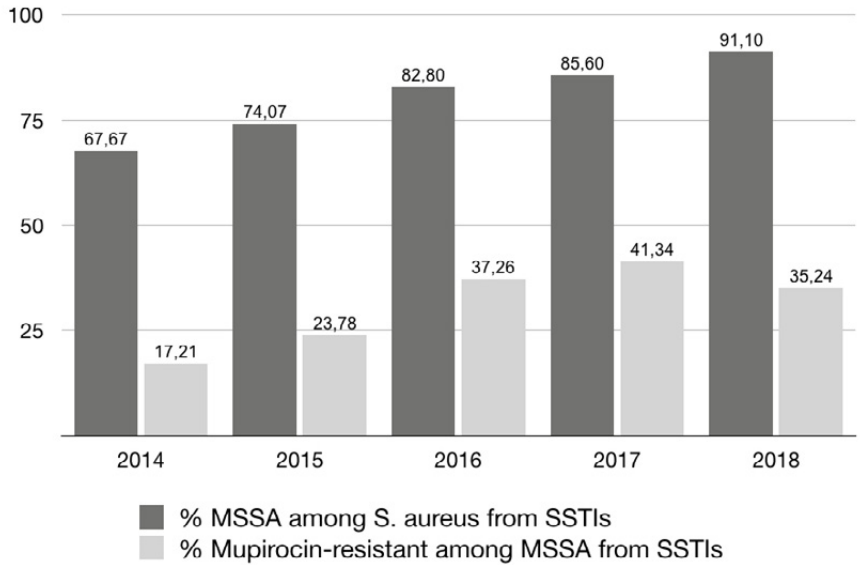
Background: *Staphylococcus aureus* is associated with several infections, ranging from skin and soft tissue infections (SSTIs) to more invasive diseases. Various pathogenic factors are known, including methicillin resistance and virulent genes' carriage. In this study, *S. aureus* from SSTIs in patients among three tertiary care hospitals in different areas of Greece (Athens, Patras, Larisa) were compared in terms of antimicrobial resistance patterns, clonal distribution, toxins and adhesin genes' carriage.

Materials/Methods: From a total of 10459 SSTIs recorded during five-year period 2014-2018, 5090 *S. aureus* were recovered. Of them, 4137 (81.28%) were methicillin-susceptible (MSSA). Antimicrobial resistance was determined by a gradient and the disk diffusion methods, according to EUCAST guidelines. Mupirocin-resistant were 1365/4137 (32.99%) of MSSA associated with SSTIs (mainly impetigo). Among 194 representative strains, genes encoding Panton-Valentine Leukocidin (PVL, *lukS/lukF-PV*), exfoliative toxins (*eta*, *etb*), adhesin FnbA (*fnbA*) and the resistance genes *mupA* (mupirocin), *fusB* (fusidic acid), *ermA*, *ermC* (macrolides/lincosamides), were defined by PCRs with specific primers. Clones were determined by MLST.

Results: From 2014 to 2017, an increase of mupirocin-resistant isolates among MSSA causing SSTIs was observed, from 17.21% to 41.34%, followed by a decrease in 2018 (35.24%) (Figure 1). All tested isolates were *mupA*-positive with mupirocin MICs ranging from 64 to >1024 mg/L. Most strains were multi-resistant, with higher resistance observed against penicillin (100%), fusidic acid (92.78%) and tobramycin (88.95%). One major clone was identified, ST121, comprising of 192/194 (98.97%) tested strains. Most isolates carried *eta* (93.3%), *etb* (97.94%), *fnbA* (88.75%), and *fusB* (98.41%). The majority of erythromycin-resistant strains carried *ermC* (34/39, 87.18%). Only one MSSA out of 194 tested, classified as ST1, was PVL-positive. One more strain belonged to ST21 being negative for toxins' genes.

Conclusions: An annual increase of mupirocin-resistant MSSA recovered from patients with SSTIs was observed from 2014 to 2017, with a decrease in 2018. The emergence of a predominant MSSA clone, ST121, resistant to mupirocin and highly resistant to tobramycin and fusidic acid was confirmed. This successful clone, comprised of PVL-negative isolates carrying resistance, exfoliative toxins and adhesin genes, predominated in SSTIs from patients in three different areas of Greece during the five-year period.



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Abstract 1341

Community and nosocomial sepsis in older adults with bacteraemia: a retrospective study in a geriatric ward

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Background: Sepsis is a global medical emergency that involves not only Intensive Care Units, but also Internal and Geriatric Wards. The incidence of sepsis is disproportionately higher in elderly adults and age is an independent predictor of mortality. Despite this, there are few available data about sepsis in elderly patients in order to help physicians to promptly diagnose and manage it.

Materials/methods: Retrospective study about 149 patients consecutively admitted to Acute Geriatric Ward from 1 January 2017 to 30 June 2019 with positive blood cultures. We evaluated clinical characteristics, autonomies, parameters and blood tests at admission and calculate the main validated scores predicting mortality and diagnosis of sepsis. We divided patients in 2 groups: community bacteremia (CB, positive blood cultures within 48h from admission) and nosocomial bacteremia (NB). Epidemiology, site of infection, antibiotic resistance and therapeutic choices has been studied.

Results: We classified 107 patients as CB and 42 patients as NB. Overall median (IQR) age was 86 (81-91) years, 51% of patients were male. 65% of the sample came from home, but were defined as frail and with limited autonomies (median (IQR) CSF 7 (6-8)). 57% were diagnosed with dementia at admission, and 54% developed delirium at onset. Classic symptoms of sepsis (fever, hypotension, tachycardia) were absent in the majority of patients. qSOFA score was >2 only in 35% and 45% of CB and NB respectively. Polimicrobial bacteremia was significantly higher in NB compared to CB patients (23.8% and 11.2%, p=.014). 65% of CB cases were due to Gram – only, while 50% of NB to Gram + only. 49,5% of CB originated from urinary tract infection, while 42,9% of NB from blood stream infection. Duration of antibiotic therapy was significantly higher in CB patients compared to NB ones. Mortality due to sepsis at day 21 was 14.3% in CB patients compared to 21.1% in the NB (p=ns).

Conclusions: Elderly patients with sepsis have clinical peculiar characteristics. Symptoms at onset are often atypical and not specific. Delirium appears in many patients, and it is an early sign of severity that should be recognized to promptly treat the leading cause.

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Abstract 1346

Multinational performance evaluation of the BIOFIRE FILMARRAY Pneumonia plus (PNplus) panel

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Abstract third-party references: On behalf of the EMEA Evaluation Program Collaborative, Supported by bioMerieux/BioFire Diagnostics LLC

Background: Identification of pathogens causing community acquired, heath-care and ventilated associated pneumonia can be problematic. The BioFire PN*plus* Panel detects 15 bacteria (with semi-quantification), three atypical bacteria, eight viral classes and seven antibiotic resistance markers (mecA/C/MREJ, CTX-M, KPC, VIM, IMP, NDM, OXA-48 like) directly from sputum-like specimens (induced or expectorated sputum; endotracheal aspirates), and bronchoalveolar lavage (BAL)-like specimens with results in about one hour.

Materials/methods: 52 laboratories from 13 countries across Europe and Israel compared the BioFire PN*plus* Panel results to standard of care (SOC) test results. SOC tests varied by site and included various combinations of culture, urinary antigen, molecular assays, and direct fluorescent antibody assays. A total of 2,501 samples (1,252 sputum-like and 1,249 BAL-like) were tested. Comparison of semi-quantification results for BioFire PN*plus* Panel and SOC bacterial pathogens were compared for 1,297 matched detections.

Results: A total of 3,278 bacterial analytes included on BioFire PN*plus* Panel were detected by at least one method. The BioFire PN*plus* Panel identified 3,128 (95%) analytes compared to 1,878 (54%) for SOC. The BioFire PN*plus* Panel detected 93 atypical bacteria and 618 viruses compared to 73 atypical bacteria and 135 viruses for SOC. Semi-quantitative values for the BioFire PN*plus* Panel were less than SOC values, equal to SOC values or greater than SOC values in 5.09%, 25.91% and 69.01% of the results, respectively. On average, BioFire PN*plus* Panel values were approximately 1 log higher than SOC values (57.75% 1-2 log; 11.26% 3-4 log). All resistance markers were detected at least once by the BioFire PN*plus* Panel and in various combinations, with mecA/C/MREJ the most prevalent in *Staphylococcus aureus* (20.35%), followed by CTM-X (8.0%) and KPC (4.3%) in applicable gram-negative bacteria.

Conclusions: Despite variations in laboratory testing methodologies across testing sites, BioFire PN*plus* Panel performed consistently with enhanced detection of all types of respiratory pathogens. In particular, limited SOC testing for viruses was shown to be a missed opportunity to define the potential cause of respiratory infection. Identification of the potential cause of pneumonia and associated resistance markers in approximately 1 hour could dramatically change antimicrobial selection and enhance patient outcomes.

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Abstract 1350

In vitro activity of ceftolozane/tazobactam against clinical isolates of carbapenem-resistant *Pseudomonas aeruginosa* from Japan hospitals

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Background: Ceftolozane/tazobactam (TAZ/CTLZ), a new-generation cephalosporins, is the first drug combined with a β-lactamase inhibitor, i.e., a cephalosporin antibacterial agent, to be effective against drug-resistant bacteria such as multi-drug-resistant *Pseudomonas aeruginosa* and ESBL-producing Enterobacteriaceae. In the present study, we examined its anti-bacterial activity against carbapenem-resistant *P. aeruginosa* and performed genetic analysis for resistant strains.

Materials/methods: Clinically isolated carbapenem-resistant *P. aeruginosa* strains (40 non-carbapenemase-producing strains) were tested. In the drug susceptibility test, an E-test (bioMérieux) was performed to measure the MIC50/90 and sen-sitivity (CLSI M100-S29). In addition, strains with a MIC of 16 mg/L were compared with a PA01 strain for mRNA expression of the AmpC gene by sequencing and qRT-PCR.

Results: The MIC50/90 values (mg/L) of TAZ/CTLZ of all 40 strains were 2/16, with a susceptibility rate of 85%. The AmpC gene was sequenced, revealing V239A and A97V mutations. The expression levels of the AmpC gene increased 8-43-fold in all strains except one.

Conclusions: The antibacterial activity of TAZ/CTLZ for carbapenem-resistant *P. aeruginosa* is higher than that of the other β-lactams, and should be effective against strains with drug resistance involving outer membrane proteins. In addition, we found that resistant strains existed before the use of TAZ/CTLZ in Japan, and that such strains were caused by mutations and increased expression of the AmpC gene, although no highly resistant bacteria were detected.

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Abstract 1354

Treatment status and prognosis of 203 cryptococcosis in non-human immunodeficiency virus-infected and nontransplant patients

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Background: To learn the treatment status and prognosis of cryptococcosis in non-human limmunodeficiency virus-infected and nontransplant patients.

Materials/methods: We retrospectively analyzed the gender,age,diagnosis,treatment and prognosis of 203 non-human limmunodeficiency virus-infected and nontransplant patients of cyptococcosis from 2012 to 2018

Results: There were 196 pulmonary cryptococcosis patients and 7 disseminated cryptococcosis patients of all the 203 non-human limmunodeficiency virus-infected and nontransplant patients. 196 pulmonary cryptococcosis patients included 127 men(64.80%) and 69 women(35.20%) and the average age of men was 49.57 years old and the average age of women was 54.52 years old.5 patients (2.55%) were diagnosed by culture,112 patients (57.14%) were diagnosed by biopsy and 79 patients (40.31%) were diagnosed by latex agglutination test.104 patients have finished the course of treatment among the 143 patients in the department of medicine, 74 patients were cured (71.15%), 27 patients were improved (25.96%), 1 patients was in persistence (0.96%) and 2 patients were treated surgically (1.92%); among the patients who have finished the course go treatment, 77patients (74.04%) use fluconazole effectively, 9 patients (8.65%) used voriconazole effectively, 2 patients (1.92%) used intraconazole effectively and 13 patients (12.50%) used amphotericin B or amphotericin B liposome effectively. 53 patients were diagnosed by the surgical pathology, 27patients (50.94%) used anti fungal after the operation, 23 patients (43.40%) didn't get any treatment and no recurrence was found, 3 patients (5.66%) were loss to follow up. Among 7 patients of disseminated cryptococcosis, 2 patients were cured, 2 patients were undergo treatment and 3 patients were withdrawn. The starting dose and maintenance dose were various in the 77 non-human limmunodeficiency virus-infected and nontransplant patients who were cured by fluconazole. 8 patients (57.14%) got renal impairment among 14 patients of pulmonary cryptococcosis who used amphotericin B or amphotericin B liposome.

Conclusions: Triazoles is always effective in the pulmonary cryptococcosis in the non-human limmunodeficiency virus-infected and nontransplant patients， few patients relapses and the prognosis is favorable.

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Abstract 1357

Roles of the FadRACB system in formaldehyde detoxification and antibiotic susceptibility in *Stenotrophomonas maltophilia*

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Background: Formaldehyde toxicity is invariably stressful for microbes. *Stenotrophomonas maltophilia*, a human opportunistic pathogen, is widely distributed in different environments and has evolved an array of systems to alleviate various stresses. This study aimed to characterize the formaldehyde detoxification system FadRACB of *S. maltophilia* with respect to formaldehyde detoxification and antimicrobial susceptibility.

Materials/methods: Presence of *fadRACB* operon was verified by RT-PCR. Single or combined deletion mutants of *fadRACB* operon were constructed for functional assay. Formaldehyde quinolone susceptibilities were assessed by observing cell viability in formaldehyde- and quinolone-containing media, respectively. Agar dilution method was used to assess the bacterial susceptibilities to antibiotics. Expression of *fadRACB* was assessed by qRT-PCR.

Results: The *fadR*, *fadA*, *fadC*, and *fadB* genes are arranged in an operon. Mutants in *fadA* and/or *fadB* were more susceptible to formaldehyde than wild-type KJ. No significant difference was observed in the ability of *fadC* single mutant to defend formaldehyde; however, simultaneous inactivation of *fadA*, *fadB*, and *fadC* further enhanced the susceptibility toward formaldehyde. In addition, compared to wild-type KJ, the triple mutant KJΔFadACB was more susceptible to quinolone and more resistant to aminoglycosides. FadR functions as a repressor for *fadRACB* operon. *FadRACB* operon has a moderate expression in aerobically-grown wild-type KJ and is further de-repressed by formaldehyde challenge, but not by antibiotics.

Conclusions: FadACB system contributes to mitigation of formaldehyde toxicity and cross-protects *S. maltophilia* from attacks of quinolone.

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Abstract 1358

Antifungal susceptibility profiles of olorofim (formerly F901318), and currently available systemic antifungals against mould and yeast phases of Talaromyces marneffei

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Background: *Talaromyces marneffei* is a thermal dimorphic fungus and is the etiologic agent of talaromycosis, a life-threatening disease which affects immunocompromised host especially those with HIV infection. The fungus is endemic in Southeast Asia and is known to be associated with bamboo rats. Talaromycosis is initially treated with amphotericin B but its use is limited due to toxic side effects. Therefore, the need for new antifungals to treat talaromycosis is urgent. Olorofim is a novel fungicidal drug which targets dihydroorotate dehydrogenase in the de novo pyrimidine biosynthesis pathway. It is highly active against *Aspergillus* and other filamentous *Ascomycetes*. However, the *in vitro* efficacy of olorofim against *T. marneffei* has yet to be reported .We therefore aimed to evaluate the susceptibility of *T. marneffei* to olorofim and other currently available systemic antifungals in its yeast as well as in mold phases.

Materials/methods: We tested 32 clinical and environmental *T.marneffei* strains recovered from southern China against 8 different antifungals according to the Clinical and Laboratory Standards Institute M38-A2 and M27-A3 guidelines.

Results: The geometric means of the minimum inhibitory concentrations/minimum effective concentrations (MICs/MECs) of the antifungals against mold phase of all *T. marneffei* strains were (in increasing order): olorofim (0.0005 mg/mL), itraconazole and posaconazole (0.016 ug/mL), voriconazole (0.05 ug/mL), 5-flucytosine (0.08 ug/mL), terbinafine (0.1 ug/mL), caspofungin (0.4 ug/mL) and amphotericin B (2 ug/mL). The geometric means MICs/MECs against the yeast phase were, as follows: olorofim (0.0007 ug/mL), posaconazole (0.016 ug/mL), Itraconazole (0.016 ug/mL), voriconazole (0.017 ug/mL), terbinafine (0.12 ug/mL), amphotericin B (0.13 ug/mL), 5-flucytosine (0.25 ug/mL), and caspofungin (4.5 ug/mL). Olorofim was the most active antifungal agent against both mold and yeast phases of all tested *Talaromyces marneffei* isolates, exhibiting an MIC range, MIC_{50}, and MIC_{90} of 0.0005-0.002 ug/mL, 0.0005 ug/mL, and 0.0005 ug/mL, respectively.

Conclusions: In summary, olorofim demonstrated potent and consistent activity against all *T.marneffei* strains *in vitro,* and its activity was maintained in two different growth phases. Further studies are warranted to evaluate the *in vivo* efficacy of olorofim against this fungus.

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Abstract 1362

Bloodstream infections caused by strong biofilm-producing bacteria increase the risk of end-organ disease and mortality in patients with haematologic malignancies

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Background: Bacterial bloodstream infection (BSI) represents a major complication in patients with hematological malignancies (HM). However, factors leading to BSI, as well as progression to end-organ disease and death, are only partially understood. The study aims at analyzing host and microbial risk factors and assesses their predicted impact on the development of BSI and mortality.

Materials/methods: A total of 96 patients with HM and BSI were included in the study. Host-associated risk factors and all-causes of mortality were analyzed by multivariable logistic regression at 30 days after onset of the first BSI in the first neutropenic episode. The multidrug-resistant (MDR) profile and biofilm production of bacterial isolates were included in the analysis.

Results: The median age was 60 years (range 20-77 years). The underlying diagnoses were acute leukemia n=53 (55%), lymphoma n=30 (31%) and myeloma n=13 (14%). Bacterial isolates from BSI were 96. *Escherichia coli* was the most common isolate (n=28, 29.2%), followed by *Pseudomonas aeruginosa* (n=16, 16.7%). MDR (n=10) caused 10.4% of bacteremia episodes. Weak biofilm producers were significantly (P<0.0001) more abundant (72.2%) than strong (27.8%) biofilm-producers. Specifically, strong biofilm-producers were 9.6% for *E. coli*, 100% for *P. aeruginosa*, 50% for *K. pneumoniae*, and 23.3% for Coagulase-negative *Staphylococcus* spp. (CoNS). Mortality at day 30 was 8.3% (8/96), and all deaths were attributable to Gram-negatives. About 22% of all BSI were catheter-related (CRBSI). The mortality rate (P=0.62) and the level of biofilm production (P=0.75) were not correlated with CRBSI. Notably, strong biofilm-producing bacteria were found to be an independent risk factor (P=0,018) associated with the end-organ disease. Besides, multivariate analysis indicated that the presence of strong biofilm-producing bacteria (P=0,013) and MDR strains (P=0,006) were independent risk factors associated with 30-day mortality.

Conclusions: Strong biofilm-producing bacteria and MDR strains caused a limited fraction of BSI in patients with HM. Strong biofilm-producing bacteria present a high risk of end-organ disease and that, together with an MDR phenotype, are significantly and independently associated with an increased risk of death. The rapid identification of biofilm-producing bacteria from BSI can offer a key biomarker to predict the clinical and therapeutic outcomes in patients with HM.

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Abstract 1363

Genetic structure characteristics and treatment for *Listeria monocytogenes* infections

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Background: Invasive *Listeria monocytogenes* (Lm) carry a high mortality despite antibiotic treatment. The aim of this study was to investigate the mechanism of pathogenicity and resistance. In addition, the effect of existing treatment options against Lm were systematically evaluated as well.

Materials/methods: Three Lm isolates were collected and 15 antibiotics susceptibility tests were done. Subsequently, the genetic characteristics were investigated by genome sequencing and bioinformatics analysis. Furthermore, the effect of meropenem, linezolid, benzylpenicillin, vancomycin, trimethoprim/sulfamethoxazole were determined using the time-kill assay.

Results: Two sequence types (STs) were identified for isolate 23949 (ST87), 26530 (ST3), 34096 (ST87), respectively. All isolates were resistant to fosfomycin and daptomycin. The resistant genes *fosX*, *mprF*, *norB* and *vgaALC* were identified in all isolates. Furthermore, 80 virulence genes were detected and 72 genes were found in all three isolates. There were 26 virulent genes associated with the structure, biosynthesis, motor switch of flagellum. And other virulent genes were involved in chemotaxis, protease, internalin and metabolism. It is of note that 8 genes were only found in 26530 isolated from cerebrospinal fluid (CSF), 7 of which were associated with haemolysin. Further in vitro time-kill assay found trimethoprim/sulfamethoxazole at serum or CSF concentrations had bactericidal effect (>3.5 log10 CFU/ml) against three tested Lm strains at 24 h.

Conclusions: The involved virulence factors were mainly associated with bacterial pathogenicity. Notably, trimethoprim/sulfamethoxazole might be greater potential therapeutic option against Lm bloodstream infection or intracranial infection.

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Abstract 1366

Epidemiology of nosocomial candidaemia in paediatrics: a multi-centre study in Iran

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Background: Nosocomial bloodstream candidaemia is a life-threatening fungal infection with high morbidity and mortality, especially among paediatric patients undergoing intensive immunosuppressive therapy. Limited data on the epidemiology of candidaemia and susceptibility profiles are available in Iran. We aimed to characterize candidaemia epidemiology, comorbidity risk factors, species distribution, and antifungal susceptibility profiles among paediatric patients in Iran.

Materials/methods: A total of 26,189 hospitalized patients under 18 years old were involved. Blood samples from patients with suspected fungal bloodstream infection were analysed using the BACTEC culture system. Fungal isolates were identified using matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF) and DNA sequencing. Antifungal susceptibility testing was performed using the Clinical and Laboratory Standards Institute broth microdilution method.

Results: Overall, 109 episodes of nosocomial candidaemia, with an incidence of 4.1 cases per 1000 admissions, were observed among paediatric patients with or without immunosuppressive therapy. The most common healthcare-associated factor was the use of a central vascular catheter (97.24%). The all-cause mortality rate was 40.36%, of which 48% was attributable to candidaemia. While *Candida albicans* (49%) was the most frequent causative agent, emerging and uncommon *Candida* species were also isolated. The mortality of candidaemia caused by non-*albicans Candida* species were significantly higher from those of candidaemia caused by *C. albicans* ($P < 0.05$). All fluconazole resistant species were non-*albicans Candida* species.

Conclusions: Uncommon *Candida* species with reduced susceptibility to antifungal agents are likely to become the major agents of nosocomial candidaemia in high-risk patients in Iran, such as paediatric cancer patients. Appropriate source control, antifungal regimens, and strengthening of antifungal stewardship policies are all needed for the management and decrease of the burden of nosocomial candidaemia.

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Abstract 1367

Gentamicin-intercalated smectite as a new therapeutic agent against *Helicobacter pylori* infection and faecal microbiome analysis after eradication in mouse model

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Background: The eradication rate of *Helicobacter pylori* with conventional standard therapy shows a decreasing trend, because of antibiotics resistance especially clarithromycin. Thus, novel antibacterial strategies against *H. pylori* are needed. We evaluate the efficacy of a gentamicin-intercalated smectite hybrid (S-GM)-based treatment regimens including toxicity of S-GM using fecal microbiome analysis in a murine model of *H. pylori* infection.

Materials/methods: To evaluate anti-*H. pylori* efficacy, mice were divided into 8 groups, and *H. pylori* eradication was assessed by *Campylobacter*-like organism (CLO) test and *H. pylori* PCR of the gastric mucosa. For the test of toxicity of S-GM, four different model was designed. One week after the end of *H. pylori* eradication, the levels of proinflammatory cytokines and the atrophic changes of gastric mucosa were examined. In addition, stool specimens were collected, and analyzed for microbiome changes in each group.

Results: The S-GM-based triple regimen decreased bacterial burden *in vivo*, compared to that in untreated mice or mice treated with other regimens. The therapeutic reactions in the CLO test from gastric mucosa were 90, 90, 80, 80, 70, and 10% in Groups III-VIII, respectively. Those of *H. pylori* PCR in gastric mucosa of mice were significantly lower in Groups III-VIII than in the Group II. In the results of toxicity of S-GM, S-GM triple therapy also reduced the level of IL-8 and the atrophic change of gastric mucosa. In the analysis of stool microbiome, abundant microorganisms of phylum level were presented, and the diversity of microbiome was preserved in the S-GM triple therapy comparing the standard triple therapy.

Conclusions: These results suggest that S-GM is a promising and effective therapeutic agent for the treatment of *H.pylori* infection.

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Abstract 1370

Features and outcomes of tuberculosis among internally displaced people in East Ukraine

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Background: From the start of military conflict now there are about 1 500 000 officially confirmed internally displaced people (IDP) in Ukraine. In 2018 there were about 35,0 % of new and 62,0 % of re-treated confirmed cases of multiple and extensive drug resistant tuberculosis (MDR/XDR TB). This study aims to analyze the features and outcomes of TB among IDP in a given TB hospital.

Materials/methods: In 2014-2018 in a given TB hospital were treated 409 patients. Among them there were 51 cases of TB in IDP. Some patients were hospitalized more than one time – discharging from hospital was done mainly (85,0%) because of migration to and out of military conflict territory. Thus, 37 patients (IDP) with TB were treated in the hospital – 28 (75,7%) males and 9 (24,3 %) females. Patients` age was 23-87 years old, middle age 41,6.

Results: 22 (59,5 %) patients were without any temporary place of living, 7 (18,9 %)– HIV infected, 9 (24,3 %) – intravenous drug users. Medical help was provided according to national protocols. HIV-infected IDP had an opportunity to get antiretroviral therapy (ART), drug users – opioid substitutional therapy, as any other Kharkiv region citizens. 32 (86,4 %) patients had MDR/XDR TB. Treatment was prescribed by the results of drug susceptibility tests and previous case`s history (TB-manager – Ukrainian national TB database). Outcomes were analyzed according to WHO recommendations: 8 (21,6%) – treatment success (2 (5,4 %) – cured, 6 (16,2 %)– finished), 29 (78,4 %)– unsuccessful treatment (6(16,2 %) – dead (2(5,4 %)– brain stroke (elderly and senile aged IDP), 2 (5,4 %) – HIV-TB co-infection, 2 (5,4 %) – very severe cases of MDR-XDR TB), 15 (40,5 %)– lost to follow up, 8 (21,6 %)– treatment failure (all of them – MDR-XDR TB)).

Conclusions: Experience of working with IDP shows ways how to improve TB management: rapid diagnostics, social adaptation of TB patients, decreasing of stigma, availability of TB drugs, opioid substitution therapy and ART in all levels of medical support. National database as a TB-manager is very helpful to identify case even if it is from different territory and gives the mechanism to improve MDR/XDR TB epidemy.

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Abstract 1376

Nasal colonisation by *Staphylococcus aureus* in nursing home residents in Crete, Greece

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Background: About 25% of healthy persons are asymptomatically colonized by in the anterior nares *S.aureus* and may spread the pathogen to other individuals, while they carry a higher risk of infection.

Materials/methods: This is a point-prevalence study detecting nasal colonization by *S.aureus* in nursing home residents conducted in 6 long-term care facilities (LTCFs) on the island of Crete, Greece. Nasal swabs were cultured in order to detect for *S. aureus* while risk factors for colonization were evaluated. Nasal swabs were also collected from healthy non-residents of LTCFs of the same age that were used as controls. Data collected included age, gender, duration of stay in LTCFs, comorbidities, antibiotic exposure, and recent hospitalization

Results: A total of 290 LTCF residents aged 65 years or more were enrolled. Mean age was 83.1 years; 30.7% were male (89 residents). The median length of stay at the LTCF was 23 months. Residents with a Charlson comorbidity index ≥3 were 24.7% (82 residents). Recent hospitalization and recent antibiotic use were recorded in 8.6% (25 residents) and 13.4% (39 residents) respectively. Among the 290 residents, 28.6% (83) were colonized by *S. aureus*, while 66.5% of them (55 residents) were MRSA carriers. Analysis of *S. aureus* and MRSA prevalence among the LTCF residents and 43 healthy controls of the same age did not reveal statistically significant differences. Statistical analysis revealed that *S. aureus* colonization was more common in women (34.3%) than in men (21.7%) and that the only factor associated with MRSA colonization was recent antibiotic exposure (23.6% if recently on antibiotics vs 3.6% if not; p=0.028).

Conclusions: Colonization by *S. aureus* is quite common in LTCFs, but the rate may not differ from that in the community. Recent antibiotic exposure significantly increases the risk for MRSA colonization.

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Abstract 1377

Pyogenic liver abscess: predictive factors of unfavorable course

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Background: Pyogenic liver abscess (PLA) is a severe disease, whose unfavorable evolution may be categorized by primary treatment failure, recurrence or death. Our objective was to assess predictive factors of unfavorable courses in patients with PLA.

Materials/methods: We conducted a retrospective population-based study in Beaujon hospital, a single tertiary care center of Paris area. All patients admitted for a PLA episode between 2010 and 2018 were included. An unfavorable course was defined by the occurrence of a primary treatment failure (clinical worsening and/or increased radiological size despite appropriate treatment, requiring modification of antimicrobial therapy and/or new drainage), a recurrence occurring at least 28 days after an initial cure, or death within 3 months after diagnosis.

Results: Overall, 317 patients were included. Median age at diagnosis was 60 years (19-92); 208 (65.6%) patients were male. Healthcare-related and nosocomial infections accounted for 86 (27.1%) and 38 (12%) of cases, respectively. A biliary origin (179/317, 56.5%) was the main mechanisms of PLA occurrence. In patients with a biliary origin, hepato-biliary tumoral obstruction and ischemic cholangitis were retrieved in 70/179 (39%) and 32/179 (17.8%) patients, respectively. *E. coli* was the first pathogen isolated (104 patients, 24.5%), followed by *Enterococcus* spp. (55 patients, 17.4%); 46/424 (10.8%) microorganisms isolated from an initial PLA episode were multi-drug resistant organisms (MDRO). An unfavorable course occurred in 91 (28%) patients: primary treatment failure and recurrence were reported in 56 (17.6%) and 28 (8.8%) patients, respectively; 32 (10%) patients died within 3 months. Factors independently associated with an unfavorable course were a healthcare-related infection (HR=1.74, p=0.033), an underlying metastatic liver (HR=2.76, p<0.001), a portal thrombosis (HR=2.46, p=0.001), an ischemic cholangitis (HR=2.16, 0.008), presence of fungi (HR=3.08, p=0.008), enterococci. (HR=1.81, p=0.020) or MDRO (HR=1.88, p=0.020); PLA drainage versus no drainage was associated with a better outcome (HR=0.52, p=0.005).

Conclusions: Unfavorable course after an initial PLA episode remains frequent and likely occurs in a healthcare setting. Identification of risk factors may help to improve management of PLA and to elaborate targeted recommendations according to patient and disease's characteristics.

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Abstract 1378

Infection incidence among patients colonised with carbapenem-resistant *Enterobacteriaceae* (CRE) and microbial aetiology

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Background: CRE are important pathogens in Hospital Acquired Infections (HAI). Intestinal colonization with CRE precedes infection and has negative effects on the morbidity and mortality. There are conflicting data in the literature on the percentage of patients developing infection after intestinal colonization. The purpose of this study is to analyze the incidence of infection in colonized subjects detected through surveillance with rectal swab and hospitalized at ASST Lariana, also considering different bacterial species involved.

Materials/methods: A retrospective research is carried out evaluating the annual and cumulative incidence of CRE infection in rectal swab-positive patients, from January 2016 to June 2019. Isolation sites, hospitalization wards and bacterial etiology are considered. The surveillance first involved the patients admitted to intensive care, but was later extended to patients from long-term care, patients with hospitalization lasting more than 30 days, patients with hospitalization in the 60 days before. Furthermore, all patients admitted to Geriatrics and Neurorehabilitation are screened. Samples taken by rectal swab are seeded on chromogenic medium, with incubation at 24 hours; bacterial identification and antimicrobial susceptibility are performed with MALDI-TOF and VITEK2 (bioMerieux).

Results: From 2016 to June 2019, respectively: 60, 74, 72 and 30 (first six months) cases of carriers of CRE were identified. The wards were: Medicine (61%), Surgery (11%), Rehabilitation (12%) and Intensive care (16%). The total incidence of CRE infection in colonized patients was 23.7%. The most involved sites of infection were the urinary tract (56.2%) followed by the lower respiratory tract. The bacterial etiology was *K. pneumoniae* with the following percentages: 96.6% in 2016, 94.4% in 2017, 93.2 % in 2018 and 80 % in the first six months of 2019, with a growing finding of *E. coli* KPC.

Conclusions: Our study showed a 23.7% incidence of CRE infection in colonized patients, higher than verified in other research, suggesting the need for further longitudinal and epidemiological investigations. The bacterial etiology was found to be in line with the literature data, showing however a tendency towards an increase in the finding of bacterial species different from *K. pneumoniae*.

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Abstract 1381

Antibiotic use in French hospitals 2012-2018: improvements to be confirmed!

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Background: Surveillance of antibiotic consumption is at the core of mandatory antimicrobial stewardship programmes in hospitals. A national standardized method was developed to describe antibiotic consumption at hospital level. In order to assess the impact of antibiotic stewardship activities, namely guidelines on broad spectrum antibiotics, changes in antibiotic consumption between 2012 and 2018 were described.

Materials/methods: Antibacterials for systemic use (J01class, WHO Anatomical Therapeutic Chemical classification, ATC-DDD system), oral imidazole derivatives and fidaxomicin were surveyed for inpatients in voluntarily participating hospitals and expressed in number of defined daily doses (DDD) per 1 000 patient-days (PD). Data were retrospectively collected from pharmacy records and administrative services each year.

Results: The number of participating hospitals increased from 1411 in 2012 to 1630 in 2018 covering 73% of national PD in 2018. Antibiotic use increased between 2012 and 2015 (+1.8%) and decreased from 2016 (-8.5%) to reach 288 DDD/1000PD in 2018. Despite an overall increase in third generation cephalosporin use (+13% between 2012 and 2018), ceftriaxone use was 10% lower in 2018 compared to 2013; carbapenem use tended to remain stable since 2015. By contrast, the consumption of piperacillin-tazobactam, linezolid and daptomycin steadily increased from 2012 (+76%, 92% and 379% respectively). Proportion of broad spectrum antibiotics (ECDC secondary indicator for hospitals) was 32% in 2012 and 34% in 2018.

Conclusions: Recent surveillance data tend to show a stabilisation and even a decrease in antibiotic consumption, namely for antibiotics targeted by guidelines (ceftriaxone in 2014, carbapenems in response to increase in carbapenem-resistant Enterobacteriaceae cases), highlighting the usefulness of specific recommendations with clear messages. However, attention should be given to the increasing use of other antibiotics, namely in the context of emergence of linezolid-resistant staphylococci. To better inform next steps in promotion of prudent antibiotic use and antimicrobial resistance control, a new national project for surveillance and prevention of antimicrobial resistance in hospitals (SPARES) was set up in 2018. Hospitals are provided with standardized methods and webtools allowing 1) a more comprehensive antimicrobial resistance surveillance and 2) cross-transmission prevention audits in order to allow identification of areas for improvements at both local and national levels.

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Abstract 1383

Whole genome sequencing and comparative analysis of echinocandin susceptible and resistant sequential *Candida glabrata* clinical isolates

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Background: *Candida glabrata* ranks as the second most common cause of candidemia in many countries. Echinocandin resistance in *C. glabrata* is emerging. The aim of this study was to compare the genomes of two sequential echinocandins susceptible and resistant *C. glabrata* related isolates.

Materials/methods: Two bloodstream *C. glabrata* isolates were serially recovered from a 72-year-old female patient with candidemia post contrary artery bypass grafting procedure (CABG) before and after caspofungin treatment (<3 months interval). Whole-genome sequencing (WGS) was performed on these two isolates to determine genetic changes using 2x250bp paired-end sequencing using MiSeq system (illumina).

Results: In vitro antifungal susceptibility testing showed an increase in MIC against caspofungin and anidulafungin for the post-treatment isolate (8 mg/L, 2 mg/L respectively) compared to the pre-treatment isolate (0.03 mg/L for both), indicating the acquisition of echinocandins resistance. Isolates confirmed to be genetically related with same MLST type. Genomic analysis of pre-treatment isolate with post-treatment isolate identified 17 nonsynonymous SNVs, including a novel undescribed F1113C substitution in FKS2 gene in addition to the previously described F625S substitution in FKS1 gene. One novel SNV was detected in ERG2 gene (G92D substitution) that belongs to the ergosterol biosynthesis-related family which is known to mediate antifungal resistance in *C. glabrata*. Multiple SNVs were present in genes related to transcriptional and translational activation in response to cellular stress such as: MSS11, MIT1, FIR1, RNR1, DNA2, RPN9, BRE2, ROX3, and CMP2, while others were found in genes related to cell wall components and have functions in membrane transportation and localization such as: SEC5, WSC4, and VMA5. Two SNVs were found in genes of unknown function.

Conclusions: *C. glabrata* has the ability to rapidly acquire echinocandin resistance. The genomic changes observed in the resistant isolate highlight the diverse mechanisms by which *C. glabrata* can adapt to the pressure of echinocandin therapy and host environment.

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Abstract 1384

The ultrastructural visualisation of Severe Fever with Thrombocytopenia Syndrome (SFTS) virus in human PBMC sample

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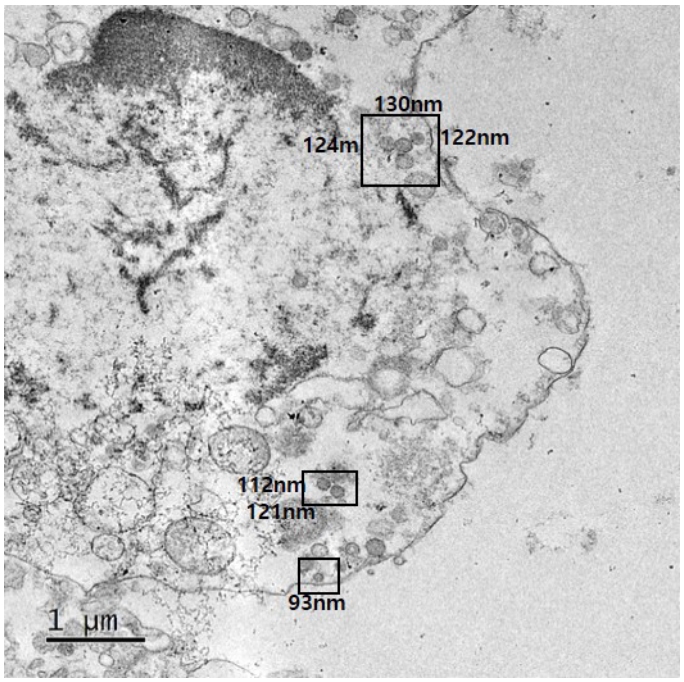
Background: Severe Fever with Thrombocytopenia Syndrome (SFTS) virus was first discovered in China. In Korea, it was first discovered in Gangwon-do in 2013 and the number of patients has been steadily increasing and has a high mortality rate of more than 30%. Before April 2017, symptoms of SFTS appeared only in humans by ticks as a medium, but since then, animals such as dogs and cats have developed symptoms of SFTS.

Materials/methods: We infected human-derived SFTS virus and dog-derived virus with vero cells and HEK cells, respectively, and then analyzed by Quantitative Real-Time PCR (qRT-PCR) analysis to identify genetic differences. Transmission electron microscopy (TEM) was also performed to confirm the morphology and composition of both cells. Furthermore, the ultrastructure of SFTS virus in human PBMC sample which is provided by Chunbuk national university hospital in Korea has been observed using TEM.

Results: SFTS is sphere and a dense nucleocapsid core of 90-120 nm which is characteristic of enveloped viruses, phleboviruses, commonly known as colonies. We also found the viral particles in monocytes from human samples.



Conclusions: The findings will help to provide a structural basis for the detection and diagnosis of SFTS infections.

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Abstract 1388

Results of an outpatient parenteral antimicrobial therapy programme in Spain

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Background: Outpatient parenteral antimicrobial therapy (OPAT) is an alternative for the conventional therapy to infectious diseases. The main advantages it offers are the reduction of the complications of conventional hospitalization, better quality of life for the patient and his family and the saving of hospital stay, with the consequent reduction of the economic cost for the health system. The results of an OPAT program are described.

Materials/methods: A retrospective, observational study of all patients attended between 2018-2019 in OPAT program of University Hospital of Cabueñes, Spain were performed. Demographics, therapy characteristics, pathogens, adverse events (AEs), and clinical outcomes were evaluated. Effectiveness was assessed by analyzing readmissions to hospital for inadequate control of underlying infection. Safety was assessed by analyzing adverse events, catheter-related complications and readmission to hospital before 30 days after the end of treatment.

Results: Eighty-six patients (55.8% females, mean age: 73 years) were included. The most frequent underlying diseases were neoplasm (25.6%), respiratory diseases (16.3%), cardiovascular diseases (14%), and diabetes (9.5%). Urinary tract infections (39.5%) were the most frequent infection follow by respiratory infections/pneumonia (30.2%), intra-abdominal infections (7%), endocarditis, septic arthritis, hepatobiliary diseases (4.7% each), prosthesis joint infection and cellulitis (3.5 % respectively) and catheter –related sepsis (2.3%). Twenty-five percent of patients had bacteremia. The most frequents microorganisms were *Escherichia coli* (24.2%), *Pseudomonas aeruginosa* (15%) *Staphylococcus aureus* (7%), *Klebsiella pneumoniae* (4.7%), *Staphylococccus epidermidis, Citrobacter freundii, Streptococcus group viridans* (3.5% each) among others. In thirty cases the microorganism produced extended spectrum beta-lactamases. The most frequent treatment was ertapenem (34.8%) follow by piperacillin-tazobactam (23.3%), ceftriaxone (19.8%) and daptomycin (7.5%). Only six patients (7%) patients had a recurrence Six patients dead due to the infection There are not significantly differences in sex, age, or underlying diseases between relapses or not. Catheter-related complications occurred in 3 patients. Mean duration of treatment was 13 days. Twenty days of antibiotic treatment was saved.

Conclusions: OPAT programs are a safe and effective alternative that saves hospital stay even in patients with bacteremia. The readmission rate is low and the level of patient satisfaction high.

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Abstract 1389

Extreme levels of diversity of *Mycobacterium tuberculosis* across a large genomic dataset: a map to disease pathogenesis and stress survival

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Background: *Mycobacterium tuberculosis (M.tb)* is a bacterial pathogen causing tuberculosis (TB), an ancient disease, which is one of the biggest infectious "killers"worldwide. It is almost 20 years since the first *M.tb* genome sequence. Many landmark studies have been undertaken, but have mainly focussed on phylogenetic analysis, drug resistance and outbreak investigation. However, a deeper understanding of the diversity present across all *M.tb* genes at a population level is required, especially in the future discovery of novel drug targets or vaccine candidates. We performed an unbiased gene-by-gene analysis of 8535 *M.tb* genomes by studying the extremes of nucleotide sequence diversity distribution - i.e. genes with low and high levels of nucleotide sequence diversity across the sequenced population.

Materials/methods: Public genomic data covering all seven *M. tb* lineages was retrieved and curated. A total of 8535 genome sequences were mapped against the reference *M.tb* genome, H37Rv, in order to identify single nucleotide polymorphisms (SNPs). The results of the initial mapping were further processed and a diversity frequency distribution of all the genes was identified.

Results: We show that levels of diversity across genes are not normally distributed and that there are genes with extreme levels of diversity and others with extreme levels of conservation. In highly variable genes, variants were found to occur at hotspots, and largely encoded functions related to disease pathogenesis and drug resistance. Such diversity may make it problematic to create a vaccine or drug that successfully targets the known diversity of *M.tb* strains. Conversely, very conserved genes are associated with the protection of the *M.tb* under stress conditions, intra-macrophage infection and the latent stage of the disease. This suggests that these genes are highly important in the TB infection cycle, and may constitute more preferential drug and vaccine targets to combat TB.

Conclusions: This study can be used as a "map" of the evolutionary trajectory of *M.tb* genes across all lineages and might inform the development of future vaccine candidates and novel anti–TB medication.

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Abstract 1395

Pathogen Box screening identifies novel antimicrobials that target *Mycobacterium chimaera*

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Background: *Mycobacterium chimaera* is a slow growing nontuberculous mycobacterium that is part of the *Mycobacterium avium* complex (MAC). *M. chimaera* Infection has been identified in patients having previously undergone cardiac surgery and it is also increasingly being detected in patients with chronic lung disease. Like many mycobacterial infections, *M. chimaera* is recalcitrant to antimicrobial therapy and require long treatment regimens. There is an urgent need to both identify novel antimicrobials and to re-purpose drugs to treat *M. chimaera* as current treatment regimens are inadequate with patient mortality as high as 50%.

Materials/methods: In this study, we screened the Pathogen Box library, which consists of 400 drug-like molecules against *M. chimaera* using a resazurin based microtiter plate assay to determine cell survival that was validated with Z-factor analysis. Selected hits were characterised with dose response curves and time kill kinetics.

Results: A total of 21 hits were identified based on a cut off of 70% or more *M. chimaera* growth inhibition when screened at the single concentration of 20 µM. Dose response curves of four compounds (MMV02248, MMV675968, MMV688179 and MMV688271) showed favourable activity against *M. chimaera*, with MMV675968 exhibiting activity similar to clarithromycin which forms part of front line treatment of *M. chimaera*. In addition, one of the hits identified was doxycycline, which is a broad-spectrum antimicrobial drug. Doxycycline generated a minimum inhibitory concentration of 6.25 µg/mL against *M. chimaera* and is bacteriostatic, based on time kill kinetic studies. Three oxazolidinone compounds linezolid, sutezolid and radezolid were also identified as hits against *M. chimaera.*

Conclusions: Here, we identified new chemical entities as well as oxazolidinone compounds that show good activity against *M. chimaera* that could lead promising new antimicrobials with further drug development. As well as identifying new compounds, we have identified the currently licensed antimicrobial doxycycline as showing efficacy against *M. chimaera.* Doxycycline is a commonly used and well-tolerated antimicrobial that should be investigated further as part of treatment regimens for *M. chimaera* infection.

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Abstract 1397

Anaplasmosis in Poland: underestimated disease?

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Background: Human cases of *Anaplasma phagocytophilum* infection are not frequently reported in Europe. However, the disease may be underdiagnosed due to the nonspecific nature of presenting symptoms. The aim of our study was to clarify the clinical picture of anaplasmosis through analysis of the symptoms and clinical signs displayed by infected patients in a cohort of tick-bitten individuals.

Materials/methods: The study included 1375 patients after a tick bite. Finally, 120 patients (8.7%) were diagnosed with anaplasmosis. Routine laboratory tests, serological and molecular microbiologic investigations were performed. Blood samples were examined by PCR for *A. phagocytophilum, Candidatus* Neoehrlichia micurensis*, B. burgdorferi*, *Babesia* spp.*, Coxiella burnetii* and *Bartonella* spp.. Positive samples were confirmed by sequencing. Serological analyses for tick-borne encephalitis virus and thin blood smears for detection of *Anaplasma* morulae were performed.

Results: Among 120 patients with HGA, there were 66 men (55%) and 54 women (45%). All patients had *A. phagocytophilum* DNA in blood samples that was detectable by standard PCR and confirmed by sequence analysis. 40 (33.3%) of patients were co-infected with *Borrelia burgdorferi*, 20 (17%) of patients were co-infected with TBEV, and one patient (0.83%) was co-infected with a *Babesia* spp. and 40 (33.3%) with *Borrelia burdgorferi*. Anaplasmosis patients presented with headaches, vertigo, nausea, vomiting, muscle pain, joints pain, and fever. Comparison of differences between patients with mono- and co-infection showed differences in symptoms and higher CRP concentration and AST activity in patients with co-infection. All patients recovered after doxycycline therapy.

Conclusions:

1. Anaplasmosis is not as rare in Europe, as it is thought to be.
2. Anaplasmosis often appears as a co-infection with other tick-borne pathogens.
3. Co-infection of *A. phagocytophilum* with *Borrelia burgdorferi* or TBEV may influence symptoms frequency.
4. PCR together with anamnesis, clinical picture and basic laboratory tests is a sufficient method for anaplasmosis diagnosis.
5. Doxycycline is an effective drug leading to complete recovery.

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Abstract 1403

Toxocariasis in children in south Russia: epidemiological and laboratory features

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Background: Clinical features of toxocariasis depend on geographic localization and age of patents. Aim: to investigate : epidemiological, clinical and laboratory features of toxocariasis in children in the South of Russia.

Materials/methods: We analyzed official statistical data in the period from 2014 to 2018 and implemented a retrospective analysis of 57 medical records of patients (40 children and 17 adults) who received treatment and were under observation in the clinic of infectious and parasitic diseases of the Rostov Scientific Research Institution of Microbiology and Parasitology, Rostov-on-Don, Russia.

Results: According to official statistics, the proportion of children aged 0 to 17 ranged from 33% to 37%Based on clinical and laboratory examination, the diagnosis was established in 26 patients (45.6%). Among patients with a verified diagnosis of toxocariasis, the proportion of children from 2 years and 5 months to 9 years old was 96.0%. An analysis of epidemiological data showed that 76.0% of children had close contact with the soil. The invasion occurred in the form of latent toxocariasis in 9 (35%) patients. In more than half of the children, the invasion was clinically manifested by geophagy (54.0%). A permanent laboratory indicator in patients with toxocariasis was the leukemoid eosinophilic type reaction. Peripheral blood eosinophilia ranged from 15.66.2 ± 9.31 with latent toxocariasis to 25.5 ± 15.0 with visceral. In some cases, this figure exceeded 60%. The coefficient of positivity (CP) in ELISA with toxocariasis antigen in patients with latent toxocariasis was higher than in the group of patients with visceral toxocariasis. No correlation between the level of eosinophilia and CP in ELISA with toxocariasis antigen was established in the each of group ($r = 0.1$).

Conclusions: The results of our analysis of the epidemiology of toxocariasis showed that preschool children (68.0%) who are in close contact with the soil (76.0%) are most susceptible to invasion, which does not correspond to the official statistical reporting data. Infestation in children is often asymptomatic (36% according to our data). If peripheral blood eosinophilia is detected, an ELISA test with a toxocariasis antigen is recommended.

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Abstract 1405

A clinical predictive model of multidrug resistance in neutropenic cancer patients with bloodstream infection due to *Pseudomonas aeruginosa* (IRONIC study)

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Abstract third-party references: On behalf of the IRONIC study group

Background: We aimed to assess the rate and predictive factors of bloodstream infection (BSI) due to multidrug-resistant (MDR) *Pseudomonas aeruginosa* (PA) in neutropenic cancer patients.

Materials/methods: We performed a multicenter, retrospective cohort study including onco-hematological neutropenic patients with BSI due to PA conducted across 34 centers in 12 countries from January 2006 to May 2018. A mixed logistic regression model was used to estimate a predictive model for developing multidrug resistance.

Results: 0 a total of 1217 episodes of BSI due to PA, 309 episodes (25.4%) were caused by MDR strains. The rate of multidrug resistance increased significantly over the study period (p=0.033). Predictors of MDRPA BSI were prior therapy with piperacillin/tazobactam (odds ratio [OR], 3.48; 95% confidence interval [CI], 2.29-5.30), prior antipseudomonal carbapenem use (OR, 2.53; 95% CI, 1.65-3.87), fluoroquinolone prophylaxis (OR, 2.99; 95% CI, 1.92-4.64), underlying hematological disease (OR, 2.09 95% CI, 1.26-3.44) and the presence of a urinary catheter (OR, 2.54; 95% CI, 1.65-3.91), whereas older age (OR, 0.98; 95% CI, 0.97-0.99) was found to be protective.

Conclusions: Our prediction model achieves good discrimination and calibration thereby identifying neutropenic patients at higher risk of BSI due to MDRPA. The application of this model using a web-based calculator may be a simple strategy to identify high-risk patients, who may benefit from the early administration of a broad-spectrum antibiotic coverage against MDR strains in accordance with the local susceptibility patterns, thus avoiding the use of broad-spectrum antibiotics in patients at low risk of resistance.

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Abstract 1408

Long-term suppressive treatment of cardiac surgery-related *Mycobacterium chimaera* disseminated infection

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Background: *M. chimaera* infections after cardiac surgery are characterized by high morbidity and mortality rate due to dissemination of infection and high affinity of mycobacteria to form biofilm on the prosthetic devices. Prolonged anti-mycobacteria treatment and removal of all cardiovascular prosthetic material (redo-operation) are suggested to obtain source control and avoid breakthrough infection. Nevertheless, in some patients, owing to comorbidities redo-operation is not feasible. The management of inoperable patients remains undefined especially regarding the number of drugs, the regimen and the length of anti-mycobacteria treatment. We report our experience on long term treatment of inoperable patients.

Materials/methods: We retrospectively reviewed all cases of *M. chimaera* infection following cardiac surgery diagnosed in our hospital.

Results: Nine patients were diagnosed with disseminated *M. chimaera* infection. Two females and 7 males, mean age 59 years . All patients were treated with an initial combination therapy: chlaritromycin, ethambutol and a rifamycin in addition to clofazimine or linezolid. Three underwent redo-operation, one died 48 hours after surgery owing to septic shock, the other had a breakthrough infection 9 months after surgery. One underwent redo-operation owing to a life-threatening periaortic abscess, before the diagnosis of *M. chimaera* infection was established. Among the six non re-operated patients three experienced a breakthrough infection, two of them died. Three are on long-term suppressive antibiotic therapy (chlaritromycin+ethambutol) after respectively 8, 14 and 18 months of four drugs, lead-in, anti-mycobacteria treatment. The blood, urine and stool culture are persistently negative, the clinical condition and quality of life are good, the therapy is well tolerated, no side effects occurred after respectively 21, 26 and 27 months of follow up.

Conclusions: The long follow up our of our non re-operated patients suggests that control of *M. chimaera* infection, in selected cases, is feasible with a long-term suppressive anti-mycobacteria therapy alone. We suggest that further studies should investigated the optimal timing and the criteria for redo-surgery and the final impact on patients survival. More clinical data are need to identify patients who will most benefit a conservative approach instead of implanted device substitution and to define the optimal medical therapy for inoperable patients.

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Abstract 1409

Usefulness of the 16S rRNA gene PCR and sequencing in the diagnosis of prosthetic joint infections

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Background: Microbiological cultures of prosthetic joint infections (PJI) often yields false negative results. We performed a prospective, comparative study to evaluate the usefulness of 16S RNA gene polymerase chain reaction and sequencing in the diagnosis of PJI

Materials/methods: Patients older than 18 years who underwent surgery for a suspected joint prosthesis infection according to 2012 IDSA definitions were included as cases and primary arthroplasties as controls. We analyzed all surgical samples using conventional cultured (identification was performed using phenotypic methods and MALDI-TOF MS) and 16S PCR and sequencing. Sensitivity, specificity, positive predictive value (PPV) and negative predictive value (NPV) were calculated for both methods.

Results: Twenty cases and 38 controls were included. Average age for cases 69.5 years (23-91) and 70 (24-90) for controls. We included 12 hips and 8 knees as cases and 19 hips and 19 knees as controls. Microorganisms were isolated by culture in 11/20 cases (*S. epidermidis 3*, S. *hominis* 3, S. *aureus* 2, E. *coli* 1, *E. cloacae* 1 and *Streptococcus viridans* group 1) and negative in 9. 16S PCR was positive in 18/20 cases (*S. epidermidis* 3, *S. aureus* 3, *S. hominis* 3, *Cutibacterium acnes* 3, *Streptococcus viridans* group 1, *E. faecalis* 1, *E. coli* 1, *E. cloacae* 1 and non-culturable microorganisms 2. Of the 9 negative cultures 16S PCR was positive in 7: *Cutibacterium acnes* 3, *E. faecalis* 1, *S. aureus* 1 and non-culturable microorganisms 2. In one case *Cutibacterium acnes* was detected by PCR in addition to the microorganism isolated by culture. Cultures and PCR were negative in 100% of the controls. For 16S PCR sensitivity was 90 %, specificity 100%, PPV 100 % and NPV 95%. For culture sensitivity was 55 %, specificity 100%, PPV 100 % and NPV 80.45

Conclusions: In our study 16S PCR and sequencing was a useful tool in the diagnosis of PJI in cases with negative culture and in polymicrobial infections, allowing the identification of bacteria not detected in the culture.

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Abstract 1416

Hospital organisation, management and implementation of culture of excellence in infection control and prevention of hospital-acquired infections at Ziv medical centre, Israel

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Background: Infections associated with health-care institutes are a threat to the medical treatment safety and manifest in 5-10% of the hospitalized patients. During the last three years we implement culture of excellence on infection control. The intervention was based on the ministry of health incentive model on infection control in Israel which include 33 measurement elements stratified to 8 categories: Inaction control team**,** hospital facility, hand hygiene training and compliance, computing support, quality parameters of microbiology laboratory, antibiotic stewardship, health care worker immunization and environmental cleaning and disinfection.

Materials/methods: Three years of implementation the culture of excellence and closing gaps in infection control elements supported by the hospital management. To achieve goals and excellence in infection control we empower nurses in infection control in each department, facility improvement, active surviellance of MDR bacteria, bacteremia and central line associated blood stream infection (CLABSI) and hand hygiene, implementation of guidelines of antibiotic treatment and stewardship, immunization of health care worker, training of physicians and nurses on central line insertion, maintenance and infusion therapy including total parenteral nutrition.

Results: Comparing data from 2016 to 2019, the immunization coverage of health care workers (HCW) rise from 33% to 92% respectively. CLABSI declined from 6 per 1,000 line days to 0.8. Hospital acquired UTI decline from 2.4/1000 hospital days at 2018 to 1.2 at 2019, Carbapenemase producing Enterobacteriaceia (CPE) decline from 27.8 /100K hospital days to 19.1, Carbapenem resistant *Acinetobacter baumannii* declined from 17.6/100k hospital days to 6.3. The score of excellence rise from 54.1% to 81.2%, being one of the higher score comparing with other governmental hospitals.

Conclusions: Management support and creating positive organization culture in infection control, bridging the facility gaps, training of staff, surveillance of processes and outcomes and monitor the quality of environmental cleaning are the main elements for hospital infection prevention of resistant bacteria and CLABSI, HCW protection from vaccine preventable diseases.

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Abstract 1419

Dose optimisation of cefotaxime in critically ill patients: a population pharmacokinetic study

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Background: Cefotaxime is a beta-lactam antibiotic used in critically ill patients to treat infections. Literature data on the pharmacokinetics (PK) of cefotaxime in these patients are lacking. A two-centre prospective, observational study in critically ill patients was undertaken. The aim of this study was to describe the PK of cefotaxime and propose a dosing regimen in critically ill patients.

Materials/methods: Critically ill patients treated with cefotaxime dosed 1g q6h or q4h were included. Five samples were drawn per patient during one dosing interval. PK parameters were estimated using NONMEM. Monte Carlo simulations (n=5000) were performed using Miclab 2.36 (Medimatics, NL) to determine Probability of Target Attainments (PTA). The percentage of patients reaching 100%*f*T>MIC was used to compare different dosing regimens for *Enterobacterales* and *S. aureus*.

Results: 92 patients (57 males), median age (range) of 64 (23-85) years, weight 76 (45-150) kg and creatinine clearance 57 (4-347) ml/min were included. A total number of 437 observations were analyzed. The best structural model was a two-compartment model with a combined error, and interindividual variability (IIV) on clearance (CL), central volume (V1), and intercompartmental clearance (Q). Correlations between IIV were included. CL increased with higher CKD-EPI (creatinine clearance) and higher albumin concentration and could explain 48% of IIV on CL. The estimates population parameters were 7.08 ml/min for CL; 15.7 L for V1; 25.0 L for V2 and 4.81 L/h for Q. For *Enterobacterales* (ECOFF 0.25 mg/L), 100% of patients reached the target with 1g q6h (15 minutes infusion time). For *S. aureus* (ECOFF 4 mg/L) a PTA of 64.2% and 88.8% was reached for the regimen 1g q6h and 1g q4h, respectively. With an increased dose of 2g q4h 97.3% of critically ill patients reached the target for *S. aureus*.

Conclusions: In critically ill patients, cefotaxime PK is best described by a two-compartment model with CKD-EPI and albumin concentration as covariates influencing clearance. All dosing regimens are adequate to treat *Enterobacterales*. However, this study indicates that for *S. aureus* the dosing regimen needs to be increased to 2g q4h administered over 15 min.

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Abstract 1420

High-resolution influenza mapping of a city reveals socioeconomic determinants of transmission within and between urban quarters

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Background: With two-thirds of the global population projected to be living in urban areas by 2050, understanding the transmission patterns of influenza within cities is crucial for effective prevention strategies. Here, in unprecedented spatial resolution, we analysed the socioeconomic determinants of influenza transmission in a European city (Basel, Switzerland). We aimed to described the incidence rates of influenza cases and transmission patterns in context to socioeconomic determinants.

Materials/methods: Our dataset included all PCR confirmed influenza cases from 2013 to 2018. We conducted a large city-wide survey with more than 30000 distributed questionnaires (2015/2016 season). Whole genome sequencing (WGS) data of 663 viral isolates was used to analyse the transmission network (2016/2017 season). We combined geographical and epidemiological data with WGS of influenza viruses at the scale of urban quarters and statistical blocks, the smallest geographic subdivisions within a city.

Results: We observed annually re-occurring geographic hotspots of influenza incidences, mainly associated with net income, and independent of population density and living space. In the questionnaire, vaccination against influenza was positively associated with household income and negatively linked to the likelihood of influenza-like illness within an urban quarter. Of WGS samples (n=663), a diverse set of 54 clusters (within 10 SNPs cut-off) were observed within the city. The phylogeny of isolates reflected the global diversity. A generally high exchange rate and complex transmission dynamic between different urban quarters was observed. Significant within quarter transmission was observed for two quarters with low socioeconomic scores and lower pre-seasonal herdimmunity as determined by heagglutination inhibition assays.

Conclusions: High-resolution city-level epidemiological studies combined with social science surveys such as this will be essential for understanding infectious disease transmission chains and delivering tailored public health information and vaccination programs at the municipal level.

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Abstract 1430

Outcome impact of a highly bactericidal scheme as initial treatment of acute staphylococcal PJI

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Background: *S. aureus* is one of the most common pathogens involved with acute PJI. Management usually involves DAIR and antibiotic treatment. Here we present the evaluation of our experience with a scheme of treatment that combines a high bactericidal combination followed by a antibiofilm combination.

Materials/methods: Between April 2011 and October 2018, 48 acute PJIs caused by *S. aureus* were treated with DAIR in our center, (15TKA and 33 THA). Time between index surgery and DAIR, antibiotic treatment scheme and follow-up were revised. We have compared the results between the new antibiotic scheme (5 days of daptomycin + cloxacilin followed by levofloxacine+rifampicin) with the previous combinations, based in the use of less-bactericidal combinations, mainly comprising vancomycin plus rifampicin or levofloxacin plus rifampicin.

Results: 23 patients were treated with DAIR diverse antibiotic combinations, after a mean period of 22.7 days after index surgery (range 12-39) and received a mean of 102.8 days af antibiotic treatment (range 35-180). 16 of them (63.6%) were free of infection after 30.6 months of follow-up(range 2-60). 25 patients were treated with DAIR and a new antibiotic scheme, which includes 5 days of daptomycin + cloxacillin (a combination with high bactericide power), followed by levofloxacine+rifampicin, with anti-biofilm properties, during a mean period of 101.4 days (range 45-180). 21 of them (84%) were free of infection after 11.3 months of follow-up (range 1.5-30). Although the limited sample size does not let us talk in terms of statistical signification, the difference in the healing rate depending on antibiotic treatment shows high clinical relevance. We have observed that this difference is higher when the period between index surgery and DAIR is less than 30 days (89.3% vs 63.2%).

Conclusions: The combination of daptomycin +cloxacilin plus levofloxacine+rifampicin, which combines an initial high bactericidal therapy followed by an antibiofilm activity, shows higher healing rates for treatment of acute PJIs caused by *S. aureus* and treated with DAIR.

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Abstract 1431

Diagnosis of acute dengue infection in Navarra

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Background: The aim of this study is to analyze the new diagnosis of dengue virus infection in our hospital from January 2016 to September 2019.

Materials/methods: Retrospective study of 255 samples from 227 different patients with possible dengue virus infection; 82 PCR and 173 serology tests were performed. Clinical history of each patient was studied to obtain clinical and epidemiological information. Cases of dengue were defined by clinical symptoms, epidemiological link and positive PCR and/or IgM detection and/or seroconversion. PCR was performed by TropicalFeverCore real-time PCR kit (FastTrack Diagnostics); for serology tests we used Dengue IgM and IgG capture ELISA kit (Panbio) and Dengue Virclia® IgM and IgG monotest (Vircell).

Results: Among all patients studied, 23 (10.1%) were diagnosed of dengue infection; mean age was 38.6 years (SD±11.4 years) and 13 were females (56.5%). Regions of birth were: Europe (60.9%), Africa (8.7%) and South America (30.4%). All patients had travelled to any dengue endemic country in Africa (17.4%), Asia (30.4%) and South/Central America (52.2%). In all cases the onset of symptoms happened during the journey or within 10 days after returning.

Main clinical manifestations were fever (100%), arthralgia/myalgia (60.9%), headache (43.5%) and cutaneous rash (34.8%); 10 cases (43.5%) presented thrombocytopenia and leukopenia. No clinically severe manifestations were observed.

Regarding diagnosis, 7 (30.4%) were performed by PCR and 15 (65.2%) were based on serology: 11 (73.3%) with IgM+/IgG+ and 4 (26.7%) with IgM+/IgG-. One case (4.3%) was confirmed by both PCR and serology. Different serum samples were available only in 2 patients (8.7%) and in both serconversion was demonstrated.

Conclusions:

- All diagnosis were of imported dengue infection in travellers returning from endemic countries.
- Due to the short period of viremia the possibility of PCR based diagnosis is low. 65.2% of diagnosis were performed only by serological assays, 26.7% of which were based only on IgM reactivity.
- The availability of a second serum sample should be taken into account as an improvement in diagnostic procedure to allow confirmation of diagnosis in these cases by seroconversion.

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Abstract 1432

Antimicrobial susceptibility of *Cutibacterium avidum* isolated from prosthetic joint infections: differences between biofilms and planktonic bacteria

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Background: *Cutibacterium avidum* is a Gram positive anaerobic rod and known to colonize human moist skin such as the groin. Rarely, it causes abscesses, and hip and shoulder peri- prosthetic joint infections (PJI), and is usually susceptible to Penicillin. However, data about antibiotic susceptibility against planktonic and biofilm *C. avidum* are limited.

Materials/methods: We tested the activity of different antibiotics against planktonic and biofilm *C. avidum* in vitro (n=11 isolates from different PJI cases, identified by MALDI-TOF MS). Minimal inhibitory concentrations (MIC) and minimal bactericidal concentrations (MBEC) were evaluated according to the microdilution method by EUCAST, using Mueller Hinton cation adjusted broth with a final bacterial inoculums of 10^4 CFU per well. The minimal biofilm inhibitory concentration (MBIC) and the minimal biofilm eradication concentration (MBEC) were assessed following the protocol previously described by Coenye *et al.* (Res Microbiol. 2007 May; 158(4):386-92). Plates were incubated at 37ºC for 48 hours under anaerobic conditions.

Results: The MIC, the MBC, and MBIC were low for amoxicillin-clavulanic acid, clindamycin, levofloxacin, linezolid, rifampin, and vancomycin (table 1). However, the MBEC to eradicate the biofilm *C. avidum* were high with > 32mg/l except for rifampin with 0.5 mg/L.

Antibiotic	MIC_{90}	MBC_{90}	$MBIC_{90}$	$MBEC_{90}$
Penicillin	0.125 mg/L	0.5 mg/L	0.125 mg/L	> 32 mg/L
Amoxicillin-clavulanic acid	0.5 mg/L	0.5 mg/L	1 mg/L	256 mg/L
Clindamycin	0.5 mg/L	2 mg/L	2 mg/L	>256 mg/L
Levofloxacin	0.25 mg/L	1 mg/L	0.5 mg/L	>32 mg/L
Linezolid	0.5 mg/L	4 mg/L	0.25 mg/L	>256 mg/L
Rifampin	0.03 mg/L	0.03 mg/L	0.03 mg/L	0.5 mg/L
Vancomycin	1 mg/L	2 mg/L	1 mg/L	256 mg/L

Conclusions: While all tested antibiotics showed bactericidal activity against planktonic *C. avidum* cells, eradication of biofilm *C. avidum* was only possible with rifampin. Currently, we are investigating the value of rifampin for cure of *C. avidum* PJIs in a large multicenter study.

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Abstract 1435

Increased serum hydrogen sulfide as determinant of resolution of ventilator associated pneumonia caused by *P. aeruginosa*

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Background: Previous data of our group in mice (Renieris G, et al. ECCMID 2018; abstract P0904) showed that host production of hydrogen sulfide (H_2S) is modulating host defense against *Pseudomonas aeruginosa*. However, clinical data on the significance of host-derived H_2S are lacking. This study investigated the role of host-derived H_2S in the outcome of ventilator associated pneumonia (VAP).

Materials/methods: From a prospective cohort of 700 Greek patients with VAP, 219 cases caused by *P. aeruginosa* (group A, n=65), *Klebsiella pneumoniae* (group B, n=60) and *Acinetobacter baumannii* (group C, n=94) were selected. Pathogens grew at $\geq 10^5$ cfu/ml in tracheobronchial secretions. H_2S was measured by the blue methylene method in serum the first 24 hours.

Results: Serum levels of H_2S were significantly higher in the resolved VAP cases of group A compared to the non-resolved cases (55.63 ± 10.93 vs 20.98 ± 4.30μM respectively; p: 0.030). Respective values for group B were 16.03 ± 1.36 vs 16.15 ± 2.15 (p: 0.965) and for group C 17.90 ± 1.05 vs 17.16 ± 1.77 (p: 0.711). Further ROC curve analysis of group A indicated that serum H_2S above 45μM could better discriminate resolved cases; 17 patients had more and 48 patients less than 45μM H_2S. VAP resolved in 16 (94.1%) and in 27 (56.3%) patients, respectively (p: 0.004). Logistic regression analysis showed that serum H_2S above 45μM was an independent protective factor for VAP resolution (Table).

	HR	95% CIs	p
Serum H_2S day 1 > 45 μM	0.03	2.70 – 0.37	0.006
APACHE II day 1 > 23	2.98	0.54 – 16.38	0.210
SOFA day 1 > 10	7.05	1.37 – 36.32	0.020
Isolation of *P. aeruginosa* in blood	3.14	0.59 – 16.62	0.179
HR: Hazard ratio; CI: Confidence intervals			

Conclusions: Circulating H_2S in a novel independent determinant of the outcome of VAP caused by *P. aeruginosa*. This may open new boundaries in personalized therapeutics of VAP.

The study was funded by the ITN Horizon 2020 Marie-Curie European Sepsis Academy

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Abstract 1437

Multi-centre study of common pathogen epidemiology in hospitalised children with acute respiratory tract infection in winter from 2017 to 2018, China

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Background: Acute respiratory tract infections (ARTIs) are a major public health problem and a leading cause of morbidity and mortality in children under the age of 5 years, with the highest number of deaths occurring in developing countries. This study aimed to analyze the epidemiological characteristics of pathogens among children hospitalized with ARTIs during the winter, with the aim of providing a reliable basis for clinical diagnosis and treatment and for rational antibiotics use.

Materials/methods: A total of 563 hospitalized children with ARTIs in the children's hospitals of Shanghai, Hangzhou, and Soochow were enrolled between November 2017 and February 2018, and nasopharyngeal aspirates were collected. Real time PCR assays were performed to detect 14 common pathogens, including *Mycoplasma pneumoniae* (MP), *Chlamydia pneumoniae* (CP), *Legionella pneumophila* (LP), *Chlamydia trachomatis* (CT), respiratory adenovirus (ADV), influenza virus A and B (IFV-A and IFV-B), human parainfluenza virus types 1-3 (HPIV 1-3), human rhinovirus (HRV), respiratory syncytial virus (RSV), and human metapneumovirus A and B (hMPV-A and hMPV-B).

Results: Of the 563 specimens obtained from the patients, 467 (82.95%) were positive for at least one pathogen. RSV was the most commonly detected pathogen (48.66%), followed by HRV (21.49%). The detection percentages for each of the respiratory pathogens varied considerably by age. RSV was the most common pathogen detected in the children aged less than 6 months. Co-infections were found in 20.6% of the patients. Of these coinfections, the combination of RSV and HRV was the most common.

Conclusions: The detection percentages of respiratory viruses and atypical bacteria in ARTI children was relatively high during the winter in the children's hospitals in Shanghai, Hangzhou, and Soochow. The pathogen incidence varied depending on patient age and ARTI manifestation.

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Abstract 1439

Risk factors for hospital readmission following complicated urinary tract infection: a multinational, retrospective cohort study

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Background: Patients surviving hospitalization are frequently readmitted. About 20% of patients are re-hospitalized during the first month after discharge. These readmissions have a vast implication by negatively influencing the patients' quality of life and imposing a significant economic burden on the health care system. Understanding the avoidable risk factors for readmission may inform policy for optimal care during hospitalization and proper post-discharge ambulatory care.Therefore, we aimed to determine potentially preventable risk factors for 60-day readmission in patients surviving hospitalization for complicated urinary tract infection (cUTI).

Materials/methods: This was a multinational, multicentre retrospective cohort study conducted in Europe and the Middle East. Our cohort included survivors of hospitalization due to cUTI during the years 2013-2014. The primary outcome was 60-day readmission following index hospitalization. Patient characteristics that could have influenced readmission: demographics, infection presentation and management, microbiological and clinical data; were collected via computerized medical records from infection onset up to 60 days after hospital discharge.

Results: Overall, 742 patients were included. The median age of the participants was 68 years (interquartile range, (IQR) 55-80) and 43.3% (321/742) of patients were males. The all-cause 60-day readmission rate was 20.1% (149/742) and more than half were readmitted for infection [57.1%, (80/140)]. Recurrent cUTI was the most frequent cause for readmission [46.4% (65/140)]. A quarter of non-infection related readmissions were for urinary tract abnormalities or instrumentation. Statistically significant risk factors associated with 60-day readmission in the multivariable analysis were: older age (OR 1.02 for an one-year increment, CI 1.005-1.03), diabetes mellitus (OR 1.63, 95% CI 1.04-2.55), cancer (OR 1.7, 95% CI 1.05-2.77), previous UTI infection in the last year (OR 1.8, 95% CI: 1.14 - 2.83), insertion of an indwelling bladder catheter (OR 1.62, 95% CI 1.07-2.45) and insertion of percutaneous nephrostomy (OR 3.68, 95% CI 1.67-8.13). Length of hospital stay and discharge to long term facilities were not statistically associated with readmission.

Conclusions: Patients surviving hospitalization for cUTI are frequently re-hospitalized, mostly for recurrent urinary infections associated with a medical condition that necessitated urinary interventions. Interventions to avoid re-admissions should target these patients.

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Abstract 1442

Clinical impact of rapid susceptibility testing in Gram-negative bloodstream infections

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Abstract third-party references: St. George's University of London, National Institute for Health Research (NIHR) Collaboration for Leadership in Applied Health Research and Care (CLAHRC) South London, UK

Background: Rapid antimicrobial susceptibility testing (AST) might have the potential to improve patient care when results are available and communicated to clinicians in a timely manner. The aim of service evaluation is to assess the clinical impact of rapid susceptibility testing in patients with Gram-negative BSI.

Materials/methods: A prospective service-evaluation was conducted from March 2018 to December 2018 at St. George's Hospital, London. Alfred 60AST system had been introduced to routine clinical management for AST of Gram-negative bacteria, directly from positive blood cultures. In routine practice, the Alfred 60AST was only run Monday-Friday before midday and results were communicated to clinicians in the same working day of positive blood culture. Patients in which the culture became positive after midday were tested by conventional AST (Phoenix). Times-to-antibiotic and clinical outcomes were compared between rapid and conventional AST. Odds ratio for discontinuation of antibiotics were generated.

Results: 191 patients were included, 93 in the rapid group and 98 in the standard group. The two groups did not differ with regard to co-morbidity, severity, source of infection, source control, multidrug-resistant organisms. The median time between blood culture collection and the reporting time of AST results was 36h (IQR; 16 – 123) in the rapid group and 63h (IQR; 34 – 5760) in the standard, p<0.001. Time to optimal antibiotic was shorter in the rapid group 43h (IQR; 3-339) vs 66.5h (IQR; 0-872), p=0.023. Aminoglycosides were stopped earlier in the rapid group 32h (IQR; 0-795) vs 54h (IQR; 4-216), p=0.002. Effective antibiotic escalation guided by AST results was initiated earlier in the rapid group 36h (IQR; 0-335) vs 51h (IQR; 2-408), p=0.028. Rapid AST and escalation of non-aminoglycosides by 48h were predictors for discontinuation of aminoglycosides at 48 hours (OR, 2.1 ; 95% [CI 1.1- 3.9], p=0.03) and (OR, 3.4 ; 95% [CI 1.7- 6.9], p<0.01) in binary logistic regression. No differences were found in 28-day mortality, length of stay, time to discharge, time to effective antimicrobial or time to stop all antibiotics.

Conclusions: Rapid susceptibility testing resulted in faster discontinuation of aminoglycosides and a shorter time to escalate beta-lactam therapy and to start optimal antibiotic.

Demographics	RAPID n = 92	STANDARD n = 98	p-value
Male	50 (54%)	49 (49.5%)	0.565
Age in years (Mean; SD)	65.4 (SD 20)	63.7 (SD 25)	0.607
Charlson index score (Mean; SD)	5.7 (SD 2.8)	5.6 (SD 2.9)	0.665
Pitt bacteraemia score (> = 2)	43 (43%)	49 (50%)	0.36
Escherichia coli in blood culture	62 (67%)	56 (57%)	0.142
Extended-spectrum-betalactamase organism (ESBL)	16 (17%)	12 (12%)	0.773
Urinary source of blood stream infection	48 (52%)	49 (50%)	0.938
Empiric effective antimicrobial	84 (90%)	84 (86%)	0.378
Antimicrobial outcomes *			
Time to AST communication results	36 h (IQR; 16 - 123)	63 h (IQR; 34 - 5760)	**<0.001**
Time to first effective antibiotic	2 h (IQR; 0 – 97)	3 h (IQR; 0 – 83)	0.205
Time to stop aminoglycosides	32 h (IQR; 0 - 795)	54 h (IQR; 4 - 216)	**0.002**
Time to effective escalation	36 h (IQR; 0 - 335)	51 h (IQR; 2 - 408)	**0.006**
Time to Optimal antimicrobial	43 h (IQR; 3 - 339)	67 h (IQR; 0 - 872)	**0.023**
Clinical outcomes			
Mortality at 28 days	7 (8%)	13 (13%)	0.240
Length of stay	11 (IQR; 0-47)	10.5 (IQR; 0-71)	0.84

*(times-to-event was measured from the time of blood culture collection)

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Abstract 1448

Antimicrobial susceptibility of bacteria isolated from patients with pneumonia in Brazil, Argentina, and Mexico: results from the SENTRY programme in Latin America (2015-2018)

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Background: The SENTRY Antimicrobial Surveillance Program monitors the frequency of occurrence and antimicrobial susceptibility of organisms from various infection types worldwide. We evaluated the frequency of occurrence and antimicrobial susceptibility results for organisms isolated from patients hospitalized with bacterial pneumonia in 3 Latin American countries.

Materials/methods: A total of 977 bacterial isolates were consecutively collected (1/patient) in 2015-2018 from 7 Latin American medical centres located in Brazil (n=427; 3 centres), Argentina (n=281; 2 centres) and Mexico (n=269; 2 centres). Organisms were tested for susceptibility by reference broth microdilution method in a central laboratory (JMI Laboratories). EUCAST and CLSI breakpoints were applied.

Results: The most common organism was *P. aeruginosa* in Brazil and Argentina, and *A. baumannii* in Mexico (Table). *P. aeruginosa, S. aureus, K. pneumoniae,* and *A. baumannii* represented the top 4 organisms in all 3 countries and accounted for 71.2-80.7% of the collection. Gram-negative bacilli (GNB) represented 75.6%, 81.9% and 92.6% of organisms; and non-fermentative (NF) GNB represented 45.4%, 43.8%, and 49.1% of organisms in Brazil, Argentina, and Mexico, respectively. *P. aeruginosa* susceptibility to ceftazidime, piperacillin-tazobactam, and meropenem were 87.0%, 79.7%, and 79.7% in Brazil, 72.3%, 69.1%, and 62.8% in Argentina, and 81.2%, 85.4%, and 79.2% in Mexico, respectively. Only 7.5% of all *A. baumannii* isolates (0.0-12.5%) were meropenem-susceptible. Besides colistin (96.9-100.0%S), the most active agents tested against *A. baumannii* were minocycline and tobramycin, with susceptibility rates (CLSI) of 100.0% and 68.8% in Brazil, 56.0% and 36.0% in Argentina, and 69.2% and 33.8% in Mexico, respectively. Overall MRSA rates were 22.2% in Brazil, 25.0% in Mexico, and 40.4% in Argentina, and decreased during the study period. *K. pneumoniae*, susceptibility (EUCAST) to ceftriaxone and meropenem were 34.0% and 54.0% in Brazil, 44.1% and 73.5% in Argentina, and 49.3% and 84.9% in Mexico, respectively. CRE rates were 17.1%, 12.1%, and 12.0% in Brazil, Argentina, and Mexico, respectively.

Conclusions: GNB represented a large proportion (75.6-92.6%) and NF-GNB accounted for almost half of organisms isolated from patients with pneumonia, and resistance rates were extremely high among these organisms. In contrast, a decreasing trend was observed in MRSA rates.

Rank	Frequency of top 7 organisms stratified by country		
	Brazil (n=427)	**Argentina (n=281)**	**Mexico (n=269)**
1	*P. aeruginosa* (32.3%)	*P. aeruginosa* (33.5%)	*A. baumannii* (28.3%)
2	*S. aureus* (21.1%)	*S. aureus* (16.7%)	*K. pneumoniae* (27.1%)
3	*K. pneumoniae* (11.7%)	*K. pneumoniae* (12.1%)	*P. aeruginosa* (17.8%)
4	*A. baumannii* (7.5%)	*A. baumannii* (8.9%)	*S. aureus* (7.4%)
5	*S. marcescens* (4.9%)	*P. mirabilis* (6.8%)	*E. cloacae* (5.6%)
6	*E. cloacae* (3.5%)	*E. coli* (5.7%)	*E. coli* (4.8%)
7	*S. maltophilia* (3.3%)	*S. marcescens* (5.7%)	*S. maltophilia* (2.6%)

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Abstract 1449

Do patients colonised by carbapenemase-producing *Klebsiella pneumoniae* have greater crude mortality? ANGEL-KpS Study

Ángela Cano Yuste*[1], Manuel García[2], Marina Gallo-Marín[1], Isabel Machuca[1], Irene Gracia-Ahufinger[3], Julian Torre-Giménez[4], Azahara Frutos[4], Lara Kindelán-Segador[4], Elena Perez-Nadales[4], Alejandra M.Natera[4], Juan José Castón[1], Jesús Rodríguez-Baño[5], Luis Martinez-Martinez[3], Julián De La Torre Cisneros[1], Belén Gutiérrez-Gutiérrez[5]

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Background: Carbapenemase-producing *Klebsiella pneumoniae* (KPC-Kp) infections are associated with high mortality rate. Colonization has been associated with higher risk of death.We evaluated the association of intestinal colonization by KPC-Kp with crude and attributable mortality and investigated the impact of infection in this association.

Materials/methods: Observational, prospective, longitudinal cohort study of patients at risk of colonization by KPC-Kp, at Reina Sofia University Hospital in Cordoba,Spain from July'2012 to November'2017.Patients were studied by rectal swab and followed-up for 90 days; rectal swab was repeated in negative patients during the follow-up (weekly in the intensive care and hematology units and before completing the follow-up in the rest of services).Cox regression was used to study variables associated with mortality from any cause. Survival curves were represented according to Kaplan-Meier.A competitive risk analysis was performed to study mortality risk factors specifically related to KPC-Kp infection.

Results: 1244 patients (1078 not colonized and 166 colonized) were included. None of the non-colonized patients developed KPC-Kp infection, while 74 (44.6%) of the colonized did.The crude 90-day-mortality was: 194/1078(18%) in non-colonized and 69/166(41.6%) in colonized.The variables associated with crude mortality in the Cox regression analysis were: KPC-Kp infection with INCREMENT score>7 (HR:1.84; 95%CI:1.19-2.86; p=0.006), hospitalization in a high-risk service (HR:3.16;95%CI:2.31-4.32; p<0.001), neutropenia (HR: 2.49;95%CI:1.56-3.98; p<0.001), neoplasia (HR:1.42;95%CI:1.08-1.88; p=0.01), chronic kidney disease (HR:1.56;95% CI:1.14-2.14; p=0.005), age (HR:1.02; 95%CI:1.01-1.03; p<0.001) and mechanical ventilation (HR:2.37 ; 95%CI:1.83-3.06; p<0.001).Competitive risk analysis using a risk subdistribution model (SHR) found that infection with INCREMENT score> 7 (SHR:66.13;95%CI:32.23-135.70; p<0.001) but not colonization was associated with attributable mortality. The period July'2012-August'2014 was also associated with attributable mortality (SHR:3.19; 95%CI:1.62-6.28; p<0.001).After this period, the attributable mortality decreased from 8.5% to 1.4%, coinciding with the onset of intestinal decontamination in patients at risk and treatment with ceftazidime-avibactam.

Conclusions: Being colonized was a necessary, but not sufficient condition, to develop an infection due to KPC-Kp infection and die.Intestinal colonization by KPC-Kp was not associated with increased mortality by itself.The risk of death from KPC-Kp is increased when colonized patients develop severe KPC-Kp infection (INCREMENT>7), and the lower mortality observed since August 2014 could be due to changes in the clinical management.

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Abstract 1452

Mandatory computerised decision support system is necessary for sustained control of carbapenems and piperacillin-tazobactam usage in a multi-faceted hospital antimicrobial stewardship programme: interrupted time series with segmented regression analysis

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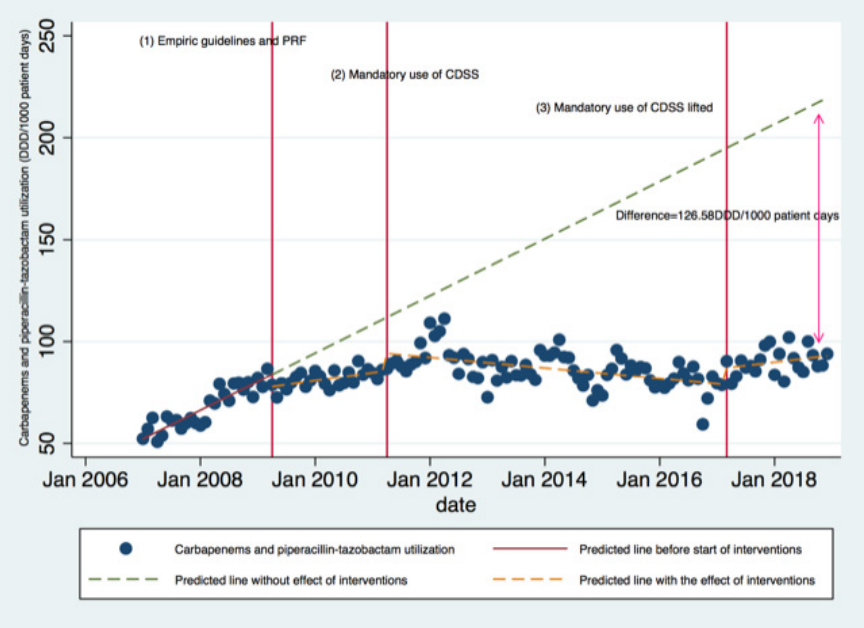
Background: As the use of piperacillin-tazobactam and carbapenems was rising in a public tertiary-care hospital in Singapore, antimicrobial stewardship (AMS) interventions targeting these two classes were introduced; empiric antibiotic guidelines and prospective review and feedback (PRF) in April 2009, and mandatory use of computerised decision support system (CDSS) in April 2011. Mandatory CDSS was lifted in March 2017 for half of the hospital's wards for a 6-month cluster-randomised study. We aimed to examine the impact of the interventions on the utilisation of carbapenems and piperacillin-tazobactam.

Materials/methods: Monthly utilisation of carbapenems and piperacillin-tazobactam in defined daily doses (DDD) per 1,000 patient-days from January 2007 to December 2018 were obtained from the hospital's database. The impact of AMS interventions was analysed by segmented regression analysis of interrupted time series.

Results: The starting level of the carbapenems and piperacillin-tazobactam utilization in January 2007 was 52.19 DDD/1,000 patient-days, and the average rate of increase was 1.17 per month prior to any interventions. When empiric antibiotic guidelines and PRF were implemented in April 2009, there was a reduction of 6.01 (95% confidence interval [CI]: -9.82, -2.20) in the same month, with an increase of 0.33 per month (95% CI: 0.18, 0.48) post-intervention. When mandatory CDSS usage was implemented, the utilisation level increased by 8.45 (95% CI: 2.82, 14.08) in the same month, followed by a reduction at a rate of 0.22 per month (95% CI: -0.33, -0.10). When mandatory CDSS usage was lifted in March 2017, the utilisation level increased by 8.29 (95% CI: 2.63, 13.94) in the same month, and the utilisation rate changed to an increase of 0.28 per month (95% CI: 0.02, 0.55).

By the end of the study period, we estimated an absolute reduction of 126.58 DDD/1,000 patient-days in the monthly utilisation of carbapenems and piperacillin-tazobactam due to the impact of the AMS interventions.



Conclusions: The AMS strategies led to a significant reduction of carbapenems and piperacillin-tazobactam utilisation over 10 years. However, the significant increase in utilisation when mandatory CDSS was lifted highlights the importance of having a mandatory CDSS combined with other strategies to ensure sustained control of antibiotic use.

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Abstract 1453

Development and implementation of an electronic admission-screening tool for *Candida auris* at a large healthcare system in Miami, Florida

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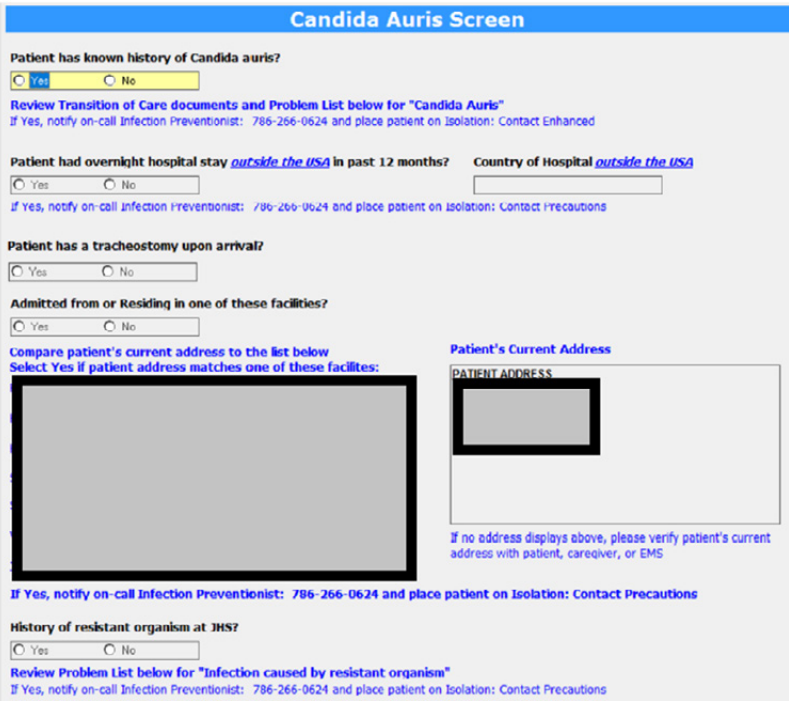
Background: *Candida auris (C.auris)*, an emerging multidrug-resistant yeast, is considered an urgent public health threat worldwide. We describe the use of an electronic tool to screen all patients for risk factors associated with *C.auris* upon admission to all facilities within a large health system in Miami, Florida.

Materials/methods: Starting August, 2019, we implemented a mandatory questionnaire within the electronic medical record (EMR) applied to all patients at the time of triage to any of our facilities. The tool asked in a conditional branching fashion if the patient had: 1. History of *C.auris*; 2. Overnight hospital stay outside the continental USA in last 12 months; 3. Tracheostomy present on admission and transferred from a facility with high risk for C.auris; and 4. Recent history of extensively-resistant-organism. Answering "yes" to any of the questions automatically generated an order for contact precautions and requested notification to the infection control department (IPD). As follow up, the IPD verified placement in proper isolation precautions and coordinated collection of screening cultures from axilla and inguinal areas. Screening cultures were processed by the Antibiotic Resistance Laboratory Network in Tennessee, USA. If the screening culture was positive, the patient remained in enhanced contact precautions for the duration of admission; if the result was negative, isolation precautions were discontinued.

Results: A total 37390 patients (47428 encounters) were screened with the questionnaire from implementation to November 17th, 2019. Only 103 patients met criteria for isolation precautions and *C.auris* screening cultures; of those, four patients had previous history of *C.auris*, 23 had overnight hospital stay outside the USA (Bahamas, Canada, China, Colombia, Cuba, Dominican Republic, Haiti, Honduras, Jamaica, Nicaragua, Spain, US Virgin Islands, and Venezuela), and 76 had tracheostomy and were transferred from a facility with risk for *C.auris*. Of the 103 screening cultures collected, only the ones with previous history of *C.auris* were positive; all four cases were transferred from local long-term-care facilities.

Conclusions: Electronic screening tools incorporated in the EMR are effective means to detect carriers of highly resistant/transmissible organisms, thus facilitating early implementation of infection control interventions aimed to prevent the spread to such organisms within healthcare facilities.



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Abstract 1454

What are the risk factors associated with development of infection by carbapenemase-producing *Klebsiella pneumoniae*? ANGEL-KpS study

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Background: Carbapenemase-producing *Klebsiella pneumoniae* (KPC-Kp) infections are associated with high mortality risk. We previously reported that colonization by KPC-Kp is necessary but not sufficient for development of KPC-Kp infection. In this study, we analyzed the risk factors associated with development of infection during 90 days of follow-up.

Materials/methods: Observational, prospective, longitudinal cohort study of patients at risk of KPC-Kp colonization, from a tertiary hospital in the South of Spain from July'2012 to November'2017. All patients with risk factors for colonization were subjected to colonization study. Only those who became colonized by KPC-Kp at the beginning or during the follow-up were included in this analysis. Differences in the risk of infection were evaluated by CART analysis, according to different time periods. The infection risks were represented by Kaplan-Meier curves. Logistic regression was used to identify variables associated with the development of KPC-Kp infection after assessing that proportional hazard assumption for Cox regression was not fulfilled.

Results: 166 KPC-Kp colonized patients were included. Previously, CART established a high-risk period from July'2012 to August'2014, where the infection rate was 53% in comparison to the period from September'2014 to November'2017 in which it decreased to 38.5%. Among 118 patients who became colonized at the beginning of follow-up, 45 (38.1%) developed infection versus those colonized "during follow-up" (60.4%; 29/48). Through logistic regression, the variables associated with development of KPC-Kp infection were: colonization detection during follow-up (OR:2.68;95%CI:1.07-7.00;p =0.04), Giannella risk score (OR:1.42;95%CI:1.27-1.62;p<0.001), high risk period (OR:3.60;95%CI:1.25-11.11;p= 0.02), high risk ward (OR:4.97,95%CI:1.82-14.90;p=0.003) and urological manipulation after admission (OR:2.96;95%CI:0.95-10.75;p=0.07). A multivariate logistic regression analysis confirmed the same risk factors for developing KPC-Kp infection in patients with high risk of death (INCREMENT-CPE score>7).

Conclusions: According to our results, in addition to a high Giannella score, the moment in which the colonization occurs and the ward where the patient is admitted, would be factors to assess when considering empirical treatment to cover KPC-Kp in the case of a suspected infection.

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Abstract 1457

Necrotising external otitis (NEO): analysis of risk factor for relapse in 66 patients managed during a 12 year period in a reference centre

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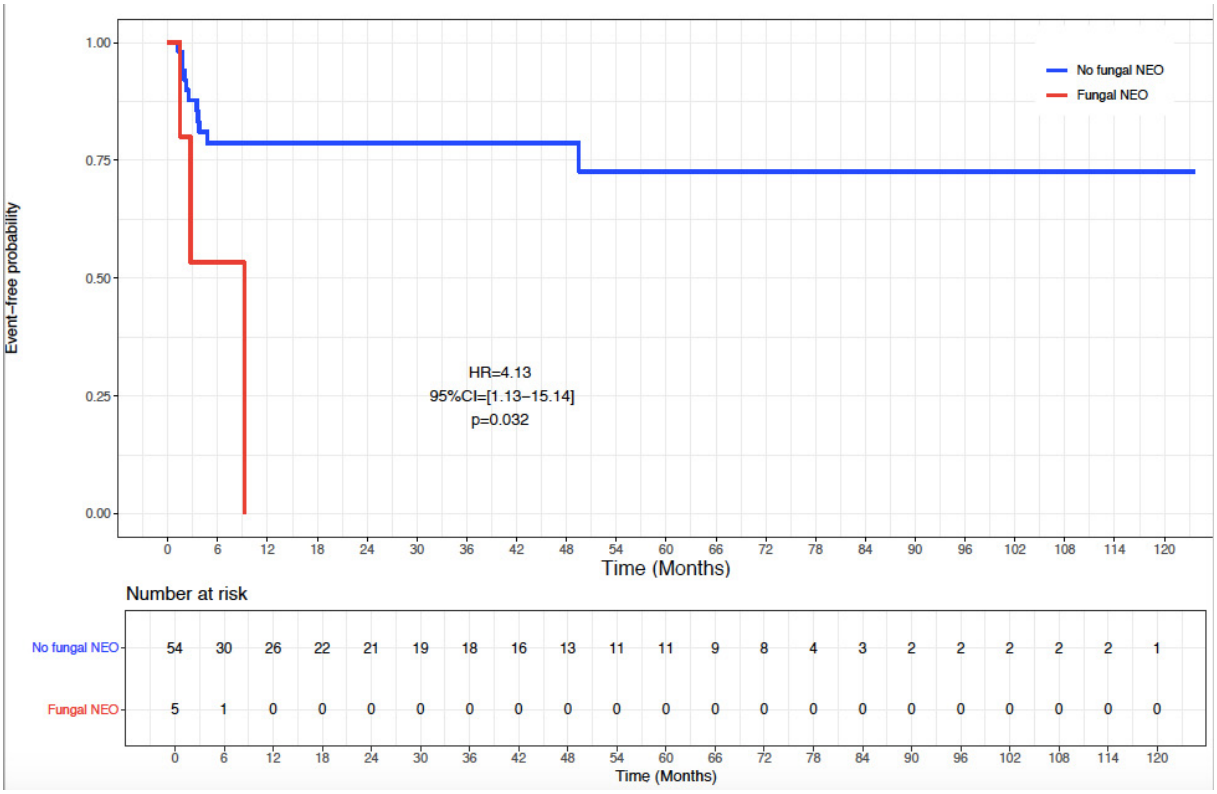
Background: NEO is a complex bone and joint infection (BJI) of the skull base that occurred generally in the elderly and/or diabetic patients. There are few data in the literature about its therapeutic management. The aim of our study was to determine risk factor for relapse.

Materials/methods: Retrospective cohort study in a reference center for the management of complex BJI. Consecutive cases of NEO over 2006 to 2018 period were included. Diagnosis was done during otoscopy, supplemented by a dedicated imaging. Risk factor for relapse were analyzed by using Cox regression survival analysis with adjusted Hazard Ratio (aHR) and Kaplan Meier curve.

Results: Among the 66 patients included (median age, 74 years), most of them had diabetes (n=46, 72%), including 35 (53%) under insulin therapy; 11 (17%) had temporomandibular arthritis, 10 (15%) cranian nerve paralysis, 2 (3%) cerebrals thrombophlebitis, and 2 (3%) contiguity abscess. Samples were obtained during otoscopy: dedicated swab (n=49, 74%), 8 (12%) surgical biopsies, and 3 (4%) both of them. *P. aeruginosa* was involved in 44 patients (67%; all susceptible), 5 patients (7,5%) had fungal NEO at baseline (3 *A. fumigatus*; 2 *C. albicans*). All patients were treated (average duration 13 weeks), oraly and intravenously for 60 of them (91%), mostly with ceftazidime-ciprofloxacin. A subsequent surgery was required in 8 patients (12%), including 3 mastoidectomy. During a median follow-up of 27 months, 16 patients experienced a relapse (*P. aeruginosa* in cultures in 5 patients). Elevated ASA score, as endocranial complication, were potential risk factors for relapse: aHR 1.9 (CI, 0.9 to 3.9; P=0.07) and aHR 1,4 (CI, 0.4 to 4.9; P=0.6), respectively. Using a combination of antibiotics tended to have a protective effect: aHR 0.3 (CI, 0.1 to 1.2; P=0.08). Having a fungal infection at baseline was the only significant risk factor for relapse: aHR of 4.1 (CI, 1.1 to 15; P=0.03) (figure).

Conclusions: NEO is a severe BJI mainly due (but not exclusively) to *P. aeruginosa* in elderly and/or diabetic patients. Fungal infections at baseline significantly impact the outcome.



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Abstract 1458

A retrospective cohort study investigating the clinical features, outcomes and risk factors leading to a poor outcome in pyogenic liver abscesses (2017-2019)

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Background: The aim of this study was to describe the clinical features and outcomes of individuals with a pyogenic liver abscess (PLA) in a tertiary centre, and to identify factors associated with mortality.

Materials/methods: A retrospective analysis of data obtained from clinical records of patients was performed, followed by multivariable regression analysis of patient and treatment-related factors.

Results: Fifty-three patients were included, with a mean age of 69 years and a male preponderance. At presentation, symptoms had been present for a median of 7 days; 75% were febrile and 58% had sepsis. Initial blood tests revealed abnormal liver function tests in 87% and an elevated C-reactive protein in 98%. Diagnostic imaging was carried out a median of 2 days following admission; 69% had an abscess >5cm diameter, 41% had multiple PLAs and 11% had metastatic abscesses. An underlying cause was identified in 91%; with a contiguous spread from a biliary source the most common. A microbiological diagnosis was confirmed in 74%; *E.coli* and *Streptococcus anginosis* group bacteria were most commonly isolated, while 15% had multiple bacteria cultured. Treatment involved complex, prolonged antibiotic therapy (>4 weeks in 66%) combined with percutaneous drainage in 43% and source control surgery in 23% (mainly cholecystectomy). The patients that had percutaneous drainage had significantly larger abscesses but drainage was not associated with significant differences in clinical outcome or duration of either antibiotic therapy or hospital admission. Mortality was 19%, 11% suffered *C.difficile* infection and only 53% had an uncomplicated clinical course. Follow-up imaging was carried out in 92%; at the time of the final scan there was complete resolution of the abscess in only 45%. Non-survivors were more likely to have cancer than survivors, but no other factors significantly impacted on survival.

Conclusions: PLA is associated with a considerable morbidity and mortality and requires complex antibiotic treatment alongside selective percutaneous drainage. Further research is required to confirm features that can risk stratify patients at diagnosis and to define the optimal treatment strategies.

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Abstract 1459

Two novel fastidious anaerobes from the genus Bacteroides isolated from chicken gastrointestinal tracts

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Background: Anaerobic bacteria inhabiting digestive tract of humans or animals have been a challenging object of microbiological studies for years. *Bacteroides* spp. make up half of microbiome and majority of these species is hardly cultivated in laboratory conditions. Aim of this work was to thoroughly characterize three *Bacteroides* spp. (AN20, AN421 and AN502) isolated on media with rumen fluid from chicken gastrointestinal tracts that showed novel properties and that were assigned as candidates for novel species

Materials/methods: A polyphasic taxonomic approach was applied to characterize isolated strains. All three were subjected to biotyping (micro,- and microscopy, Gram-staining, API 20A and RAPID 32A tests, fermentation products), chemotaxonomy based methods (analysis of proteins, fatty acids and menaquinones) and genomic methods (sequencing of the 16S rRNA gene, whole-genome sequencing and phylogenetic analyses).

Results: Initial analysis of the 16S rRNA sequences showed that the closest relative of AN20 is *Bacteroides uniformis* (90.3% similarity) and of AN421 and AN502 *Bacteroides eggerthii* (93.4%). These results suggested that cultivated strains may represent novel species of the genus *Bacteroides*. Phylogenetic analysis of 16S rRNA gene sequences showed that studied strains formed two separate clades within the genus *Bacteroidetes*, however they clustered along with *Bacteroides coprophilus, Bacteroides coprocola* and *Bacteroides plebeius.* Final confirmation of novelty was done by comparison of whole genomes based on ANI and dDDH values. ANI values between all three strains and *B. coprophilus* DSM 18228^T, *B. coprocola* DSM 17136^T and *B. plebeius* DSM 17135^T were between 70.0-72.0%. Moreover, AN421 and AN502 showed 97.7% identity between each other, whereas AN20 showed 74.1 and 75.3% similarity to AN421 and AN502 confirming these belong to two different species. Biochemical and chemotaxonomy-based methods showed differences between novel strains as well as towards their closest relatives which is important for their proper identification.

Conclusions: In this study, novelty of two *Bacteroides* species was clearly proved. These two fastidious species were thoroughly described in order to characterize their unique properties. ANI values showing less than 95% genomes similarities as required for species delineation definitely confirmed two novel species for which the names *Bacteroides pullorum* (AN421^T) and *Bacteroides brunensis* (AN20^T) are proposed.

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Abstract 1460

Imported schistosomiasis in children: a French prospective multi-centre study of prevalence, clinical features and diagnostic methods

Claire Leblanc*[1], Sophie Brun[2], Olivier Bouchaud[2], Arezki Izri[2], Marion Caseris[3], Maya Husain[3], Alice Bergevin[3], Luu-Ly Pham[4], André Paugam[5], Luc Paris[6], Stéphane Jauréguiberry[7], Vincent Levy[8], Coralie Bloch Queyrat[8], Vichita Ok[8], Marouane Boubaya[8], Simon Escoda[9], Frederic Sorge[10], Alexis Mandelcwajg[11], Albert Faye[12], Patricia Mariani[12], Loïc De Pontual[1]

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Background: Data on imported schistosomiasis are scarce especially in children. Screening in at risk population is recommended but the best diagnostic strategy remains uncertain and not evaluated in children. The aim of the study was to estimate the prevalence of imported schistosomiasis in children at risk in Paris and suburbs, and to compare diagnostic methods.

Materials/methods: All children at risk of schistosomiasis who consulted in four hospitals in the region of Paris were prospectively included from June 2017 to June 2018. Clinical and biological data were collected anonymously using an online software after parental and child consent. Direct parasitological diagnosis was urinary and feces microscopy and real-time polymerase chain reaction. Serological diagnosis was performed by Western blot, ELISA, indirect hemagglutination, immunochromatography and rapid test diagnosis circulating cathogen antigen. The Western blot assay and the microscopy were the reference methods used to estimate schistosomiasis prevalence. A latent class model has been used to evaluate each test performances.

Results: A total of 114 patients were included (sex ratio: 2.9 and mean age: 13.2 years). Most of the children were newly arrived migrants from Sub-Saharan Africa. The prevalence of schistosomiasis was 26.3%. Half of the positive patients were asymptomatic. The performances of ELISA and Western blot assays were equal (sensitivity: 83%; specificity: 99%) according to statistical analysis using latent class models. Serum immunochromatography had interesting performances (sensitivity: 100%; specificity: 89%).

Conclusions: Imported schistosomiasis is a common pathology in at risk children which confirms the need for systematic screening. Clinicians should be aware of such high prevalence in children at risk. And Serum immunochromatography seems to be the most cost/effective as a mass screening method.

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Abstract 1461

Utility of multiplex PCR in the screening, diagnosis and follow-up of malaria in patients attended in a tropical medicine referral centre

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Background: Due to the increase in trips to endemic zones and migrations, the diagnosis of malaria is on the rise in our setting. PCR with its high sensitivity (higher than immunochromatography and microscopy) is a widely used diagnostic tool, especially in non-endemic countries.

The objective of this work is to evaluate the usefulness of PCR in the detection of low parasitaemias (observed in semi-immune patients, in patients with incomplete prophylaxis / treatment and in post-treatment control) and in the identification of mixed infections in patients attended in a Tropical Medicine Referral Centre.

Materials/methods: Data from patients attended between July-2017 and July-2019 with a request for malaria PCR were reviewed. Two periods, July-2017 to June-2018 and July-2018 to July-2019 were established for the analysis. Results were evaluated together with those obtained by other techniques such as immunochromatography for antigen detection (SD Bioline®) and microscopic examination of thin and thick blood smears. During this period, two PCRs were used, an in-house Nested-Multiplex-PCR in the National Microbiology Centre and a commercial Multiplex-PCR (Bio-Evolution®) in our hospital.

Results: In the first period, a total of 203 PCRs were performed with a 11.82% positivity rate. 176 were screening PCRs in health exams (86.7%), 22 diagnostic PCRs (10.84%) and 5 follow-up PCRs (2.46%). 9.09% of the screening PCRs were positive (all non-mixed infections). 8 diagnostic PCRs were positive (36.36%), all of them also positive by microscopy.

In the second, a total of 290 PCRs were performed with a 15.52% positivity rate. 203 were screening PCRs (70%), 71 diagnostic PCRs (24.48%) and 16 follow-up PCRs (5.52%). 13.3% of the screening PCRs were positive (5 mixed and 22 non-mixed infections). 16 diagnostic PCRs were positive (22.54%), 9 of them (56.25%) being also positive by microscopy and 14 by antigen detection (87.5%).

In both periods, the agreement was total at species identification level between PCR and microscopy and the follow-up PCRs were always negative.

Conclusions: Malaria PCR has demonstrated its usefulness in post-treatment follow-up and in the detection of submicroscopic mixed and non-mixed malaria infections, with an increase in the positivity rate in the second period.

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Abstract 1465

Plasmodium vivax diversity, population structuration and history of origin in Sudan

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Background: *Plasmodium vivax* was less common in Sub-Saharan African countries due to the lack of Duffy antigen receptor for chemokine's (DARC) on red blood cells. In last year *P.vivax* emerged in Africa. In Sudan in the recent years the parasite is becoming widely distrusted and number of cases showed risen trend and can reach up to 20% of total positive malaria cases. It is not known whether this expansion is due to parasite evolution or population migration to Sudan. In this study use microsatellite DNA loci are polymorphic, neutral and distributed throughout the genome and have been useful for determining haplotypes diversity, population structure,history and ancestral origin of parasite population.

Materials/methods: *P. vivax* microsatellite typing was conducted on 113 field isolates collected from two districts in Sudan: 21 from Halfa (2013) and 92 from Khartoum (2013 and 2015).Microsallite DNA (MS) loci across the parasite genome were amplified and length variation of labeled PCR products was measured on an ABI PRISM 3730XL DNA Analyzer. MS data diversity, HE, haplotype across loci, Analysis of Molecular Variance (AMOVA) indexes and Principal Coordinate Analysis (PCoA) were generated with Gen AIEX. Linkage disequilibrium (LD) was obtained using LIAN software version 3.5. Geographical clusters and ancestral origin of Sudanese isolates were determined using STRUCTURE 2.2 software.

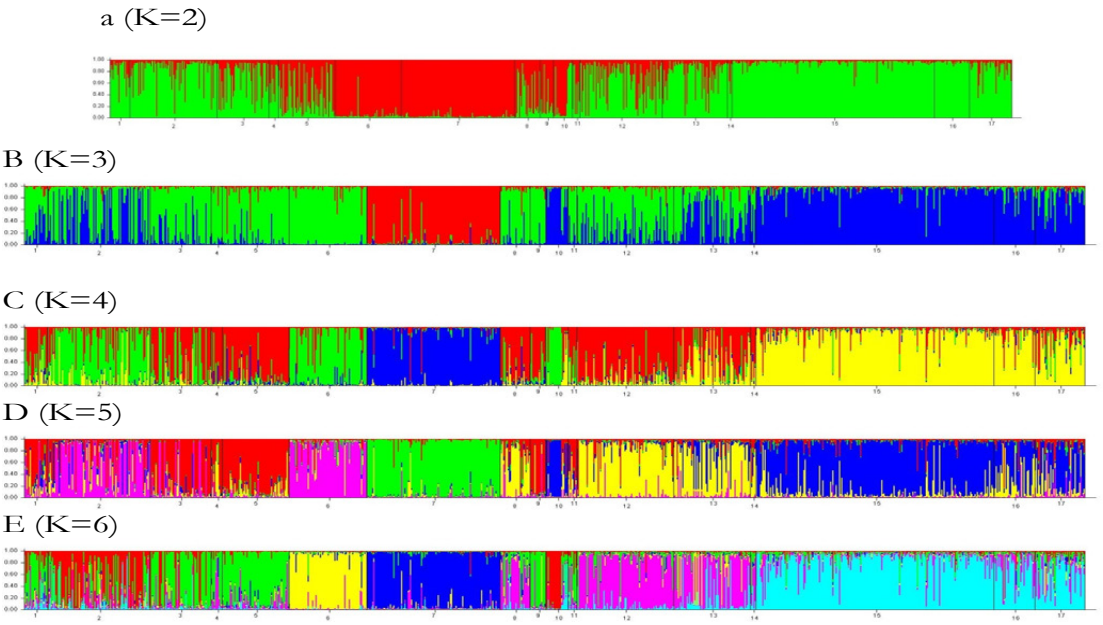

Figure 1 (A-E). Population structure of 17 populations analysed at K=3 level. Cluster 1 (Red) includes *P. vivax* isolates from Peru, Brazil, and Central America. Cluster 2 (Green) includes *P. vivax* isolates from New Halfa, Khartoum, other parts of Sudan and Africa, Madagascar and isolates from Peru. Cluster 3 (Blue) includes *P. vivax* isolates from Cambodia, Vietnam, Indonesia, Papua New Guinea low land, Papua New Guinea high land and Solomon Island.

Results: Microsallite DNA analysis showed multiple haplotype per locus varying in number from 9 to 22 (mean = 12.57). A total of 49 (67.1%) isolates revealed mixed clonal infection. The virtual heterozygosity (HE) values ranged from 0.71 to 0.88 (mean HE ± SE = 0.8450 ± 0.0460) while multilocus linkage disequilibrium (LD) showed ISA value of 0.1486 ($P < 0.001$). The AMOVA analysis showed that most of the genetic variation (96%) lies within parasite population .Clustering analysis of Sudanese versus Ethiopian population showed distinct different clusters for each population while clustering analysis of Sudanese versus worldwide isolates showed distinct signature and global pattern.

Conclusions: Microsatellite-based analysis of *P.vivax* parasites from Sudan showed extensive genetic diversity and ancestral origin of Sudanese *P.vivax* population represent the worldwide clusters and this seem to suggest a double origin from Africa (or Europe) and Asia.

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Abstract 1471

Relationship between intestinal microbiota and infantile colic

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Abstract third-party references: Supported by The Lebanese National Council for Scientific Research (CNRS)

Background: Infantile colic is a clinical condition in which a healthy infant suffers from paroxysms of excessive frequent crying that may be accompanied by irritability, flushing of the face, meteorism, drawing-up of the knees and arching the back. Approximately 10-30% of newborns will develop symptoms of infantile colic. In most cases, physicians are unable to determine the cause of the colicky behavior. An aberrant intestinal microbiota has been associated with infantile colic.

Materials/methods: This study compared 42 colicky infants with a control group composed of 46 non-colicky infants, all born at 37-42 weeks of amenorrhea, born by spontaneous delivery (n=33 newborns) or by caesarean section (n=54), exclusively breast fed (n=10) or exclusive formula fed (n=45) or receiving both feeding modes (n=33). Fecal samples were collected in pediatric private clinics between January 2018 and September 2018 and microbiota was analyzed by 16S rRNA gene quantitative PCR (qPCR).

Results: Age was significantly higher in colicky infants (p=0.014), while other parameters such as, birth rank, number of siblings, birth weight and crowding index did not differ between both groups. Infants were mainly colonized by anaerobes such as *Clostridium of cluster I, Bifidobacterium* and *Bacteroides/ Prevotella* group and facultative anaerobes such as *Lactobacillus* and enterobacterales. Differences were found by qPCR between colicky and non-colicky infants (figure 1). Colicky infants are more colonized by *Lactobacillus* (p=0.015), enterobacterales (p=0.019), *Klebsiella* (p=0.002) and *Clostridium of cluster XI* (p=0.002); whereas non colicky infants are more colonized by *Bifidobacterium* (p=0.005) and *Clostridium leptum* group (p=0.05). Parents with depression and anxiety had 3 times more probability of having a colicky infant (p=0.03). This could be bidirectional and can be the consequence of infantile colic and not the cause.

Conclusions: Our findings show that differences exist between the intestinal microbiota of colicky and non-colicky infants. On the long term, characterization of the intestinal microbiota in infants with colic may allow the implementation of prevention strategies to minimize the incidence and reduce crying in infants.

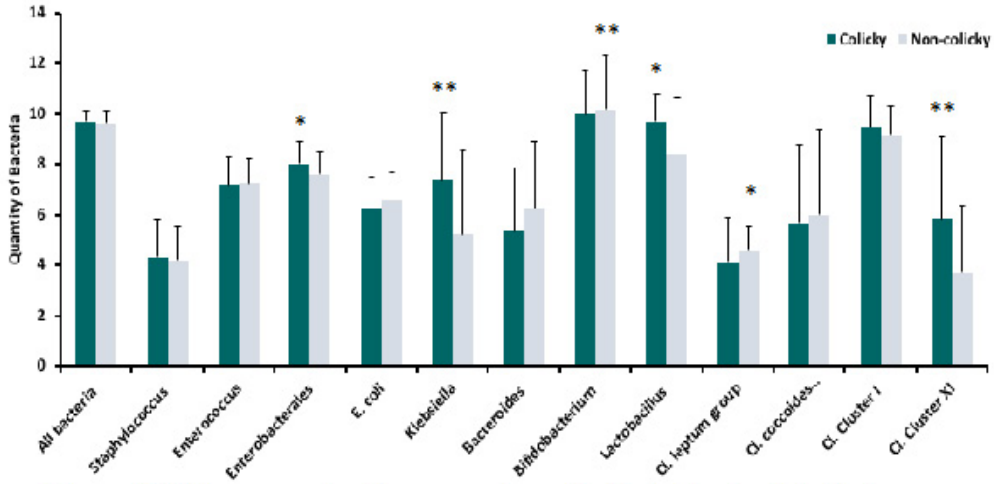

Figure 1: Histograms showing percentage of colonization by intestinal microbiota in colicky infants (green) and non-colicky infants (grey). Results of the Student test or Mann-Whitney test are shown by asterisk. * = p<0.05; ** = p<0.01.

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Abstract 1474

Knowledge and awareness of inadvertent use of yellow fever vaccine among renal transplant recipients

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Background: Yellow fever (YF) is a vaccine-preventable disease but the live attenuated YF vaccine is contraindicated in immunosuppressed patients due to the increased risk of life-threatening YF vaccine-associated viscerotropic disease in this population. The objective was to (i) estimate the prevalence of renal transplant recipients (RTR) inadvertently vaccinated against YF, (ii) evaluate the evolution of these patients, (iii) awareness of those unvaccinated to not to be vaccinated, and (iv) evaluate the knowledge of those patients about the contraindication of YF vaccine to them.

Materials/methods: A cross-sectional telephone contact study was conducted with 200 RTR, selected from the highest risk of YF vaccine exposure based on state vaccination policies against the YF outbreak in Brazil in 2017/2018. A questionnaire with information on previous use of YF vaccine before or after transplantation was applied. If the patient did not receive the vaccine post-transplantation, he was instructed not to get vaccinated; if the patient was vaccinated post-transplant, a second questionnaire was conducted to check for possible adverse events potentially associated with inadvertent vaccination. For each patient, up to 3 telephone contact attempts were performed. If the patient was not available in either of them, the attempt to contact was terminated.

Results: There were 116 successful telephone contacts (58%). A total of 11 vaccinated patients were identified - 5 in the pre-transplant and 6 in the post-transplant period. All patients received the full dose of the vaccine. Among those vaccinated pos-transplant, only 1 reported adverse events (nausea) after receiving the vaccine. 100% of post-transplant vaccinated patients reported not knowing the vaccine contraindication due to their clinical condition. Among the unvaccinated patients, this rate was 12.4%.

Conclusions: There is no specific antiviral treatment for YF, which makes vaccination the main tool for disease prevention and control. However, despite increasing evidence that transplant recipients have tolerated YF vaccine, data are not strong enough to recommend this vaccine in transplant recipients**.** Thus, counseling RTR on the contraindication of YF vaccine is important to prevent inadvertent use of the vaccine in this population, while additional studies on the real effects of YF vaccination on RTR are pending.

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Abstract 1475

An audit of latent tuberculosis management at a tertiary referral centre in Ireland

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Abstract third-party references: Royal College of Surgeons in Ireland

Background: Ireland is a low-incidence Tuberculosis (TB) country. Effective treatment of patients at high risk of latent TB infection (LTBI) reactivation is important for low-incidence TB countries because TB due to ongoing transmission is thought to be less frequent compared to high incidence TB countries.

Materials/methods: Our aim was to evaluate the effectiveness of LTBI management at our tertiary referral outpatient department (OPD) using national guidelines as an audit standard. We included all patients seen in the infectious diseases OPD who were referred querying a diagnosis of LTBI. Patients had to have attended the OPD at least once in between the 01/07/2018-31/12/2018. A retrospective review of each patient's electronic record was performed. Data extraction was performed independently by two auditors. A data collection tool was designed using Microsoft Excel. We calculated the cost of screening and managing the patients referred to our OPD. We calculated the cost considering the cost of investigations, staff and treatment using national costing guidelines.

Results: We identified 25 patients who met our inclusion criteria. 14/25 (64%) were male. The median age at time of first review was 52 years (IQR=24). All patients had a valid indication for LTBI screening. 22/25 (88%) were offered LTBI treatment, 22/22 accepted treatment, 17/21 (81%) completed treatment. The treatment used was isoniazid for a duration of 6 months for 12/21 (57%), isoniazid for 9 months 6/21 (29%) and rifampicin and isoniazid for 3 months in 3/21 (14%). A risk assessment for hepatoxicity was documented in 20/21 (96%). 1 patient had gastrointestinal upset on rifampicin. There were no other adverse events. There were 109 appointments attended by these 25 patients. The median number of appointments attended was 4 (IQR=2.5). The cost of screening, testing and managing the 25 patients referred was €34,466.62. The lowest cost treatment was Isoniazid plus Rifampicin for 12 weeks. The mean cost per patient seen in the clinic was €1,378.66. The mean cost per LTBI successfully treated was €2,027.45.

Conclusions: Our TB clinic is effective in the assessment and safe management of latent TB in accordance with national guidelines.

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Abstract 1479

Risk factors associated with daptomycin non-susceptible *Staphylococcus aureus* bloodstream infections

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Background: Daptomycin (Dap) is being increasingly utilized for treatment of methicillin-resistant *Staphylococcus aureus* (MRSA) infections. Consequently, daptomycin non-susceptible (DNS) SA strains have recently emerged, leading to limited treatment options for complicated MRSA infections. The purpose of this study was to evaluate risk factors associated with DNS SA bloodstream infections (BSI) at Henry Ford Health System in Michigan.

Materials/methods: Retrospective case-control study was conducted from 07/07/2008 through 09/18/2019 to identify clinical characteristics and risk factors in hospitalized patients with DNS SA BSI using electronic medical records (EMR). Patients with daptomycin-susceptible (DS) MRSA were used as controls. Data were analyzed using univariate analysis. Multivariate regression analysis was constructed using the PROC LOGISTIC from the univariate analysis. Statistical analysis was done using SAS 9.4 software.

Results: Thirty-one patients with DNS SA BSI were identified during the study period and compared to 59 patients with DS MRSA BSI. There was no significant difference in baseline characteristics and risk factors between the 2 groups with the exception of nursing home (NH) residence (p = 0.01), presence of central venous catheter (CVC) (p = 0.004) foley catheter (p=0.02), diabetes mellitus with end-organ damage (p=0.01), hemodialysis (p=0.04) or MRSA in the past year (p=0.03). Open wounds were more common in the DS MRSA group (p=0.026). Antibiotic use within 90 days was not significant with the exception of vancomycin (p=0.02). There was significant daptomycin MIC change in the DNS SA group (odds ratio (OR=15.67; 95% confidence interval, 3.19-76.89; p = 0.007). Mean bacteremia duration was 7.4 and 3.8 days (OR=1.2; 95% confidence interval, 1.07–1.35; p = 0.004) for case patients and controls, respectively. Multivariate analysis implicated NH residence (OR=13.03; 95% confidence interval, 2.24–75.57; p = 0.004) and CVC (OR=3.2; 95% confidence interval, 1.05–9.89; p = 0.04) as risk factors for DNS SA infection.

Conclusions: DNS SA is an emerging pathogen associated with indwelling devices, poorly controlled diabetes mellitus, hemodialysis, history of MRSA, vancomycin use and longer duration of bacteremia. NH residence and CVC use confer risk for DNS SA acquisition. Further studies to determine strain relatedness and identify resistance genes and virulence factors are warranted.

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Abstract 1480

A novel celecoxib-derivative kinase inhibitor, AR-12 (OSU-03012), is active against *Mycobacterium abscessus* complex *in vitro*

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Background: Therapeutic options for *Mycobacterium abscessus* (*M. abscessus*) infections are extremely limited and therapy outcomes often end in failures. New or repurposed drugs are in urgent need. AR-12 (OSU-03012), a novel celecoxib-derivative kinase inhibitor, has a broad spectrum of antibiotic activity against various pathogens. In this study, we investigated the *in vitro* and intracellular potency of AR-12 against *M. abscessus* complex.

Materials/methods: The susceptibility, stability and pre-exposure assays of AR-12 against *M. abscessus* complex were performed. We also conducted the minimum bactericidal concentration (MBC) and Time-kill kinetics assays to evaluate the bactericidal/Static activity of AR-12. Using checkerboard synergy assay, we tested in vitro synergistic interactions between AR-12 and five clinically important antimycobacterial agents against *M. abscessus*. Finally, we evaluated the effect of AR-12 on intracellular survival of *M. abscessus* complex in macrophage infection experiments.

Results: AR-12 exhibited high *in vitro* killing activity against *M. abscessus* isolates, with MIC50 of 4 and 8 mg/L for both subspecies. Stability testing showed that at 30°C AR-12 maintained its susceptibility within three days, and gradually lost its antimicrobial activity over time. MBC and Time-kill kinetics assays demonstrated AR-12 dominantly exhibited a bactericidal activity. Pre-exposure to AR-12 didn't induce more pronounced resistance of *M. abscessus* subspecies. There were no antagonistic interactions of AR-12 with clarithromycin, amikacin, imipenem, cefoxitin and tigecycline. Although AR-12 was inferior to amikacin in *in vitro* Time-kill kinetics assays, its intracellular cfu was significantly lower than that of amikacin.

Conclusions: AR-12 is active against *M. abscessus in vitro*, and showed excellent stability and compatibility with clinically important antimycobacterial agents. AR-12 may be a potential candidate for a novel treatment modality of *M. abscessus* complex infections.

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Abstract 1481

Obstructive pyelonephritis associated with ureteral stones: microbiology, treatment and prognosis

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Background: Acute pyelonephritis (APN) is often associated with obstruction of the upper urinary tract due to presence of urinary stones. It causes severe complications such as bacteraemia, sepsis, and septic shock. This study aimed to investigate the clinical outcomes and antibiotics susceptibilities of causative microorganisms in obstructive pyelonephritis associated with ureteral stones.

Materials/methods: This retrospective cohort study included female patients diagnosed with community-acquired APN at a tertiary care hospital from 2008 to 2017. A comparison between cases of APN associated with obstruction of the upper urinary tract due to presence of ureteral stones and cases of APN without complications was performed. Propensity score matching was used to adjust the heterogeneity within each group.

Results: Of the 588 female patients with community-acquired APN, 107 patients were diagnosed with obstructive pyelonephritis associated with ureteral stones (OPU) and 481 patients were diagnosed with uncomplicated APN. *Escherichia coli* was the most common pathogen in both groups (61.7% vs. 65.5%, p = 0.502). *Proteus* species were determined as the causative agent in 9.3% OPU cases and 0.4% cases with uncomplicated APN (p < 0.001). After propensity score matching, Enterobacteriaceae strains isolated from OPU cases were more resistant to ciprofloxacin (51.9% vs. 16.0%, p < 0.001). In addition, extended-spectrum β-lactamase (ESBL) was detected in 22.2% and 21.0% of the Enterobacteriaceae strains isolated from OPU cases and cases with uncomplicated APN, respectively (p = 1.000). The overall in-hospital mortality (3.7% vs. 4.9%, p = 0.699) and urinary tract infection recurrence rates within 1 year were similar in OPU and uncomplicated APN groups (16.0% vs. 21.0%, p = 0.545).

Conclusions: Antibiotic treatment for patients with obstructive pyelonephritis associated with ureteral stones may be empirically selected in accordance with the treatment protocol for general pyelonephritis. Clinicians should exercise caution before prescribing ciprofloxacin for the treatment of obstructive pyelonephritis associated with ureteral stones.

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Abstract 1485

Comparison of β-lactamase-producing *Escherichia coli* ST131 C1-M27 and ST131 non-C1-M27 by whole genome analysis using next-generation sequencing in Japan

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Background: In recent years, ESBL-producing *Escherichia coli* ST131 has become prevalent worldwide. Recent studies using whole-genome sequencing (WGS) analysis revealed that since the 2000s, clade C has become the most dominant lineage among the ST131 isolates, and one report shows that clade C1-M27 is increasing. In the present study, to pursue factors that spread the epidemic strains globally, we conducted a genome analysis of the C1-M27 epidemic strain and the non-epidemic strain non-C1-M27 using WGS and attempted to detect the mutations.

Materials/methods: We used 99 strains isolated from West Japan. The clades determined using PCR were A (n = 7), B (n = 6), C1 (n = 18), C1-M27 (n = 34), and C2 (n = 34). We used SnpEff, which classifies proteins by the level of gene mutation, to extract specific proteins. We extracted those proteins that were classified as "HIGH". We analyzed the protein mutation sites, functions, and protein interactions identified *in silico* using SeaView, S-VAR, and STRING.

Results: The proteins extracted were AMP nucleosidase and GABA permease. As a result, the 68th proline of the non-C1-M27 strain was a common amino acid in AMP nucleosidase, but it was mutated to serine in the C1-M27 strain. GABA permease, the 85th alanine, was mutated to threonine. AMP nucleosidase was predicted to have no effect on protein function by point mutation, whereas GABA permease was predicted to effect protein function. Although GABA permease is possessed by all *E. coli*, a p.Ala68Thr mutation was observed in all clade C1-M27 and C1 6 strains, whereas it was not observed in the other clades. We used STRING to analyze the protein-protein interactions of GABA permease. The results suggested that GABA permease is indirectly associated with acid-resistance systems.

Conclusions: GABA permease is a high-affinity uptake system for GABA. The prediction of protein function from point mutations suggests that the point mutation revealed here affects the function of GABA permease, and protein-protein interaction prediction suggested a relation with acid-resistance systems. We surmise that the specific point mutation extracted in this research may be related to the worldwide pandemic.

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Abstract 1486

Colistin resistance increases fatality in bloodstream infections due to carbapenem-resistant *Klebsiella pneumoniae*

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Background: Mortality due to K. pneumoniae bacteremia is on rise. Defining risk factors for colistin resistance and mortality is of paramount importance particularly in regions with high rates of carbapenem resistance.

Materials/methods: Patients diagnosed with "carbapenem-resistant K. pneumoniae (CRKp) bacteremia were divided into two groups as "colistin susceptible (ColS)" and "colistin resistant (ColR)". Retrospective casecontrol study was conducted to compare characteristics and outcomes. Multiple logistic regression model was used to define independent risk factors for acquired colistin resistance and mortality.

Results: A total of 82 patients (39 ColS and 43 ColR) were included. Mean age was 61.5 years and 50 (61%) were male. Colistin resistance was significantly increased with age (p = 0.074) and duration of hospitalization (p = 0.007). Prior colistin use was significantly higher (p = 0.007) in ColR group. Mortality rates at 14-day, 28-day and final follow up were 55%, 66% and 70% respectively. Colistin resistance significantly increased 28-day (p=0.009) and in-hospital (p = 0.040) mortality. PFGE analysis revealed an outbreak with K. pneumoniae ST78 and ST45 clones. OXA-48-like carbapenemase was positive in 60% of the strains and related with increased mortality. No significant difference was found between the outcomes of treatment modalities (monotherapy, double-triplequadruple combined therapy) in terms of 14th-day, 28th-day and total survival.

Conclusions: Colistin resistance increases 28-day and in-hospital mortality in CRKp bacteremia. Existing antibacterial combinations have no apparent superiority to each other. Clinical or microbiological response to treatment within seven days, along with prompt source control, favors survival.

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Abstract 1488

Geographical clustering of hantavirus isolates from Apodemus agrarius identified in the Republic of Korea indicates the emergence of a new hantavirus genotype

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Background: Several studies on hantavirus evolution have shown that genetic reassortment plays an important role in the evolution and epidemiology of this disease. Hantaan virus, a prototype hantavirus carried by *Apodemus agrarius,* is found throughout China, Russia, and Korea. The aim of this study was to investigate the distribution of hantaviruses in rodents in the Republic of Korea (ROK) and perform phylogenetic comparisons using the geographical distribution of their natural reservoir rodent hosts as a point of reference

Materials/methods: To understand the genetic epidemiology of human pathogenic hantaviruses, we examined viral isolates from rodent reservoirs, captured at three different locations in the ROK, between 2017 and 2018. Each sample collected was subjected to reverse-transcription nested polymerase chain reaction (RT-N-PCR) targeting the L- and S-segments of the hantavirus genome. Positive isolates from Gwangju, Boseong-gun (Jeollanam-do Province), and Jeju Island were confirmed as Hantaan virus using DNA sequencing. Phylogenetic analysis showed that all isolates grouped together as Hantaan virus. The isolates from Jeju, Boseong-gun, and Gwangju tended to cluster together, but with each region forming a distinct cluster. In addition, these three clusters were distinct from other Hantaan isolates reported in previous studies from Korea and its neighboring countries China and Russia. This suggests the emergence of a new hantavirus genotype in southwestern ROK.

Conclusions: Hantaan viruses exhibit a considerable degree of geographical clustering, and there may be a novel Hantaan genotype in southwestern ROK. This study helps expand our knowledge regarding the emergence of new hantavirus strains and their degree of geographical variation.

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Abstract 1495

Swiss Pathogen Surveillance Platform: development of a surveillance database for molecular epidemiology of multidrug-resistant pathogens

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Background: Transmission of virulent and resistant pathogens can be described using molecular epidemiological methods. In particular, whole genome sequencing (WGS) allows high resolution typing. As the interactions between compartments (e.g. human, animal, food, and environment) are complex, molecular typing data alone often does not explain the route of transmission. Interoperable processes, standardized epidemiological vocabulary and metadata are key requirements for unmasking this complexity.

Materials/methods: Within a NRP72-funded project, we are developing and implementing a molecular surveillance platform for Switzerland allowing the integration of WGS typing and epidemiological data at high spatiotemporal resolution. Within the consortium framework (i) requirements are defined regarding the WGS workflows, data analysis and interpretation and (ii) a prototype for a web-based surveillance platform is established and (iii) the platform is tested using a set of methicillin-resistant *Staphylococcus aureus* (MRSA) isolates from all involved centers.

Results: The required functional specifications of the platform were agreed: minimal datasets on epidemiological data and visualization aspects of spatiotemporal information. Legal and governance frameworks were evaluated. Bioinformatics functionalities of the platform were determined and implemented based on open source software. These include whole genome typing methods (e.g. cgMLST, SNP-tree) and more classical methods such as MLST typing, that allow comparison to older datasets. A first prototype of the surveillance platform is hosted at a BioMedIT node of the Swiss Institute of Bioinformatics (SIB) to ensure secure data access and computational power. Data is managed and searchable through a user dashboard including visualization powered by an integrated version of Nextstrain. A current set of >200 MRSA isolates (genomic and metadata) will expand to >1000 isolates over the next few months.

Conclusions: Transferring powerful backend bioinformatic tools to an easily accessible and comprehensive frontend solution is critical for use by people with various knowledge backgrounds. The surveillance platform has been designed to be highly interactive and intuitive. The legal framework had to be carefully evaluated for epidemiological/research tools, as different laws are applicable. With this platform, we are increasing public health networking within Switzerland and enabling fast detection and real time tracking of outbreaks on various scales. Expansion to other pathogens is planned.

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Abstract 1499

Antibiotic resistance of 34,539 *Campylobacter* spp. isolated from human sources: National Surveillance Data of Switzerland from 2007 to 2018

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Background: In Switzerland, acute gastroenteritis is commonly caused by bacteria, mainly, *Campylobacter* spp., with about 7,500 registered episodes annually, is of importance due to substantial healthcare costs. In recent years, more antimicrobial resistance (AMR) has been reported. However, little is known about temporal trends and geographical patterns of AMR within Switzerland.

Materials/methods: We used prospectively collected data from the ANRESIS antibiotic surveillance framework in Switzerland from 2007 to 2018. The network covers about two thirds of reported laboratory data. We conducted pre-defined, descriptive and exploratory statistical analyses. No *a priori* hypothesis was tested. For each year and geographic region the frequency of isolates resistant to specific antibiotics was calculated. Finally, we examined the association of AMR with demographic and epidemiological variables and invasiveness.

Results: The full dataset contained 34,539 human isolates of 11 *Campylobacter* spp. plus isolates identified to genus level only. The main analysis focused on *C. jejuni* (n=26,661) and *C. coli* (n=2,235) representing 99% of all isolates characterized on species level. A subset of 329 (1.1%) isolates was invasive. Per year, 2,273 to 3,308 isolates were collected for antibiotic resistance testing. Over time, we observed an increasing rate of resistance to ciprofloxacin and tetracycline in both species, to doxycycline in *C. jejuni* and to clarithromycin in *C. coli*. With exceptions, most geographic patterns of AMR were homogeneous. Noteworthy, in the South of Switzerland, as compared to the rest of Switzerland, a relatively higher rate of resistance to erythromycin was observed in *C. coli*. Further, in central-East and central-West Switzerland, as compared to the rest of Switzerland, a relatively lower rate of resistance to tetracycline was observed in both species. Our data provide no evidence for an association of AMR with demographic or epidemiological variables or in invasiveness.

Conclusions: We observed temporal and geographical differences in AMR patterns. As campylobacteriosis is epidemiologically often linked to handling and consumption of raw or undercooked chicken meat, travels abroad and no human-to-human transmission is known, these differences in AMR may be linked to practise changes outside of human medicine. Follow-up studies should include isolates from food samples.

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Abstract 1501

HIV is a risk factor for death among persons with candidaemia in South Africa

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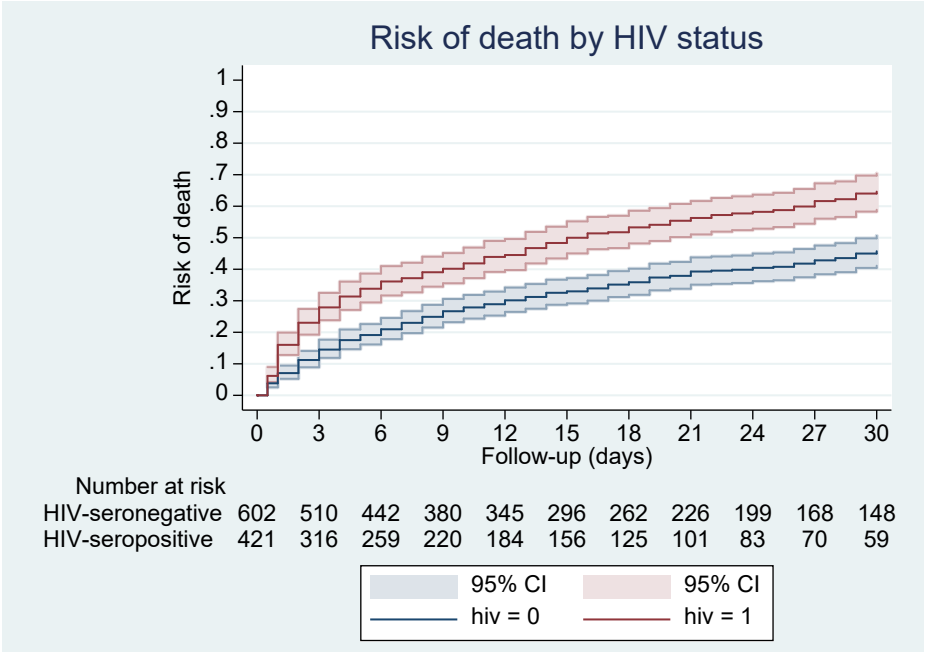
Background: Mortality among critically-ill persons with candidaemia is high. We aimed to determine the effect of HIV on 30-day mortality risk among persons with candidaemia in South Africa.

Materials/methods: We included persons aged ≥18 months with an episode of culture-confirmed candidaemia at 29 sentinel hospitals, 1 January 2012 - 31 December 2017. Surveillance officers collected clinical data by interview/chart review. *Candida* isolates were identified at a reference laboratory. We used random-effects logistic regression to adjust for sentinel hospital and participant-level confounders, treating follow-up as a fixed length of time (30 days). We plotted Kaplan-Meier survival curves by HIV status.

Results: Of 2563 cases, clinical data were available for 1846 (72%). Of these, we retained 1040 cases with both HIV status and outcome data (56%). Of 1040 cases, 458 (44%) were HIV-seropositive. Among 404 with available data, 301 (75%) were antiretroviral treatment-experienced. Among 267 with a recorded CD4 count close to candidaemia diagnosis, the median CD4 count was 133 cells/µl (IQR, 42-309); 63% (166/267) had a CD4 count <200 cells/µl. The overall case-fatality ratio was 458/1040 (44%). The median age of 1037 participants was 37 years (IQR, 23-52 years) and 542/1040 (52%) were male. Overall, 50% (514/1023) were admitted to an intensive care unit (ICU) at time of diagnosis. The 30-day case-fatality was 37% (230/614) and 54% (228/426) for HIV-seronegative and -seropositive cases respectively (crude odds ratio [OR] 1.92, 95% compatibility interval [CI] 1.50-2.47, p<0.001). After adjusting for sentinel hospital, age, sex, year of diagnosis, ICU admission, receipt of systemic antifungal treatment and *Candida* species (n=907), the 30-day mortality was 1.89 times higher (95%CI 1.38-2.60; p<0.001) among HIV-seropositive vs. -seronegative participants. The stratum-specific mortality OR was higher among HIV-seropositive individuals not admitted to ICU (OR 2.27, 95%CI 1.47-3.52; p<0.001) than those who were (OR 1.56, 95%CI 1.00-2.43, p=0.05). HIV-seropositive individuals had a 60% reduced adjusted odds of ICU admission than those HIV-seronegative (OR 0.40, 95%CI 0.25-0.64, p<0.001).

Conclusions: HIV-seropositive individuals had a two-fold increased adjusted risk of all-cause mortality within 30 days of candidaemia diagnosis, compared to their HIV-seronegative counterparts. HIV-seropositive individuals with candidaemia should be considered for ICU admission.



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Abstract 1502

Microbiological validation of the BIOFIRE FILMARRAY Pneumonia Panel plus: a single-centre experience

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Background: Culture-based identification and AMR-testing requires up to 72h. In addition, respiratory samples may have low sensitivities due to (i) small sample amounts being cultured and (ii) background (over)growth of oropharyngeal flora. Broad-panel PCR assays may overcome these gaps. We aim to evaluate the microbiological performance of the Biofire® FilmArray® Pneumonia Panel plus (BFPP) compared to culture-based techniques.

Materials/methods: We used consecutive collected bronchoalveolar lavage (BAL) and tracheal secretion (TS) samples from February-August 2019. Detection rates of the BFPP (200uL per sample) was compared to culture (BAL: 1uL and TS: approx. 50uL; internal gold-standard) on 5% sheep blood agar, CNA, Haemophilus, and MacConkey plates. The BFPP covered 15 bacterial (semi-quantitative), 3 atypical bacterial and 9 viral and 7 AMR targets (qualitative) and was performed according to company instructions.

Results: We compared 690 respiratory samples, corresponding to 18,630 BFPP targets. BFPP detected 517 targets (347 bacteria, 2 atypical bacteria, and 168 viruses). In comParison to culture, the BDPP found significantly more bacterial targets (+114%, 347/690 vs. 162/690). Some species were more frequently detected with BFPP: *Haemophilus influenzae*, *Moraxella catarrhalis*, *Streptococcus agalactiae*, *Streptococcus pyogenes,* and *Staphylococcus aureus* with additional 375%, 533%, 100%, 250% and 89%, respectively. These were often detected at low quantities in PCR (10e4 to 10e5 CFUs/mL). Samples with higher background flora (>50,000 CFUs/mL) showed a higher mismatch between the culture and BFPP results. Overall specificity and sensitivity were 98.1% and 89.9%, respectively. We detected only 5 AMR genes (3x CTX-M/2x mecA), of which 3 were confirmed by culture (2x CTX-M/1x mecA).

Conclusions: BFPP allows a rapid assessment of most common pneumonia pathogens and AMR genes. The difference in detection rates is most likely due to substantial differences in the culture workup or small quantities of target bacteria overgrown by oropharyngeal flora. The question remains if *S. aureus* and *H. influenzae* are pathogens or bystanders at low concentrations or presence of substantial background flora. Careful evaluation of clinical evidence for infection should be considered to avoid overtreatment of patients. The BFPP may benefit from a background flora target.

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Abstract 1503

Efficacy of pulsed xenon ultraviolet disinfection of multidrug-resistant bacteria and *Clostridioides difficile* spores

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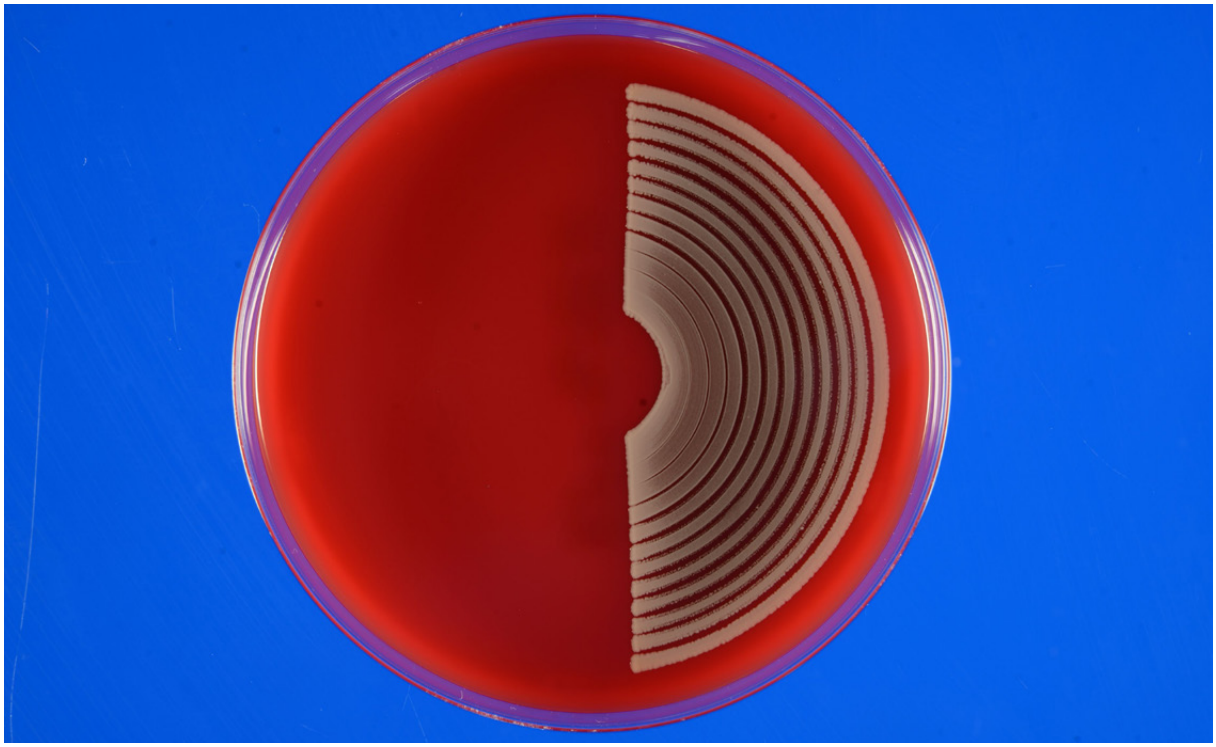
Abstract third-party references: This study was funded in part by a grant from Terumo Co., Ltd., Tokyo, Japan. Terumo Co., Ltd.

Background: Contamination of healthcare environments by multidrug-resistant organisms (MDRO) and *Clostridioides difficile* is a risk for healthcare-associated infections. The efficacy of pulsed xenon ultraviolet (PX-UV) disinfection in healthcare environments has mainly been studied in the United States. However, there are few reports about PX-UV disinfection in Japan. The aim of this study was to investigate in vitro the efficacy of PX-UV disinfection of MDRO and *C. difficile* spores commonly isolated in Japanese hospitals.

Materials/methods: We investigated reductions in microbial counts after exposure to PX-UV of the following clinically-isolated organisms on seeding agar plates: methicillin-resistant *Staphylococcus aureus* (MRSA), vancomycin-resistant *Enterococcus faecium*, carbapenemase-producing *Klebsiella pneumoniae*, extended spectrum β-lactamase-producing *Escherichia coli*, multidrug resistant *Acinetobacter baumannii*, and *C. difficile* spores. We also visually assessed the attenuation of sterilization by shielding of MRSA and carbapenemase-producing *K. pneumoniae* from PX-UV exposure. The left half of the plate was exposed to pulsed xenon ultraviolet light and the right half the plate was covered with aluminum foil during the exposure.

Results: PX-UV disinfection for 5 min induced >5-log growth inhibition of all the MDRO. PX-UV disinfection for 15 min induced >3-log growth inhibition of *C. difficile* spores. Where a plate was shielded from PX-UV exposure the bacteria showed confluent growth (Figure, the right side), but no colonies were observed on unshielded (exposed) parts of the plates (Figure, the left side).

Conclusions: PX-UV is a powerful disinfectant of clinical MDRO. *C. difficile* spores were more resistant to PX-UV disinfection than vegetative bacteria. Further evaluation for the efficacy of PX-UV disinfection on reducing the contamination of real-world surface and the incidence of healthcare-associated infection are needed.



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Abstract 1507

Personalised production and administration of bacteriophages: lesson learned from a unique European academic collaboration to treat a patient with pandrug-resistant *Pseudomonas aeruginosa* spinal infection

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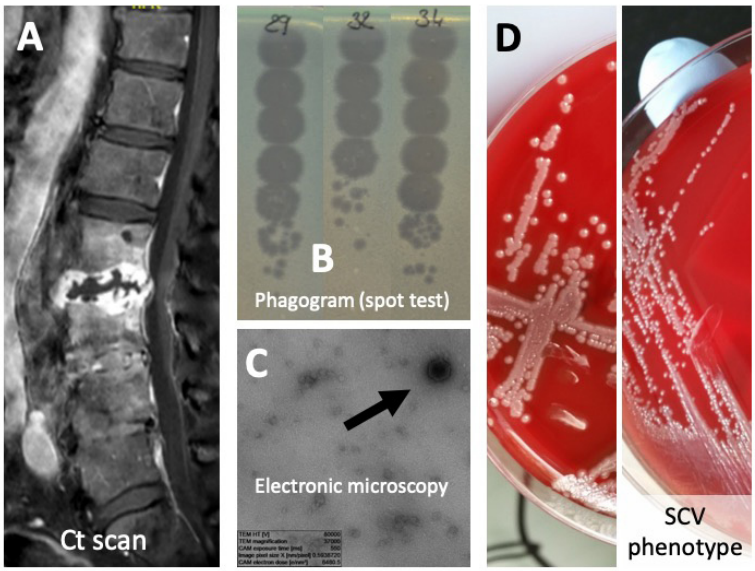
Background: As lytic phages act synergistically with antibiotics on biofilms, they could be a potent adjunct treatment for bone and joint infections (BJI). Currently, phage Active Pharmaceutical Ingredients (APIs) production follows minimal requirements of quality and safety, which guarantee adequate composition and acceptable levels of residual contaminants.

Materials/methods: A 74-year-old man experienced *P. aeruginosa* bacteremia in January 2018. In summer 2018, spondylodiscitis with spinal abscess due to pandrug-resistant *P. aeruginosa* was diagnosed (panel A). Industrial phages under development were inactive, but 3 active phages (Phi4029, Phi4032 and Phi4034) were identified by the laboratory of G. Resch (panel B, C). Dedicated production of the APIs, in compliance with a monograph describing the production process and Quality Control (QC) system for incorporation in magistral preparations, was done at Queen Astrid military hospital in Brussels under the supervision of the French National authority (ANSM) in collaboration with the hospital pharmacist.

Results: The patient was treated by open debridement and one local application of the phage cocktail after magistral preparation (dilution in 7 mL; final titer of 10^7 PFU/mL). Cefiderocol was started after the surgery for a duration of 6 weeks. One month after, a new surgery, using intersomatic cages for stabilization, was performed. The patient had no systemic (no fever, CRP 10 mg/L) nor clinical signs of infection. The same phage cocktail with same dilution and titer was locally used. Cefiderocol was pursued pending the culture results. Unfortunately, *P. aeruginosa* still grew in culture from bone biopsies with small colony variant phenotype (panel D), but remained susceptible to the phage cocktail and cefiderocol. Colistin was added and phages were administered intravenously in 3-hours infusions (30 mL, phage titers 10^8 PFU/mL) every day during 28 days. Antibiotics (cefiderocol and colistin) were stopped at 3 months. The outcome was favorable after 6 months, and the patient is walking without pain (video available).

Conclusions: Personalized phage therapy is a potential adjunct treatment for patients with complex BJI due to pandrug-resistant bacteria. In addition to industrial phages under development, academic collaborative research is crucial to develop personalized phage therapy.



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Abstract 1508

Serum active Granzyme A: a new biomarker that contributes to the pathogenesis of peritoneal sepsis

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Background: Peritonitis is one of the most common leading cause of sepsis. Recent evidence suggests that Granzyme A (GzmA), a serine protease mainly expressed in NK cells and T cells, could act as a proinflammatory mediator and could play an important role in the pathogenesis of sepsis. This work aims to analyze the role of serum GzmA as a biomarker and therapeutic target in peritoneal sepsis.

Materials/methods: Concentration and enzyme activity of soluble GzmA were sequentially analyzed in serum from healthy donors and patients with peritonitis and were correlated with the Sequential Organ Failure Assessment (SOFA) score.
Peritonitis was induced in C57Bl/6 (Wt) and GzmA-KO mice by cecal ligation and puncture (CLP). Mice were treated intraperitoneally with antibiotics and with serpinb6b, a specific GzmA inhibitor, for 5 days. Mouse survival was monitored during 14 days and the levels of serum proinflammatory cytokines and bacterial load in blood and spleen were analyzed at 6 and 24h from CLP.

Results: We have found high levels of GzmA in serum of patient with peritonitis. Most importantly, we observed that GzmA activity in serum correlates with SOFA score, suggesting that active GzmA could play an important role in sepsis development in peritonitis patients and could be a new biomarker of sepsis severity.
In order to analyze the therapeutical potential of soluble GzmA in peritoneal sepsis, we used the CLP mouse model. After peritonitis induction, GzmA-KO mice exhibit increased survival compared with Wt mice, which correlated with reduced levels of proinflammatory cytokines in serum. The analysis of bacterial load in blood and spleen showed no differences between Wt and GzmA-KO mice suggesting that GzmA does not play an important role in bacterial control.
Treatment with serpinb6b reduced mortality, which correlated with reduced cytokine serum levels in serum, confirming the therapeutical potential of gzmA to treat peritoneal sepsis.

Conclusions: Our findings confirm that soluble GzmA plays an important role in the pathogenesis of sepsis and could be a new therapeutic target and a biomarker for the treatment of peritoneal sepsis.

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Abstract 1513

First case of *Gemmiger formicilis* bacteraemia identified using partial 16S rRNA gene sequencing

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Background: *Gemmiger formicilis* is a Gram negative, strictly anaerobic, pleomorphic, budding-like organism previously isolated from human faeces and from chicken caecal contents. *G. formicilis* has not previously been reported as causing human infection. We report here the first case of *G. formicilis* bacteraemia.

Case report: A previously healthy 20 year old man was admitted with diarrhoea, abdominal pain, fever, chills, and rigors. On admission, he was febrile, with temperature 39.4 °C, and inflammatory markers were raised. Blood cultures were taken.
The anaerobic blood culture bottle taken on admission flagged positive after 42 hours of incubation. Gram stain of the positive blood culture broth showed microorganisms with an unusual morphology. The microorganisms appeared to be Gram variable cocci of varying sizes arranged in chains. The positive blood culture broth was sub-cultured onto solid media as per our laboratory's routine processes, including incubating in anaerobic conditions. No growth was detected on sub-culture despite incubation for up to two weeks. A repeat sub-culture was also negative.

We extracted DNA directly from the positive blood culture bottle broth, and partial 16S rRNA gene sequencing identified the microorganisms as *G. formicilis*. This identity was in keeping with the distinctive Gram stain appearance, and with it being a fastidious, strictly anaerobic microorganism which may require stringent growth conditions.
The patient had been treated with oral ciprofloxacin prior to admission, and was subsequently treated with intravenous ceftriaxone and oral moxifloxacin. He recovered well from this acute episode and was discharged on hospital day 11.

Conclusions: *G. formicilis* has not previously been reported as causing human infection. This might be because it is rarely pathogenic, but might also be because of difficulties with microbial growth and identification due to its fastidious, strictly anaerobic nature. This first case of *G. formicilis* bacteraemia highlights that this species may be able to cause clinically significant infection. Furthermore, direct partial16S rRNA gene sequencing was necessary to identify the microorganisms in the blood culture broth. This case highlights the increasing need to integrate molecular diagnostics into routine clinical diagnostic bacteriology.

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Abstract 1517

Five versus seven days nitrofurantoin for urinary tract infections in women with diabetes: a non-inferiority study

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Background: In the Netherlands, the first choice therapy for cystitis in women with Diabetes Mellitus (DM) is seven days of nitrofurantoin. However, general practitioners often treat these patients as an uncomplicated cystitis with five days nitrofurantoin. The comparative effectiveness of either policy is unknown. The aim of this study was to compare the effectiveness between five and seven days of treatment.

Materials/methods: Data from the Julius General Practitioners' Network, consisting of 75 GP practices, was retrospectively collected between January 2013 and June 2019. Inclusion criteria were nitrofurantoin prescription of five or seven days for cystitis, female sex, age > 12 and DM based on International Classification of Primary Care code T90. Patients with other reasons than DM for a seven day prescription were excluded, e.g. male gender, pregnancy, urologic abnormalities and immunosuppression.. The primary endpoint early treatment failure was defined as a new prescription for a UTI within 28 days. The secondary endpoint was overall treatment failure within 90 days. Crude risk differences were estimated using linear regression. The adjusted risk differences were calculated by inverse probability weighting to account for confounders. The non-inferiority margin for the primary outcome was set at 2% absolute risk difference.

Results: We included 8,255 patients of whom 3,893 were treated for five days and 4,362 for seven days. Patients treated for seven days were overall older, used more co-medication and had more comorbidities. Treatment failure within 28 days occurred in 734 patients (18.9%) with five day treatment and 815 (18.7%) with seven day treatment (crude risk difference: 0.1% (95% CI -1.5 to 1.9); adjusted risk-difference: -0.1% (95% CI -1.8 to 1.6)). Treatment failure within 90 days was 1239 (31.8%) and 1344 (30.8%) for five and seven day treatment, respectively (crude risk difference: 0.2% (95% CI -1.5 to 1.9); adjusted risk-difference: 1.1% (95% CI -0.9 to 3.2)).

Conclusions: Five days treatment is non-inferior to seven days treatment with nitrofurantoin for early treatment failure in diabetic women with cystitis. Non-inferiority could not be demonstrated for overall treatment failure within 90 days, neither was there a statistically significant difference.

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Abstract 1518

Clinical and microbiological characteristics in men with non-obstructive acute pyelonephritis

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Background: Acute pyelonephritis (APN) is the most common cause of bacteremia in hospitalized patients. The objectives of this study were to investigate the differences in the clinical and microbiological features of hospitalized men with community-onset (CO) and healthcare-associated (HA) non-obstructive APN, as well as predictive factors associated with bacteremia.

Materials/methods: Five urological centers participated in this study. Men with non-obstructive APN as a discharge diagnosis were identified from January 2011 to December 2017 using an electronic medical records system. We compared the clinical and microbiological data in men with CO- and HA-APN.

Results: Of the 245 men with non-obstructive APN, 175 had CO- and 70 had HA-APN. The HA group was significant older, had longer hospital stay and had a higher frequency of underlying disease, bacteremia, and ICU care than the CO group. Bacteria were identified in 154 of 245 patients (62.9%), and the most commonly cultured included *Escherichia coli* (41.7% and 50.0% in the CO and HA groups, respectively). The susceptibility of the cultured bacteria to fluoroquinolone was 68.7% in the CO group and 45.3% in the HA group (p=0.005). The proportion of ESBL-producing bacteria was 22.7% and 53.5% in the CO and HA groups, respectively (p<0.001). In the CO and HA groups, the sensitivity of piperacillin/tazobactam was 94.9% and 90.0%, respectively (p=0.297). Amikacin showed more than 95% sensitivity to bacteria isolated from both groups (p=0.555). The multivariate analysis revealed that age ≥65 years (p=0.043) and chronic liver disease (p=0.029) were independent predictive factors for bacteremia.

Conclusions: The HA group showed a higher incidence of antibiotic resistance and bacteremia than the CO group. However, the proportion of resistance for fluoroquinolone and ESBL-producing bacteria was high in both groups. Piperacillin/tazobactam and amikacin may be a feasible option as an empirical antibiotics for men with non-obstructive APN regardless of disease severity.

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Abstract 1519

Evaluation of the Qiastat-Dx Gastro-intestinal Panel at the University Hospital of Liege (Belgium)

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Background: The QIAstat-Dx Gastro-intestinal panel (QIAstat-Dx GI panel, Qiagen) detects the 24 most common gastro-intestinal pathogens by using qualitative real-time-PCR in stool samples. The system delivers results within 70 minutes with Ct values and amplification curves. The purpose of this study was to evaluate the QIAstat-Dx GI panel at the University Hospital of Liege (CHULiège) in comParison with the results obtained with the current techniques available in the laboratory.

Materials/methods: From 06/23/19 to 07/04/19, all stools addressed to the Microbiology lab for bacteriological, parasitological or virological analysis were tested with the QIAstat-Dx GI panel and the current diagnostic methods. These methods included bacteriological culture, *Clostridium difficile* antigenic tests (GDH and toxins A/B, Meridian), microscopy and rapid tests (Alere) for parasites.

Results: A total of 180 samples collected from 126 patients were included. Out of these samples, 51 (28%) were tested positive with the QIAstat-Dx panel with 61 pathogens detected in total. Co-infections were identified in 8 patients (4.5%). Four *Campylobacter* detected by PCR were not confirmed by culture nor by antigenic tests. Besides, 4 out of 13 *C. difficile* toxin-positive results detected by the GI panel were not confirmed by antigenic test or by culture. The results are summarized in the table 1. All discrepancies were in favor of the GI panel which show better sensitivity.

	Positive GI panel N (%)	Positive detection by current methods N (%)	Discrepancies N (%)
Escherichia coli (enteroaggregative, enteropathogen, enterotoxinogen and enteroinvasive)	26 (43)	(0)*	26
Campylobacter species	13 (21)	9 (14)	4
Clostridium difficile	13 (21)	9 (14)	4
Salmonella species	1 (2)	0	0
Virus (Norovirus, Adenovirus, Sapovirus)	6 (10)	6 (9)	0
Giardia lamblia	2 (3)	1 (1.6)	1
Total	61 (34)	25 (40)	35

*not detectable by current methods
Table 1. Summary of the results.

Conclusions: The QIAstat-Dx GI panel can detect many pathogens with higher sensitivity than the current non-PCR lab methods. The availability of Ct levels allows the evaluation of the nucleic acids content helping for differentiation between colonization and infection. The panel has a potential to improve the patient quality of care with reduction of turn-around time to result.

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Abstract 1521

Predictors of mortality in solid-organ transplant recipients with bloodstream infections due to carbapenemase-producing Enterobacterales: the impact of *cytomegalovirus* disease and lymphopenia

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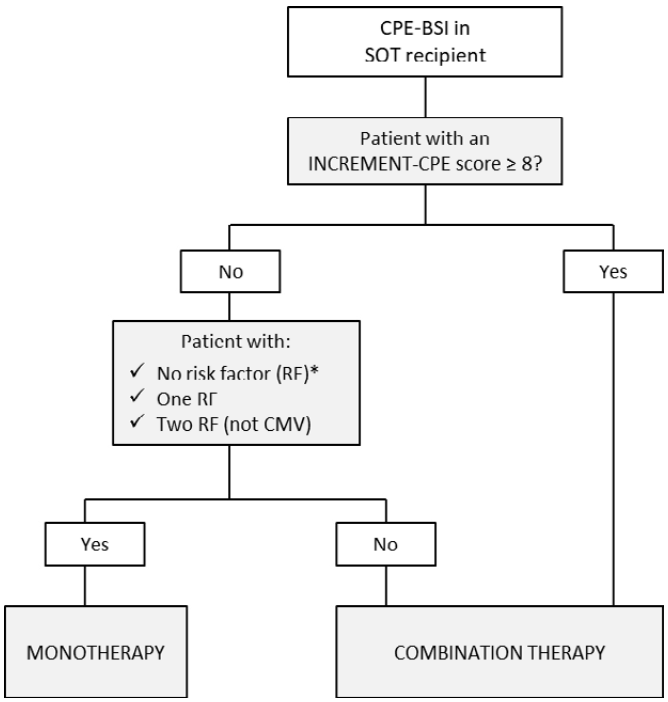
Background: Treatment of carbapenemase-producing *Enterobacterales* bloodstream infections (CPE-BSI) in solid-organ transplant recipients (SOT) is challenging. The objective of this study was to develop a specific score to predict mortality in SOT recipients with CPE-BSI.

Materials/methods: A multinational, retrospective (2004-2016) cohort study of CPE-BSI among SOT adult recipients (INCREMENT-SOT, ClinicalTrials.gov NCT02852902) was performed. The main outcome variable was 30-day all-cause mortality. The INCREMENT-SOT-CPE mortality score was developed using logistic regression and calculating the area under the ROC curve (AUROC). The impact of targeted therapy (monotherapy versus combination therapy) was analysed using Cox-regression.

Results: The INCREMENT-SOT-CPE score was developed using logistic regression. The global cohort included 216 patients. The final logistic regression model included the following variables: INCREMENT-CPE mortality score ≥8 (8 points), no source control (3 points), inappropriate empirical therapy (2 points), cytomegalovirus disease (7 points), lymphopenia (4 points), and the interaction between INCREMENT-CPE score ≥8 and CMV disease (minus 7 points, indicating that CMV disease does not further increase the risk of death if the INCREMENT-CPE-score is ≥8, but do so only if the score is <8). This score showed an area under the receiver operating characteristic curve of 0.82 (95% CI 0.76-0.88) and classified patients into three strata: 0–7 (low mortality), 8-11 (high mortality) and 12-17 (very-high mortality). We performed a stratified analysis of the effect of monotherapy versus combination therapy among 165 patients who received appropriate therapy. Monotherapy was associated with higher mortality only in the very-high (adjusted HR 2.82, 95% CI 1.13-7.06, P=0.03) and high (HR 9.93, 95% CI 2.08-47.40, P=0.004) mortality risk strata.

Conclusions: A mortality risk score of CPE-BSI in SOT recipients was developed. We propose a score-based algorithm (Figure 1), which can be used for therapy guidance.

Figure 1. Algorithm for clinical management of SOT patients with bloodstream infection due to carbapenemase-producing *Enterobacterales* (CPE-BSI), based on INCREMENT-SOT-CPE mortality risk score.



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Abstract 1522

Do *cytomegalovirus* infection and valgancyclovir exposure increase the risk of BK viraemia and associated nephropathy after kidney transplantation?

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Background: Both CMV and BK polyomavirus (BKV) adversely affect graft outcomes after KT. Indirect immunomodulatory effects attributable to CMV would predispose to non-CMV infections. Recent studies have suggested that VGCV prophylaxis may increase the risk of BKV viremia and BKV-associated nephropathy (BKPyVAN) due to a presumptive drug-specific immunosuppressive effect. However, these apparently contradictory associations remain controversial. We investigated whether KT recipients exposed to CMV replication and/or VGCV therapy experienced higher incidence of BKV infection.

Materials/methods: Prospective cohort study including 423 consecutive KT recipients from November 2014 to September 2019 in which CMV and BKV DNAemia were periodically monitored throughout the first year. VGCV prophylaxis was given for 6 months to D+/R- patients and for 3 months to R+ patients receiving antithymocyte globulin. The remaining patients were pre-emptively managed. The impact of CMV replication and VGCV therapy (prophylaxis or treatment) during the first 90 and 180 pos-transplant days on the subsequent occurrence of BKV viremia and BKPyVAN was analyzed.

Results: VGCV prophylaxis was administered to 235 patients (55.6%), whereas 188 (44.4%) were managed by preemptive therapy. In the latter group, 47 (25.0%) and 53 (28.2%) received VGCV treatment for CMV infection and/or disease during the first 90 and 180 days. One-year incidence rates for CMV and BKV DNAemia were 48.9% (n = 207) and 18.4% (n = 78). Only one patient (0.2%) developed BKPyVAN. The incidence of BKV viremia beyond days 90 (17.7% vs. 14.2%; *P*-value = 0.355) and 180 (9.7% vs. 8.9%; *P*-value = 0.785) was not different between patients that had previously received or not VGCV therapy, respectively. Likewise, no significant differences were found in the occurrence of BKV viremia beyond days 90 (12.9% vs. 17.9%; *P*-value = 0.218) and 180 (8.4% vs. 10.2%; *P*-value = 0.542) between patients with or without CMV exposure over the preceding periods. The lack of impact of VGCV therapy or CMV exposure during the first 90 and 180 days was confirmed after adjusting for various clinical covariates by Cox regression.

Conclusions: This large prospective study does not support an association between previous CMV replication or VGCV exposure and subsequent BKV viremia after KT.

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Abstract 1523

High-resolution subtyping of *Escherichia coli* using optical DNA mapping

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Background: Typing of bacteria on the sub-species level generally requires sequencing, but there is a need for faster and easier methods for efficient infection control in clinics. We have previously demonstrated that optical DNA mapping (ODM) can differentiate bacterial species with high specificity, and here extend this approach to subtyping of *Escherichia coli*.

Materials/methods: The DNA extraction was carried out in agarose plugs to protect the DNA from fragmentation and generate ultra-long DNA molecules (>200 kb). The DNA was then stained with YOYO-1 and netropsin to generate an emission profile along the DNA that reflects the sequence: a DNA barcode. To visualize the barcode, the DNA was stretched in nanofluidic channels and imaged using fluorescence microscopy.
The barcodes were aligned to a database of theoretical barcodes from >2000 bacterial species where the included *E. coli* genomes were typed using the Warwick MLST scheme. Only barcodes with high-quality matches to a single species were retained after quality filtering. Barcodes matching discriminatively to *E. coli* were further analyzed and reported if all high-quality matches were to the same sequence type (ST).

Results: ODM was performed for clinical *E. coli* isolates, including clinically important STs. Preliminary experiments on eight isolates, belonging to ST38, ST131, ST156, ST405, ST410, and ST648, comprised of on average 37 mapped molecules per sample. The proportion of barcodes that matched discriminatively to a single ST was on average 25%. Importantly, the proportion of discriminative barcodes that matched the correct ST – i.e. the true positive rate – was 100% for all samples, except one where nine out of ten discriminative barcodes matched the correct type.

Conclusions: We demonstrate how ODM can classify *E. coli* down to the ST level. Sample preparation and data collection are significantly faster than for sequencing methods, which opens up possibilities for clinical use, in particular in infection control. Importantly, the approach is general and can likely be transferred to other clinically relevant bacterial species.

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Abstract 1524

Epidemiology of carbapenemase-producing Enterobacterales in the Netherlands in 2018

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Abstract third-party references: on behalf of the Dutch CPE Surveillance Study Group

Background: The current epidemiology of carbapenemase-producing Enterobacterales (CPE) in Europe varies from sporadic imported cases, to sporadic hospital outbreaks, (inter-) regional spread between hospitals, and CPE being endemic in health-care settings. Here, we describe the epidemiology of CPE in the Netherlands in 2018 based on the enhanced CPE surveillance system.

Materials/methods: All Dutch medical microbiological laboratories are requested to submit Enterobacterales isolates with a MIC for meropenem >0.25 mg/L and/or MIC for imipenem >1 mg/L to the National Institute for Public Health and the Environment (RIVM). MALDI-ToF, MIC for meropenem, carbapenemase inactivation method (CIM), and PCR for carbapenemase-coding genes are performed on all isolates and whole genome sequencing (WGS) is done for all CIM+ isolates. An epidemiological questionnaire is requested for all CIM+ isolates. Reported data were based on the first unique CIM+ species-gene combination per person in 2018 and epidemiological data were analysed on person level.

Results: 578 Enterobacterales isolates were submitted of which 306 were unique CPE isolates obtained from 266 persons (mean age 60 years and 53% male). *K. pneumoniae* was most frequently identified (40%), followed by *E. coli* (29%) and *E. cloacae* complex (12%), and 19% were other species. The genes most often detected coded for OXA-048 (40%), NDM (34%; 20% of all CIM+ isolates was NDM-5, 12% NDM-1), VIM (6%) and KPC (6%). Epidemiological characteristics were available for 161 persons (61%). Forty-five persons (28%) were sampled for diagnostic reasons. Screening because of presumed risk, usually upon admission, was the reason for sampling in 115 (71%) persons. Hospitalization abroad was the most common risk factor (*n*=93; 58%), with Turkey (*n*=20) and Morocco (*n*=14) most often reported. In 50 persons no risk factor was identified (31%). Risk factors reported in <4% of the persons include contact with a foreign country in a different way in the past year, relation with a known outbreak of CPE, work-related exposure to livestock animals, and already known carrier of CPE.

Conclusions: Genes coding for OXA-048 and NDM were most frequently detected in CPE isolates submitted to the RIVM. Recent hospitalization abroad is the main risk factor for CPE in the Netherlands.

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Abstract 1526

Impact of unrestricted movement of carbapenemase-producing Enterobacteriales (CPE) carriers on transmission of CPE in nursing homes: a prospective cohort study

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Background: In September 2018, the National Infection Prevention and Control Committee (NIPC) of Singapore recommended standard precautions and unrestricted movements for CPE carriers in NH. We studied the impact of this recommendation on Carbapenemase-producing *Enterobacteriales* (CPE) transmission among NH residents.

Materials/methods: This prospective cohort study was conducted in a 255-bedded nursing home in Singapore. Eligible consenting residents were followed for 3 months. Stool and environmental samples (sink steel traps and shower drain traps) were collected at baseline and weeks 2, 8 and 12. We collected demographic, comorbidity, hospitalization, antibiotics and travel history at baseline and during follow-ups. We used CHROMID® CARBA SMART to detect CPE, with environmental samples undergoing an additional selective broth enrichment step prior to culture. CPE were identified with MALDI-TOF and PCR for carbapenemase genes. CPE acquisition was defined as having a positive CPE stool sample after an initial negative screening at recruitment. Statistical analysis was done with STATA15.

Results: Between April and July 2019, 32 residents including 6 known CPE carriers (identified in a recent acute hospital stay): 5 bla_{NDM} and 1 bla_{OXA-48}) were recruited and followed-up. Among the known CPE carriers, only 1 remained persistently stool-positive for bla_{OXA-48} while the rest reverted to negative throughout the study. After a total follow-up of 2699 patient-days, one resident acquired bla_{NDM}-producing *Enterobacter cloacae* at week 12, giving an acquisition rate of 0.37 per 1000 person-days (95%CI 0.05, 2.63). A total of 164 environmental samples were collected from 28 sink steel traps and 13 shower drains. Of the 28 sink steel traps, 6 were positive for CPE (5 were bla_{NDM} and 1 was bla_{KPC}). The shower drain traps remained negative for CPE throughout the study.

Conclusions: The recommendation to allow standard precautions during patient care and unrestricted movement of CPE carriers in nursing home appears to be acceptable because we were unable to demonstrate patient-to-patient transmission in this study. However, larger studies with longer follow-up periods are necessary to definitively confirm this finding.

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Abstract 1528

ComParison of host immune responses *in vivo* versus ex vivo lipopolysaccharide stimulation in humans using an immune transcriptomic profiling panel

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Abstract third-party references: European Sepsis Academy, European Union's Horizon-2020 research and innovation program grant agreement No. 676129

Background: Patients that suffer from sepsis exhibit an early hyper-inflammatory immune response which can lead to organ failure and death. In our study, we assessed the immune modulation in the human *in vivo* endotoxemia model and compared it to *ex vivo* lipopolysaccharide (LPS) stimulation using 38 transcriptomic markers.

Materials/methods: Eight volunteers were challenged with intravenous LPS *in vivo*. In parallel, blood from another 8 volunteers was challenged *ex vivo*. Blood was collected before and after 4 hours of LPS challenge and tested with the Immune Profiling Panel (IPP) using the FilmArray® system.

Results: The use of IPP showed that markers from the innate immunity dominated the response to LPS *in vivo*, mainly markers related to monocytes and neutrophils. Comparing the two models, *in vivo* and *ex vivo*, revealed that most of the markers were modulated in a similar pattern (68%). Some cytokine markers such as *TNF*, *IFN-γ* and *IL-1β* were under-expressed *ex vivo* compared to *in vivo*. T-cell markers were either unchanged or up-modulated *ex vivo*, compared to a down-modulation *in vivo*. Interestingly, markers related to neutrophils were expressed in opposite directions, which might be due to the presence of cell recruitment and feedback loops *in vivo*.

Conclusions: In both models, the majority of IPP markers showed similar patterns of expression post-LPS challenge, except for several markers related to neutrophils and T-cells. The IPP tool was able to capture the early immune response in the human *in vivo* endotoxemia model, which is a translational model mimicking the immune response observed in septic patients.

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Abstract 1529

First report of blaNDM-1 and blaOXA-181 harbouring P. vermicola from Nepal

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Background: The genus *Providencia* encompasses five common species i.e., *P. alcalifaciens, P. rettgeri, P. stuartii, P. rustigianii*, and *P. heimbachae*. They are frequently isolated from wounds, respiratory tract, urinary tract, stool of humans, poultry, faeces from reptiles, throat, perineum, axilla and blood of humans. Other species and antimicrobial resistance in this genus are uncommon, especially in clinical samples. We executed whole genome analysis of a pan-drug resistant *Providencia* spp. isolated from a septic patient in Nepal.

Materials/methods: In Nepal, the strain was isolated from urine sample and phenotypically identified as *Providencia spp.* The strain was found resistant to 14 antimicrobials including colistin in disk-diffusion method. The pan-drug resistant *Providencia* spp. was transported to our laboratory for further investigations. We cultured the bacteria on McConkey in 35°C for overnight and prepared a pure stock. The susceptibility of the bacteria to 33 antimicrobials was measured by automatic microbiological system. We searched for ESBL and carbapenemase encoded genes in association with the isolate by disk-synergistic test and modified carbapenamase inactivation method (mCIM), respectively. Genomic DNA of the strain was extracted by boiling method and was sequenced using the PacBio RS II platform.

Results: Susceptibility test revealed that the isolate was susceptible only to monobactum and fosfomycin and was resistant to all other groups of antimicrobials including 3rd-4th generation cephalosporin, carbapenems, aminoglycoside, fluoroquinolone, colistin, etc. Disk synergistic test and mCIM conferred the isolate as non-ESBL encoded and carbapenamase producing isolate, respectively. 16S rRNA sequencing revealed the isolate is highly identical to the *P. vermicola* (99.65%). A total of 13 resistance genes including *qnrD*, *aac(6')-Ib*, bla_{NDM-1}, $bla_{OXA-181}$, etc. were detected in association with the isolate. No typable plasmid replicons, including IncF was detected.

Conclusions: To our knowledge, this is the first *Providencia* strain concomitantly harboring bla_{NDM-1} and $bla_{OXA-181}$ encoding genes. First clinical *P. vermocola* was isolated in 2015 from India and we are reporting the second clinical and most resistant species in the genus *Providencia* from Nepal. The findings suggest that the preparedness to emerging MDR organisms mandates more microbiological surveillances in Asia.

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Abstract 1531

Clinical and microbiological characteristics and outcomes for community-onset sepsis patients in a teaching hospital in Latvia: a retrospective, single-centre, cohort study

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Background: Sepsis is a complex life-threatening condition characterised by systemic inflammatory immune response, which may cause organ failure, septic shock and death. The objective of the study is to assess the mortality and associations between clinical and microbiological characteristics in patients with community-onset sepsis (COS) admitted to Pauls Stradins Clinical University Hospital (PSCUH).

Materials/methods: In retrospective cohort study we identified 395 adult patients with sepsis-related ICD-10 codes upon discharge, admitted to PSCUH between September 2017 and September 2018. Further analysis was performed on 289 COS cases, identified using consensus definitions (Sepsis-3). We collected demographic data, information on clinical presentation, risk factors, time-to-culture (TTC), blood culture (BC) turn-around-time (TAT) and mortality.

Results: The median age of the COS cohort patients was 74 years (IQR 59.0-82.5) with median Charlson Comorbidity Index of 6 points (IQR 4-8), 49.8% were male. The intrahospital mortality reached 47.2%. The reason of hospitalization was documented as infectious disease for 50.8% of COS cases; nevertheless, the BC were not taken in 12.2% of those patients. The most common sites of COS origin were pneumonia (22.7%) and urinary tract infection (16.3%). In 79.2% of cases BC were performed; furthermore, patients without BC were significantly older (p=0.004). Antimicrobials prior to the BC were administered in 36.2% of cases. From 173 BC performed 59.0% returned positive with *Staphylococcus aureus* MS, *Escherichia coli* and *Streptococcus pneumoniae* as the most common isolates – 47.1%, 27.5% and 14.7%, respectively. The rate of positive BC was significantly higher in COS survivor group (p=0.045). Median TTC was 4.8 hours (IQR 2.8-16.4). TTC was not dependent on age, comorbidities, previous exposure to long-term healthcare facilities, clinical presentation, source of infection or presence of septic shock. Median TTC in COS patients initially admitted for non-infectious reason was 5.4h (IQR 3.6-18.6). Median TAT was 93.7h (IQR 78.3-115.0).

Conclusions: Intrahospital mortality was remarkably higher than reported in other sepsis cohorts. Additional training is needed about the recognition of the community-onset sepsis and importance of blood cultures to improve outcomes, especially in the geriatric population. The data collection will be continued and larger cohort remains to be assesed.

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Abstract 1532

Bacteriophages in real-life: positive and negative experience in a difficult to access old-new therapeutic

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Background: Bacteriophages therapies as an alternative or in combination with antibiotics are regaining a place in the arsenal of occidental Infectious Diseases (ID) specialist's after decades of neglect. In the last year bacteriophages as treatment increased in France with more than fifteen patients treated.

Materials/methods: Demographic and clinical data, bacteriophages indication, microbiological aspects including antibiotic susceptibility, procedure to obtain bacteriophages, health care authority statement and outcome after therapy are reported.

Results: Between November 2018 and November 2019, eight cases were discussed in our center. Four patients had bone and joint infection, two a central nervous system infection, one pulmonary abscess and one chronic sinusitis. After reviewing medical chart by a dedicated board, bacteriophages therapy was considered as an option for five patients out of eight. The three remaining cases could be treated with antibiotics optimization. These five cases were subsequently presented and validated by the French national drug agency (ANSM) who authorized compassionate use. Bacteriophages active against patient's bacterial strains were available in three cases. In two cases, bacteriophages were provided by a French pharmaceutical biotech company. In the last case bacteriophages were available in a Swiss research lab. They were active *in vitro* but the patient's family finally refused the treatment. Patients treated with Bacteriophages presented *(i)* a *Staphylococcus aureus* extradural empyema (ED) and osteitis and *(ii)* a prosthetic knee infection. Both previously experienced relapses despite adapted antibiotic treatment. Both patients received a combination of two different Bacteriophages through local instillation in association with active antibiotic therapy. The prosthetic infection relapsed one month after phage instillation while the patient with the ED is cured without relapse at one year follow up.

Conclusions: Bacteriophages therapy is a neglected therapy which came back in our therapeutic arsenal through the multi and pan resistance problem. One of the major limits for Bacteriophages use nowadays is the absence of bacteriophages active against clinical stains as experienced in our experience. Open source libraries of bacteriophages available for clinicians and patients might resolve this limitation. Finally bacteriophages were currently used as salvage therapy in desperate situation which might explain the experienced relapse.

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Abstract 1533

Anakinra for the treatment of protracted paradoxical inflammation in HIV-associated tuberculosis

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Background: Paradoxical inflammation including immune reconstitution inflammatory syndrome (IRIS), is well described in HIV-associated tuberculosis(TB). At the severe end of the disease-spectrum significant morbidity and mortality may occur particularly in TB of the central nervous system (CNS), or when protracted high dose corticosteroids are used. Interleukin-1 (IL-1) mediated inflammation has been implicated in the pathophysiology of IRIS. We describe two cases where anakinra (recombinant human IL-1 antagonist) successfully controlled life-threatening protracted paradoxical inflammation.

Materials/methods: Case reports

Results:
Case 1: A 33-year-old woman from Ethiopia was diagnosed with HIV (baseline CD4 count of 60 cells/mm^3) and fully-sensitive TB with cervical, thoracic and abdominal adenopathy and splenic micro-abscesses. She was treated with standard anti-TB therapy. Following antiretroviral therapy initiation, she had protracted IRIS with fever and massive adenopathy. No alternative infective, malignant or inflammatory cause was found. Pus from repeated lymphnode aspirations showed acid fast bacilli but no further growth of mycobacteria, consistent with IRIS. Over 3 years it was not possible to wean prednisolone below 20mg, nor achieve control of inflammation despite montelukast and colchicine. Protracted inflammation lead to nephrotic syndrome with AA amyloidosis on renal biopsy. This prompted initiation of anakinra, with rapid normalisation of inflammatory markers, proteinuria and quality of life.

Case 2: A 41-year-old man from Zimbabwe with known HIV (virologically suppressed with CD4 count of 275 cells/mm^3) was diagnosed with isoniazid-monoresistant miliary TB. He had cerebral tuberculomata on magnetic resonance imaging(MRI). He was treated with rifampicin, moxifloxacin, pyrazinamide, ethambutol and dexamethasone. He had no neurological deficit at treatment initiation. Over 18 months had progressive episodic neurological deterioration whenever he weaned off corticosteroids with ataxia, aphasia, hemiparesis and inability to live independently. Serial MRI showed unstable tuberculomata is both hemispheres, cerebellum, pons and medulla. Brain biopsy demonstrated necrotizing granulomata with no mycobacterial growth consistent with a paradoxical inflammatory reaction. Anakinra was initiated after unsuccessful trial of thalidomide. Since anakinra initiation he had continual neurological and functional improvement with resolution of tuberculomata on MRI.

Conclusions: We describe, to the best of our knowledge the first reported usage of anakinra to control life-threatening paradoxical inflammation in HIV-associated TB.

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Abstract 1541

One Health surveillance of extended-spectrum beta-lactamase-producing Enterobacteriales in urban and rural Malawi

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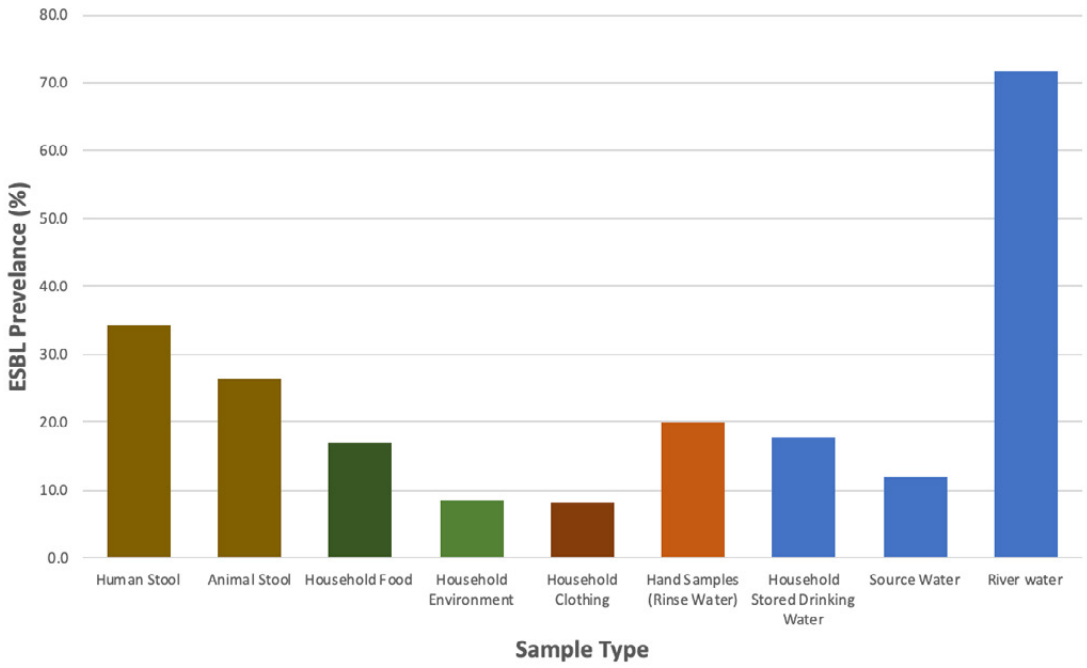
Background: The greatest burden of drug-resistant infections is predicted to occur in low- and middle-income countries (LMICs). Given the limited availability of carbapenems and local resistance to 3rd generation cephalosporins, extended spectrum betalactamase (ESBL) blood stream infections are often untreatable. It is therefore essential to understand the key drivers and environmental reservoirs of ESBL resistance within these settings to interrupt community transmission. We describe a one-health focused observational study of households in Malawi to describe the dynamics of ESBL *E. coli* (ESBL-E) and ESBL *Klebsiella pneumoniae* (ESBL-K) and their ecological niche.

Materials/methods: Longitudinal, microbiological surveillance of 195 households in urban (65), peri-urban (65) and rural (65) Malawi. Each household undergoes 3-4 visits over a 6-month period.
At each visit human and animal stool, alongside an extensive environmental sweep of the household, and broader external environment are taken. Household sampling includes food, drinking water, clothing and key hand contact surfaces, whilst broader environmental sampling comprises nearby soil, drainage systems and local river water. Samples undergo concentration and enrichment culture (buffered peptone water), before plating onto ESBL chromogenic agar. ESBL-E and ESBL-K isolates are identified morphologically, and ESBL-K are confirmed with PCR.

Results: Microbiological surveillance of 112 households (1,700 samples) indicates a high prevalence of ESBL-E and ESBL-K within human stool (34.5% n=162), animal stool (26.4% n=43), on household food (17.1% n=29), in household drinking water (17.8% n=21), on participant clothing (8.2% n=8), on household environmental surfaces (8.6% n=38) and within the broader environment (71.6% n=53) (Figure 1).

Conclusions: In urban and rural Malawi there is a very high prevalence of ESBL Enterobacteriales in humans, animals and the environment. These data will be placed in the context of water sanitation and hygiene behaviour, human health and antimicrobial usage in order to develop a dynamical transmission model.



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Abstract 1544

Clinical factors associated with empirical antibiotics resistance in febrile patients with urinary tract calculus

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Background: To investigate the clinical and microbiological features in the febrile patients with urinary tract calculus, as well as factors that affect empirical antibiotics resistance.

Materials/methods: A retrospective analysis was performed of 203 patients hospitalized between January 2011 and December 2016 for antibiotic treatment of febrile urinary tract infection with urinary calculus at 3 institutions. We investigated patient age, sex, body mass index, underlying diseases, stone-related factors and results of urine and blood culture examination and antibiotic sensitivity test.

Results: Bacteria were identified in 152 of 203 patients (74.9%), and the most commonly cultured included *Escherichia coli* (44.1%), followed by *Enterococci* spp. (11.8%), *Proteus* (8.6%), S. agalactiae (6.6%), *Klebsiella* spp. (5.3%), *Pseudomonas* spp. (4.6%), coagulase-negative *Staphylococci* (4.0%), *Staphylococcus epidermidis* (4.0%), *Serratia* (2.6%), *Enterobacter* (0.7%), *Acinebacter* (0.7%), mixed infection (7.2%) and other spp. (5.4%). The multivariate analysis revealed that multiplicity of calculus was independent predictive factor for fluoroquinolone resistance (p=0.008). Recurrent infection was determined to be significant predictor of cefotaxime resistance on multivariable analysis (p=0.041).

Conclusions: Based on the results from the present study, fluoroquinolone should not be considered as the empirical treatment in febrile patients with urinary tract calculus. Also, combination antibiotic therapy is recommended in case with recurrent infection, because cefotaxime resistance can occur.

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Abstract 1545

Does iodine-impregnated incision drape prevent periprosthetic joint infection? One-year follow-up of 1187 patients in a randomised controlled trial

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Background: PJI is a devastating incident for the patients and in a population that is getting older and the incidence of arthroplasty surgery is rising it is vital to keep the infection rate as low as possible. Despite prophylactic measures as pre-operative decontamination, antisepsis and prophylactic antibiotics the infection rate has been constant at 1-2%.
The primary aim of this study was to examine whether the use of iodine impregnated incision drape (IIID) decreased the risk of periprosthetic joint infections (PJIs). The secondary aim was to investigate whether intraoperative contamination could predict postoperative infection.

Materials/methods: We performed a prospective, randomized two arm study (IIID vs control group) of 1187 patients undergoing primary knee arthroplasty surgery. A database with patient demographics and surgical observations was established with the purpose of following the patients for ten years. Patients, who developed an infection within the first year of surgery were analysed for correlation with the intraoperative bacterial findings and the use of IIID.

Results: 31/1187 (2.6%) patients were re-operated during the follow-up period. 18/31 (58%) patients were deemed infected and received antibiotic treatment. 9/18 of infected patients were female. Of the 18 infected patients 2 were contaminated at primary surgery. 9 of the 18 infected patients were operated with IIID at the primary surgery. No correlation was found between the use of IIID at primary surgery and subsequent infection (OR 0.95, 95% CI 0.38-2.46, P=0.95) Chi square test showed no correlation between contamination and infection (OR 0.86, 95% CI 0.20-3.79, P=1).

Conclusions: We found no effect of the use of IIID and subsequent development of PJI. Nor did we find a correlation between the intraoperative contamination and development of PJI within the first year of follow-up. Longer follow-up time and larger studies are needed to determine if IIID can prevent postoperative infection.

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Abstract 1546

Bronchial abundance of Streptococcus as a potential biomarker for lung cancer

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Background: Lung cancer has been associated to dysbiosis of the lung microbiota, but available data are scarce. The aims of this work were: i) to define the microbiota of the central bronchial tumour, in comParison with the contralateral bronchus of the same patient and with a cohort of controls; ii) to analyse the differences between the oral and pulmonary microbiota, and iii) to find potential microbiota-related biomarkers for lung cancer.

Materials/methods: We obtained bronchial samples by bronchoscopy from tumour and from contralateral lung of 25 patients diagnosed of central lung cancer. Sixteen healthy controls were also included, each contributing with a biopsy of their healthy bronchi. One salivary sample per participant was also obtained. None received antibiotics within the month prior sampling. Bacterial composition was determined by PCR amplification and sequencing of the V3-V4 regions (16S rDNA) using a MiSeq platform (Illumina). Bioinformatics was performed using QIIME2. Differential abundance was assessed by Linear discriminant analysis Effect Size (LEfSe). ROC curves were plotted using SPSS (v.22).

Results: After quality evaluation of the sequencing process, 22 tumour tissue (affected bronchi), 25 contralateral bronchi, and 25 saliva samples from patients (n=25), and 12 bronchi and 16 saliva samples from controls (n=16) were finally included. Alpha-diversity analysis showed higher Chao1 and Shannon indices in patients' bronchi than controls' ($p<0.001$), whereas no significant differences were observed between patients' and controls' saliva ($p>0.05$). Beta-diversity analysis (UniFrac distance) showed that both affected and contralateral bronchial microbiota were different from controls ($p<0.001$). Saliva from patients and controls were also different ($p<0.005$). LEfSe analysis showed a higher density of Firmicutes (particularly *Streptococcus*), in detriment of Proteobacteria, in patients' samples. ROC curves using the relative abundance of *Streptococcus* (Figure1) showed that >14.6% of *Streptococcus* in bronchus predicted lung cancer with 90.9% sensitivity and 83.3% specificity (AUC=0.848, using affected and control bronchi data). Otherwise, streptococcal abundance in saliva did not perform well as biomarker.

Conclusions: Lung and oral microbiota showed an enrichment of Firmicutes and a reduction of Proteobacteria in lung cancer patients. Streptococcal abundance in lung samples obtained by bronchoscopy could be a potential biomarker for lung cancer diagnosis.

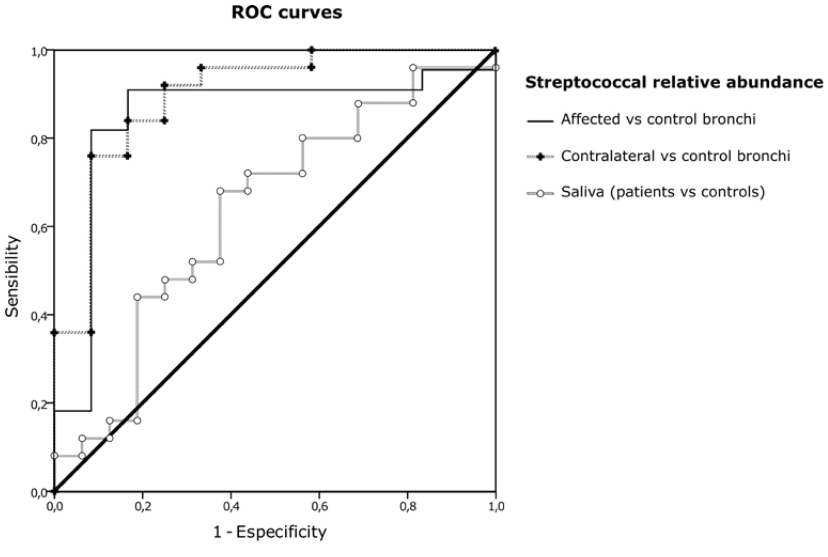

Figure1. ROC curves to discriminate patients from controls using their relative abundance of *Streptococcus*.

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Abstract 1548

ComParison of antibiotic susceptibility of *Escherichia coli* between community-acquired and post-prostate biopsy acute bacterial prostatitis

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Background: To compare the antibiotic susceptibility of *Escherichia coli* (*E. coli*) between community-acquired acute bacterial prostatitis (CA-ABP) and ABP following transrectal ultrasound-guided prostate biopsy (Bx-ABP).

Materials/methods: A total of 4,383 patients underwent prostate biopsy from January 2005 to June 2014. Among these patients, 34 had Bx-ABP; of which 22 patients had *E. coli* identified in their urine or blood culture. *E. coli* was also identified in 91 out of 209 patients with CA-ABP in urine or blood culture. We investigated patient and microbiological characteristics.

Results: The Bx-ABP (50.1%) group showed a higher bacteremia prevalence than the CA-ABP group (13.2%) ($p<0.001$). Significant differences in the antibiotic sensitivity to *E. coli* between the two groups were observed for fluoroquinolone, cephalothin, and gentamicin. The antibiotic sensitivity of fluoroquinolone in the Bx-ABP group was only 27.3%. Amikacin, imipenem, meropenem, amoxicillin/clavulanic acid, and piperacillin/tazobactam showed more than 95% antibiotic sensitivity in both groups. Bx-ABP was an independent predictive factor for bacteremia by multivariate analysis.

Conclusions: *E. coli* in Bx-ABP showed a higher incidence of antibiotic resistance and bacteremia than those in CA-ABP. Carbapenem may be a treatment of choice for patients suspected of having sepsis. Considering the recent emergence of carbapenem-resistant bacteria, piperacillin/tazobactam or amikacin may be considered.

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Abstract 1556

Rapid carbapenemase detection using the CARBA5 lateral flow device

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Abstract third-party references: Supported by NG Biotech

Background: Colonisation and infection with carbapenemase-producing organisms is now frequently reported in the UK, with many diagnostic microbiology laboratories routinely screening for these organisms. Following validation of the NG-Biotech CARBA5 lateral flow device for the detection of the 'Big 5' carbapenemases, we implemented the test into our diagnostic service. Here, we report our carbapenemase detection rate for all rectal screens since March 2019.

Materials/methods: All Enterobacteriales recovered from rectal swabs, as part of our carbapenemase-producing organism screen, were identified by MALDI-ToF and underwent antibiotic susceptibility testing by disk diffusion. Isolates that matched our presumptive carbapenemase algorithm were tested on the CARBA5 according to the manufacturer's instructions.

Results: Between March 2019 and October 2019, 3993 patient rectal swabs were screened for carbapenemase-producing organisms. Of these, 132 (3%) were positive for a carbapenemase-producing organism according to the CARBA5 device, including 12/132 that possessed two carbapenemase-producing organisms. Enzymes detected included OXA-48 (70%), NDM (21%), IMP (2%) and 6% of isolates possessed both OXA-48 and NDM. One presumptive carbapenemase-producer, that was resistant to ertapenem and meropenem, was negative on the CARBA5 device. This isolate was confirmed as negative for the common carbapenemases by the Public Health England reference laboratory.

Conclusions: The CARBA5 lateral flow device was successfully validated and implemented as part of our routine diagnostic service. Importantly, this test enables rapid identification of the most common carbapenemases in our Trust, and in the UK, which reduces the turnaround time for this test, as well as enabling prompt and appropriate infection control interventions.

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Abstract 1557

Incidence of bloodstream infection from multidrug-resistant bacteria in haematological patients with rectal colonisation

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Background: Spread of multidrug-resistant (MDR) bacteria has a relevant impact on the clinico-therapeutic management in the hospital setting with epidemiological surveillance playing a crucial role in its containment. Patients with hematological malignancies are at high risk of infection due to deep immunodepression and long hospitalization periods. In Italky, approximately 5-10% of these patients are colonized by MDR bacteria (carbapenem-resistant [CR], extended sprectrum beta-lactamase producers [ESBL] and vancomycin-resistant enterococci [VRE]); blood stream infection (BSI) develops in 25% of these patients with 60% of these infections being caused by colonizing MDR bacteria. In this study, the incidence of rectal colonization and subsequent MDR-BSI was evaluated in hematological adult patients referred to our laboratory.

Materials/methods: MDR-bacteria colonization was evaluated in 828 hematological patients referred to our laboratory over a two-year period (2017-18) by rectal swab screening; in these patients, blood cultures were analyzed for BSI development following MDR bacteria colonization.

Results: Overall, 43/817 patients (5.3%) were colonized by CR, 232/746 (31.1%) ESBL and 56/441 (12.7%) VRE. Thirthy patients (3.6%) presented colonization by multiple MDR bacteria. Considering species, *K.pneumoniae* (KP) represented 78% of CR, *E.coli* (EC) 75.3% of ESBL (53% of all MDR bacteria) and *E.faecium* (EF) 98.2% of VRE.Over the study period, at leas one episode of BSI developed in 223/828 patients (26.9%), with MDR bacteria in 17.9% of the cases (4.8% of all the patients). Among 43 MDR isolates, 30 were involved in BSI following colonization. Overall, the mean rate of BSI in colonized patients was 12% (3/32 KP CR, 16/174 EC ESBL, 9/45 KP ESBL).

Conclusions: Over the study period, at least one case of rectal colonization from MDR bacteria was found in 35.7% of patients with a high prevalence of ESBL producers (70.4%); this rate of colonization is higher than in other countries, in which however CR bacteria are prevalent (59%). The rate of BSI (26.9%) is similar to that reported in literature (25-26%), however BSIs from MDR bacteria following colonization result lower in comaprison to those reported in literature (15-20%). Further studies are required to define the impact of colonization and subsequent BSI on the patient outcome.

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Abstract 1559

Pooled saliva *cytomegalovirus*-PCR: a viable laboratory technique for universal *cytomegalovirus* screening of healthy newborns

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Background: The vast majority of congenital CMV (cCMV) infected infants have no overt manifestations at birth; still, CMV-related sensorineural hearing loss (SNHL) may be present. Valganciclovir initiated to neonates with moderate-severe cCMV disease has the potential to ameliorate long-term hearing outcome, yet with the customary target screening, many neonates with SNHL cases are missed. Given its ease of collection, saliva is recommended as the preferred screening specimen. Accordingly, we aimed to investigate the screening of healthy full-term neonates employing a pooled saliva specimen technique.

Materials/methods: This was a prospective laboratory universal CMV PCR screening conducted at a secondary hospital in Northern Israel, March 2019 until June 2019. All neonates underwent saliva sampling upon arrival to the nursery. Specimens were extracted in pools of 10 and individually (40µL and 400 µL, respectively) by the QiaCube (Qiagen) automated extractor. Specimen extracts were analyzed for the presence of CMV DNA by the RealStar® CMV-PCR Kit 1.0 (Altona Diagnostics) using the Rotorgene 6 plex real-time platform (Qiagen). In cases where the pooled specimen was positive, the pool was opened and the individual specimens evaluated to determine the source(s) of CMV. A definitive cCMV was defined only after confirmation with positive urine testing.

Results: Of the 1000 saliva samples, there were 6 urine-confirmed congenital CMV patients attained by both laboratory techniques. The specificity of both techniques, was high with the pooled specimen yielding 98.94 (95% CI: 94.2-99.97%) and the individual sampling 98.1% (95% CI: 97.0-98.8%), respectively. The rate of false positive results was statistically significantly higher in individual sampling in comParison to the pooled specimens, 19/25 (76.0%) versus 1/7 (14.3%; p<.003), respectively. Similarly the PPV of the individual sample was only 22.4% in comParison to 98.2% in the pooled specimens.

Conclusions: Pooled saliva CMV PCR of full-term healthy newborns appears to be an effective laboratory technique for identification of asymptomatic cCMV infection. The pooling technique affords a higher specificity by decreasing the rate of saliva false-positive samples and may have the potential to improve the laboratory workflow and decrease costs. Further studies are needed to evaluate the clinical correlation of this widespsread cCMV screening technique.

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Abstract 1562

Acquired resistome of *Escherichia coli*

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Background: *Escherichia coli* is an ubiquitous bacterium found in the intestinal microbiota of vertebrates. Accordingly, *E. coli* is widely exposed to antibiotics and has evolved by acquiring different antibiotic resistance genes (ARGs). In the past, the exhaustive characterization of these genes was difficult because based on targeted PCRs. With the availability of next-generation sequencing, the identification of resistance genes has become easier. Here, we aimed at characterizing the census ARGs acquired by *E. coli*, leveraging a publicly available *E. coli* genome database.

Materials/methods: We downloaded the 82,084 genomes of Enterobase that includes *E. albertii*, *E. marmotae*, *Escherichia* clades, *E. fergusonii*, *E. coli*, *Shigella* or unspecified. *E. coli* genomes were identified by the ClermonTyper tool and *in silico* PCR. Plasmid incompatibility groups were determined by PlasmidFinder and ARGs by the Diamond tool using both the AMRFinder and ResFinderFG databases (minimum 80% nucleotide identity and/or 80% coverage). In order to reduce selection bias of the strains in the database, the proportions of ARGs were normalized within each phylogroup. The different associations were studied with R.

Results: We identified 70,307 *E. coli* genomes that carried 311,348 antibiotic resistance genes: 382 genes sharing 100% identity with known genes (n = 164,534) and 328 genes for which variants of known genes were identified (n = 146,814). *bla*$_{TEM-1}$ was the most recovered gene (n = 16,766). We observed limited beta-lactamase diversity with only 22 different families.

However, we have identified a gene encoding a class A beta-lactamase from *Bacteroides* in a strain isolated in Germany. In addition, we observed the frequent presence of ARGs conferring resistance to antibiotics used in Gram-positive bacterial infections: rifampin (*arr*) and macrolide-lincosamines (*lnu*, *mef, mphA*, *erm*, *vga* and *msr*). Finally, we observed associations between ARGs as well as correlations between ARGs and plasmid incompatibility groups.

Conclusions: Using a substantial set of *E. coli* genomes, we could describe the acquired resistome of *E. coli*. While the diversity of acquired beta-lactamases – encoding genes was low, we could observe the frequent presence of ARGs conferring resistance to antibiotics not primarily targeting *E. coli*, reflecting the selective pressure exerted on *E. coli* in the gut.

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Abstract 1563

Risk factors for readmission among OPAT patients in the Netherlands

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Background: In the Netherlands, home treatment with intravenous antimicrobial therapy is a relatively new concept. Although several studies have shown that outpatient parenteral antimicrobial therapy (OPAT) can be administered safely, people receiving antimicrobials at home remain at risk for adverse events. The Infectious Disease Society of America (IDSA) guidelines recommend weekly follow-up of all OPAT patients, to monitor and reduce adverse events. The aim of our retrospective study is to determine rates of OPAT-related complications and to identify risk factors for readmission in patients discharged with OPAT.

Materials/methods: Electronic patient records from all patients, age > 18 years and discharged with OPAT during the period of 2016-2018 were included. Complications consisted of antibiotic-related adverse drug events (ADE) or catheter-related (infection, thrombosis, mechanical). Multivariate analysis was performed to identify demographic risk factors for readmission.

Results: A total of 247 patients were included in the analysis; mean age was 60 years. Most common reason for OPAT was bone and joint infections (17%). Penicillins (40%), cephalosporins (28%) and vancomycin (13%) were the most commonly prescribed antimicrobials. A total of 37 patients (15%) were discharged with aminoglycosides or vancomycin. The overall complication rate was 16%. Forty-one percent of readmission was OPAT-related (ADE, catheter- or mechanical complications). The overall readmission rate was 10%, respectively. Among the patients receiving aminoglycosides or vancomycin, 51% (19/37) received weekly therapeutic drug monitoring (TDM). The readmission rate in this group was 32%. Receiving aminoglycosides or vancomycin was found to be an independent predictor of readmission (p<0.05, OR 5.7; CI, 2.46-13.78). Age, gender, indication and discharge to skilled nursing facility were not found predictive for readmission in multivariate analysis.

Conclusions: OPAT patients receiving aminoglycosides or vancomycin have a higher risk of readmission, compared to the general OPAT population. Further research needs focus on the prevention of readmission by performance of weekly TDM and monitoring according to IDSA guidelines.

Table 1. Complications and readmission rate in patients discharged with OPAT from 2016 until 2018 at the VU Medical Center.

	Total n=247
Complications	40 (16%)
Catheter-related	22 (55%)
Adverse drug events (ADE)	15 (38%)
Other (not-OPAT related)	3 (8%)
Readmission	25 (10%)

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Abstract 1564

Bordetella holmesii in suspected cough: a frequent pathogen?

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Background: *Bordetella holmesii* is responsible for bacteremia in asplenic or sickle cell patients. *B holmesii* can also be found in nasopharyngeal samples of patients with a symptomatology compatible with whooping cough. Diagnostic PCR kits typically target IS*1001* and IS*481*, which does not distinguish *B. pertussis* from *B. holmesii*. This lack of distinction leads to biases in vaccine efficacy analyzes, as the vaccine does not protect against *B. holmesii*. We investigated the frequency of detection of *B. holmesii* from March to August 2019, in outpatients (93%) and hospitalized patients (7%), following the implementation of PCR assays targeting IS*481* and IS*1001* but also hIS*1001*, which allows distinction between *B. holmesii* and *B. pertussis.*

Materials/methods: Automated DNA extraction from nasopharyngeal samples was performed on the Janus Chemagic 360 from 1 mL of sample with an elution volume of 100 µL. Automated amplification was performed using a CFX 96 ™ with the Viasure *Bordetella* kit. The absence of *B. pertussis* DNA in the 10 samples was controlled by the National Reference Center of whooping cough.

Results: Of the 7,161 nasopharyngeal samples analyzed, we detected *B. holmesii* in 10 samples, (0.14%), *B. pertussis* in 819 (11.4%) and *B. parapertussis* in 34 (0.47%). No co-infection was identified. The age of patients infected with *B. holmesii* was 24.7 years, whereas mean age was 27.5 and 14.9 years for *B. pertussis* and *B. parapertussis*, respectively. Cases were evenly distributed over time. The geographical origin of the *B. holmesii* cases was Paris, Ile de France outside Paris, South East, Aquitaine , Loire Valley and Great East .

Conclusions: *B. holmesii* was rarely found in the population studied, and represented only 2% of *Bordetella* infections among adults and adolescents, consistent with recent reports from Spain, Switzerland, Australia and Japan.

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Abstract 1566

A mock-outbreak of carbapenem-resistant *Klebsiella pneumoniae*: using whole genome sequencing to correlate clinical and environmental samples and provide clues to improve infection control in real-time

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Background: ONEIDA is a Portuguese consortium of research institutions aiming to collaborate with hospitals to integrate bacterial real-time genotyping based on whole genome sequencing (WGS) to support infection control.
In Portugal, the incidence of nosocomial infections due to carbapenem-resistant *Klebsiella pneumoniae* (CRKP) is increasing exponentially.

We conducted a pilot study to simulate the investigation of a CRKP outbreak in a Portuguese hospital with two main goals: to test the capacity to obtain and interpret WGS data in a short period of time; to evaluate the relevance of concomitant analysis of hospital environmental samples to unveil potential routes of transmission.

Materials/methods: Ten CRKP clinical strains routinely isolated in the hospital microbiology laboratory were provided to simulate an outbreak situation. In parallel, 40 environmental samples (from sinks and sink drains) were obtained from the wards where the infected patients had stayed.

Environmental samples were plated in selective media and pure cultures suggestive of CRKP were isolated. DNA was extracted from clinical and environmental isolates and sequenced (Illumina NextSeq). Genomes were assembled using INNUca v3.1. MLST, cgMLST and antimicrobial resistance were determined using Pathogenwatch.

Results: The first conclusions were obtained within 48 hours: eight clinical samples were confirmed to be CRKP; the other two were *K. aerogenes*. The eight CRKP were of ST13 (n=6, all harboring bla_{KPC-3}), ST14 (n=1, $bla_{OXA-181}$) and ST111 (n=1, $bla_{OXA-181}$). Results regarding the 40 environmental samples were obtained within six days: half of the samples yielded colonies compatible with CRKP. By WGS, eight were confirmed to be CRKP: five were ST13, one was ST117 and two were ST323. All harbored the bla_{KPC-3} gene. Environmental CRKP were isolated mostly from sink drains (n=6). Importantly, ten out of the 11 clinical and environmental ST13 CRKP clustered closely together by cgMLST differing from each other in 0-19 alleles (out of 1972 core genes).

Conclusions: This pilot study demonstrated the ability of ONEIDA academic researchers and health care professionals to work closely together to investigate an outbreak in real time. The results further indicate that concomitant environmental sampling is informative to determine transmission routes allowing for rapid implementation of targeted infection control measures.

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Abstract 1568

Transcriptome analysis of pneumococci isolated from meningitis patient's cerebrospinal fluid identifies multiple genes important for pathogenesis, including a novel operon of unknown function

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Background: Pneumococcal meningitis (PM) remains a significant cause of mortality and long-term morbidity, despite antibiotics and corticosteroids. We sequenced the *S. pneumoniae* transcriptome in patient CSF during PM, to investigate which highly expressed genes are implicated in damaging inflammatory responses.

Materials/methods: CSF from adults with PM was collected prior to antibiotics and stored at -80ºC in PAXgene®. Total RNA was isolated and sequenced after ribodepletion on the Illumina Nextseq platform. Transcripts were mapped against multiple *S.pneumoniae* genomes, normalised and quantified. The clinical transcriptome was analysed against infection-relevant conditions in the *in-vitro* D39 transcription model PneumoExpress. Gene-deletion mutant bacteria were generated by targeting selected genes that were highly expressed during PM in a serotype 1 (ST5316) *S. pneumoniae* meningitis isolate. The mutant phenotypes were investigated using *in-vitro* models of neutrophil phagocytosis, growth in human CSF (hCSF), and in a murine model of PM.

Results: CSF transcriptomes were available for 11 adults with PM (median age 32 years, 60% male, 70% HIV-1 co-infected, 10/11 non-survivors, median bacterial load $1.6x10^7$ copies/ml CSF (IQR $4.1x10^6$ – $7.0x10^7$). Transcripts mapping was optimal against Serotype 1 strains (gamPN10373, P1031). Genes with very high expression included multiple genes encoding proteins involved in avoidance of opsonophagocytic killing (BgA, PsaA, PspC, CiaRH, NanA, ply, pep0, Pbp1A, CbpA) as well as several genes with unknown function. Highly upregulated genes were clustered and tested against a set of *in-vitro* conditions mimicking different infection models. Clinically expressed genes most closely correlated with *S. pneumoniae* D39 gene expression in the presence of A549 epithelial cells. Gene deletion mutants were constructed in two highly upregulated genes not previously described to be involved in PM, *bgaA* (encodes a betagalactosidase) and the operon SP_1800-5 (no previous published data). Neither mutant strain grew in ex-vivo human CSF, opsonophagocytic killing of both mutants was enhanced compared to WT bacteria, murine data pending.

Conclusions: *S.pneumoniae* expresses multiple virulence proteins in the CNS compartment during meningitis. Expression of an operon with previously unknown function implies that *S.pneumoniae* may invoke meningitis-specific responses in CSF. Further investigation of the meningitis-specific bacterial response may present novel therapeutic targets for this devastating disease.

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Abstract 1569

Effectiveness of chlorhexidine-impregnated dressing and a bundle of interventions for prevention of central line-associated bloodstream infections

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Background: The aim of this study was to assess the effectiveness of chlorhexidine-impregnated dressing and bundle practice to reduce the rate of central line associated bloodstream infections (CLABSIs).

Materials/methods: We performed a bundle of interventions to reduce the CLABSIs by the year 2012. As one component of the bundle, we started using the chlorhexidine impregnated catheter dressing. We used a form describing how to apply central venous catheter for the practicing physicians and nurses, and we organized several information meetings. Then we have compared the rate of CLABSI before and after the intervention.

Results: In total 76 CLABSI events were detected between January 1, 2011 and June 31, 2019. Twenty-six cases were detected before the intervention period which was between January 1 2011 and December 31 2011, and 50 cases were detected after the intervention period in seven and a half years (January 1, 2012 and June 31, 2019). Following interventions, the annual CLABSI rate was 2.60/1000 catheter days in pre-intervention period and 0.49/1000 catheter days (p=0.037) in post-intervention period. Additionally, the CLABSI rate among hematology-oncology inpatients decreased from 3.39 to 0.76 (p=0.010) in the same term.

Conclusions: The use of chlorhexidine impregnated dressing and bundle form decreased the rate of CLABSIs significantly. This protocol became the standard of care in our hospital.

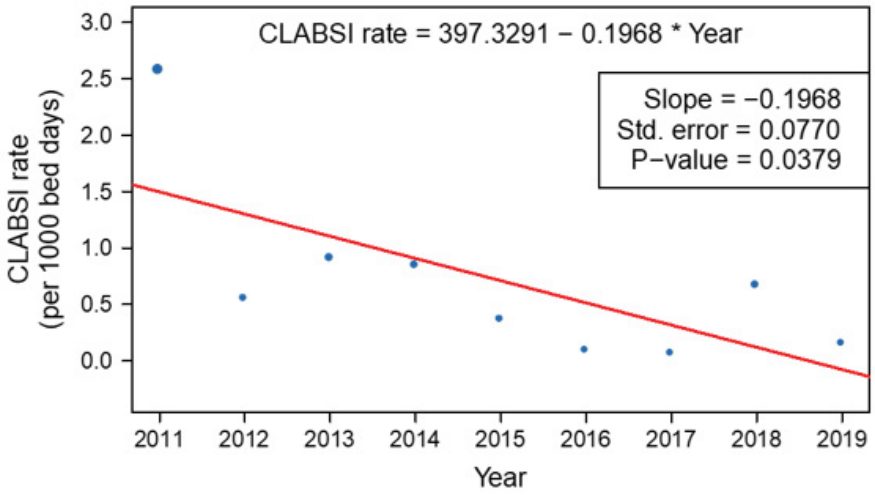

Figure 1: The CLABSI rates per 1000 catheter days among inpatients during the study period.

Ps: P values and average values have had calculated according to six-month term period.

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Abstract 1571

Effect of hybrid organo-inorganic sol-gel coating loaded with antifungals on *Candida* strains

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Abstract third-party references: Funded by a grant from the Mutua Madrileña Foundation

Background: *Candida albicans* and *C. parapsilosis* are the major etiological agents of fungal prosthetic joint infections (PJI). Although infrequent, these infections are difficult to diagnose and treat and display high recurrence rates. Here we evaluate two sol-gel coatings loaded with fluconazole and anidulafungin in order to treat fungal biofilms formed during PJI.

Materials/methods: A hybrid organo-inorganic sol-gel coating was fabricated from a mixture of two organopolysiloxanes: 3-methacryloxypropyltrimethoxysilane and tetramethoxysilane in a molar ratio of 1:2, and the addition of tris (trimethylsilyl) phosphite in a molar ratio of 52:1 (organopolysiloxanes:phosphorus compound). Control coatings without additions of antifungal (P2) and three coatings loaded with three saturation percentages (50, 75 and 100%) of anidulafungin (A) or fluconazole (F) were used.
Biofilm formation of *C. albicans* ATCC 10231 (Cal ATCC) and *C. parapsilosis* ATCC 22019 (Cpar ATCC) was induced in a 96-well plate using 0.5 McFarland of yeasts in RPMI 1640 + 2% glucose for 48 h. After incubation, medium was renewed and the lid of the plate was replaced by a MBEC™ biofilm Incubator lid whose pegs had been coated a day before by dipping it in wells filled with 200 µL of each treatment, followed by incubation at 37 °C for 48 h.
Biofilm viability was determined by adding 10 µl of Alamar Blue per well and measuring the fluorescence after 3 h. Experiments were performed in triplicate. ComParisons of the viability percentage were performed by using *t*-Student test with a level of statistical significance of 0.05.

Results: The presence of P2 was sufficient to produce a significant decrease (between 10-15%) of *C. albicans* ATCC 10231 biofilms, while the addition of antifungal contributed slightly to this effect. P2 alone did not affect biofilm viability of *C. parapsilosis* ATCC 22019 and the presence of antifungal decreased viability by up to 99% in the case of fluconazole.

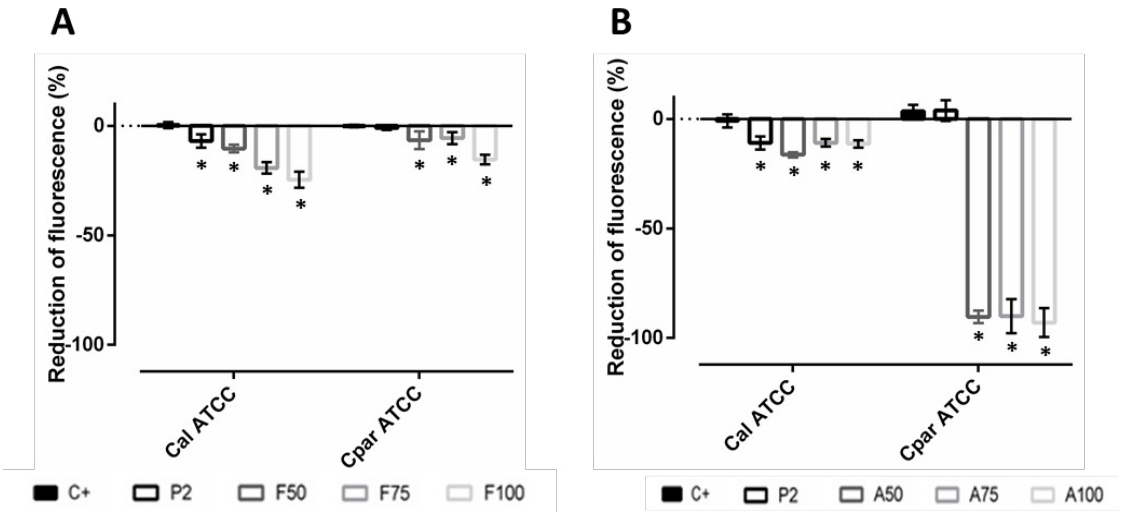

Figure 1. Biofilm viability after treatment with fluconazole-loaded (F50, F75, F100) (A) or anidulafungin-loaded (A50, A75, A100) (B) sol-gels. *: P<0.05.

Conclusions: The sol-gel coating loaded with antifungals is able to reduce fungal biofilm viability, being a promising tool for locally treating *Candida* PJI.

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Abstract 1573

Prevalence and outcome of ampicillin-susceptible but penicillin-resistant *Enterococcus faecalis* bacteraemia: a multi-centre retrospective study

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Background: Ampicillin-susceptible but penicillin-resistant *Enterococcus faecalis* (PRASEF) strains have been recently related to higher mortality in enterococcal bacteremia. The primary purpose of this study was to assess the prevalence and outcome of PRASEF bacteremia.

Materials/methods: This observational, retrospective, multicenter study was conducted between January 2010 and July 2019 in two Italian and one Spanish hospital. All hospitalized patients with monomicrobial bacteremia caused by ampicillin-susceptible *E. faecalis* were enrolled. Penicillin-susceptibility was defined based on CLSI criteria. Primary endpoint was clinical failure, defined as composite outcome consisting of a) modification of antibiotic therapy due to lack of efficacy, b) relapse, endocarditis or mortality within 90 days from the index blood culture.

Results: Study population consisted of 204 patients: median age was 73 years (IQR 60-81), 69% of the patients were male and median Charlson comorbidity index was 10 (IQR 10-12). Main bacteremia sources were urinary tract (32%), primary (29%), and gastro-intestinal tract (18%). PRASEF were observed in 28 (14%) cases. There were no differences in terms of demographics, source and severity of bacteremia among PRASEF and non-PRASEF groups. Median (IQR) length of hospitalization was significantly longer [18 (9-31) vs 28 (13-45), p 0.02] in PRASEF vs. non-PRASEF groups.
Clinical failure occurred in 61% and 37% of patients in the two groups (p 0.033), respectively. Mortality at 90 days was also significantly higher in the PRASEF population (46% vs 26%, p 0.004). No differences were found among the other elements of composite outcome. Multivariate logistic regression analysis adjusted for Charlson comorbidity index, diabetes, sepsis or septic shock, isolation of PRASEF, immunosuppression, source of bacteremia, showed that isolation of PRASEF [OR 2.46 (95% CI 1.04-5.81) p 0.04], Charlson comorbidity index [OR 1.143 (95% CI 1.05-1.23) p 0.001], and sepsis or septic shock [OR 2.84 (95% CI 1.32-6.09) p 0.007] were independent risk factors for clinical failure.

Conclusions: Our study confirms the unfavorable outcome of bacteremia due to PRASEF strains and emphasizes the need for a timely evaluation of minimum Inhibitory concentrations (MICs) for penicillin and ampicillin. Further studies are needed in order to assess *ad hoc* therapeutic regimens for this peculiar resistance phenotype.

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Abstract 1574

Nontoxigenic *Clostridioides difficile* strains against C. difficile colonisation: an experimental study

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Background: Nontoxigenic *Clostridioides difficile* strains (NTCD) are non-pathogenic and cannot acquire the toxin A and B genes. Their role in preventing *C. difficile* recurrence was demonstrated among hospitalized patients (Gerding et al., JAMA 313(17):1719-1727).

In a previous study we described a high *C. difficile* intestinal colonization rate of preterm neonates, mostly due to two NTCD. We hypothesized that these strains could be protective against *C. difficile* colonization and conducted an *in vivo* experiment in a hamster caecitis model to determine their potential protective role.

Materials/methods: 40 hamsters were treated by clindamycin to induce an intestinal dysbiosis (D-5). They were divided into 5 groups: 1 positive control group (n=8, A) was infected only by a toxigenic strain (PCR-ribotype 027), 2 groups (n=7, B and C) were administered only one NTCD each, and 2 groups (n=9, D and E) were administered one NTCD each (D-3), followed by the 027 strain (D0). Animals were daily monitored for 19 days (clinical activity score and weight). Stool colonization was determined from D-1 until death or sacrifice. After sacrifice (if euthanasia criteria were met or at D19), caeca were collected for histological analysis.

Results: All animals (8/8) in group A died within 2 days. The survival rate was significantly increased in groups D (4/9 deaths, p=0.029) and E (1/9 death, p=0.0004). The mean colonization rate of the toxigenic strain in the group A was $1.6x10^7$ CFU/g of stool, and was equivalent in the other groups. At D2, the colonization rate of NTCD in groups B, C, D and E was $2.3x10^7$, $2.4x10^7$, $1.5x10^8$ and $6.2x10^7$, respectively. In the group D, the toxigenic strain was steadily detectable at a lower rate in 4 animals (10^4-10^6 CFU/g), whereas in the group E, only 2 animals were colonized and only at D2. Histological analysis of the caeca revealed that co-infected animals with no clinical signs had no tissular alterations.

Conclusions: Both NTCD provide a potential protection against *C. difficile* colonization. *In vitro* studies and genome analysis are ongoing to try to elucidate the protective mechanisms.

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Abstract 1576

Ceftolozane/tazobactam for multidrug-resistant *Pseudomonas aeruginosa* in a swine model of severe pneumonia

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Abstract third-party references: BITRECS, IDIBAPS, Barcelona, Spain, CIBERES, Madrid, Spain, Merck & Co, Kenilworth, NJ, USA

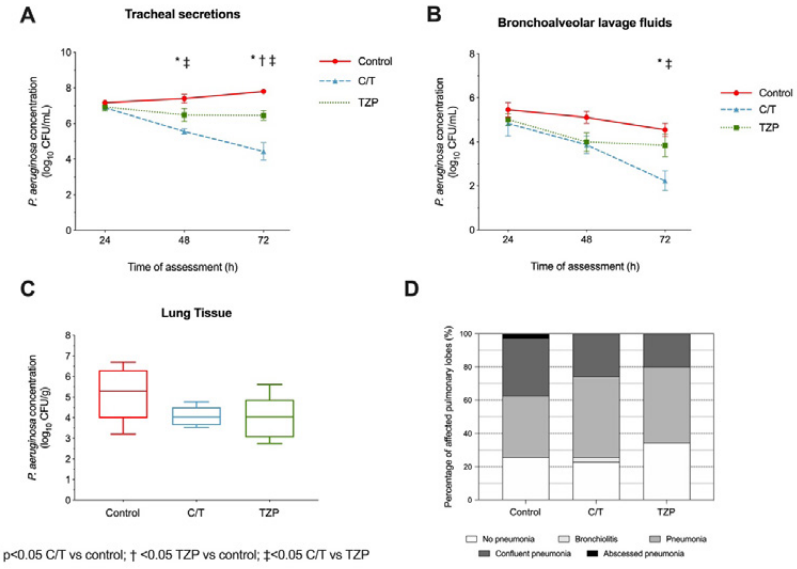
Background: Nosocomial pneumonia is one of the most common hospital-acquired infections, associated with high morbidity and mortality. Gram-negative pathogens, particularly *Pseudomonas aeruginosa*, cause life-threatening infections specifically in hospital settings. Ceftolozane/tazobactam (C/T) is a novel antibiotic with activity against multidrug resistant (MDR) *P. aeruginosa* but still not fully characterized against other first-line antibiotics for nosocomial pneumonia.

Materials/methods: Twenty-one pigs (32.9±1.7 kg) were anesthetized and mechanically ventilated up to 76h. Severe pneumonia was developed by intra-bronchial inoculation of a clinical *P. aeruginosa*, intermediate to piperacillin/tazobactam (TZP) but susceptible to C/T. Following clinical pneumonia diagnosis, animals were randomly assigned into three groups: placebo (control), 50/25 mg/kg C/T and 200/25 mg/kg TZP. Antibiotic doses had previously been humanized. Ceftriaxone was administered to avert endogenous colonization. Inflammatory markers were measured throughout the study. *P. aeruginosa* was cultured in tracheal secretions and bronchoalveolar lavage (BAL) fluid and development of antibiotic resistance compared among groups. Upon autopsy, *P. aeruginosa* was cultured in lungs and histopathology injury scored.

Results: Development of pneumonia and treatment substantially affected systemic cytokines. In particular, IL-1β was significantly downregulated by C/T and returned to baseline levels after 48h of treatment, in comParison with control and TZP animals (p=0.031). Bacterial burden in tracheal secretions and BAL fluids varied among study groups (p<0.001) and times of assessments (p<0.001) (Figure 1A-B). Specifically, C/T-treated animals achieved the greater eradication in both matrixes. In contrast, *P. aeruginosa* burden in lung tissue was 5.30[4.00-6.30], 4.04[3.64-4.51], and 4.04[3.05-4.88] CFU/g in the control, C/T, and TZP groups, respectively (p=0.299), without histopathological differences (p=0.556) (Figure 1C-D). An increase in resistance to TZP was found in 3 animals.

Conclusions: In a swine model of MDR *P. aeruginosa* severe pneumonia, C/T decreased respiratory secretions' bacterial burden, while averting development of resistance and possibly reducing systemic inflammation. Yet, after only 2 days of treatment, *P. aeruginosa* tissue concentrations were moderately affected.

Figure 1. *P. aeruginosa* burden (log_{10} CFU/mL; mean ± standard deviation) in tracheal aspirates (A), bronchoalveolar lavage fluids among study groups (B). (C) *P. aeruginosa* burden (log_{10} CFU/g; median [interquartile range]) in lung tissue among study groups. (D) Severity of histopathological findings among treatment groups.



* p<0.05 C/T vs control; † <0.05 TZP vs control; ‡<0.05 C/T vs TZP

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Abstract 1577

Efficacy of beta-lactam/beta-lactamase inhibitors to treat extended-spectrum beta-lactamase-producing Enterobacterales bacteraemia secondary to urinary tract infection in kidney transplant recipients

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Abstract third-party references: This work was supported by Plan Nacional de I+D+i 2013-2016 and Instituto de Salud Carlos III, Subdirección General de Redes y Centros de Investigación Cooperativa, Ministerio de Ciencia, Innovación y Universidades, Spanish Network for Research in Infectious Diseases [REIPI RD16/0016/0008; RD16/0016/0001, RD16/0016/0002, RD16/0016/00010] - co-financed by European Development Regional Fund "A way to achieve Europe", Operative program Intelligent Growth 2014-2020; ESCMID Study Group for Infections in Compromised Hosts [ESGICH grant to J.M.A.]; Sociedad Andaluza de Trasplante de Órgano Sólido [SATOT grant to L.M.M.]; ESCMID Study Group for Bloodstream Infections and Sepsis (ESGBIS); and ESCMID Study Group for Antimicrobial Resistance Surveillance (ESGARS).

Background: Urinary tract infection (UTI) is the most common source of bloodstream infection (BSI) in kidney transplant recipients (KTR). Episodes caused by extended-spectrum β-lactamase-producing *Enterobacterales* (ESBL-E) are particularly frequent in these patients. We sought to evaluate risk factors for therapeutic failure and examine the impact of regimens based on carbapenems versus β-lactam/β-lactamase inhibitors (BLBLI) in a large multinational cohort of KTR diagnosed with BSI secondary to UTI.

Materials/methods: We retrospectively evaluated 306 KTR with BSI secondary to UTI caused by ESBL-E, admitted to 30 centers from January 2014 to October 2016 (INCREMENT-SOT, ClinicalTrials.gov NCT02852902). Therapeutic failure (lack of cure or clinical improvement and/or death from any cause) at days 7 and 30 from BSI onset were primary and secondary study outcomes, respectively. Univariate and multivariate logistic regression models were applied to identify factors predicting therapeutic failure. A propensity score (PS) was used to control the therapy indication bias.

Results: Carbapenem monotherapy (68.6%, primarily meropenem) was the most frequent active therapy used, followed by BLBLI monotherapy (10.8%, mostly piperacillin-tazobactam). Therapeutic failure at day 7 was 9.0% (13.8% at day 30) with carbapenems and 3.0% (9.1% at day 30) with BLBLI. Mortality at days 7 and 30 was 1% and 3%, respectively. Hospital-acquired BSI [adjusted OR (aOR): 3.89; 95%CI: 1.41-10.76] and Pitt bacteremia score at BSI onset (aOR: 1.53; 95%CI: 1.24-1.88) were independently associated with therapeutic failure at day 7. Age-adjusted Charlson Index (aOR: 1.25; 95%CI: 1.05-1.48), Pitt score (aOR: 1.72; 95%CI: 1.35-2.17) and lymphocyte count ≤500 cells/μL at presentation (aOR: 3.16; 95%CI: 1.42-7.06) were independently associated with therapeutic failure at day 30. In PS-adjusted analysis, BLBLI could not be found to be associated with increased risk of failure at day 7 or 30 (PS-adjusted OR: 0.79; 95%CI: 0.23-2.64 and PS-adjusted OR: 0.64; 95%CI: 0.23-1.77, respectively).

Conclusions: Significant differences in the risk of therapeutic failure at 7 and 30 days, according to the use of active therapy with BLBLI *versus* carbapenem-containing regimens, could not be identified in this large multinational cohort of KTR diagnosed with BSI secondary to UTI due to ESBL-E.

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Abstract 1578

Aspirin reduces cardiovascular events in patients with pneumonia: a prior events rate ratio analysis in a large primary care database

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Abstract third-party references: NIHR, NIHR HPRU

Background: Ischaemic stroke and myocardial infarction are common after pneumonia, and are associated with mortality. Aspirin may attenuate this risk, leading to significant reduction in post-pneumonia complications. Limited evidence from secondary care suggests that aspirin may have a beneficial effect, but studies so far have been small, and none have focussed on primary care.

Materials/methods: A prior event rate ratio (PERR) analysis, performed in the Clinical Practice Research Datalink (CPRD), a large UK primary care database, from inception until January 2019, linked to Office for National Statistics (ONS) mortality data. All patients over 50 with a coded diagnosis of pneumonia and adequate data quality, with follow-up data for at least one year after pneumonia, were included. The study period covered from one year before to 6 months after the pneumonia date.
The PERR approach allows for control of measured and unmeasured confounding, as the ratio of events prior to and after a given event is considered, and each participant is a self-control. Diabetes, smoking, hypertension, previous cardiac and cerebral ischaemic events, age, gender, and socioeconomic deprivation were included as covariates. Time-to-event analysis was performed. The primary outcome was the combined outcome of ischaemic stroke and myocardial infarction. Secondary outcomes were ischaemic stroke and myocardial infarction individually.

Results: 48,260 patients were included in the final analysis. 8,099 of these were aspirin users, with 35,197 non-aspirin users, and 4,964 patients censored for intermittent aspirin use. Despite being older and more comorbid, aspirin users had a reduced risk of the primary outcome (adjusted hazard ratio, HR 0.68; 95% confidence interval 0.55 - 0.83) in the PERR analysis. For both secondary outcomes, aspirin use was also associated with a reduced risk (HR 0.52 (0.34 – 0.77) and 0.71 (0.55 – 0.94) for myocardial infarction and stroke respectively).

Conclusions: Aspirin use is strongly associated with reduced ischaemic events after pneumonia, in a primary care setting. Further work should explore the prophylactic benefits of aspirin prescription in pneumonia, in a prospective, randomised fashion.

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Abstract 1580

Optimising the use of triazole therapeutic drug monitoring using quality improvement methodology

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Background: Posaconazole and voriconazole are triazole antifungals indicated for prophylaxis and treatment of mycotic infections. Therapeutic drug monitoring (TDM) and individualised dosing are recommended to ensure clinical efficacy and prevent toxicity. Local audit data revealed 38% (*n*=8) of haematology inpatients administered triazoles received TDM at our tertiary London hospital. We undertook a Quality Improvement (QI) project to optimise triazole TDM.

Materials/methods: Haematology inpatients administered posaconazole or voriconazole were identified retrospectively from pharmacy dispensing records to calculate baseline TDM compliance over 16 weeks. Compliance was calculated by dividing number of patients who received TDM by the number of patients eligible for TDM based on local guidelines: 1) 3-7 days post-treatment initiation, 2) repeated week 2, and 3) repeated every 4 weeks. Therapeutic ranges were taken from ESCMID guidelines (Ullman et al. *Clin Microbiol Infect*; 2018).
QI methodology was used to improve compliance with Trust guidelines. This included the development of a driver diagram and questionnaire to identify barriers to conducting TDM appropriately. Interventions were designed to prompt TDM when indicated.

- Intervention 1 (week 17): a pharmacist prospectively identified patients on triazoles from the electronic prescribing system (Cerner PowerChart) for discussion on a joint infection-haematology ward round. Additionally, a text reminder was built into Cerner.
- Intervention 2 (week 27): patients requiring TDM were sent directly to the haematology consultant.

Results: 111 encounters (*n*=38 patients) were prospectively reviewed over the course of 16 weeks. 51 levels were taken out of 87 recommended (59%). Subtherapeutic levels (*n*=13) and potentially toxic levels (*n*=4) were managed by dose adjustment (*n*=10). Remaining deviations were managed with repeat levels or alternative treatment.
Following the first intervention, compliance remained above the mean, demonstrating a shift (figure 1). Mean compliance was recalculated at almost three-times baseline (24% to 65%).

Conclusions: This QI project has improved appropriate use of TDM. Future work will focus on expanding to outpatient areas and other specialities such as respiratory medicine. Pharmacist-led TDM clinics incorporating other tests (e.g. liver function) could be used to ensure outpatients are effectively monitored and doses optimised.

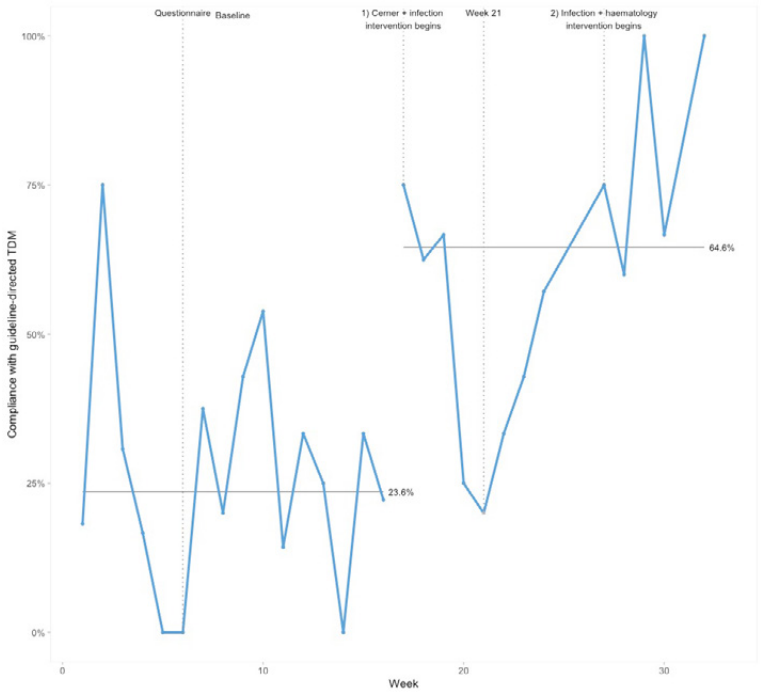

Figure 1. Week 21 excluded (no referrals due to Bank Holiday).

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Abstract 1581

The difficulties of differentiating central nervous system infection from disease relapse in a cohort of adult patients with haematological malignancy: 10 years' experience from a central London hospital

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Background: CNS infections occur in up to 15% of patients with haematological malignancy undergoing allogenic haemopoetic stem cell transplant (HSCT). Delays to identification of causative pathogens may contribute to worse outcomes, however diagnostic samples can be difficult to obtain. We sought to describe MRI head (MRH) features seen in a cohort of adult patients with haematological malignancy in who CNS infection was suspected.

Materials/methods: We undertook a retrospective case review of patients with haematological malignancy undergoing MRH for suspected CNS infection between 2007-2017. Cases were identified through electronic MRH database using a text search. MRI images were classified according to anatomical disease, reports divided into either high or low/equivocal suspicion of CNS infection by two radiologists (unaware of the final diagnosis). Laboratory and clinical records were subsequently searched for definitive diagnostic data.

Results: 5787 MRH scans were identified, 1855 in patients with haematological-malignancy, of which 147 were for suspected CNS infection. After duplicate scan removal, 110 patients were included. Median age 52 years (13-81), 51% were female, 81% were inpatients. 50% were <12 months post bone marrow transplant (BMT) including allo-HSCT. Leukaemia (46%) and lymphoma (44%) predominated. 20/20 (100%) of extra-dural lesions were caused by disease relapse, other anatomical patterns were equally split between infection and relapse. Of 31 patients with MRH reports of high clinical suspicion of infection on MRH, 24/31 (77%) had proven infection, the remainder had tissue diagnosis of disease relapse or no cause found. Of those with low/equivocal suspicion of infection on MRH, seven had subsequently proven infection. CNS infection was diagnosed in 30 (26%) patients, disease relapse in 15 (14%) and alternative diagnosis/no cause found in 65 (59%). Of patients with proven CNS infection, viruses were identified in 15/30 (50%) (CMV 7/15, HSV (1), JC (3) and HHV6 (4), bacteria and fungi were rare (6). Patients with CNS infection more frequently presented within 12 months of BMT (50%) than those with disease relapse (20%).

Conclusions: Reported imaging finding on MRH are relatively non-specific in patients with subsequently proven CNS infection. Multi-centre prospective data are required to confirm these findings and inform treatment guidelines.

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Abstract 1583

Evaluation of the filmarray GI panel in the microbiological diagnosis and management of the patient with infectious gastroenteritis

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Background: To evaluate the usefulness of a molecular diagnostic panel for the diagnosis and management of patients with gastrointestinal infections.

Materials/methods: Retrospective observational study of molecular panels for syndromic diagnosis of infectious gastroenteritis (GEI) Filmarray ™ GI Panel, Biofire diagnostics (Biomérieux) conducted from January to October 2019. The results of the traditional microbiological techniques and variables obtained from the clinical history were also reviewed.

Results: RT-CRP was performed on 54 non-shaped feces, one sample per patient. The age range was from 10 months to 92 years with a median of 33.30 years. Thirty of them were men and 24 women. Cultures were performed in 94% of the cases, viral antigens in 50%, parasites in 26% and *Clostridioides difficile* toxins in 48%. The indications for requesting the microarray were the severity of the condition (invasive diarrhea and / or dehydration) in 50% of the cases, base immunosuppression in 30%, travel history in the previous week in 7% and others in 13%.
The panel was negative in 57% of cases, detected *Campylobacter sp* in 21%, *C. difficile* toxin in 8%, *Salmonella sp* 4% and other enteropathogens (8%). Seven coinfections were detected by the molecular panel (13%) and none by traditional techniques.
There was an agreement between the results of the microarray and traditional microbiological methods in 84% of cases (kappa 0.687).

Table 1: Distribution of positive tests by classical techniques and by CRP

Tests	Number of traditional tests*	Positive traditional test n (%)	Positive CRP tests n (%); n total=54
Culture	51	13 (25%)	21 (39%)
Viral antigens	27	0 (0%)	3 (6%)
Parasites	15	0 (0%)	1 (2%)
C. difficile toxin	25	3 (12%)	7 (13%)

* CRP was performed in all cases (54) but traditional tests only when expressly requested under clinical criteria (the table reflects the total of tests of each type performed)

There was a therapeutic modification in 63% of the cases in which the panel was requested due to the severity of the diarrhea, in 54% of the cases in which the CRP was performed due to travel history, in 40% when the cause was immunosuppression and when the cause was unknown, no therapeutic change was assumed.
The filmarray results had an average delay of 12 hours *vs* an average of the traditional techniques of 26 hours (range: 2-72).

Conclusions: The agreement between traditional techniques and CRP is substantial (kappa: 0.6) although it is far from perfect. The average time saved by CRP, its greater range of potential diagnoses per test and the possibility of detecting coinfections can allow effective and faster clinical decisions.

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Abstract 1587

The pharmacodynamics of omadacycline against *Escherichia coli* and *Acinetobacter baumannii* studied in an *in vitro* pharmacokinetic model of infection

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Background: Omadacycline (OMC) is a broad spectrum aminomethylcycline tetracycline antimicrobial. OMC is approved for clinical use by the US FDA in community-acquired bacterial pneumonia and skin and skin structure infections as intravenous and oral formulations. The pharmacodynamics (PD) of OMC have been extensively studied against Gram-positive pathogens but less information is available for Gram-negatives. Here we describe the pre-clinical PD of OMC against *E. coli* and *A. baumannii*.

Materials/methods: An *in vitro* dilutional single compartment PK model was used. Exposure ranging experiments - freedrug Area Under Curve to MIC ratio (fAUC/MIC) 0-1200 were performed. Five strains of *E. coli* and 5 strains of *A. baumannii* were used. In addition, time-kill curves were conducted with a single strain of either *E. coli* or *A. baumannii* over a concentration range 0-80 mg/L OMC. 2% oxyrase was added to broth to stabilise OMC. The primary endpoint was - log change in viable count at 24h.

Results: *E. coli* OMC MICs ranged from 0.25-2 mg/L and *A. baumannii* OMC MICs ranged from 0.5-1 mg/L. In time-kill experiments with both *E. coli* and *A. baumannii,* OMC showed concentration dependant killing up to 80 mg/L: OMC was less bactericidal against *A. baumannii* than *E. coli*. The fAUC/MIC for 24h static, -1 log and -2 log reduction in *E. coli* bacterial load were 22.5±15.9, 38.1±28.3 and 83.6±64.4. For *A. baumannii* the fAUC/MIC for 24hr static and -1 log drop in bacterial load were 108.1±38.6 and 266.3±27.1. Emergence of resistance was observed with both *E. coli* and *A. baumannii* strains. OMC MICs of strains recovered at the end of 24-48h exposure to OMC were increased 2-32 fold.

Conclusions: The size of the OMC fAUC/MIC for static effect against *E. coli* is in alignment with published *in vivo* data from a murine thigh infection model. fAUC/MIC targets are higher for *A. baumannii* than *E. coli*. These OMC fAUC/MIC targets may be useful for translational modelling of possible OMC doses for therapy of these Gram-negative pathogens.

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Abstract 1591

Global estimation of antimalarial drug effectiveness for the treatment of uncomplicated *Plasmodium falciparum* malaria, 1991–2019

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Background: Monitoring spatiotemporal variation in antimalarial drug efficacy and effectiveness is of importance to understand and sustain the gains in reducing malaria burden globally. Therapeutic efficacy studies (TES) are the gold-standard for measuring drug efficacy and appropriate for characterizing global variations. This study utilizes data from 232 TES comprised of 89,713 individuals to estimate the effectiveness of artemisinin-based and non-artemisinin-based antimalarials in malaria-endemic countries between 1991 and 2019.

Materials/methods: Bayesian spatiotemporal models were fitted separately for the artemisinin-based and non-artemisinin-based antimalarial drugs, and used to predict effectiveness at the pixel-level (5km x 5km). Median and interquartile range (IQR) of the effectiveness are presented.

Results: The global effectiveness levels of artemisinin-based antimalarials were high: 87.3% (IQR: 75.4-93.9) in 1994 and 94.6% (IQR: 89.2-97.4) in 2019. However, country-to-country variations exist. In Africa, the Democratic Republic of the Congo, Republic of Congo, Uganda, and parts of the Central African Republic face challenges of relatively low effectiveness. In Asia, effectiveness of these drugs remained >90% for an extended period. However, effectiveness fluctuations were observed from the mid-1990s to 2008/2009 with Cambodia, Malaysia, and Indonesia being the most affected countries. Use of artemisinin-based combination therapies (ACTs) with a competent partner drug and having multiple ACTs as first-line treatment were associated with sustained high levels of effectiveness. High levels of access to healthcare, human resource capacity, education, and proximity to cities were associated with increased effectiveness. Global effectiveness of non-artemisinin drugs remained low over time, 69.9% (IQR:48.5-89.3) in 1994 and 71.6% (IQR: 57.9-91.5) in 2019. These drugs are not effective in several Sub Saharan African countries and Asia but remained effective in Central and South America.

Conclusions: This study provides evidence that ACTs are effective for treating uncomplicated *Plasmodium falciparum* malaria. Other antimalarial drugs such as chloroquine and sulphadoxine-pyrimethamine remain useful for *P. falciparum* malaria in only a few locations. Low effectiveness is driven by type of drug, health system performance and climate factors. These results are useful to guide countries' treatment policies and as critical inputs for malaria prevalence and incidence models utilized to estimate national levels of malaria burden.

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Abstract 1593

Beyond the contact precaution: what does the surveillance culture tell us about multidrug-resistant microoganisms in critically ill patients? Data of the Public Hospital of São Paulo City, Brazil

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Background: Surveillance cultures (SC) are routinely used to screen multidrug resistant microorganisms (MDR). The purpose of this study was to evaluate the epidemiological and molecular aspects between events of colonization and healthcare-associated infection (HAI) caused by the same MDR in critically ill patients.

Materials/methods: Study was performed in two ICUs (clinical and surgical) of a public tertiary hospital between January 2016 and May 2018. All patients had SC collected for institution of contact precautions in positive cases of MDR. The healthcare associated infections are notified according to CDC criteria. The bacterial identification was performed using mass spectrometry and the minimal inhibitory concentration of antibiotics was determined using the Vitek 2 System. The detection of the carbapenemases, VanA and VanB genes were determined by real time PCR and the genetic relatedness of the strains were characterized by Pulsed-Field Gel Electrophoresis (PFGE) only for available strains at the time.

Results: Thirty six patients colonized by MDR developed HAI by MDR, the mean between MDR colonization and HAI was 21,9 days. The most prevalent HAI was central line-associated bloodstream infections (CLABSI) in clinical ICU and surgical site infection (SSI) in surgical ICU. Twenty eight HAI episodes were caused by the same colonizing bacteria with identical antimicrobial susceptibility profile (ASP) (Table 1), 14 episodes could be analyzed by PFGE and the concordance rate was 100%. Other eight HAI episodes were caused by non-concordant MDR.

Conclusions: MDR colonization prevention measures are essential and must be performed prior to colonization in critically ill patients. The presence of colonization should be valued by the clinician to an appropriate choice of initial empirical therapy and stewardship in critically ill patients.

Table 1: Concordant microorganism distribution between colonization and infection

Microorganism	Colonized patients	HAI concordant by ASP	HAI concordant by PFGE	PFGE concordant HAI topography
Klebsiella pneumoniae (KP-KPC)	28	24	10	CLABSI 6 VAP 2 UTI 1 SSI 1
Vancomycin resistant Enterococcus (VRE)	4	2	2	CLABSI 1 IE 1
Carbapenem resistant Acinetobacter baumannii	1	1	1	CLABSI 1
Carbapenem resistant Pseudomonas aeruginosa	1	1	1	CLABSI 1
Carbapenem resistant Enterobacter cloacae (KPC)	2	0	0	0

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Abstract 1594

Ceftobiprole compared with vancomycin plus aztreonam in the treatment of acute bacterial skin and skin-structure infections: results of a phase III, randomised, double-blind trial (TARGET)

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Abstract third-party references: Supported by Basilea, Submitted on behalf of J. Scott Overcash and co-authors

Background: The development of novel, broad-spectrum antibiotics with efficacy against both Gram-positive and Gram-negative bacteria has the potential to enhance treatment options for acute bacterial skin and skin structure infections (ABSSSIs). Ceftobiprole, the active moiety of the prodrug ceftobiprole medocaril, is an advanced-generation cephalosporin with broad *in vitro* activity against Gram-positive (including methicillin-resistant *Staphylococcus aureus*) and Gram-negative pathogens, and is approved in many European and several non-European countries for the treatment of pneumonia. The present study (TARGET) evaluated the utility of ceftobiprole in patients with ABSSSIs.

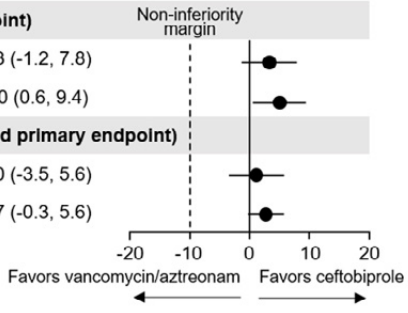
Materials/methods: TARGET was a randomised, double-blind, active-controlled, parallel-group, multicentre, phase 3, non-inferiority study that compared ceftobiprole with vancomycin plus aztreonam (NCT03137173). Main efficacy endpoints were: early clinical response 48–72 hours after therapy initiation (≥20% reduction in primary lesion area, survival, no concomitant antibacterials, and no unplanned ABSSSI surgery); and investigator-assessed clinical success (complete or near complete resolution of baseline signs and symptoms, with no further antibacterial treatment) at the test-of-cure (TOC) visit 15–22 days after randomisation. Non-inferiority was defined as the lower limit of the 95% confidence interval for the difference in success rates (ceftobiprole minus vancomycin/aztreonam) >10%. Safety was also assessed through adverse event and laboratory data collection.

Results: 679 patients were randomised to ceftobiprole (n=335) or vancomycin/aztreonam (n=344), of whom 676 received ≥1 dose of study medication. Median treatment duration was 6.0 and 7.0 days, respectively, with a median duration of 3.0 days for aztreonam in the comparator group. Main efficacy endpoint results are shown in the figure. Documented or presumed microbiological eradication rates at the TOC visit were similar between treatment arms (90.2% vs 86.6%). The proportion of patients experiencing ≥1 treatment-related adverse events (n [%]: 66 [19.8%] vs 62 [18.1%]) was also similar between treatment arms. Treatment-related serious adverse events were uncommon, reported in only 1 and 2 patients in the ceftobiprole and vancomycin/aztreonam arms, respectively.

Conclusions: TARGET demonstrated that ceftobiprole is non-inferior to vancomycin/aztreonam in the treatment of ABSSSIs, both in terms of early clinical response and investigator-assessed clinical success at the TOC visit. Both treatment arms displayed similar microbiologic success and had similar safety Profiles.

Figure: Main efficacy endpoint analyses

	Ceftobiprole n/N (%)	Vancomycin/ aztreonam n/N (%)	Adjusted difference (ceftobiprole minus vancomycin/aztreonam) (95% CI)[a]
Early clinical response (FDA-defined primary endpoint)			
ITT	306/335 (91.3)	303/344 (88.1)	3.3 (-1.2, 7.8)
CE[b]	267/283 (94.3)	262/293 (89.4)	5.0 (0.6, 9.4)
Investigator-assessed clinical success (EMA-defined primary endpoint)			
ITT	302/335 (90.1)	306/344 (89.0)	1.0 (-3.5, 5.6)
CE	277/283 (97.9)	279/293 (95.2)	2.7 (-0.3, 5.6)



Abbreviations: CE, clinically evaluable; CI, confidence interval; ITT, intent-to treat.

[a]Proportion differences (95% CI) (ceftobiprole minus vancomycin/aztreonam) were computed using the Cochran-Mantel-Haenszel weights method adjusted for geographical region and actual type of ABSSSI.

[b]Secondary endpoint. The objective for the FDA-defined primary endpoint was based on a non-inferiority assessment of the ITT population only. The EMA-defined primary endpoint was based on a non-inferiority assessment in both the ITT and CE populations.

Abstract 1598

Routine use of whole genome sequencing for *Salmonella* Enteritidis surveillance in the Netherlands in 2019

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In the Netherlands, national laboratory surveillance for *Salmonella* Enteritidis was based on conventional serotyping and Multi Locus Variable Number Tandem Repeat Analysis (MLVA). In January 2019, whole genome sequencing (WGS) was implemented as routine typing method for *S.* Enteritidis. Here we describe the relation between WGS-based cluster detection and MLVA types, and the presence of genetic and phenotypic β-lactamase resistance in *S.* Enteritidis isolates from Dutch national surveillance in 2019.

Submitted *Salmonella* isolates were serotyped using Luminex and conventional methods, minimum inhibitory concentrations (MIC) for antibiotics were determined on a selection of isolates. For those serotyped as *S.* Enteritidis, MLVA type was determined and WGS was performed using Illumina technology. An in-house pipeline based on SPAdes 3.10.0 was used for quality control, trimming and de novo assembly. Detection of resistance genes was performed using the bacterial analysis pipeline of the Center for Genomic Epidemiology. WGS Clustering was investigated with core genome multi-locus sequence type (cgMLST) using Ridom Seqsphere 6.0.2. with the Enterobase *S. enterica* cgMLST V2 scheme.

From January until October 2019, 1,171 *Salmonella* isolates were received, of which 399 *S.* Enteritidis (35%). A total of 377 isolates were from unique patients, resulting in 349 sequences (93%) of good quality. A β-lactamase gene was detected in 45 *S.* Enteritidis isolates (13%), in one isolate coding for extended spectrum β-lactamase. For 35 of these isolates the MIC for ampicillin was determined, for which 29 (83%) were phenotypically resistant according to EUCAST breakpoints. Using a threshold of five alleles distance in cgMLST, 43 clusters of ≥ 2 isolates were detected, containing a total of 254 isolates (73%). With MLVA, 60 types were found comprising 23 clusters of ≥ 2 isolates, 312 isolates (89%) were part of these clusters. Using WGS, clusters ranged from 2-36 isolates, and 15 clusters (35%) contained multiple MLVA types ranging from two to five types within the same cluster.

WGS showed a higher discriminatory power than MLVA. This is especially important during outbreak investigation to avoid misclassification of outbreak-related cases. Moreover, WGS allows us to monitor resistance and virulence genes.

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Abstract 1599

High levels of resistance to recommended antimicrobial agents in *Pseudomonas aeruginosa* from patients with bronchiectasis

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Background: Non-cystic fibrosis bronchiectasis (BE) is a chronic structural lung condition that facilitates chronic colonization by different microorganisms and courses with frequent exacerbations and recurrent infections. One of the main pathogens involved in chronic colonization and acute exacerbations is *Pseudomonas aeruginosa*. When not eradicated during early infection *P. aeruginosa* can accumulate high rates of resistance to the most antipseudomonal agents.

Materials/methods: A prospective observational study was carried out in Hospital Clinic. A total of 44 strains of *Pseudomonas aeruginosa* were isolated and characterized from sputum of BE patients. The antimicrobial susceptibility to: Aztreonam, ciprofloxacin, meropenem, imipenem, amikacin, tobramycin, pipertaz, ceftazidime and colistin was performed using the Kirby-Bauer method with the ATCC 27853 strain as a control. Interpretation of results was carried out according to the European Committee on Antimicrobial Susceptibility Testing (EUCAST). Molecular characterization of each resistance mechanism was screened by PCR, electrophoresis in 2% agarose gels and sequencing.

Results: The frequency of *Pseudomonas aeruginosa* resistant isolates was: Aztreonam (68,18%), ciprofloxacin (45,45%), meropenem (31,81%), imipenem (31,81%), amikacin (20,45%), tobramycin (20,45%), pipertaz (11,36%), ceftazidime (11,36%) and colistin (2,27%). The strains showed different antimicrobial profiles: PS (9,09%), MR (61,37%), MDR (20,45%) and XDR (9,09%). Mutations in *gyrA, gyrB*, *ParC* and *ParE* genes were found in ciprofloxacin resistant *P. aeruginosa* strains. The most frequent mutation in *gyrA* was A33G, in *gyrB* S466F, in *parC* S87W and in *parE* D539E. Our study showed that a higher number of mutated genes was related to the increased of MIC in the QRDR. The presence of different β-lactamases was detected: *oxa50* (95,45%), *ges* (90,74%), *imi* (23,8%), *gim* (4,76%) and *sim* (4,76%), in the strains resistant to β-lactams. The *aac(3)-Ia, aac(3)-Ic, aac(6")-Ib* and *ant(2")-Ia* genes were related to aminoglycoside resistance.

Conclusions: the high level of resistance to first-line antimicrobials recommended in BE guidelines and the great diversity of mechanisms of resistance found, threatens the treatment of BE and the eradication of *P. aeruginosa*.

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Abstract 1603

In vitro Activities of ceftazidime-avibactam and comparator agents against Enterobacterales and *Pseudomonas aeruginosa* from Turkey collected through the ATLAS global surveillance programme 2013-2018

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Background: Avibactam (AVI) is a non-β-lactam, β-lactamase inhibitor that can restore the activity of ceftazidime (CAZ) against organisms that possess Class A, C, and some Class D enzymes. This study examined the *in vitro* activity of CAZ-AVI and comparators against Enterobacterales and *Pseudomonas aeruginosa* collected in Turkey through the ATLAS global surveillance program from 2013 to 2018.

Materials/methods: A total of 2,205 non-duplicate, clinically isolated Enterobacterales and 567 *P. aeruginosa* were collected from six sites in Turkey during 2013-2018. Susceptibility testing was done using broth microdilution according to CLSI guidelines and interpreted using EUCAST 2019 breakpoints. CAZ-AVI was tested with a fixed concentration of 4 mg/L AVI. The presence of genes encoding resistance mechanisms was previously assessed via multiplex PCR, followed by amplification of the full-length genes and sequencing.

Results: Susceptibility data are provided in the table. CAZ-AVI exhibited potent activity against all Enterobacterales (MIC_{90}, 0.5 mg/L; 98.2% susceptible). When MBL-positive isolates were removed from analysis, susceptibility to CAZ-AVI was 100%. CAZ-AVI showed consistently higher % susceptibilities than all comparators against MBL-negative meropenem-nonsusceptible isolates (CRE) and isolates positive for OXA-48. CAZ-AVI also showed good activity against the majority of *P. aeruginosa* isolates (MIC_{90}, 8 mg/L; 94.2% susceptible).

Organism (n)	Drug (MIC90 [mg/L] %susceptible)				
	CAZ-AVI	CAZ	MEM	AMK	CST*
Enterobacterales (2,205)	0.5/98.2	128/62.9	1/92.0	8/92.4	>8/80.3
Enterobacterales, MBL-NEG (1951)	0.5/100	64/66.0	0.5/93.6	8/93.6	>8/80.5
Enterobacterales, MBL-positive (31)	>128/16.1	>128/0	>8/3.2	>32/29.0	>8/45.2
CRE, MBL-negative (125)	2/100	>128/12.0	>8/0	>32/73.6	>8/40.7
Enterobacterales, OXA-48 (77)	2/96.6	>128/17.2	>8/28.7	>32/78.2	>8/49.0
E. coli (764)	0.25/99.7	64/57.5	0.06/98.8	8/92.0	1/99.9
K. pneumoniae (648)	1/96.5	>128/50.3	>8/79.3	16/89.4	>8/83.2
Enterobacter spp. (172)	0.5/98.8	64/73.8	0.12/97.1	2/97.7	1/96.5
P. aeruginosa (567)	8/94.2	64/79.7	>8/69.5	16/87.7	2/96.4
P. aeruginosa, MBL-negative (504)	8/94.8	64/81.0	>8/71.6	16/89.9	2/95.9

*colistin not tested in 2013; colistin tested vs. 1876 Enterobacterales in 2014-2018
CAZ-AVI, ceftazidime-avibactam; CAZ, ceftazidime; MEM, meropenem; AMK, amikacin; CST, colistin; MBL, metallo-β-lactamase. % susceptible defined using EUCAST 2019 breakpoints

Conclusions: CAZ-AVI showed potent *in vitro* activity against Enterobacterales and *P. aeruginosa* collected in Turkey, including isolates resistant to last-in-line agents.

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Abstract 1607

Evaluating prophylactic post cardiac transplantation amphotericin B treatment by simulation

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Background: Antifungal treatment is recommended to prevent invasive aspergillosis, a condition which occurs frequently and is associated with a poor prognosis in the first 3 months following cardiac transplantation. Current recommendations do not include a once a week administration of liposomal amphotericin B (L-AmB), despite its favorable safety profile. The objective of the current study was to simulate the efficacy of a once a week administration of L-AmB using a pharmacokinetic-pharmacodynamic (PK-PD) approach.

Materials/methods: Based on the population PK model published by Würthwein *et al.*, 1000 plasma and tissue kinetic profiles were simulated over a 7-day period after administration of a single dose of 7.5 mg / kg of L-AmB as a 1-hour infusion. For each simulated plasma profile, the Area Under the Curve (AUC) for total concentrations over 24 hours was calculated from D1 to D7. These AUCs were compared with L-AmB PK-PD efficacy target (AUC / MIC> 167) to determine the percentage of simulated profiles achieving this target (i.e. probability of target attainment). The theoretical duration of effectiveness was determined using both the simulated tissue kinetic profiles and a concentration higher than the MIC for more than 90% of the profiles.

Results: At D1, more than 90% of the plasma profiles met the PK-PD target for Minimum Inhibitory Concentrations (MICs) ≤ 0.5 mg/L. This percentage dropped to 80.2% when the MIC was increased to 1 mg/L (i.e. Aspergillus breakpoint). At D7 and for a MIC corresponding to the breakpoint, only 3.3% of the plasma profiles achieved the PK-PD target. The treatment efficacy assessed at tissue level does not extend to 7 days regardless of the MICs tested. Indeed, efficacy is theoretically maintained during 3.2 and 1.3 day(s) for MICs of 0.25 to 0.75 mg/L. For MICs ≥ 1 mg/L, less than 90% of the simulated profiles reached tissue concentrations ≥ 1 mg/L.

Conclusions: Regardless of plasma or tissue PK-PD target, our simulations suggest that a once a week administration of L-AmB does not guarantee antifungal efficacy throughout the entire one-week period. These results need to be confirmed in clinical practice.

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Abstract 1608

Identification of host-specific genetic elements of *Campylobacter jejuni* in Germany based on whole genome data

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Background: The zoonotic pathogen *Campylobacter jejuni* is the leading cause of bacterial food-borne infections in humans worldwide. *Campylobacter* are most commonly transmitted through the consumption of undercooked poultry meat or raw milk products. *In silico* multi locus sequence typing (MLST) of *C. jejuni* strains from different sources has revealed association of certain sequence types (STs) with specific hosts or a host-generalism lifestyle. While host restriction of *C. jejuni* lineages is known, the survival mechanisms allowing them to adapt to gut environments of different hosts have not been completely understood.

Materials/methods: To generate more in-depth knowledge about these mechanisms, 330 *C. jejuni* strains from different hosts (100 each from human, chicken, cattle and 30 from pig) across Germany were randomly selected, and whole genome sequencing (WGS) was performed. Additionally, 166 isolates from a Canadian study were included to extend the dataset and compare it with international samples. Host-specificity was investigated by a stratified random sampling approach on top of a *k-mer* based genome-wide association study (GWAS) to increase the accuracy of the identification of host specific determinants.

Results: We discovered that a strong host association can be observed in the core genome as well as in the accessory genome. The identified genetic elements encode for proteins, which play important roles in mobility, energy metabolism and genetic information processing. Although, we could discover a strong recombination barrier between *C. jejuni* lineages within the same host, identical allelic gene variants could be found amongst those genes.

Conclusions: Our research shows, that host-adaptation in *C. jejuni* takes place in a wide range of cellular functions within the whole pan-genome. This indicates that the adaptation towards a specific host niche is most likely a long evolutionary and multifactorial process rather than a spontaneous evolution or selection pressure.

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Abstract 1610

An international quality control pilot programme for the measurement of antimicrobial drugs

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Background: There is an increased interest in developing assays to determine plasma concentrations of antimicrobial drugs; used for pharmacokinetic research purposes as well as in clinical practice when performing TDM. Participation in an interlaboratory quality control (QC) program is an essential component of quality assurance. Therefore, we developed the first international QC program for the measurement of antimicrobial drugs.

Materials/methods: Antimicrobial drugs involved in the first two rounds of this pilot program were ceftazidime, ciprofloxacin, flucloxacillin, piperacillin, tazobactam, sulfamethoxazole, n-acetyl sulfamethoxazole and trimethoprim. Two QC samples (one sample per round) were prepared by spiking drug-free plasma with all eight antimicrobial drugs in either low or high concentrations. All participants were provided feedback anonymously on their performance. All weighed-in concentrations were considered true values. Acceptable accuracy was defined if measurements were within the 80-120% limits of the true weighed-in concentrations. A one-tailed unpaired t test was performed on the absolute inaccuracies to determine a difference between the high versus low concentrations.

Results: A total of 143 laboratories were approached. Seventeen laboratories participated in the first round and 22 laboratories in the second round. A total of 129 analyses were performed in both rounds. A total of 81% of the measurements was determined accurately. The measurements of flucloxacillin showed the best performance; 100% (21 out of 21) of the samples was determined accurately. The measurements of ceftazidime showed the worst performance; 56% (14 out of 25) of the samples was determined accurately. The measurements of the higher antibiotic concentrations showed a trend towards better performance than of the lower concentrations (p=0.052).

Conclusions: The initial results of this pilot program showed a relatively good performance of the participating laboratories compared to previous program initiated by us (HIV, TB and fungal). Nevertheless, still one out of five (19%) measurements was inaccurate. By participating in the program these laboratories were alerted, which may help them to improve their methods. Our results emphasize the importance of an ongoing QC program. In future rounds we will consider incorporating other antimicrobial drugs as well as the possibility the report free concentrations.

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Abstract 1612

Review of enquiries to the UK national travel advice line by healthcare professionals regarding immunocompromised travelers

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Background: Overseas travel is rising; UK residents made >70 million trips abroad in 2017. Concurrently, there has been a rise in individuals with primary/ acquired immunosuppression. The National Travel Health Network and Centre (NaTHNaC) offers a nurse-led telephone advice line for clinicians to discuss travellers with special health needs. A cohort of immunosuppressed patients from 2013 was described previously – we aimed to update this.

Materials/methods: Retrospective review of advice line data collected between January 2016 and December 2018 involving immunosuppressed travellers.

Results: 2107/17250 (12.2%) calls involved immunosuppressed travellers; a proportionate rise since 2013 (8.1%). On review, 1085/2107 individuals (51.5%) did not fulfil CDC/ green book criteria for immunosuppressive condition/ treatment. The majority of enquiries originated from General Practice (82.1%), concerned male patients (55.7%), aged 21-59 (50%). The majority of travel was to Africa (40%), and overall, most trips were 1-4 weeks duration (60.7%). The most common purpose of travel was tourism (49%). 792 callers (77.5%) asked for advice on vaccinations, most frequently Yellow fever (431, 54.4%). A significant number of callers also asked about malaria prophylaxis (404, 39.5%). There were 147 travellers with a diagnosis of HIV in the cohort; CD4 count was available for 44 (29.9%). 123 patients had asplenia/ splenic dysfunction, 63 patients had renal failure, 128 chronic liver disease/ diabetes (or both), and 642 were severely immunocompromised, most frequently due to an immunosuppressive treatment (403, 62.8%).

Conclusions: Findings were broadly similar to 2013. As might be expected, there was a rise in travellers receiving monoclonal antibodies or small molecule inhibitors and individuals post solid organ/ stem-cell transplant. Criteria for immunosuppressive states and the risks facing these travellers do not appear be well understood. The majority of enquiries regarded live vaccinations (e.g. Yellow Fever) which account for a small minority of the total risk encountered by these individuals. Information provided (e.g. CD4 count, drug dose, timing of stem-cell transplant) by referring healthcare professional was frequently incomplete limiting advice that could be offered. A checklist of information to collect prior to contacting the NaTHNaC advice line may help to identify immunocompromised travellers and tailor guidance.

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Abstract 1614

Suitability of citrate buffered piperacillin/tazobactam via continuous infusion in outpatient parenteral antimicrobial chemotherapy (OPAT)

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Abstract third-party references: On behalf of Members of the BSAC Working Group on Drug Stability Testing

Background: Piperacillin/tazobactam is a broad-spectrum penicillin/beta-lactamase inhibitor combination antibiotic with activity against a wide range of pathogens including multi-drug-resistant Gram-negative organisms. Optimal administration of piperacillin/tazobactam is at 6-8 hourly intervals, which is unfeasible for OPAT services. This study assessed the stability of piperacillin/tazobactam solution for injection for up to 13 days followed by continuous 24-hour infusion in two different commercially available elastomeric devices. The stability for both actives must comply with the UK National Health Service (NHS) Yellow Cover Document (YCD) requirements throughout the study.

Materials/methods: Piperacillin/tazobactam was diluted in 0.3% w/ citrate-buffered saline (pH 7.0). Two clinically useful concentrations of drug (25 mg/mL and 90 mg/mL) were compounded into two different elastomeric devices (FOLFusor, Baxter and Easypump®II, B.Braun). Devices were refrigerated for 13 days at 2-8°C, followed by 2-3 hours at room temperature and 24 hours at 32°C (representing a simulated infusion period). All testing was in accordance with NHS YCD requirements.

Results: Results show piperacillin/tazobactam diluted in 0.3% w/v citrate-buffered saline pH 7.0 is stable for 13 days at 2-8°C, plus a 24-hour administration period in both elastomeric devices tested.

Conclusions: This study confirms piperacillin/tazobactam solutions for injection when prepared in buffered aline in two elastomeric devices at both concentrations has the potential to allow for single infusion at 32°C over a 24-hour period following extended storage at 2-8°C, making this practical for use in OPAT.

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Abstract 1620

In vitro Activities of ceftazidime-avibactam and comparator agents against Enterobacterales and *Pseudomonas aeruginosa* from Israel collected through the ATLAS global surveillance programme 2013-2018

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Background: Avibactam (AVI) is a non-β-lactam, β-lactamase inhibitor that can restore the activity of ceftazidime (CAZ) against organisms that possess Class A, C, and some Class D enzymes. This study examined the *in vitro* activity of CAZ-AVI and comparators against Enterobacteriaceae and *Pseudomonas aeruginosa* collected in Israel through the ATLAS global surveillance program from 2013 to 2018.

Materials/methods: A total of 2,585 non-duplicate, clinically isolated Enterobacterales and 663 *P. aeruginosa* were collected from five sites in Israel during 2013 to 2018. Susceptibility testing was done using broth microdilution according to CLSI guidelines and interpreted using EUCAST 2019 breakpoints. CAZ-AVI was tested with a fixed concentration of 4 mg/L AVI. The presence of genes encoding resistance mechanisms was previously assessed via multiplex PCR, followed by amplification of the full-length genes and sequencing.

Results: Susceptibility data are provided in the table. CAZ-AVI exhibited potent activity against all Enterobacterales (MIC_{90}, 0.5mg/L; 99.7% susceptible). When MBL-positive isolates were removed from analysis, susceptibility to CAZ-AVI was 100%. CAZ-AVI showed consistently higher % susceptibilities than all comparators other than colistin against MBL-negative meropenem-nonsusceptible isolates (CRE) and isolates positive for KPC. CAZ-AVI also showed excellent activity against the majority of *P. aeruginosa* isolates (MIC_{90}, 4 mg/L; 98.8% susceptible).

Organism (n)	Drug (MIC_{90} [mg/L]/% susceptible)				
	CAZ-AVI	CAZ	MEM	AMK	CST*
Enterobacterales (2,585)	0.5/99.7	64/70.6	0.12/98.7	8/95.2	> 8/82.4
Enterobacterales, MBL-negative (2,205)	0.25/100	64/78.1	0.12/99.1	8/95.2	> 8/82.9
CRE, MBL-negative (20)	2/100	>128/0	>8/0	>32/35.0	2/92.9
Enterobacteriaceae, KPC (18)	4/100	>128/0	>8/0	>32/33.3	2/92.3
E. coli (779)	0.25/100	32/72.7	0.06/99.6	8/95.3	1/99.7
K. pneumoniae (702)	0.5/100	128/50.0	0.12/97.4	8/92.9	1/99.2
Enterobacter spp. (202)	1/98.5	128/65.4	0.12/97.5	4/98.5	1/92.1
P. aeruginosa (663)	4/98.8	32/84.8	8/82.8	8/94.3	2/97.4

*colistin not tested in 2013; colistin tested vs. 2,173 Enterobacteriaceae in 2014-2018.
CAZ-AVI, ceftazidime-avibactam; CAZ, ceftazidime; MEM, meropenem; AMK, amikacin; CST, colistin; MBL, metallo-β-lactamase. % susceptible defined using EUCAST 2019 breakpoints

Conclusions: CAZ-AVI showed potent *in vitro* activity against Enterobacterales and *P. aeruginosa* collected in Israel, including isolates resistant to last-in-line agents.

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Abstract 1625

Effects of prospective review and feedback and mandatory computerised decision support system for carbapenems and piperacillin-tazobactam on other broad-spectrum antibiotic use: interrupted time series with segmented regression analysis

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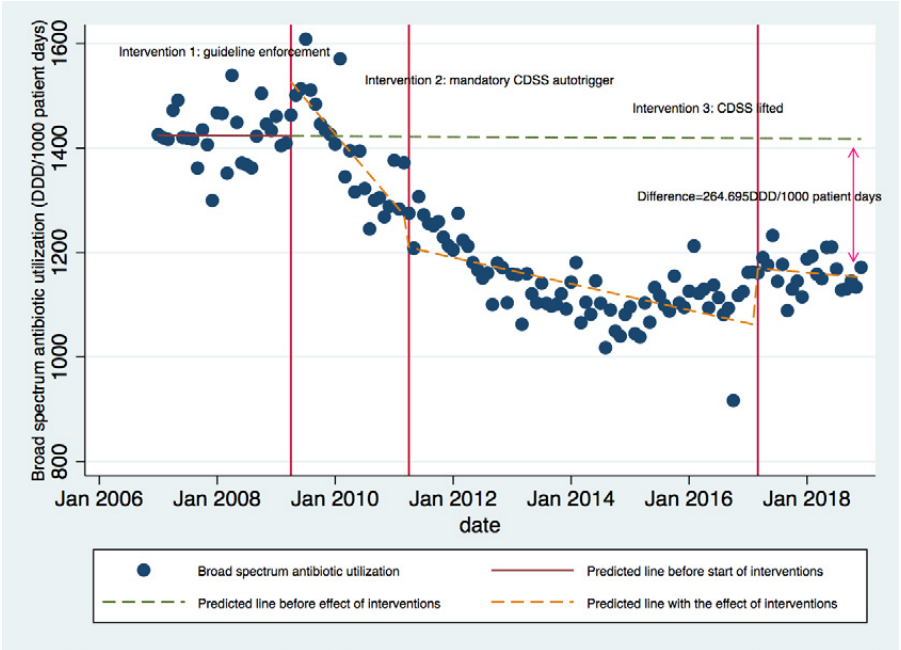
Background: As the use of piperacillin-tazobactam and carbapenems was rising in a public tertiary-care hospital in Singapore, antimicrobial stewardship (AMS) interventions targeting these two classes were introduced; empiric antibiotic guidelines and prospective review and feedback (PRF) in April 2009, and mandatory use of computerised decision support system (CDSS) in April 2011. Mandatory CDSS was lifted in March 2017 for half of the hospital's wards for a 6-month cluster-randomised study. We aimed to examine if AMS interventions targeting piperacillin-tazobactam and carbapenems impacted the utilisation of other broad-spectrum antibiotics.

Materials/methods: In addition to piperacillin-tazobactam and carbapenems, monthly utilization of other broad-spectrum antimicrobials (co-amoxiclav, 3rd and 4th generation cephalosporins, fluoroquinolones and vancomycin) in defined daily doses (DDD) per 1,000 patient-days from January 2007 to December 2018 were obtained from the hospital's database. We investigated the impact of AMS interventions using segmented regression analysis of interrupted time series.

Results: The baseline of other broad-spectrum antibiotic use was 1424.51 DDD/1,000 patient-days in January 2007. When empiric antibiotic guidelines and PRF were implemented in April 2009, there was an increase in the level of utilisation by 103.46 (95% confidence interval [CI]: 49.23, 157.68) in the same month, followed by a reduction at a rate of 11.1 per month (95% CI: -15.12, -7.08). Co-amoxiclav accounted for most of the changes in the broad-spectrum antibiotic use. After the implementation of mandatory CDSS, the reduction rate of other broad-spectrum antibiotic utilisation slowed to 2.10 per month (95% CI: -3.13, -1.07). When mandatory CDSS usage was lifted in March 2017, there was an increase in the level of other broad-spectrum antibiotic use by 109.20 (95% CI: 57.79, 160.61) in the same month with no significant changes in the monthly utilisation rate.

By the end of the study period, we estimated absolute reductions of 126.58 DDD/1,000 patient-days in monthly utilisation of carbapenems and piperacillin-tazobactam, and 264.70 DDD/1,000 patient-days of other broad-spectrum antibiotic use due to the impact of the AMS interventions.



Conclusions: Despite AMS interventions being centred on piperacillin-tazobactam and carbapenems, unexpected reduction of other broad-spectrum antibiotic utilisation was observed.

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Abstract 1626

Epidemiological aspects of ascariasis in the south of Russia

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Background: More than a quarter of the world's population is at risk of ivasion with the soil-transmitted helminths. Ascaris lumbricoides is the main species infecting people and it is represent a significant public health problem.
Aim: to assess the epidemiological situation of ascariasis and determine the risk factors for invasion with Ascaris lumbricoides of the population in the South of Russia based on serological and parasitological investigations.

Materials/methods: Over the past 5 years a serological screening was carried out of 2600 serum samples of conditionally healthy residents of the southern Russia. Human samples were analyzed with a commercial ELISA test to detect anti Ascaris lumbricoides IgG antibodies . For the same period, 7800 parasitological studies of environmental objects (wastewater and their sediments, soil, sand, surface water) were carried out by the flotation method.

Results: According to official statistics the incidence rate of ascariasis in Russia ranges from 12.7 to 18.4 per 100 000 population over the past 5 years. Also, it is worth noting that about 70% of patients are children.
As a result of the research, it was found that the detection rate of anti Ascaris lumbricoides IgG antibodies in the serum of residents of the South of Russia in average 19.8% for the period from 2014 to 2018.
Parasitological investigation of environmental objects found that the intensive indicators of contamination by ascaris eggs amounted from 2 to 15 eggs per liter/kg for wastewater and their precipitation and 1-10 eggs per kg/liter for soil, sand and surface water.

Conclusions: Significant proportions of seropositive individuals, as well as the presence of facts of detection of ascaris eggs in environmental objects indicate the maintenance of a potential risk of infection of the population of southern Russia with ascariasis. In addition, the results mean the necessity to continue monitoring for ascariasis.

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Abstract 1627

In vitro activity of aztreonam-avibactam and comparator agents against Enterobacterales from Europe collected during the ATLAS global surveillance programme 2015-2018

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Background: β-lactamase-producing Enterobacterales frequently co-carry resistance to antimicrobials from other classes, limiting treatment options. Avibactam inhibits class A, class C, and some class D serine β-lactamases, including extended-spectrum β-lactamases and KPC-type and OXA-48-like carbapenemases, while aztreonam is refractory to hydrolysis by metallo-β-lactamases (MBL). Aztreonam-avibactam is being developed for use against drug-resistant isolates of Enterobacterales, especially those co-producing MBLs and serine β-lactamases. This study evaluated the *in vitro* activity of aztreonam-avibactam and comparators against Enterobacterales collected in 2015-2018 in Europe as part of the Antimicrobial Testing Leadership and Surveillance (ATLAS) program.

Materials/methods: Non-duplicate clinical isolates were collected from 134 medical centres in 25 countries. Susceptibility testing was performed by CLSI broth microdilution and interpreted using EUCAST 2019 breakpoints. Aztreonam-avibactam was tested at a fixed concentration of 4 mg/L avibactam. PCR and sequencing were used to determine the β-lactamase genes present in all isolates with meropenem MIC >1 mg/L, and *Escherichia coli*, *Klebsiella* spp. and *Proteus mirabilis* phenotypically positive for ESBL activity (2015) or with aztreonam or ceftazidime MIC >1 mg/L (2016-2018).

Results: Aztreonam-avibactam was active *in vitro* against Enterobacterales isolates (MIC_{90}, 0.12 mg/L), with 99.9% (31230 of 31252), including all isolates that produced MBLs, inhibited by ≤8 mg/L of aztreonam-avibactam. Aztreonam-avibactam tested with MIC_{90} values of 0.5 mg/L against subsets of cephalosporin-resistant, aminoglycoside-resistant, colistin-resistant, and MBL-positive Enterobacterales and MIC_{90}s of 1 mg/L against meropenem-resistant isolates and those resistant to three last-line agents (meropenem, amikacin and colistin) (Table). In most cases, the tested comparators showed susceptibility of <80% against these subsets of resistant isolates.

Phenotype (n)	MIC_{90} [mg/L]/% Susceptible[a]													
	ATM-AVI		ATM		FEP		MEM		AMK		CST		TGC[a]	
	MIC_{90}	% S	MIC_{90}	% S	MIC_{90}	% S	MIC_{90}	% S	MIC_{90}	% S	MIC_{90}	% S	MIC_{90}	% S
Enterobacterales, All (31252)	0.12	NA[b]	64	74.2	>16	78.1	0.12	96.1	8	95.1	>8	82.5	1	78.7
FEP-R (5703)	0.5	NA	>128	2.9	>16	0.0	>8	79.7	32	79.2	8	88.6	2	68.4
MEM-R (877)	1	NA	>128	7.3	>16	1.9	>8	0.0	>32	36.0	>8	66.8	2	39.7
AMK-R (948)	0.5	NA	>128	13.9	>16	7.9	>8	43.3	>32	0.0	>8	68.9	4	46.2
CST-R (677)[c]	0.5	NA	>128	32.4	>16	37.4	>8	56.1	>32	65.6	>8	0.0	2	57.5
AMK-R, MEM-R, CST-R (134)[c]	1	NA	>128	5.2	>16	0.0	>8	0.0	>32	0.0	>8	0.0	4	34.3
MBL-positive (379)	0.5	NA	>128	15.8	>16	1.6	>8	10.3	>32	36.9	>8	78.6	4	46.2

ATM-AVI, aztreonam-avibactam; ATM, aztreonam; FEP, cefepime; MEM, meropenem; AMK, amikacin; CST, colistin; TGC, tigecycline; R, resistant; MBL, metallo-β-lactamase; n, number of isolates.

[a] % Susceptible was defined using EUCAST 2019 breakpoints. Tigecycline breakpoints for *E. coli* and *C. koseri* were applied to all species.

[b] NA, no breakpoints available.

[c] Excluded Proteeae and *Serratia* spp. with intrinsic resistance to colistin.

Conclusions: Based on MIC_{90} values, aztreonam-avibactam was the most potent agent tested against resistant and MBL-positive subsets of Enterobacterales collected in Europe, including isolates resistant to one or multiple last-resort agents from different drug classes. The promising *in vitro* activity of aztreonam-avibactam warrants further development of this combination for treatment of infections caused by drug-resistant Enterobacterales.

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Abstract 1629

Cardiovascular Disease risk in liver transplant recipients for hepatitis B,C and delta virus-associated cirrhosis

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Background: Cardiovascular disease (CVD) is a cause of morbidity and mortality after liver transplantation (OLT), mostly in patients transplanted for NASH, obesity and diabetes-associated liver disease. Few data exist on CVD among patients transplanted for viral hepatitis. Our aim is to clarify the CVD risk and subclinical vascular damage among OLT recipients for HCV, HBV, HDV-associated liver disease.

Materials/methods: OLT patients due to viral hepatitis admitted for follow-up to University of Campania in the period June-July 2019 were prospectively enrolled. An estimation of cardiovascular risk was assessed using the main risk charts (Framingham, ASCVD, Heart Score), and by performing the ecocolordoppler of epiaortic vessels to assess subclinical endothelial damage. A Intima-Media Thickness [IMT] ≥1 mm was considered pathological. A carotid was classified as being affected by atherosclerotic plaque if the localized thickening was ≥1.3 mm.

Results: An overall of 76 patients were considered of whom 31 (40.8%) were transplanted for HCV, 14 (18.4%) for HBV, 24 (31.6%) for dual infection HBV-HDV, 5 (6.6%) for dual infection HBV-HCV and 2 (2.6%) for triple infection HBV-HDV-HCV. 30 patients (39.5%) had a familiarity for CVD, 39 (51.3%) for diabetes mellitus and 18 (23.7%) for dyslipidemia; 27 (35.5%) patients had diabetes and 19 (25%) were active smokers. More than half of the patients (63.1%) were taking antihypertensive therapy and 19.7% a lipid-lowering drugs. An overall of 43 patients (56.6%) were considered at high cardiovascular risk according to Framingham, 28 patients (36.9%) to ASCVD and 10 (13.1%) to Heart Score. Only 4 patients (5.3%) showed a normal carotid ultrasound, while 27 patients (35.5%) had a IMT and 45 (59.2%) an atherosclerotic plaque.

Conclusions: OLT recipients for HCV, HBV±HDV-associated liver disease are at high risk of CVD. Comparing the high percentage of subclinical carotid lesions with data of the risk charts, the latter seem to underestimate the real extent of the endothelial damage. In the pathogenesis of CVD in these patients, a chronic inflammatory status, could play a key role. It's important to raise the awareness of CVD risk in OLT patients to prevent CVD and improve the timing of early diagnosis of premature vascular lesions.

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Abstract 1630

Knowledge about transmission and determinants of tuberculosis among Pakistani adults: evidence from demographic and health survey

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Background: Knowledge about symptoms and transmission of tuberculosis determines health-seeking behavior and helps in the prevention of tuberculosis transmission in the community. Such data is useful for policymakers to formulate information, education and communication strategies for tuberculosis control.

Materials/methods: A secondary data analysis of Pakistan demographic and health survey, 2017/18 was carried out. Questions about self-reported tuberculosis, transmission, and curability of tuberculosis were analyzed. Correct knowledge (without misconceptions) about tuberculosis transmission was used as a dependent variable and the explanatory variables tested were demographic data, education, wealth quintiles, frequency of exposure to media and the curability of tuberculosis. Determinants of correct knowledge without misconceptions were tested by univariate and multivariate analyses.

Results: The percent of correct knowledge of tuberculosis (TB) was 51.7. The 'Correct knowledge about TB transmission' was TB transmission "Through the air when coughing or sneezing" but had no misconceptions about TB transmission. The number of respondents who had "heard of an illness called tuberculosis" was 13,596 (90.2%). Of these 3015 (20.0%) participants did not know the correct mode of TB transmission. The common misconceptions about transmission were "Through food" (31.7%), "Sharing utensils" (35.7%), and "Touching a person with tuberculosis" (9.1%). Only 7793 (51.7%) participants had correct knowledge about TB transmission. Being rich (aOR 1.39, 95% CIs 1.26-1.52), urban residence (aOR 1.22, 95% CIs 1.12-1.32), age (25-49 years) (aOR 1.48, 95% CIs 1.35-1.62), education (secondary and higher) [(aOR 1.53, 95% CI 1.37-1.70) and (aOR 3.08, 95% CI 2.68-3.50)], and "Tuberculosis can be cured" (aOR 3.33, 95% CIs (2.89-3.83) were significantly associated with correct knowledge without misconceptions.

Conclusions: Knowledge about TB transmission is considerably poor, and misconceptions remain persistent. Among the traditional mass media, the frequency of watching television was associated with correct knowledge about TB transmission. Strategies to deliver information, education and communication campaigns could be improved.

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Abstract 1631

Insights into vaginal metabolic profiles throughout pregnancy

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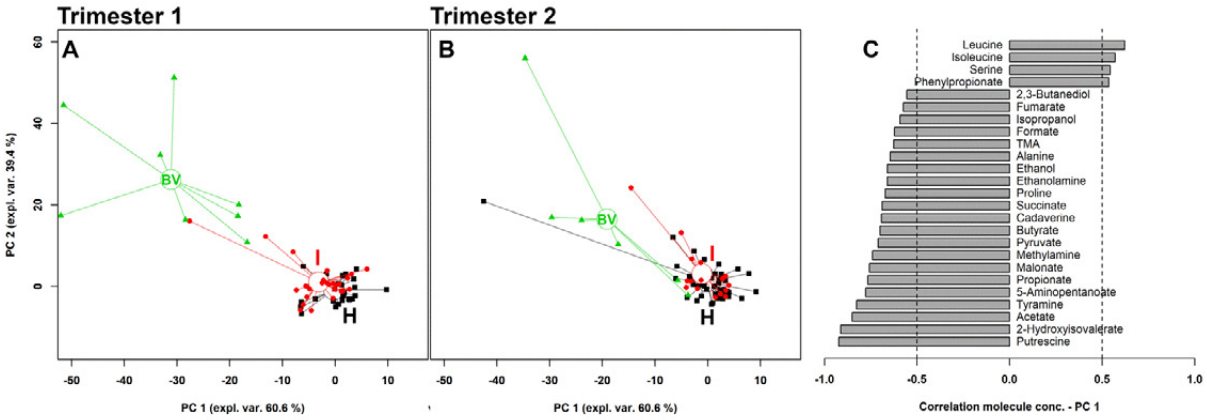
Background: During pregnancy, the vaginal microbiome plays an important role in both maternal and neonatal health outcomes. The vaginal microbiome undergoes significant changes during pregnancy, including a significant decrease in overall diversity, increased stability, and enrichment with *Lactobacillus* spp.
Since the changes in the microbial profiles are usually associated with significant shifts in the composition of vaginal metabolites, the aim of this study was to characterize the vaginal metabolic profiles throughout pregnancy at two different gestational ages, correlating them with a microscopic evaluation of the vaginal bacterial composition.

Materials/methods: A total of 67 Caucasian pregnant women, with a mean age of 31.3 years, and presenting to the Family advisory health Centres of Ravenna for prenatal care were enrolled. After a clinical examination, a vaginal swab was collected at gestational ages 9-12 weeks (first trimester) and 20-24 weeks (second trimester) from each woman. The composition of the vaginal microbiome was evaluated by a Gram stain scoring system (Nugent score), assessing for the presence of different bacterial morphotypes (*Lactobacillus* spp., *Gardnerella vaginalis* and *Mobiluncus* spp.). Based on this score, women were divided into 3 groups: 'H' (normal lactobacilli-dominated microbiota), 'I' (intermediate microbiota), 'BV' (bacterial vaginosis).
Starting from the cell-free supernatants of the vaginal swabs, a metabolomic analysis was performed by means of a ^{1}H-NMR spectroscopy. Differences among experimental groups were assessed via PCoA and a two-ways ANOVA test.

Results: From the first to the second trimester of pregnancy, a greater number of women showed a normal lactobacilli-dominated microbiota (33 vs 45 women), with a reduction of cases of dysbiosis. These microbial shifts were clearly associated with profound changes in the vaginal metabolic profiles. Globally, over the weeks, a significant reduction in the levels of BV-associated metabolites (e.g. putrescine, acetate, propionate, methylamine, butyrate, formate, cadaverine) was observed. At the same time, the vaginal metabolome was characterized by higher concentrations of leucine, isoleucine, serine and phenylpropionate, typically found in healthy vaginal conditions.



Conclusions: Throughout pregnancy, the vaginal metabolic composition became less diverse and more homogeneous, reflecting the shift towards a lactobacilli-dominated microbiome.

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Abstract 1632

In vitro activity of tigecycline and comparator agents against Gram-negative and Gram-positive isolates from China in 2018

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Background: The TEST (Tigecycline Evaluation and Surveillance Trial) global surveillance program monitors *in vitro* activities of tigecycline and a panel of marketed antimicrobial agents against clinically significant Gram-negative and Gram-positive bacterial pathogens. In this analysis we review recent TEST program data for Gram-negative and Gram-positive isolates tested by clinical laboratories in China.

Materials/methods: Clinically significant Gram-negative (n=2,959) and Gram-positive (n=989) isolates were cultured from multiple infection sites by 24 clinical laboratories in China in 2018. Isolates were identified to species level and MICs determined in each clinical laboratory using broth microdilution panels (supplied by IHMA, Schaumburg, IL, USA) following CLSI guidelines. Isolates were limited to one per patient. Data were submitted to IHMA for analysis. MICs were interpreted using current EUCAST (2019, v 9.0) and US FDA (tigecycline) MIC breakpoint criteria.

Results:

Organism (n)	% Susceptible							
Gram negative	**TGC**	**AMK**	**FEP**	**CAZ**	**CRO**	**LVX**	**MEM**	**TZP**
Enterobacterales (2,549)	97.4[a]	90.2	53.8	52.8	47.8	52.0	87.1	73.6
CRE (329)	95.4[a]	46.0	0.3	1.2	0	9.1	0	2.4
Acinetobacter spp. (410)	NA[b]	29.3	NA	NA	NA	14.9	15.9	na
Gram positive	**TGC**	**AMC**	**AMP**	**LVX**	**LNZ**	**VAN**		
Enterococcus spp. (370)	90.0	NA	60.3	45.1	98.4	97.8		
S. aureus (619)	96.6	NA	NA	72.0	99.8	100		

CRE, carbapenem-resistant Enterobacterales (meropenem MIC >2 mg/L), NA, MIC breakpoints not available; TGC, tigecycline; AMK, amikacin; FEP, cefepime; CAZ, ceftazidime; CRO, ceftriaxone; LVX, levofloxacin; MEM, meropenem; TZP, piperacillin-tazobactam; AMC, amoxicillin-clavulanate; AMP, ampicillin; LNZ, linezolid; VAN, vancomycin.
[a] US FDA MIC breakpoints applied. 91% (670/736) of *Escherichia coli* had tigecycline MICs ≤0.5 mg/L (EUCAST tigecycline-susceptible MIC breakpoint).
[b] No MIC breakpoint available, MIC_{90} = 2 mg/L.

Conclusions: *In vitro* susceptibility of Enterobacterales was highest to tigecycline (97.4%); isolates were less susceptible to amikacin, meropenem, and the other agents tested. 12.9% of Enterobacterales isolates in China were CRE; 95.4% of CRE were susceptible to tigecycline. >90% of enterococci and *S. aureus* were susceptible to tigecycline; linezolid and vancomycin were slightly more active *in vitro* than tigecycline against common Gram-positive cocci. Country specific monitoring of susceptibility patterns among common bacterial pathogens provides useful information for determining empiric treatment strategies.

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Abstract 1633

Utilising the full potential of model-based dosing tables: an interprofessional collaboration to develop and integrate meropenem dosing tables into clinical routine

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Background: Meropenem is an antibiotic used to treat infections in intensive care patients. Pharmacokinetic (PK) variability observed in critically ill patients leads to a high risk of suboptimal exposure. Recent observational data at the Charité-Universitätsmedizin Berlin shows that >70% of patient's exposure is outside the C_{min} target range (1x-5x MIC). Consequently, improvement of current dosing practices is urgently needed. Model-based Bayesian dosing software for dose optimization have been suggested [1] to improve dosing practices, however several barriers exist [2] hindering implementation in clinical practice. We aimed to develop easy-to-use model-based dosing tables to optimise meropenem treatment at intensive care units (ICU) at Charité. To ensure suitability and user-friendliness a close collaboration with the antimicrobial stewardship (AMS) and ICU teams of the hospital was pursued.

Materials/methods: A previously developed meropenem PK model was used to perform Monte Carlo simulations considering PK parameter uncertainty [3]. In close discussion with the AMS and the ICU teams multiple clinically relevant dosing regimen (n=15) were evaluated with respect to target attainment ($fT_{>MIC}$=98%) and its probability (PTA≥90%). Dosing regimen reaching a PTA≥90% were further discriminated with regards to probability of reaching the predefined target range (1x-5x MIC) and potentially toxic C_{min} values (>16 mg/L or >64 mg/L).

Results: Optimised and easy-to-use model-based dosing tables are now available for clinical routine dosing at Charité-Universitätsmedizin Berlin. Dosing regimen stratified for a patient`s creatinine clearance and determined/assumed MIC are summarised in one concise table. Our result showed that for the same daily dose, (i) prolonged (4h) or continuous infusions reached higher PTA than short-time infusions and (ii) four-times-daily dosing was superior in PTA to three-times-daily-dosing. Both can easily be integrated into clinical routine. 2-g meropenem loading doses provided little further benefit over 1-g loading doses and consequently were not further considered.

Conclusions: Model-derived dosing tables are a promising tool to improve dosing in ICU patients. To fully utilise their potential and integrate them into clinical routine a close collaboration between all parties of an interprofessional team is needed. The developed dosing tables are currently prospectively evaluated.

[1]Roberts et al. (2014).
[2]Kumar et al. (2019).
[4]Ehmann et al. (2019).

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Abstract 1635

Feasibility studies of the WHO practical toolkit for antimicrobial stewardship programmes in healthcare facilities in low-and middle-income countries

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Background: The overuse and misuse of antimicrobials are a main driver for development of antimicrobial resistance (AMR). Antimicrobial stewardship (AMS) has emerged as a systematic approach to optimize antimicrobial use. To meet the increasing need for practical guidance on how to implement effective AMS programmes, the World Health Organization (WHO) developed a draft toolkit for AMS programmes in hospitals in low- and middle-income countries (LMIC). In this study, we evaluated the feasibility of implementing the toolkit in four LMIC settings.

Materials/methods: The study used a descriptive qualitative study design with semi-structured interviews with national- and hospital-level stakeholders. Four countries were included: Bhutan, the Federated States of Micronesia, Malawi, and Nepal. A total of 12 national policy makers, 20 hospital administrators and managers, and 64 hospital staff were interviewed.

Results: All study participants identified AMS as an important priority and responded that the AMS toolkit would be helpful in improving AMS programmes within their countries and hospitals. Key facilitators for implementing AMS included strong national and hospital leadership and support, and hospital staff engagement in AMS committees. Key barriers included lack of human and financial resources, limited access and supply of medicines particularly in remote regions, difficulty enforcing regulations for prescription only antibiotic sales, and inadequate AMS competencies training. Key recommendations to strengthen AMS included dedicated AMS financial resources, identification of dedicated hospital AMS leaders and champions, stepwise approach for AMS implementation based on country and hospital context, establishing mechanisms for reporting and feedback, and initiating AMS training workshops and AMS curricula. Key recommendations to improve the draft WHO toolkit included the need for guidance to prioritize AMS activities based on available resources, stronger linkage between existing programmes e.g. Infection Prevention and Control, and further guidance on establishing AMS committees.

Conclusions: The draft toolkit was well received throughout the four study countries. The overall consensus was that the toolkit will be an important asset as countries and hospitals move forward to combat AMR and implement AMS programmes. However, many barriers will need to be addressed at both the national and hospital levels in order to facilitate implementation.

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Abstract 1636

HPV OncoPredict: analytical performance of a novel diagnostic tool allowing accurate determination of sample cellularity and normalised high-risk human papilloma virus genotype-specific viral load

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Abstract third-party references: This Project is conduct in collaboration with GeneFirst as part of the EU funded programme (SME Instrument Grant GA 806551)

Background: Cervical cancer (CC) kills 330,000 people annually and requires persistent infection with high-risk Human Papillomavirus (hrHPV) for its development. Type-specific hrHPV viral load has been suggested to be a useful risk triage indicator for the development of high-grade squamous intraepithelial lesion (≥HSIL) as well as a clinically useful marker to monitor post treatment ("test-of-cure").

Most presently commercially available hrHPV tests do not provide type-specific hrHPV viral load or quantitative sample cellularity assessment as a measure of sample adequacy.

HPV OncoPredict is a new in-vitro diagnostic tool allowing accurate sample adequacy assessment and hrHPV type-specific viral load (E6/E7 DNA) determination. The aim of this study is to evaluate the intra- and inter-laboratory analytical performance of HPV OncoPredict prototype using international standards and reference samples.

Materials/methods: HPV OncoPredict prototype analytical performance has been evaluated using NIBSC (National Institutes of Biological Standards and Controls) standards for HPV16 (06/202) and HPV18 (06/206), WHO LabNet Proficiency Panels as well as commercially available Verification/Validation standards (Microbix) for HPV 16, 18, 31, 33, 39, 45 and HPV 67 (negative control).

Results: HPV OncoPredict was able to quantitatively assess and correctly identify hrHPV types 16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59 as well as a human gene, used to normalize viral load and assess sample adequacy. HPV OncoPredict assigned type-specific viral loads and human Genomic Equivalents (hGE) comparable to those indicated in the WHO LabNet 2018 report. Moreover, HPV OncoPredict demonstrated 100% accuracy in genotyping all 12 hrHPV types, as defined by IARC, on testing both NIBSC and Microbix control standards. Inter-laboratory performance is presently under evaluation in 2 external University Laboratories using 2019 WHO LabNet Proficiency Panel.

Conclusions: HPV OncoPredict analytical performance has demonstrated accurate assessment of sample's cellularity and hrHPV type-specific viral loads, using both international standards and commercial controls. These promising results will support HPV OncoPredict future clinical validation studies aimed at evaluating the correlation between normalized viral loads and cervical lesions. References: This project is conducted in collaboration with GeneFirst as part of a EU funded Horizon 2020 SME Instrument Project (SME Instrument Grant GA 806551).

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Abstract 1644

Prediction of antibiotic resistance in *Helicobacter pylori* by whole genome sequencing and open-source bioinformatics tools

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Background:

					ResFinder		RGI	
Nº OF STRAINS	AMX	CLA	LEV	TET	MTZ	MUTATION		MUTATION	
6	S	R	S	S	R	4/6	A2147G	4/6	A2147G
					1/6	A2146G	1/6	A2146G	
					1/6	No mutations	1/6	No mutations	
5	S	R	S	S	S	5/5 A2147G		5/5 A2147G	
2	S	S	S	S	R	No mutations		No mutations	
1	R	R	S	S	S	A2147G		A2147G	
6	S	S	S	S	S	No mutations		No mutations	

Increasing antimicrobial resistance in Helicobacter pylori (Hp) is a worldwide problem. Whole genome sequencing (WGS) has recently emerged as a diagnostic tool in clinical microbiology for drug resistance prediction in bacteria. The aim of this study was to compare phenotypic drug susceptibility testing results with the presence of genetic resistance determinants identified in Hp genome using two open-source bioinformatics tools.

Materials/methods:
20 Hp strains isolated from gastric biopsies were selected. Antimicrobial susceptibility testing was performed on blood agar plates using the following E-tests: clarithromycin (CLA), metronidazole (MTZ), levofloxacin (LEV), amoxicillin (AMX) and tetracycline (TET). EUCAST breakpoints were used. After DNA extraction, WGS was performed using Illumina-MiSeq platform. Resistance Gene Identifier (RGI) 5.1 and ResFinder 3.2 were used to identify resistance mutations.

Results:
The following table shows the results from susceptibility testing (susceptible=S, resistant=R) and the resistance mutations found:

Conclusions: Both tools detected a clarithromycin resistance mutation in all clarithromycin-resistant strains, except in one. The most frequent clarithromycin mutation was A2147G. Metronidazole resistance is due to a combination of various complex mechanisms, so it is difficult to predict it with genotypic data. No resistance was detected in the amoxicillin-resistant strain. Hp WGS and open-source bioinformatics tools can be useful to predict clarithromycin resistance.

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Abstract 1650

Distinct effectiveness of oritavancin against tolerance-induced *Staphylococcus aureus*

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Background: Within a sufficiently large bacterial population, some of the members will naturally adopt an alternate, metabolically-active state that favors small molecule synthesis over cell division. In *Staphylococcus aureus* this process can be sharply accelerated by multiple factors present during infection including nutrient limitation, host cationic peptide exposure and polymorphonuclear neutrophil internalization. These isogenic "tolerant" subpopulations have variable responses during antibiotic exposure and can remain viable in the presence of typically bactericidal concentrations. Survivors of the antibiotic exposure can restart cell division upon cessation of antibiotics and cause relapse or recurrent infection. In this study we determine the ability of typical and atypical antistaphylococcal therapies to reduce the viability of tolerant *Staphylococcus aureus* bacteria.

Materials/methods: *S. aureus* strain ATCC29213 as well as four clinical isolates (two MSSA, two MRSA) were selected for analysis. Overnight cultures were diluted in pre-warmed broth (MHB50) to approximately 1×10^6 cfu/mL. Tolerance was induced by exposure to mupirocin (low [0.032 µg/mL] or high [3.2 µg/mL]) for 30 min. Tolerant cultures were exposed to vancomycin (35 µg/mL), cefazolin (25 µg/mL), daptomycin (7 µg/mL), telavancin (10 µg/mL), dalbavancin (6 µg/mL) or oritavancin (14 µg/mL) and viability was assessed by dilution plating at pre-defined time points (0, 2, 6, 24, 48 h). The minimum duration for 3-log viability reduction from baseline ($MDK_{99.9}$) and culture viability at 48h were calculated independently for each of three biological replicates.

Results: The rate of bacterial killing ($MDK_{99.9}$) was reduced for all study antibiotics by the addition of mupirocin in a dose-dependent manner. In contrast to all other regimens, including lipoglycopeptide comparators, oritavancin was the only antimicrobial agent that maintained a similar extent of bacterial killing against tolerant staphylococci.

Conclusions: Antimicrobial tolerant staphylococci exhibit a decreased rate of killing by antistaphylococcal agents. However, oritavancin remained effective at maintaining a similar extent of killing. Further studies to investigate the role of otritavancin against recurrent or relapse staphylococcal infection is warranted.

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Abstract 1651

CANDIMAD study: a prospective multi-centre laboratory based survey of antifungal resistance in *Candida* spp. causing invasive candidiasis in Madrid

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Background: Active surveillance studies are necessary to know local epidemiology and help clinicians start appropriate empirical antifungal treatment. Resistance rates in Candida spp. come mainly from isolates causing candidaemia and figures in Spain are relatively old (CANDIPOP study, 2014). We assessed the epidemiology and antifungal resistance of recent yeast isolates causing invasive infections in patients at hospitals located in Madrid, Spain.

Materials/methods: We studied 312 isolates from 282 patients (23 presented ≥2 isolates and 19 showed mixed cultures) admitted to 15 hospitals located in the Madrid metropolitan area from January 2019 to October 2019. Isolates sourced from blood (52.6%), abdominal samples (29.8%), peritoneal samples (10.9%) and other digestive tract samples (6.7%) were identified by MALDI-TOF and antifungal susceptibility to amphotericin B, azoles, micafungin, anidulafungin and investigational agent, ibrexafungerp (previously SCY-078) was tested according to EUCAST EDef 7.3.1 (Breakpoints table v.10.0). FKS genes were sequenced in echinocandin-resistant Candida isolates.

Results: The species distribution of isolates was C. albicans (48.7%, n=152), C. glabrata complex (19.2%, n=60), C. parapsilosis complex (17.6%, n=55), C. tropicalis (7.1%, n=22), C. krusei (2.9%, n=9), other Candida spp. (3.2%, n=10), and non-Candida yeasts (1.3%, Rhodotorula mucilaginosa [n=2], and Trichosporon inkin [n=2]). Overall, triazoles, candins and ibrexafungerp showed high activity. Ibrexafungerp was more active against C. parapsilosis than candins. Fluconazole resistance was detected in 6.1% of Candida isolates (n=19; C. krusei [n=9], C. glabrata [n=4], C. parapsilosis [n=2], C. albicans [n=1], C. tropicalis [n=1], C. guilliermondii [n=1], and C. inconspicua [n=1]) sourcing from blood (n=11), abdominal samples (n=6), and peritoneal samples (n=2). Rate of echinocandins resistance was lower than 1% and was found in isolates sourcing from blood (n=2) and abdominal samples (n=1): C. krusei (n=2; L701M FKS1) and C. glabrata (n=1, WT). Resistant isolates were from patients from nine out of the 15 hospitals. Non-Candida yeasts showed intrinsic echinocandin resistance. No resistance to amphotericin B was detected (Figure).

Conclusions: We found a low percentage of overall resistance (<7%), with anecdotal echinocandin resistance rate. Resistant isolates sourced from blood (4%), abdominal samples (2%), and peritoneal samples (0.6%), and were distributed across different hospitals. No multi-drug resistant species were found.

	Minimun Inhibition Concentration (mg/L)																%R/ NWT
	≤0.002	0.004	0.008	0.016	0.03	0.06	0.125	0.25	0.5	1	2	4	8	16	32	64	
C. albicans **(n=152)**																	
Amphotericin B	-	0	0	0	0	1	32	89	29	1	**0**	-	-	-	-	-	0
Fluconazole	-	-	-	-	-	6	90	46	8	0	1	0	**0**	**1**	**0**	-	0.7
Voriconazole	-	118	24	2	6	0	1	1	**0**	**0**	**0**	-	-	-	-	-	0
Posaconazole	-	3	78	66	4	1	**0**	**0**	**0**	**0**	**0**	-	-	-	-	-	0
Isavuconazole	94	37	16	2	2	0	0	1	0	0	-	-	-	-	-	-	ND
Micafungin	14	102	28	8	**0**	**0**	**0**	**0**	**0**	**0**	-	-	-	-	-	-	0
Anidulafungin	39	84	19	10	0	**0**	**0**	**0**	**0**	**0**	-	-	-	-	-	-	0
Ibrexafungerp	-	-	-	0	19	68	50	10	5	0	0	0	0	-	-	-	ND
C. glabrata **complex (n=60)**																	
Amphotericin B	-	0	0	0	0	1	6	40	13	0	**0**	-	-	-	-	-	0
Fluconazole	-	-	-	-	-	0	0	0	0	3	7	37	7	2	**3**	**1**	6.7
Voriconazole	-	0	0	0	2	18	29	7	1	3	**0**	-	-	-	-	-	0
Posaconazole	-	0	1	0	0	0	6	25	22	5	**1**	-	-	-	-	-	1.7
Isavuconazole	1	1	0	1	14	25	9	7	1	1	-	-	-	-	-	-	ND
Micafungin	0	1	48	11	0	**0**	**0**	**0**	**0**	**0**	-	-	-	-	-	-	0
Anidulafungin	0	0	0	9	47	3	**1**	**0**	**0**	**0**	-	-	-	-	-	-	1.7
Ibrexafungerp	-	-	-	0	0	0	0	12	25	23	0	0	0	-	-	-	ND
C. parapsilosis **complex (n=55)**																	
Amphotericin B	-	0	0	0	0	0	5	32	17	1	**0**	-	-	-	-	-	0
Fluconazole	-	-	-	-	-	0	3	22	21	3	1	3	**0**	**0**	**1**	**1**	3.6
Voriconazole	-	6	23	17	4	2	1	2	**0**	**0**	**0**	-	-	-	-	-	0
Posaconazole	-	0	1	8	30	14	**1**	**0**	**1**	**0**	**0**	-	-	-	-	-	3.6
Isavuconazole	9	23	17	4	1	1	0	0	0	0	-	-	-	-	-	-	ND
Micafungin	-	-	-	1	0	0	0	3	16	24	11	**0**	**0**	-	-	-	0
Anidulafungin	-	-	-	1	0	0	0	0	1	21	29	3	**0**	-	-	-	0
Ibrexafungerp	-	-	-	0	0	1	5	42	6	1	0	0	0	-	-	-	ND
C. tropicalis **(n=22)**																	
Amphotericin B	-	0	0	0	0	0	2	12	8	0	**0**	-	-	-	-	-	0
Fluconazole	-	-	-	-	-	0	0	7	12	1	1	0	**0**	**0**	**1**	-	4.6
Voriconazole	-	0	0	0	4	15	2	0	**1**	**0**	**0**	-	-	-	-	-	4.6
Posaconazole	-	0	2	8	10	1	**0**	**0**	**1**	**0**	**0**	-	-	-	-	-	4.6
Isavuconazole	1	9	5	6	0	0	0	1	0	0	-	-	-	-	-	-	ND
Micafungin	0	0	1	17	4	0	**0**	**0**	**0**	**0**	-	-	-	-	-	-	0
Anidulafungin	0	0	6	12	4	0	**0**	**0**	**0**	**0**	-	-	-	-	-	-	0
Ibrexafungerp	-	-	-	0	0	0	1	10	8	3	0	0	0	-	-	-	ND
C. krusei **(n=9)**																	
Amphotericin B	-	0	0	0	0	0	0	1	7	1	**0**	-	-	-	-	-	0
Fluconazole	-	-	-	-	-	0	0	0	0	0	0	1	0	0	7	1	ND
Voriconazole	-	0	0	0	0	0	3	5	1	0	0	-	-	-	-	-	0
Posaconazole	-	0	0	0	0	6	2	1	0	0	**0**	-	-	-	-	-	0
Isavuconazole	0	0	0	0	2	3	4	0	0	0	-	-	-	-	-	-	ND
Micafungin	0	0	1	0	0	3	5	0	**0**	**0**	-	-	-	-	-	-	0
Anidulafungin	0	0	0	0	2	5	**2**	**0**	**0**	**0**	-	-	-	-	-	-	22.2
Ibrexafungerp	-	-	-	0	0	0	0	0	5	4	0	0	0	-	-	-	ND

Values shaded in grey indicate either resistant isolates or non-wild type isolates according to clinical breakpoints or tentative ECOFFs (EUCAST Breakpoints table v 10.0, November 2019).
ND: Not done as either breakpoints or ECOFFs were not available. R: Resistant. NWT: Non-wild type.

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Abstract 1653

High diagnostic yield of splenic core biopsy in patients with pyrexia or inflammation of unknown origin: a descriptive analysis of imaging (including FDG-PET) and pathological findings at a major tertiary centre

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Background: A proportion of patients with pyrexia and/or inflammation of unknown origin (PUO) are without a diagnosis following clinical and laboratory evaluation. Imaging, including with FDG-PET, may identify and characterise splenic abnormalities. Many specialists are reticent to undertake splenic biopsies because of the perceived risk. We aim to report on the diagnostic yield of targeted splenic biopsy in patients with febrile or inflammatory presentations showing splenic abnormalities, and explore predictors of definitive diagnosis.

Materials/methods: Cases were identified by searching the pathology archive at University College London Hospital over the 10 year period 2009-2019. We combined search terms 'biopsy' and 'spleen' and excluded non-core biopsy samples. We used electronic patient records to identify those investigated for unexplained fever or inflammation and collated data on prior and subsequent diagnostic tests, final diagnosis, complications and 6 month survival.

Results: 20 patients meeting these criteria were identified. All patients had splenomegaly. Microbiological diagnoses were made by culture or PCR. A diagnosis was made from splenic biopsy in 15 (75%) cases. Of the remaining cases, 1 biopsy showed reactive features only and responded to steroids; 2 were diagnosed at subsequent splenectomy, and 2 received a delayed final diagnosis from prior investigations. An infectious cause was found in 20%. 15 patients had a FDG-PET scan. While diagnostic yield was higher in those with the most abnormal splenic PET findings, biopsies were diagnostic even among those with mild FDG avidity. There were no complications.

Histopathology of splenic biopsy	Final diagnosis	No. of cases
Lymphoma	Lymphoma	10
Granulomatous inflammation	Fungal infection	3
	Mycobacterium tuberculosis	1
	Sarcoidosis	1
Non-diagnostic	Lymphoma	3
	Polycythaemia vera	1
	No diagnosis	1
		20

Conclusions: We demonstrate the high utility of splenic core biopsy in diagnosing patients with inflammatory/infectious presentations and splenic imaging abnormalities who have undergone extensive investigation on other laboratory and imaging. In patients with splenomegaly, FDG-PET features cannot classify those for whom biopsies were non-diagnostic.

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Abstract 1655

ComParison of prognostic capacity of presepsin and procalcitonin in adult septic patients: results from a prospective observational study in two university clinical centres

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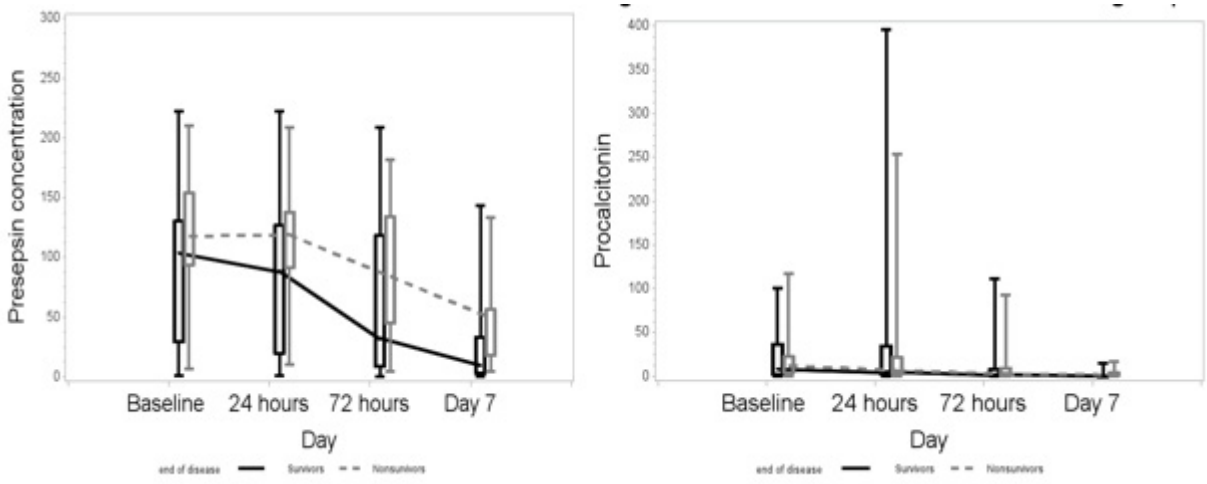
Background: Sepsis is a life-threatening condition that causes millions of death worldwide each year. Early recognition of disease is crucial for better outcome. Sepsis biomarkers are widely used for rapid diagnosis of sepsis. We evaluated a prognostic value of presepsin concentrations in patients with sepsis.

Materials/methods: A prospective observational study was conducted on 100 adult septic patients admitted at the Clinic of Infectious Diseases in Prishtina, Kosovo, and University Hospital for Infectious Diseases in Zagreb, Croatia. New Sepsis-3 definitions were used for disease stratification. Based on the disease outcome patients were grouped as survivors and non-survivors. During the disease course, sepsis biomarkers (procalcitonin and presepsin) were measured four times: on admission, after 24 hours, 72 hours, and on day 7. Multivariate generalized linear model (glimix) was performed to test the association of presepsin and procalcitonin levels during the course of the disease with outcome and multivariate logistic regression analysis was performed to test the association of initial sepsis biomarkers (presepsin and procalcitonin) with disease outcome.

Results: There were 68 survivors and 32 non-survivors. In Figure 1 are presented the differences in trends of presepsin and procalcitonin during disease course between two outcome groups. Initial and subsequent measurements of presepsin concentrations significantly differ between survivors and non-survivors. In non-survivors presepsin levels were significantly higher throughout the disease course. Procalcitonin concentrations did not differ in two outcome groups.

Figure 1. Concentration of presepsin and procalcitonin in two outcome groups



On the left side association of presepsin concentration with disease outcome. On the right side association of procalcitonin with disease outcome. Black line-survivors, black spotted line-non-survivors. Hosmer-Lemeshow test p=0.6226, with satisfactory explanatory value c=0.675.
Presepsin values but not procalcitonin values on admission werew significantly associated with death. Procalcitonin didn't show any prognostic value.

	Odds Ratio Estimates		
Effect	Point Estimate	95% Wald Confidence Limits	
Presepsin on admission	1.011	1.002	1.020
PCT on admission	0.986	0.970	1.003

Conclusions: Initial presepsin concentrations and their non-decreasing trend over the time suggests poor disease outcome.

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Abstract 1658

Accurate differentiation of carbapenemases by MALDI-TOF MS-typing: employment of bioinformatics

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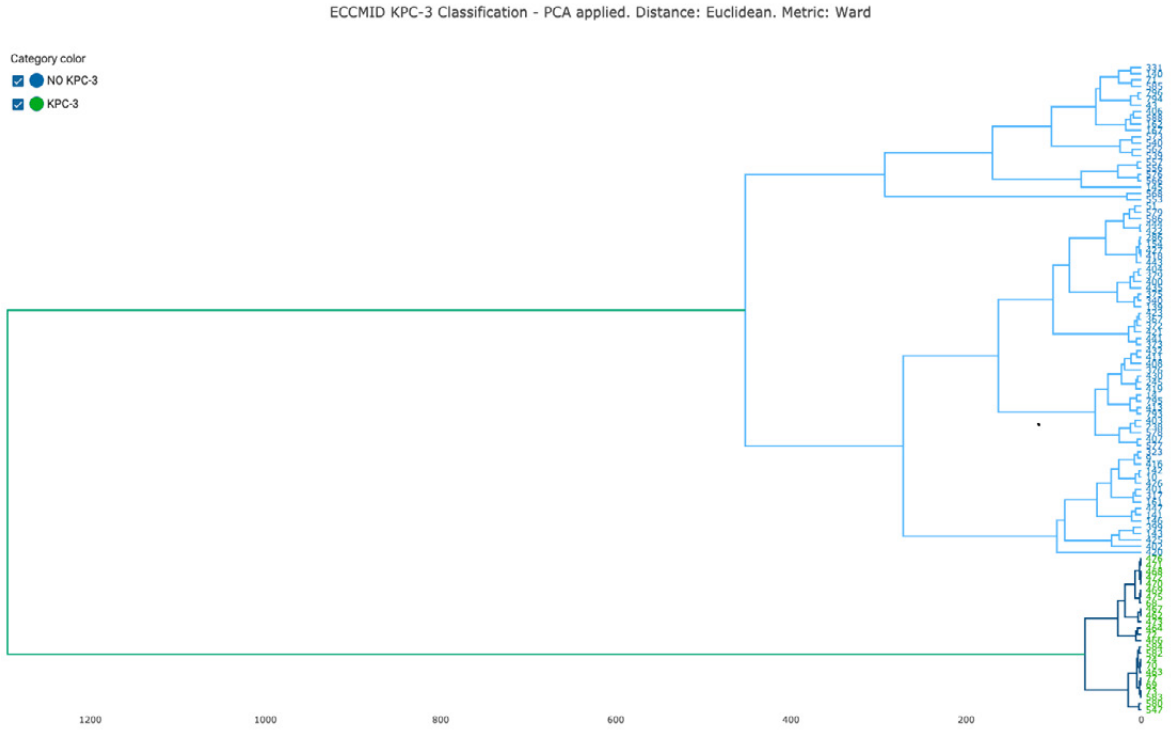
Background: Detection of Carbapenemase-Producing Enterobacterales (CPE) is one of the main goals of microbiology laboratories, as they constitute a health alarm worldwide. Rapid methods to detect resistance mechanisms and strain typing as part of routine data analysis could therefore greatly benefit infection control efforts. MALDI-TOF MS has demonstrated substantial utility for rapid organism identification. Here, we demonstrate that real-time, direct tracking of CPE is possible using MALDI-TOF MS and artificial intelligence in a manner that could be implemented for routine screening in clinical microbiology laboratories.

Materials/methods: A total of 102 previous molecular characterized CPE (20 KPC-2, 26 KPC-3 and 56 OXA-48) with different sequence types, were submitted to two different standard operating procedures, an *in-target* and a full formic acid-ethanol extraction. All isolates were spotted four times on the MALDI target plate and measured three times each. Thus, 12 spectra were acquired per sample using the automated functionality of FlexControl 3.3 software (Bruker Daltonik). Raw data was submitted to baseline subtraction using Top-Hat filter and smoothing via Savitzky-Golay filter (Clover BioSoft software). All replicates were aligned with a tolerance factor of 0.0002. The processed data set was submitted to Principal Component Analysis (PCA) and hierarchical clustering. Technical reproducibility was analyzed, along with the best extraction method in terms of spectral quality, discrimination against the gold standard (molecular characterization) and simplicity of the method.

Results: Both extraction methods provided similar results, so we chose the *in-target* extraction for further studies. KPC-3 strain was correctly classified by hierarchical clustering after applying PCA to the processed dataset and was accurately differentiated from OXA-48 and KPC-2 isolates (Image 1). Besides, potential biomarkers have been identified to classify OXA-48 different clones. In particular, the peaks 9831, 9845, 9857 y 9872m/z ± 1.5 Da discriminate ST 307, whereas 9342m/z ± 1.5Da identify ST 147.



Conclusions: Accurate differentiation of CPE by MALDI-TOF MS-typing was accomplished in as little as 10 min from isolated colonies, demonstrating the potential clinical utility for real-time screening in clinical practice. This software can be implementated in all currently available MALDI-TOF MS systems.

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Abstract 1662

Approaches to identify new onset diarrhoea among hospitalised patients and the frequency of stool sample collection for *Clostridioides difficile* infection: a pilot for the CLOUD Louisville study

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Abstract third-party references: On behalf of the CLOUD Louisville Study Group. This study was sponsored by Pfizer, Inc.

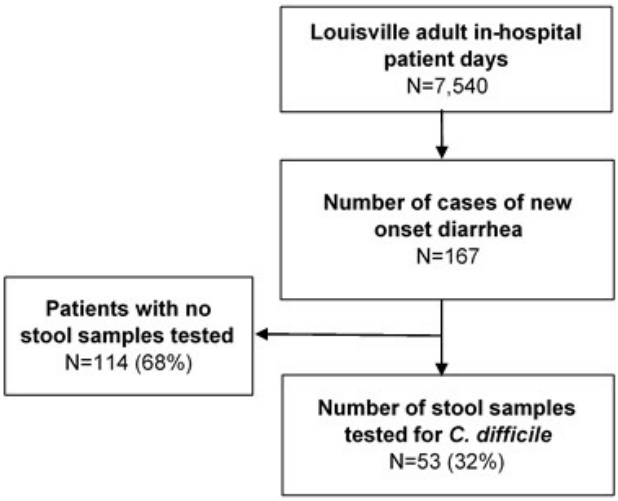
Background: Population-based surveillance studies defining the incidence of *Clostridioides difficile* infection (CDI) are important to inform policy makers. One challenge to perform these studies is the identification of all hospitalized patients with new onset diarrhea. Additionally, CDI may be underestimated if stool specimens are not collected from patients with diarrhea and tested for *C. difficile*. We conducted a pilot study to inform the development of a protocol for a population-based incidence study in all hospitals in Louisville, Kentucky. The objectives of this pilot study were to define the optimal approach to identify adult patients with new onset diarrhea and the frequency of stool collection for CDI testing.

Materials/methods: This was a cross-sectional pilot study conducted in all nine adult hospitals in Louisville, Kentucky. For seven consecutive days in December 2018, all adult Louisville inpatients were evaluated for new-onset diarrhea (≥3 loose stools within 24 hours, Bristol stool form scale 5-7) using a 3-level approach: 1) medical record review; 2) nurse interview; and 3) patient interview. The frequency of stool specimen collection for CDI testing according to local standard of care was ascertained.

Results: A total of 7,540 Louisville adult in-hospital patient days were evaluated (Figure 1). Patients with diarrhea were identified either by medical record review (50%), nurse interviews (42%) or patient interviews (8%). All cases identified by patient interviews were identified by nurses the following day. New onset diarrhea was identified in 167 patients (47% male; median age 64 years). Stool samples were submitted for *C. difficile* testing in 32% (53/167) of patients.

Conclusions: Medical record review and nurse interviews were the most effective approaches to identify inpatients with new onset diarrhea. Considering that stool specimens were collected from only one-third of the inpatients with new onset diarrhea, it is likely that CDI is underdiagnosed and the burden of CDI may be underestimated. Results were used to inform the design of the CLOUD Louisville study, an ongoing, prospective population-based surveillance study to define the incidence of CDI among hospitalized adults in the United States.

Figure 1. Study Flow Chart



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Abstract 1663

Bacterial DNA promotes tau and beta-amyloid aggregation and is suggested as a novel therapeutic target for Alzheimer's disease

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Background: Different bacteria (including facultative intracellular parasites) and fungi have been detected in the cerebrospinal fluid and postmortem brains of individuals with Alzheimer's disease (AD).
We hypothesize that DNA from these microorganisms can act as an efficient promoter for protein misfolding and AD pathogenesis. In this study, we evaluated the effect of DNA extracted from diverse prokaryotic and eukaryotic cells in tau and beta-amyloid misfolding and aggregation. Our results show that DNA from various, unrelated gram-positive and gram-negative bacteria may play a previously overlooked role, in triggering the propagation of protein misfolding and AD pathogenesis

Materials/methods: We used a protein misfolding cyclic amplification method, electron microscopy, sedimentation analysis and cell culture methods to evaluate the effects of DNA from different Gr+/- bacteria, fungi and human cells on Tau and beta-amyloid aggregation. 3xTG mouse model of AD was used to evaluate the effect of bacterial extracellular DNA destruction on tau and beta-amyloid deposition.

Results: The results showed that DNA from various (but not all) bacterial species significantly promoted tau and beta-amyloid aggregation. Thus, both ThT fluorescence and lag phase were over 5 times higher compared to untreated control ($p<0.001$). Conversely, addition of eukaryotic DNA, such as from yeast or human cells, had no effect in promoting tau aggregation. Data received indicate that the largest promoting effect was obtained in the presence of DNA from *Escherichia coli* and *Porphyromonas gingivalis*. Animal studies confirmed that the destruction of extracellular DNA decreased tau and beta-amyloid deposition in 3xTG mouse model.

Conclusions: Here we report the first evidence for the capacity of extracellular DNA from certain bacterial species to substantially promote tau and beta-amyloid misfolding, for the first time suggesting its role in AD.

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Abstract 1664

Validation of a machine learning model for prediction of mortality among patients with community-acquired pneumonia

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Background: Scoring systems such as the PSI and CURB-65 predict short-term mortality and are useful tools in guiding the diagnostic workup and initial therapy for patients with suspected community-acquired pneumonia (CAP). To be operational, scores should be able to be calculated automatically based on routine clinical data available in the electronic health record. We assess the generalizability of a previously developed mortality prediction score based on a machine-learned causal probabilistic network (CPN).

Materials/methods: Retrospective observational study. Data were collected prospectively for consecutive patients 18 years or older admitted with CAP at Hospital Universitario y Politécnico La Fe, Valencia, Spain from January 2012 to December 2018. Pneumonia diagnosis was based on a new radiological infiltrate with at least two compatible clinical symptoms. Exclusion criteria were admission in the previous 15 days, immunosuppressive treatment or human immunodeficiency virus (HIV+).
The SepsisFinder CPN (SF) was extended to include common respiratory variables; respiratory rate, pH, PaO2, SaO2, supplementary oxygen flow rate or FiO2 where available, using data collected at the Hospital Clinic of Barcelona. Results of learning were described previously (00421, ECCMID 2019).
The updated SF was used to calculate the probability of death within 30 days. Discriminatory performance for predicting 30-day mortality was assessed using the area under the ROC curve (AUC) and compared with commonly used clinical scores: PSI and CURB-65. Mortality rates were also compared for risk cut-offs defined for SF according to the percentiles associated with each PSI risk class.

Results: 1034 patients were included in the study. 30-day mortality was 4.2%. The AUC was 0.803 for SF, which did not differ significantly from that obtained for the training data (0.811). For the validation data, the AUC for SF was not significantly different to that for PSI: AUC=0.830 (p=0.42) or CURB-65: AUC=0.763 (p=0.20). When cut-offs were set to stratify the patients into groups of the same size as the PSI risk classes, the SF-selected groups had similar mortality, as shown in the table.

Conclusions: SepsisFinder shows potential for improving mortality prediction among patients with CAP using structured health data. Additional external validation studies should be conducted support generalizability.

PSI Risk Class	Patients, n (%)	30-day Mortality	SF – matched N patients, 30-day mortality
1	113 (10.9)	1 (0.9)	1 (0.9)
2	186 (18.0)	0 (0.0)	2 (1.1)
3	300 (29.0)	5 (1.7)	6 (2.0)
4	337 (32.6)	16 (4.7)	12 (3.6)
5	98 (9.5)	21 (21.4)	22 (22.2)

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Abstract 1668

Development of a user-friendly clinical decision support system (TREAT-Essential) for antimicrobial stewardship

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Background: Clinical decision support systems (CDSS) for antimicrobial stewardship can reduce unnecessary antimicrobial use and change prescribing patterns away from resistance-promoting drugs without compromising coverage, thereby improving the quality of empiric therapy and reducing costs. Despite purported benefits, CDSS are faced with a number of barriers to successful implementation. Our aim was to overcome key barriers identified for the previously developed TREAT CDSS, which provided guidance for antimicrobial therapy. The barriers were incomplete integration into the clinical workflow and interface with IT systems, limited physician acceptance of the CDSS intervention and limited management commitment.

Materials/methods: We developed a new version of TREAT, TREAT-Essential. This involved a series of four workshops concerning functionality, user-friendliness, IT architecture and calibration/clinical relevance. Workshops were conducted with relevant stakeholders including specialists in infectious diseases, clinical microbiology, and IT management.

Results: The result of the workshops was a redesigned graphical user interface and simplified decision engine. By modifying the decision engine to take the physician's diagnosis as an input rather than determining this from entered signs and symptoms. Thereby the data entry burden was reduced to a range of 5 clicks with a minimized loss of physician autonomy. Additional patient information is automatically extracted from the electronic health record and summarized as it pertains to the current infection. Keeping the detailed information out of view provided the clinician an easier overview, but easily displayed when required. Likewise, the recommended therapy is presented as a single recommendation, while probabilities for causative pathogens and expected coverage for the chosen treatment are hidden by default (Figure). The workshops also identified opportunities for deeper integration (thus less manual data input) and locations for activation within the current workflow with minimum interruption of current workflows.

Conclusions: Involving key stakeholders across disciplines (clinicians and IT developers) uncovered additional opportunities for improving the design that may have been missed with separate workshops. TREAT-Essential has improved integration into workflow and IT infrastructure and requires less user input. Whether this will improve clinical acceptance must be validated in clinical trials.

TREAT-Essential is activated directly in the electronic prescription module at the time of prescribing

1. Add background information

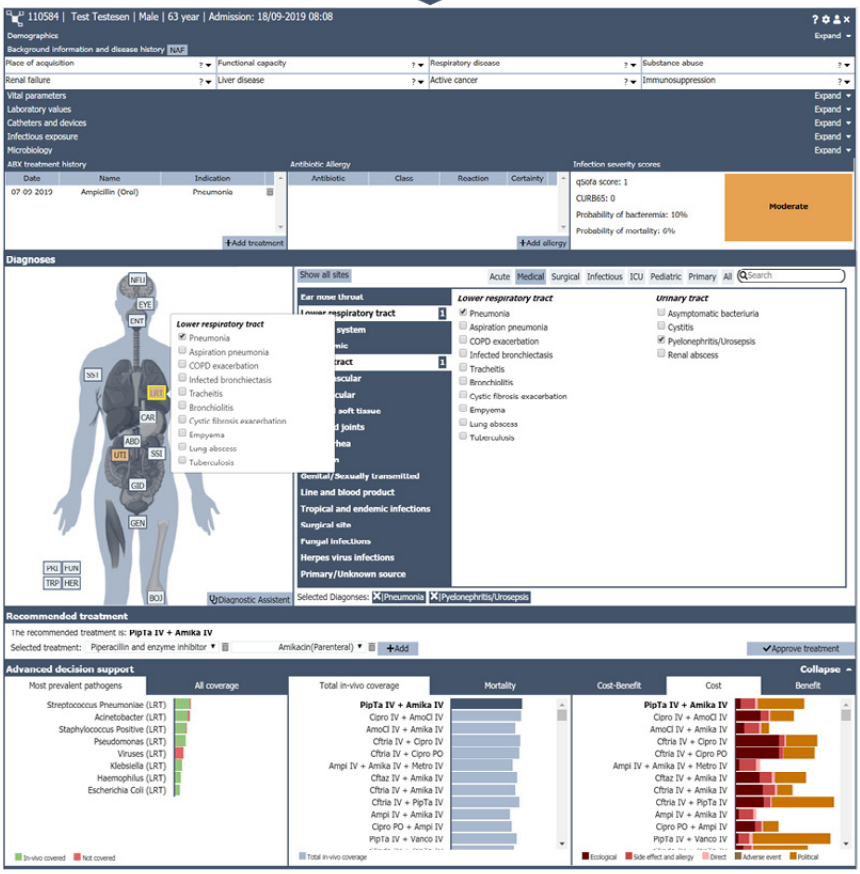
1a. (optional) Inspect summary of patient data

2. Select diagnosis

2a. Depending on diagnosis, severity, answer questions to confirm indication for antimicrobial therapy

3. View recommendation, select treatment (or no treatment), approve

3a. (optional) Inspect decision support output



User returns to the prescription module where the selected treatment is pre-filled. Audit-trail includes the recommendation and its basis for quality assurance.

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Abstract 1669

First report of the discovery of amurin peptides: direct lytic agents with broad activity against carbapenem-resistant Enterobacteriaciae, *Acinetobacter*, and Pseudomonas, including colistin-resistant strains

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Background: DLAs are new modalities in development to address antimicrobial resistance (AMR). Lysins, cell wall hydrolases enzymes, are at the vanguard of this field, with recently reported clinical Proof of Concept of the antistaphylococcal lysin, exebacase to treat MRSA bacteremia. Here, we describe amurin peptides, previously unidentified bacteriophage-encoded DLAs, distinct from lysins, with bactericidal activity against a wide range of pathogenic Gram-negatives (GN) including CDC urgent threat/WHO critical priority pathogens: colistin-resistant CRE, CRA, and CRP.

Materials/methods: Amurin were identified in the viral genome database (NCBI) and synthesized by GenScript (Piscataway, NJ). In vitro characterization of bactericidal activity, antibiofilm effects, synergy with antibiotics, and resistance profile was conducted using standard methodologies. MICs were determined against MDR/XDR clinical isolates (n=188) from 5 CDC Antibiotic Resistance Panels.

Results: We identified a novel class of DLAs comprised of amurin peptides with antimicrobial activity against all GN ESKAPE pathogens, as well as *E. coli*, *P. mirabilis*, *A. xylosoxidans*, and *S. maltophilia*. Hallmark features of amurins include rapid bactericidality (>3-$\log_{10}$ kill), synergy with ≥13 antibiotics, antibiofilm activity (MBEC values of ≤2 µg/mL), and no detectable resistance in spontaneous. Strikingly, an MIC_{90} of 1 µg/mL (range=0.125-2 µg/mL) was demonstrated for several peptides against all CDC resistance panel isolates, including XDR strains of *P. aeruginosa*, *K. pneumoniae*, *E. cloacae*, *A. baumannii*, and *E. coli* with both carbapenem and colistin resistance (examples in Table 1).

Table 1: MIC (µg/mL) analysis of amurin peptides (AM1-3) and comparator antibiotics against select colistin-resistant CRE, CRA and CRP isolates from CDC resistance panel isolates.

Strain	Strain/Resistance type	AM1	AM2	AM3	AMI	CIP	COL	LEV	MEM
K. pneumoniae	AR522 (CRE)	0.5	0.5	0.25	8	>8	>8	>8	>8
A. baumannii	AR303 (CRA)	1	1	0.25	>64	>8	>8	>8	>8
P. aeruginosa	AR239 (CRP)	1	0.5	0.25	>64	>8	8	>8	>8

Key: AMI, amikacin; CIP, ciprofloxacin; COL, colistin; LEV, levofloxacin; MEM, meropenem

Conclusions: Newly discovered amurin peptides are highly active DLAs against CRE, CRA, and CRP including colistin resistant strains, and are potential "game changers" in the efforts to combat AMR and treat pathogens for which there are no current therapeutic options.

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Abstract 1671

Imported malaria: overview of the diagnosed and suspected cases of malaria in a Spanish city (15 years of experience)

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Background: In our city , paludism is the first imported tropical disease. It is suffered all about in visiting friends and relatives (VFR). We describe 287 malaria cases and 367 suspected but not confirmed cases of malaria attended in the last 15 years.

Materials/methods: It is a retrospective, comparative and populational study of all malaria cases and not confirmed cases diagnosed during 2004-2018 period.We have used media or median values,chi square test and median test to describe and to compare both groups.

Results:
Malaria group:
287 cases of malaria were diagnosed. 72,6% VFR, 10,8% travelers VFR,15,6% inmigrants, 0,3% travelers. September (16%) and august (13,2%) were the two most frequent period of diagnosis in front of March (2,1%) and April (3.5%). 53% were men.
47.6% came from Guinea Ecuatorial , 45,1% from Nigeria.*P falciparum* 89.6%,*P vivax* 1.4%,*P ovale* 3.1%, *P malariae* 1% mixed infections 2,4%.
Median values: age 33 years, days in risk areas 30, days in Spain to diagnosis 7, days with simthoms to diagnosis 4, Leucocytes 5450 /mcl, Plaquets 109000/mcl,hemoglobin 12,2 g/dl, bilirrubin 2 mg/dl, c reactive protein (CRP) 9,1 mg/dl, LDH 281 mg/dl, and amount of parasitation 1%. Of all patientes 73,6% had thrombopenia, 52,2% had anemia and 95,7% had high values of CRP. 14,9% had splenomegaly, 94,8% fever,50,3% headache,51,4% digestive symtoms.
14 cases (4,9%) had submicroscopic malaria, the rest of them were diagnosis with antigenic test or gross gout.
11 patientes (3.8%) needed an intensive car unit treatment. 14 cases were on pregnant (10,6% of all women). 12 cases were HIV positive (2 false positive 6 were new diagnosis of HIV infection, and 4 were known HIV positive. Median of CD4 364 /mcl, and 75% under 500/mcl CD4, and 30% under 250/mcl CD4. 18 (6,3%) patients were diabetics.
Of all patients only 4,9% did apropriate prophylaxis. One death in all serie.

Comparative values with confirmed and not confirmed Malaria (Figure).

Variables with significance differeces (median)	Confirmed Malaria	Not confirmed Malaria	P difference
Platelets (c/mcl)	109.000	225000	< 0,05
C reactive protein (mg/dl)	9,1	0,54	<0,05
Splenomegaly	14,9%	1,7%	<0,05
Fever	94,8%	67,8%	<0,05
Headache	50,3%	24,6%	< 0,05
Digestive symptom	51,4%	37,1%	<0,05
Apropriate prophilaxis	4,9%	12,1%	< 0,05
Respiratory symptom	14,3%	25,3%	<0,05
All other variables	No differences	No differences	Not statystical differences

Conclusions: Malaria is a prevalent imported infectious diseases. There are important prevalent groups as HIV, pregnant,and diabetic patients. Different clinical, and analytic characteristics could help us to diagnose risk patients with and without malaria

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Abstract 1674

Georeferencing patients infected by Gram-negative bacteria producing extended-spectrum beta-lactamase, Pereira city, Colombia, 2012-2017

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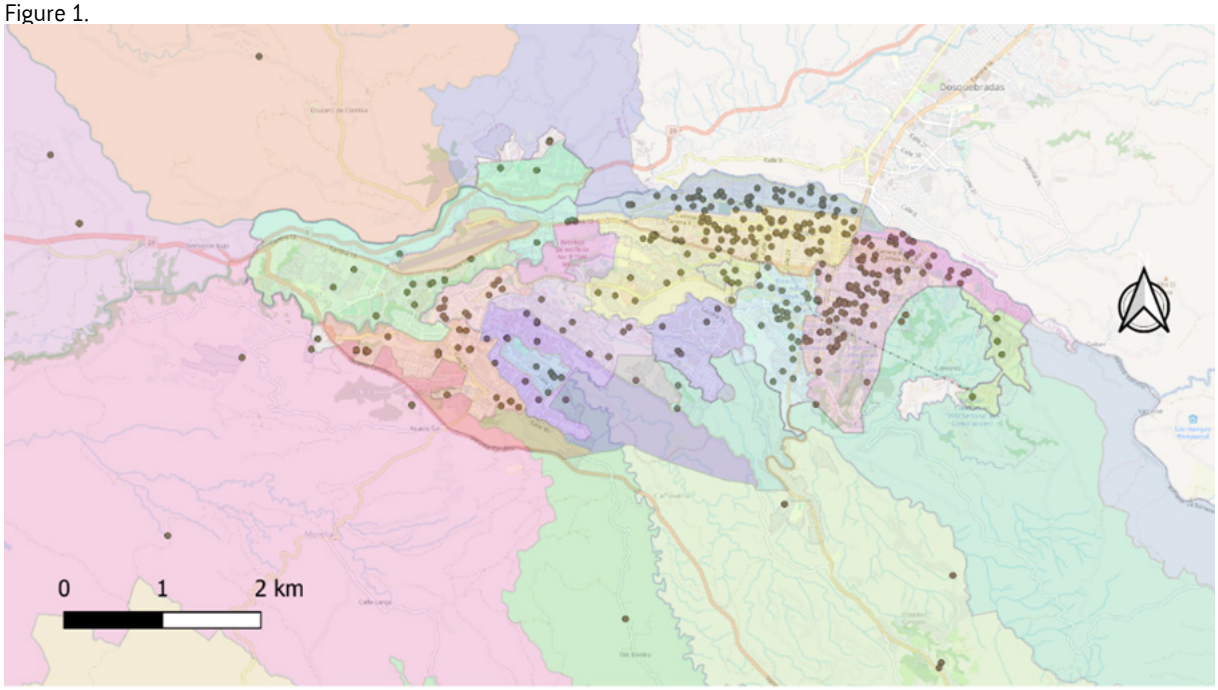
Background: Knowledge about the geographic distribution patterns of resistant Gram Negative Bacteria (GNB) is potentially valuable information that could help establish ecological factors associated with transmission and resistance acquisition in the community level. The aim of this study was to establish the existence of patterns of geographic distribution of patients with positive isolation for gram-negative bacilli resistant to third-generation cephalosporins with phenotype producing Extended Spectrum Beta lactamase (ESBL), in the city of Pereira, Colombia. Study period: 2012 to 2017.

Materials/methods: A georeferencing study was carry out. We took the database of a tertiary Hospital and a reference laboratory in the city on the isolates with phenotypic pattern of ESBL production. Ethical endorsement was obtained from the bioethics committee of the Universidad Tecnológica de Pereira Pereira. The georeferencing was done with the KOSMO GIS and QGIS open access programs.

Results: We obtained 1246 records of subjects with GNB ESBL infection. After applying the inclusion and exclusion criteria, the geographical distribution of 415 subjects with isolation from the community, from Pereira, was established (Figure 1). The highest concentration of events was found in the San Joaquin, Perla del Otún, Río Otún, Centro, Oriente, Villavicencio, Boston and Universidad districts.

Conclusions: The geographic distribution patterns of resistant GNB infections with ESBL producing phenotype are shown. The existence of local transmission foci is proposed mainly in the central and eastern areas of the city. We highlight the importance of controlling the sources of microbial resistance not only at the hospital level but also at different actors in the community.

Figure 1.



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Abstract 1675

Low horizontal transfer rate of mcr-8 may constrain the spread of mcr-8 genes

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Background: Colistin has been regarded as a highest priority important antimicrobial for human medicine by World Health Organisation since 2017. Plasmid-borne *mcr-* genes are one of the main contributors for the success of the global spread of colistin-resistance bacterial pathogens. This study aims to characterize a novel plasmid harbouring a *mcr-8* gene in klebsiella pneumoniae isolated from blowflies in Thailand, and examine the fitness effect of *mcr-8* gene on plasmid maintenance and competitiveness.

Materials/methods: hybrid assembly of Illumina and Oxford Nanopore sequencing was performed to identify a novel *mcr-8*-carrying plasmid and strain. The transferability of both co-existed *mcr-1* and *mcr-8* plasmids were investigated by conjugation experiments and qPCR. To assess the fitness effect of *mcr-8* expressionon bacterial growth, plasmid constructs and growth assays were conducted. Furthermore, the competition and persistence between *mcr-1* and *mcr-8* were investigated via 30-day passage experiments

Results: the *mcr-8* gene was identified in previous reported 17 *mcr-1*-positive *K. pneumoniae* strains isolated from blowflies in Thailand. The *mcr-8* gene is located in an IncFII: FIB plasmid (pKP100-mcr8) that co-harboured with *qnrS1*, *tet(A)*, bla_{TEM-1b} and *ampC*. pKP100-mcr8 shares low sequence similarity (less than 60% coverage) of other plasmids in the NCBI database. The plasmid pKP100-mcr8 can be transferred from *K. pneumoniae* to *Escherichia coli* J53Az^{r}, with significantly lower transfer frequency (as low as $3.4x10^{-13}$) than that of *mcr-1*-IncX4 plasmid co-existed in the *K. pneumoniae* strains (approx.$1x10^{-4}$). The expression of *mcr-8* did not affect bacterial growth rate, suggesting that there is no significant fitness burden conferred by the expression of *mcr-8* gene. Furthermore, both *mcr-1* and *mcr-8* are very stable in an *in-vitro* competition model over a period of ff300 generations.

Conclusions: The emergence of this newly identified *mcr-8.1*-positive plasmid from blowflies raise a great concern to our public health. Our data show that *mcr-8* has fitness advantage and ability of maintenance and persistence, however, when comparing to its co-existed *mcr-1* gene, its rate of horizontal transfer is relatively low, which explain the low occurrence of *mcr-8* in the globle level. It further suggests that horizontal transfer is a key factor for the global dissemination of AMR genes.

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Abstract 1677

ESwab collection device allows both detection of human papilloma virus with molecular assays and culture with WASP automation

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Background: A multitasking specimen collection device that supports different testing methods is an asset for a centralized microbiology laboratory. Copan ESwab™ kit, consists of a FLOQSwab® and a tube with 1 ml Amies liquid medium for the collection of clinical specimens, resulting in a homogeneous sample suspension suitable for gram smear, antigens detection, bacteria culture, and molecular assays for the detection of microbial infectious agents. The objective of this study was to validate the performance of genital specimens collected with ESwab™ for the detection HPV genotypes with the Roche Linear Array and the detection of bacteria culture processed on the WASP™ automated system.

Materials/methods: In this study were analysed 427 genital samples, (383 females, 44 males) received in the SANADOR Molecular Laboratory from Gynecology, Dermatology and Urology Departments for HPV genotyping. ESwab™ codes 490CE for females and 491CE for males were used for sample collection. Nucleic acids were extracted from 200 ul of each ESwab™ sample using the High Pure PCR Template Preparation kit. Fifty µL of the extracted DNA were used for PCR amplification and analyzed for HPV genotyping with Roche Linear Array assay**.** HPV genotypes were visualised after reverse hybridisation in a Beeblot automated system**.** All ESwab™ samples were processed on the WASP™ for bacteria culture on Columbia and Sabourand agar plates.

Results: In the 427 samples investigated, 241 were negative and 186 were HPV positives. At least one HPV genotype was detected in 44% of patient's samples. Most prominent HPV HR, present, in single or multiple co-infections, were HPV 16 (44/186), 51 (35/186), 52 (27/186), 31 (25/186), 39 (23/186), 58 (19/186), 18(18/186), 35 (12/186). HPV53 was most prominent (38/186) for the possible HR and 54 (33/186) for the LR. In the males 20/44 HR genotypes, and 10/44 possible HR were detected. In the 241 HPV negative samples, culture detected 13 *Candida spp*, 10 *Streptococcus B*, 4 *Candida spp+Streptococcus B* and 1 *E. coli.*

Conclusions: Data generated in this study demonstrated that ESwab™ is a versatile collection device that can be used for both the detection of HPV genotypes with molecular assay and bacteria culture with WASP™ automation.

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Abstract 1678

Decreasing reporting time of blood cultures by workflow optimisation with the WASPLab system

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Background: One of the goals of lab automation is fast reporting to clinicians while maintaining high quality and efficiency. We describe the impact of WASPLab® and consecutive extension of the working hours of lab technicians in the bacteriology laboratory on reporting time of identification (ID) and antimicrobial susceptibility testing (AST) results of blood cultures (BC).

Materials/methods: At the University Hospitals Leuven, positive BCs are streaked manually on at least a blood and MacConkey agar and incubated afterwards. Based on tracking in the laboratory information system, the time from BC positivity to ID and AST results reporting to the clinician were calculated. Three 5-months periods were compared: period 1 with conventional incubation and reading at 8.30h, 14h and 17h; period 2 with WASPLab® incubation and reading at 8.30h, 14h and 17h of BCs positive during the day (same staff and working hours as period 1) and period 3 with WASPLab® incubation of all plates and reading at 8.30h, 14h, 17h and 21h (extended working hours). Plates are photographed in WASPLab® at 4, 6, 10, 16, 24 and 48 hours of incubation. ID is performed with MALDI-TOF MS and AST with Vitek2® or disk diffusion.

Results: Median time between BC positivity and reporting of ID decreased from 19h50min in period 1 to 17h41min and 12h55min in respectively period 2 and period 3 (Table). The percentage of IDs reported within 8 hours increased from 0.7% to 7.2% and 16.5% in the consecutive periods. In period 3, 83.5% of IDs were reported within 24 hours compared to 63.4% in period 1. Also a decrease in median time between BC positivity and reporting of AST was seen from 40h32min in period 1 to 37h07min and 33h17min in respectively period 2 and 3.

Conclusions: Introduction of WASPLab® without change in staff and working hours resulted in a decreased reporting time of blood cultures. Extending the working hours of the bacteriology lab from 8:30-17:30 to 7:00-23:00, made it possible to further optimize the use of WASPLab®, which altogether resulted in a decrease of median reporting time of ID and AST of 7 hours compared to conventional workup.

Table 1: Comparison of time to results for identification (ID) and antimicrobial susceptibility testing (AST) of blood culture isolates in period 1 (conventional incubation and reading), period 2 (use of WASPLab® system) and period 3 (use of WASPLab® system with extended opening hours) for incubation and reading of agar plates.

	Period 1 June – October 2017	**Period 2** June – October 2018	**Period 3** June – October 2019
Method of incubation and reading of BC	Conventional	WASPLab®	WASPLab® (ext)
Working hours of technician in bacteriology lab	8.30h - 17.30h	8.30h - 17.30h	7h - 23h
Reading moments of the plates	8.30h, 14h and 17h	8.30h, 14h and 17h	8.30h, 14h, 17h and 21h
Number of positive BC	4905	4310	4269
Reporting of ID results			
- Median time between BC positivity and reporting ID	19h 50min	17h 41min	12h 55min
- Percentage of samples reported			
Within 8 hours	0.7%	7.2%	16.5%
Within 12 hours	10.0%	25.1%	45.2%
Within 16 hours	33.8%	43.5%	65.0%
Within 24 hours	63.4%	70.9%	83.5%
Reporting of AST results			
- Median time between BC positivity and reporting AST	40h 32min	37h 07min	33h 17min
- Percentage of samples reported			
Within 24 hours	3.0%	7.7%	15.1%
Within 36 hours	38.2%	47.4%	59.2%
Within 48 hours	70.7%	72.8%	78.5%

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Abstract 1679

First evidence of systemic efficacy of a pathogen-targeted, engineered lysin (GN-370) against carbapenem-resistant *Pseudomonas aeruginosa* in a rabbit pneumonia model

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Background: Lysins are direct lytic agents which have shown efficacy against gram-positive bacteria *in vivo* and in a recent Phase 2 clinical study in MRSA bacteremia. However, lysins were considered to be inactive against gram negative (GNs) pathogens when administered systemically *in vivo*. GN-370, a novel engineered lysin, was evaluated as systemic treatment for *P. aeruginosa* alone or in addition to meropenem, in a rabbit pneumonia model.

Materials/methods: Pneumonia was induced in New Zealand White rabbits by endotracheal inoculation with PA20 ($3x10^9$ CFU). At 6h post-infection, rabbits were randomized to receive: no therapy (pretreatment); vehicle alone; meropenem alone (20 mg/kg, 3 doses x q8h, subcutaneously); GN-370 alone (3 or 10 mg/kg, single intravenous dose); or GN-370 plus meropenem at the same doses. Lung, kidney, and spleen tissues were collected 24h after the last dose of meropenem, were quantitatively cultured (log_{10} cfu/gram of tissue; and mean counts (+/- SD)) and compared in the various groups.

Results: GN-370 was well tolerated. All GN-370-treated animals survived until end of study, whereas only ff40% of vehicle-control animals survived. In animals receiving either meropenem or GN-370 alone, the mean bacterial lung counts decreased by ff1.5-2-log_{10} CFU/g (vs pretreatment or vehicle-treated controls, $p \leq 0.0016$). GN-370 (10 mg/kg) in addition to meropenem was synergistic, with bacterial counts in all target tissues decreasing by an additional ff2 log_{10} CFU/g vs meropenem or GN-370 alone ($p \leq 0.02$).

Treatment	Bacterial Burden (log_{10} CFU/g)		
	Lungs	Kidney	Spleen
6hr pretreatment control (n=4)	7.77±0.55	4.13±0.59	4.57±0.70
Vehicle control (n=5)	7.86±0.62	6.41±0.90	6.39±0.59
Meropenem 20mg/kg, SC X 3doses every 8hrs. (n=6)	5.88±0.98	3.92±0.63	3.62±0.21
GN-370 (3mg/kg,IV,once) (n=8)	6.36±1.04	5.06±1.05	5.23±1.25
GN-370 (3mg/kg) + Meropenem (n=9)	6.11±1.17	3.90±1.06	4.16±0.98
GN-370 (10mg/kg,IV,once) (n=6)	6.08±1.47	3.46±0.78	3.76±0.44
GN-370 (10mg/kg + Meropenem (n=8)	3.97±1.62	1.99±1.00	1.89±1.01

Conclusions: These data represent the first evidence that GN-targeted lysins can be engineered to result in systemic efficacy *in vivo*. GN-370 was well tolerated and effective against *P. aeruginosa* when administered intravenously alone, and had marked synergy with meropenem in the rabbit pneumonia model. *P. aeruginosa* causes serious, life-threatening and ever-increasing antibiotic-resistant invasive infections, especially nosocomially. This study provides *in vivo* proof-of-concept for the further development of GN-370 to treat invasive *P. aeruginosa* infections. Moreover, these data represent a key proof of principle for GN-targeted lysins as new modalities to combat antimicrobial resistance in such pathogens.

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Abstract 1680

Total knee and hip arthoplasty after septic arthritis: retrospective analysis of 53 cases managed in a reference centre for bone and joint infections

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Background: Arthroplasty after or during treatment of septic arthritis (SA) raises diagnostic and therapeutic questions. The objective was to describe characteristics of patients undergoing total knee (TKA) or hip arthroplasty (THA) after SA, results of cultures taken at implantation, management of antibiotic therapy and outcome after arthroplasty.

Materials/methods: Retrospective monocentric study from January 2005 to May 2019, including all the patients undergoing TKA or THA with a history or SA or current SA on the same joint.

Results: 51 patients, 31 men (61%), with a median age of 64 years, operated on 53 joints (32 knees, 21 hips) were included. SA occurred after joint infiltration (n=13), surgery (n=8), hematogenous spread (n=12), from a contiguous source (n=9) or was of undetermined origin (n=11). Median time between SA and arthroplasty was 31 [0-832] weeks. It was ≤2 years in 47 and ≤6 months in 21 cases. Arthroplasty was performed in 6 cases while the patient was still on SA treatment. Synovectomy and one-stage arthroplasty was carried out in 47 cases, two-stage arthroplasty in 6 cases. Intraoperative cultures were positive in 8 cases (15%) with the same microorganism in 3, a different one in 4, and SA was diagnosed on these cultures in one case. No antibiotic prophylaxis was administered, but all the patients received postoperative antibiotic therapy, targeting the SA microorganism and the skin flora. Median duration of treatment was 10 days, if cultures remained sterile, 82 days, if they confirmed an infection. To date, 32 patients (60%) were followed for ≥ 12 months. No SA relapse was observed. Five patients (3 TKA, 2 THA) developed a prosthetic joint infection with a different microorganism 5 months to 7 years after arthroplasty.

Conclusions: Arthroplasty may be considered after or during SA, even within a short period of time. Intraoperative cultures were positive in 15% of the cases. One-stage arthroplasty can be performed if a thorough synovectomy is realized, intraoperative samples are taken systematically, and an antibiotic therapy is administered until the cultures results are available. We observed no SA relapse, but new prosthetic joint infections occurred.

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Abstract 1681

Clinical utility of syndromic meningitis/encephalitis testing in children

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Background: Rapid diagnosis and treatment of central nervous system infections is critical. The BioFire FilmArray Meningitis/Encephalitis Panel (FA-M/E) is a molecular syndromic test that can rapidly detect 14 pathogens in cerebrospinal fluid (CSF). Here, we sought to analyze the clinical utilization and impact of FA-M/E in children.

Materials/methods: Between June 2016-December 2017, FA-M/E was tested on 449 patients (Test group) and 412 patients received no FA-M/E testing (Control group). Chart abstraction was conducted to compare patient medical history, antimicrobial course, and length of stay (LOS).

Results: FA-M/E testing in the Test group detected 62/449 (14%; 14 bacteria, 48 virus) targets compared to 8/412 (2%; 5 bacteria, 3 virus) in the Control group. The top three most common targets detected by FA-M/E were Enterovirus (n=25), HHV-6 (n=14), and *Streptococcus agalactiae* (n=7). The number of immunocompetent patients were slightly lower in the Test group compared to Control (57.9% vs 66.5%). The median time to discontinuation (TTD) of key antibiotics in patients with negative test results was shorter by 21.8 hours (32.7 vs 54.5 hrs, *P=0.0002*) in Test group. These drugs include gentamicin (32.2 vs 54.4 hrs, *P=0.03*), ampicillin (34.4 vs 54.4 hrs, *P=0.0002*), cefepime (28.9 vs 55 hrs, *P=0.002*), and meropenem (154 vs 215 hrs, *P=0.52*). For a positive viral result, the median TTD of antibiotics in the Test group was 34.7 hours from time of test ordered. Results were not compared to Control group due to the low number of viral positives. Patients previously not placed on antibiotic therapy but tested positive for bacterial target were started on appropriate antibiotics 69 hours earlier in the Test group (14.5 vs 83.5 hrs, *P=0.2*). Rapid FA-M/E results in the Test group resulted in a decrease in LOS by 4 days (2.7 vs 6.7 days, *P<0.001*) in positive patients. In the Test group, patients positive for viral targets were discharged 11.2 days (2.6 vs 13.8 days, *P=0.002*) earlier than those positive for bacterial targets.

Conclusions: FA-M/E significantly reduced time to identification of M/E pathogens. Use of FA-M/E was associated with accelerated optimization of therapy and decreased LOS in pediatric patients.

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Abstract 1683

Rapid molecular diagnosis of Neisseria meningitidis, *Streptococcus pneumoniae*, Listeria monocytogenes, *Enterovirus* and parechovirus from blood in patients of the paediatric emergency department of a tertiary hospital

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Background: Early microbiological diagnostic of febrile illness in children under 3 years may be challenging, especially when no infectious focus is identified. New molecular techniques allow us to detect the most common pathogens in short time. The objective of this study was to evaluate the performance of molecular detection of *Neisseria meningitidis, Streptococcus pneumoniae, Listeria monocytogenes*, Enterovirus and Parechovirus from blood in patients of the pediatric emergency department of a tertiary hospital.

Materials/methods: We selected children under 3 years with fever (≥38ºC) without focus attending to the pediatric emergency department from January to October 2019. In addition to the routine analyses a 5ml whole blood tube was collected. Nucleic acids were extracted on MagNApure® system under standard conditions and two different Progenie-Molecular® assays (bacterial and viral) were conducted on the SmartCycler®. We compared the results of the bacterial PCR to the gold standard blood culture and to the clinical manifestations

Results: 202 patients (123 male 79 female) were included on the study with a mean age of 0.96 years. There were 26 patients with positive samples (12.9%).

Total patients	*Streptococcus pneumoniae*	*Neisseria meningitidis*	*Listeria monocytogenes*	Enterovirus	Parechovirus
202	5	1	0	12	8

Only one patient with a positive assay for *Streptococcus pneumoniae* had a positive blood culture, one was contaminated, and the rest were negative. Three were clinically significant and two were doubtful about having also another infectious cause. There was no previous record of antibiotic consumption. All of them but one were vaccinated.
The patient with a positive *Neisseria meningitidis* assay had also a positive blood culture.
There were no positive blood cultures for the detected bacterial agents in the patients with negative bacterial assay or positive blood cultures when any of the viral targets were positive.

Conclusions: This diagnostic approach may be useful in this kind of patients when combined with the standard procedures, especially when an early viral diagnosis, which were almost a 10% in our series, may reduce the antibiotic burden at childhood. This molecular assay may outperform the blood culture particularly if the sample is from the early stages of the illness.

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Abstract 1684

A retrospective study of pyogenic liver abscess caused by *Klebsiella pneumoniae* as a primary pathogen: computed tomography and clinical differentiation

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Background: The incidence of *Klebsiella pneumoniae* pyogenic liver abscesses (KP-PLA) is increasing. However, its diagnosis and treatment are often delayed, leading to complications. To retrospectively compare computed tomographic (CT) features of KP-PLAs with those of abscesses caused by other bacterial pathogens (non-KP-PLAS) and to further identify prognostic factors for PLA.

Materials/methods: Data of 219 study patients including clinical presentation, comorbid conditions, metastatic infection, treatment duration, and mortality were retrospectively collated. CT characteristics of abscesses were recorded. Etiology was established by pus and/or blood culture. The differentiating CT features and clinical findings were compared between the monomicrobial KP-PLA and non-KP-PLA groups. Furthermore, factors related to in-hospital case fatality were analyzed.

Results: Our study identified thin-walled abscesses, absent rim enhancement, metastatic infection, and absence of underlying biliary tract disease as significant predictors of KP-PLA. With 3/4 criteria applied in combination, a specificity of 96.5% was achieved for KP-PLA diagnosis. The in-hospital mortality rate was 3.7%. In present study, multivariate analysis revealed that diabetes mellitus (P=.031), multiple abscesses (P=.026), internal gas bubbles (P=.041), metastatic infection (P=.004), and septic shock (P=.002) were significantly associated with mortality.

Conclusions: Our study suggested that thin-walled abscess, metastatic infection, absence of rim enhancement, and absence of underlying biliary tract disease are potentially useful CT findings for early KP-PLA diagnosis.

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Abstract 1685

Comparing outcomes and clinical characteristics associated with carbapenemase-producing and non-carbapenemase-producing carbapenem-resistant *Enterobacteriaceae* bacteraemia

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Background: Carbapenem-Resistant Enterobacteriaceae (CRE) bacteremia is associated with significant morbidity and mortality. CRE are classified as either carbapenemase-producing (CP-CRE) or non-carbapenemase-producing (non-CP-CRE). There are limited studies comparing the outcomes and characteristics of patients with each type of infection.

Materials/methods: We performed a chart review of 146 patients with CRE bacteremia from January 2010-July 2019. CRE was defined using the current CDC definition. The modified carbapenem inactivation method was performed on each CRE isolate to determine carbapenemase production. Electronic medical records were reviewed to obtain clinical characteristics and outcomes including prior antibiotic use, comorbidities, prior location, treatment, hospital course, and outcomes including in-hospital mortality, recurrence of bacteremia, and readmission.

Results: Of 145 cases included in our analysis, 87/145 (60%) were CP-CRE and 58/145 (40%) were non-CP-CRE. Patients with CP-CRE had a higher median Pitt Bacteremia score (4 vs. 2, p=<.001), were more likely to have been admitted from a healthcare facility (49.4% vs. 27.5%, p=.008), and to have received antibiotics in the 90 days prior to bacteremia onset (89.7% vs. 72.4%, p=.007). Patients with CP-CRE were less likely to receive active empiric therapy (19.54% vs. 51.72%, p=<.005) and active targeted therapy (74.4% vs. 86.2%, p=.08). Non-CP-CRE was associated with a 2.6 times higher hazard of death within 30 days compared to CP-CRE (hazard ratio, 2.6; 95% CI, 1.4,4.9). Additional outcomes data are presented in Table 1.

Table 1. Outcomes

Characteristic	Non-CP-CRE (n=58)	CP-CRE (n=87)	p-value
Survival until hospital discharge	38(65.5%)	51(58.6%)	0.403
Survival until 14 days after bacteremia	39(67.2%)	66(75.9%)	0.255
Survival until 30 days after bacteremia	39(67.2%)	54(62.1%)	0.525
Time to death, days	5(1-9.5)	12(2-20)	**0.029**
Time to discharge alive, days	8.5(5-17)	16(9-29)	**0.005**
LOS, days	13.5(7-43)	25(15-52)	**0.009**
LOS post positive blood cx, days	7.5(4-13)	14(8-25)	**0.002**
Recurrence of CRE BSI within 90 days	2(5%)	8(13.8%)	0.158

Conclusions: Patients with CP-CRE were more likely to have exposure to healthcare facilities and antibiotics, have more severe illness at bacteremia onset and were less likely to receive active therapy. There was no significant difference in mortality between groups but non-CP-CRE was associated with a higher likelihood of death within 30 days.

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Abstract 1693

Imipenem/relebactam pharmacokinetic/pharmacodynamic analyses from an *in vivo* neutropenic murine thigh infection model

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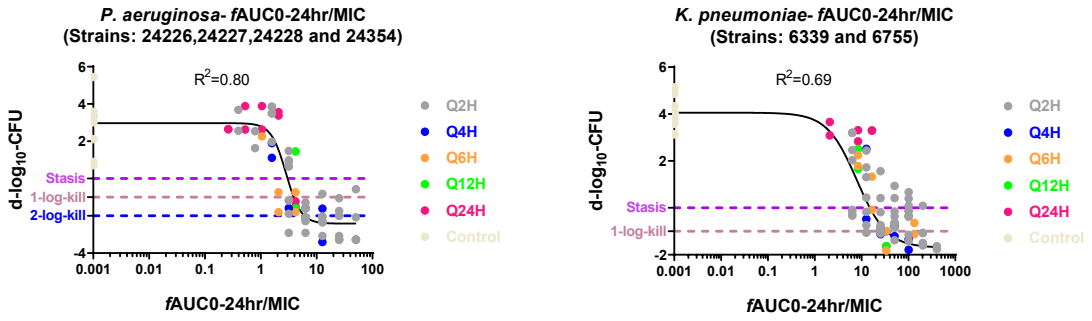
Background: Relebactam is a small molecule beta-lactamase inhibitor. The combination of relebactam with imipenem (*in vitro*) and imipenem/cilastatin (*in vivo*) showed significant antibacterial activity against imipenem nonsusceptible strains. We conducted pharmacokinetics/pharmacodynamics (PK/PD) analyses utilizing data from an *in vivo* neutropenic murine thigh infection model to derive relebactam PK/PD targets associated with stasis, 1-log kill and 2-log kill.

Materials/methods: Previously conducted PK/PD murine thigh studies were used for generation of the pooled PK/PD dataset. This dataset was obtained using two isolates of *Klebsiella pneumoniae* and four isolates of *Pseudomonas aeruginosa* at imipenem doses within two-fold of the humanized dose with varying total daily doses and dosing frequency of relebactam. Correlation analyses using the pharmacokinetic (PK) exposure and response (change in $\log_{10}$ colony-forming unit at 24 hours post-dose) was plotted against *f*AUC, *f*AUC/MIC, *f*Cmax, *f*Cmax/MIC, %*f*T>C_T at 1,2 and 4 mg/L for both *Pseudomonas aeruginosa* and *Klebsiella pneumoniae*. Imipenem MICs in the presence of 4 mg/L of relebactam were used to derive the *f*AUC/MIC and *f*Cmax/MIC for each strain. An Emax model with Hill coefficient was used to fit the data. Stasis, 1-log kill, and 2-log kill PK/PD targets were derived from this model.

Results: The PK/PD parameter *f*AUC/MIC was best correlated with response in this analysis. The derived stasis, 1-log kill, and 2-log kill *f*AUC/MIC PK/PD targets for *Pseudomonas aeruginosa* were 3.3. 4.3 and 7.0 respectively. This 2-log kill PK/PD target is consistent with previous analyses in an *in vitro* hollow fiber infection model.

Conclusions: PK/PD analyses using pooled data from four isolates of *Pseudomonas aeruginosa* and two isolates of *Klebsiella pneumoniae* demonstrated that *f*AUC/MIC is the best PK/PD driver for relebactam. The derived 2-log kill target can be used for dose justification and probability of target attainment (PTA) assessments for the fixed dose combination of imipenem/cilastatin/relebactam.

Figure. PK/PD Relationship of relebactam in the neutropenic mouse thigh infection model at imipenem 8 mg/kg and 15.9 mg/kg for *Pseudomonas aeruginosa*



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Abstract 1697

NK cell deficiency and cryptococcosis

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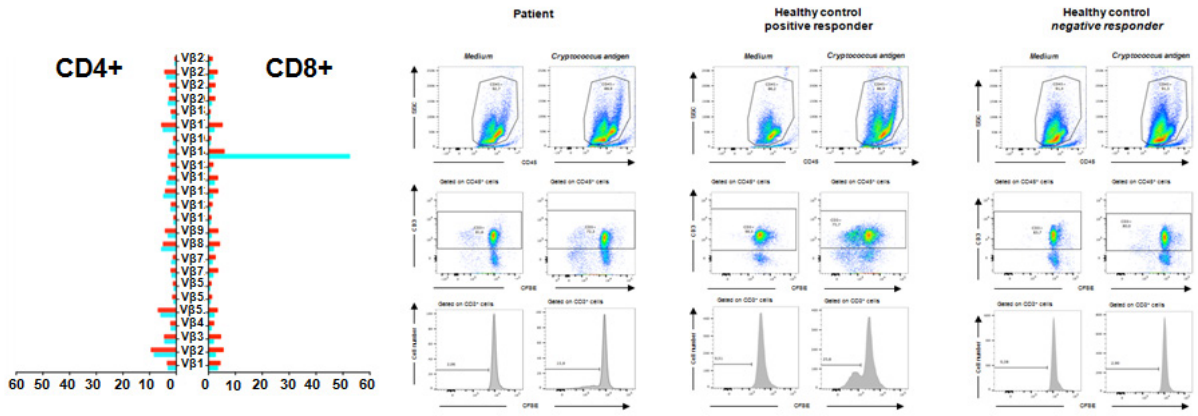
Background: Human NK deficiency (NKD) is a rare primary immunodeficiency, characterized by less than 50 NK cells and < 1% of circulating lymphocytes and usually associated with *Herpesviridae* infections. We described a new phenotype of NK deficiency in a healthy 28-year-old man characterized by a predominant Dim NKD associated with a pulmonary cryptococcosis.

Materials/methods: The patient was admitted in December 2008 for a nonproductive cough and the discovery of non-calcified nodules on chest X rays. The patient had no medical history. He had no fever and medical examination was normal. The standard biological results were in the normal values including a normal leukocyte count and a CRP of 2mg/l. A broncho-alveolar lavage revealed the presence of many *Cryptococcus neoformans var. grubii* (serotype A). Cryptococcal antigenemia and/or fungal culture were negative in Cerebrospinal fluid, blood and urine. The patient was successfully treated by fluconazole 400mg per day for 12 months. The patient remains healthy 11 years after the diagnosis without relapse or new infection.

Results: Immune system evaluation revealed an isolated NKD with 7/mm^3 (0,3%) CD3$^-$ CD56$^+$ natural killer (NK), and 1943/mm^3 (88%) CD3$^+$ T cells stable during the 10 years follow up. Related to the NKD two adaptative immunological abnormalities were noted 1) an in vitro impaired lymphocyte proliferation assays after challenge with *Cryptococcus* antigens and 2) a stable TCD8 Vβ14 expanded population accounting for 50% of circulating TCD8 lymphocytes (figure). Cryptococcosis was therefore linked to a complex immunodeficiency via a lack of direct killing of *Cryptococcus neoformans* by NK cells, an inability to mount a Th1 response normally shaped by NK cells and a possible inhibition of anti-*Cryptococcus* TH1lymphocytes response in relation to the huge TCD8 Vβ14 clonotype. This case illustrates the central role of NK cells in immunity against *Cryptococcus* and confirms the tight interplay between NK cells and adaptative immunity via TH1 modulation and regulation of CD8 expansion.

Conclusions: Two practical medical conclusions can be drawn: the need to perform NK cells determination in cases of idiopathic cryptococcosis, and the need to screen the Vβ repertoire in cases of NKD in other to better understand NKD.



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Abstract 1699

One day detection of live *Mycobacterium tuberculosis* from sputum by measuring heat-induced MPT64 secretion with ultra-sensitive ELISA

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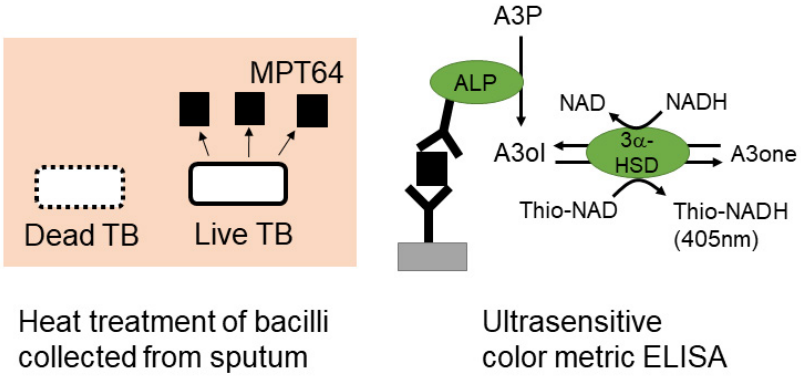
Background: Although nucleic acid amplification tests (NAATs) are now widely used, they cannot discriminate live bacilli from dead ones because nucleic acids exist in dead bacilli. Detection of only live bacilli can be achieved by only a time-consuming culture test. In the present study, we propose a de novo TB diagnosis method for the detection of only live bacilli that has the same high-detection sensitivity as a culture test and can be performed within a day.

Materials/methods: TB patient sputum was pretreated, and the specimen was heated at 46°C for 1 h to induce secretion of MPT64 protein from live *M. tuberculosis*. This protein was detected with our new ultrasensitive diagnosis method that was based on an enzyme-linked immunosorbent assay (ELISA) coupled with thionicotinamide-adenine dinucleotide (thio-NAD) cycling. We compared our data with those of a culture test (MGIT), a smear test (Kinyoun staining) and a NAAT (Xpert).

Results: The limit of detection for MPT64 in our ultrasensitive ELISA was 0.2 amoles/assay. We confirmed that heat-induced MPT64 secretion was not observed when BCG was exposed with 8 μg/mL rifampicin. Using the cutoff value of the measuring absorbance at 17 mAbs, which corresponded to ca. 330 CFU/mL in a culture method, the sensitivity was 86.9% (93/107, 95% CI: 79.0 - 92.7%), and the specificity was 92.0% (770/837, 95% CI: 89.9 - 93.7%) compared to that of MGIT. These were better than those obtained from Kinyoun staining tests and were not significantly different from those of Xpert tests. Further, the validity for drug susceptibility examination was shown by our ultrasensitive ELISA tests better than by Xpert tests because our tests detected only live bacilli.

Conclusions: A de novo, culture-free, same-day TB diagnosis method detects only live *M. tuberculosis* with a high-detection sensitivity. This method is especially useful for the patients under TB-treatment to evaluate whether it is effective or not.



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Abstract 1702

Evaluation of voriconazole therapeutic drug monitoring practice: experience of a tertiary referral centre

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Background: Therapeutic drug monitoring (TDM) is used to optimise the dosing of voriconazole. To maximize the benefit of TDM, evaluation of current TDM practice is needed. This study had three objectives: 1) to evaluate current voriconazole TDM practice by identifying patient characteristics that were associated with TDM being performed, 2) to identify potential barriers to the optimal conduct of TDM and 3) to make recommendations for practice improvement.

Materials/methods: This retrospective study was undertaken at Westmead hospital, an Australian tertiary hospital, and was approved by the local ethics committee. Medical records of inpatients who started voriconazole therapy with or without TDM between January 2017 and December 2018 were reviewed. TDM was evaluated for sample collection, turnaround time and actions taken for trough concentrations which were outside the therapeutic range of 1-5 mg/L. On-site and off-site sample analyses were compared with respect to turnaround time and costs in a scenario analysis.

Results: In total, 112 patients (median age 57 years) were included. A longer duration of voriconazole therapy rather than patient characteristics was found to predict the performance of TDM. TDM was initiated in 91 (81%) patients on a median of day 6 of voriconazole therapy with a median follow-up TDM interval of 5 days. Sample collections were frequently mistimed (n=101/253, 40%). Half (n=34/68) of the first trough concentrations were within the therapeutic range. Voriconazole dosages were adjusted for 20% (n=16/80) of trough concentrations which were outside the therapeutic range, with a follow-up measurement performed in 69% (n=11/16) of patients. Off-site sample analysis resulted in a median turnaround time of 7 days with a cost of AUD 37.10 per sample analysed. On-site implementation of immunoassay can potentially shorten the turnaround time to 3 hours and reduce the cost of TDM by up to 53%.

Conclusions: Mistimed sample collections, prolonged turnaround time and lack of recommendations when reporting results were barriers to the optimal conduct of TDM. On-site sample analysis, Bayesian software to guide dosing and antifungal stewardship are required to improve the current practice. Periodical evaluation of TDM practice should be established to ensure sustainable improvement in TDM practice.

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Abstract 1706

Extended spectrum beta-lactamase producing *Enterobacteriaceae* urinary tract infections: is cefoxitin an effective therapy?

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Background: Cefoxitin is a β-lactam antibiotic derived from substrate produced by *Streptomyces lactamdurans.* Cefoxitin resistance to β-lactamase hydrolysis is attributed to a 7α-methoxy group in the nucleus conferring activity against various bacteria including extended spectrum beta-lactamases (ESBL) producers. There is a growing interest in cefoxitin as a carbapenem-sparing agent; however, there is paucity in outcome data. Our study aim is to evaluate clinical and microbiologic cure rates for non-complicated Urinary Tract Infections (UTIs) caused by ESBL *Enterobacteriaceae* in which cefoxitin was used.

Materials/methods: We conducted a retrospective study to review all patients who were diagnosed with a UTI and received cefoxitin at our quaternary care hospital over 3 years. The primary end points were; clinical cure (defined as the resolution of urinary symptoms as documented by the treating physician) and microbiologic cure (negative repeat urinary culture if done at the end of therapy). Relapse and recurrence data were documented and defined as repeat positive urine culture and/or clinical symptoms within 2 to 4 weeks and three months respectively.

Results: During the study period we identified 26 patients with 27 infection encounters who were diagnosed with UTI secondary to ESBL producing *Enterobacteriaceae* and received cefoxitin. The sample was comprised of 18 males, mean age 66.9±18.7 years, mean weight 76.8±18.7 kg, 22 patients had UTIs with an indwelling Foley catheter, and 16 were diabetic. Identified organisms were *E.coli* (n=17) and *Klebsiella Pneumoniae* (n=10). Minimum Inhibitory Concentration (MIC) was ≤4 mg/L for all isolates except for two (MIC was 8mg/L). Cefoxitin doses ranged from 1-2 g IV q6-12 hours for mean therapy duration of 5.9±2 days. Clinical Cure was achieved in 24 of the treatment encounters (85%), and microbiological cure was confirmed in all 11 repeat cultures (100%). Five patients relapsed. Four patients had recurrence within 3 months. Mortality occurred with one patient.

Conclusions: Cefoxitin is an effective treatment for non-complicated UTIs causes by ESBL producing *enterobacteriaceae.* Randomized controlled studies are required to determine the efficacy of cefoxitin as a carbapenem-sparing agent.

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Abstract 1710

Replication of MERS and SARS Coronaviruses in bat cells offers insights to their ancestral origins

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Background: The Middle East Respiratory Syndrome coronavirus (MERS-CoV), which first emerged in Saudi Arabia 2012, has caused >2,000 cases including >800 deaths in 27 countries. Previous findings of MERS-CoV-related viruses in bats, and the ability of Tylonycteris-BatCoV HKU4 spike protein to utilize MERS-CoV receptor, human dipeptidyl peptidase 4 (hDPP4), suggest a bat ancestral origin of MERS-CoV.

Materials/methods: We developed 12 primary bat cell lines from 7 bat species, including Tylonycteris pachypus, Pipistrellus abramus and Rhinolophus sinicus (hosts of Tylonycteris-BatCoV HKU4, Pipistrellus-BatCoV HKU5, and SARS-related-CoV respectively), and tested their susceptibilities to MERS-CoVs, SARS-CoV, and human coronavirus 229E (HCoV-229E). Effort in constructing more cell lines from more relevant species and organs are on-going.

Results: 5 cell lines, including *P. abramus* and *R. sinicus* but not *T. pachypus* cells, were susceptible to human MERS-CoV EMC/2012. However, 3 tested camel MERS-CoV strains showed different infectivities, with only 2 strains capable of infecting 3 and 1 cell lines, respectively. SARS-CoV can only replicate in *R. sinicus* cells, while HCoV-229E cannot replicate in any bat cells. Bat dipeptidyl peptidase 4 (DPP4) sequences were closely related to those of human and non-human primates but distinct from dromedary DPP4 sequence. Critical residues for binding to MERS-CoV spike protein were mostly conserved in bat DPP4. Of the 5 bat cells susceptible to MERS-CoV DPP4 expression was detected, with significantly higher mRNA expression levels than those in non-susceptible cells, supporting that DPP4 expression is critical for MERS-CoV infection in bats. However, overexpression of *T. pachypus* DPP4 failed to confer MERS-CoV susceptibility in *T. pachypus* cells.

Conclusions: Our study suggested that a number of bat cell lines were susceptible to human MERS-CoV, and within those, some for camel MERS-CoV. There seems to be a correlation between susceptibility and DPP4 mRNA expression, yet other factors are at play. The broad cellular tropism of MERS-CoV should prompt further exploration of host diversity of related viruses to identify its ancestral origin. Further work is being conducted to illustrate other determinants for susceptibility and characterize the cellular response during an infection in these cell lines.

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Abstract 1713

Mass PCR testing and targeted treatment for malaria in a low transmission area in Amazonia, French Guiana

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Background: *Plasmodium vivax* (*Pv*) and *Plasmodium falciparum* (*Pf*) are the main species found in French Guiana. The major difficulty for malaria elimination in the area is the prevalence of *Pv*, which causes relapses and asymptomatic gametocyte carriers. The aim of this study was to assess the impact of PCR-based mass screen and treat (MSAT) campaigns for malaria control in the general population of a malaria endemic area.

Materials/methods: A before-after study was conducted in 13 of 16 most affected neighborhoods (2,727/4,033 inhabitants) of the most impacted municipality of French Guiana, Saint Georges de l'Oyapock. Two MSAT interventions were implemented at a one-year interval relying on PCR for malaria detection followed by treatment of malaria positive individuals. RDT or PCR-positive consenting participants received artemether-lumefantrine against *Pf* or chloroquine and, in the absence of contraindication, primaquine against *Pv*. Symptomatic malaria incidence was passively monitored through the health center from one year before the first intervention until the end of the second intervention.

Results: More than half targeted inhabitants (1,566/2,727, 57.4%) were included in the study and 1,501 participated in the first screening, of which 1,276 (81.5%) also participated in the second screening. Overall, there were 1,231 individuals with complete PCR results. During the first MSAT, the PCR-positivity rate was 6.7% (6.0% *Pv*, 0.7% *Pf* with 73% of asymptomatic carriage), compared to 2.9% (2.4% *Pv* 0.5% *Pf* with 88% of asymptomatic carriage) during the second intervention (p<0.005). All positive participants received treatment and any severe side effect was reported. During the first intervention a large seasonal malaria epidemic was reported. A significant decrease of incidence was observed by passive monitoring among study participants (95 to 43/1566 person-years, p<0,005) but not in the non-participating population (38 to 59/2467 person-years p=0.24).

Conclusions: In French Guiana, a mass PCR screening and treatment intervention was operationally feasible and could reduce *Plasmodium* sp. carriage and incidence. Limitations of this study include seasonal variations and villager mobility, which may have limited the impact of the intervention. Strategies that only target populations with RDT testing and symptomatic cases treatment alone are likely to overlook a large part of the reservoir.

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Abstract 1716

Ceftobiprole and daptomycin concentrations in valve tissue in a patient with aortic native valve endocarditis

Silvia Boni[1], Miriam Antonucci[2], Valeria Avataneo[2], Amedeo De Nicolò[2], Luigi Martinelli[3], Stefania Artioli[1], Giovanni Di Perri[2], Antonio D'Avolio*[2]

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Background: A main determinant of clinical response to antibiotic treatment is drug concentration at the infected site. Data on ceftobiprole (CFB) valve penetration are lacking. We measured CFB and daptomycin (DPT) concentrations in a native infected valve to verify their pharmacokinetic penetration and relationship with pharmacodynamic microbiological markers.

Materials/methods: One patient undergoing surgical valve substitution for native valve endocarditis (NVE) with lung and brain embolism and receiving intravenous CFB and DPT was studied. Valve and plasma specimens were collected at a variable time in the operatory day (4.00pm and 8.00pm, respectively) after CFB (500mg 8.00am and 4.00pm) and DPT (500mg 8.00am) administration. Drug concentrations were measured by high-performance liquid chromatography with tandem mass spectrometry kit for plasma (CoQua Lab srl) and a modified-method for the valve tissue evaluation. The valve tissue quantifications were performed in triplicate (in two different days), from 3 different positions on valve.

Results: The isolated microorganism was a MRSA with CFB and DPT MIC<2 mg/L and <1 mg/L, respectively. The CFB and DPT plasma concentrations were 36.2 and 14.1 mg/L, respectively and the extrapolated concentration at the operatory time were 16,4 and 19.1 mg/L for CFB and DPT, respectively; the corresponding median CFB and DPT valve concentrations were 2.26 (IQR 1.44-2.69) and 12.9 mg/L (IQR 5.51-20.9), respectively. The estimated tissue/plasma ratios for CFB and DTP were 0.14 and 0.67, respectively.

Conclusions: NVE is a serious infection with potentially fatal consequences. From the data available, we can suppose that the time above the minimum inhibitory concentration (T>MIC) was probably near to 24h in all compartments. CFB valve penetration (>14%) is not high but seems to be enough to cover MRSA CFB MIC (the patient has had a good clinical and microbiological response). For DTP, valve penetration (>67%, 12.9 mg/L) and plasma concentration (12h post-infusion) 14.1 mg/L, seems to be enough to cover MRSA sensitivity both in plasma and in tissue. DTP tissue concentration has a very high variability, probably influenced by tissue blood irroration. This is the first data on CFB valve tissue penetration, and it needs to be confirmed in other patient valve tissues.

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Abstract 1717

The effectiveness of nitrofurantoin, fosfomycin and trimethoprim for cystitis in relation to renal function

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Background: Nitrofurantoin, fosfomycin-trometamol and trimethoprim are recommended for the treatment of cystitis in primary care in the Netherlands. In patients with impaired renal function, lower urinary concentrations have been reported for all three antibiotics, which may be associated with a higher risk of treatment failure. We evaluated the effects of renal function on clinical failure rates of treatment with nitrofurantoin, fosfomycin-trometamol and trimethoprim in cystitis patients in primary care.

Materials/methods: Data was retrospectively obtained from the Julius General Practitioners' Network, consisting of 78 Dutch general practitioner (GP) practices between 2013 and 2019. Episodes were classified as uncomplicated or complicated cystitis if antibiotics were prescribed according to Dutch guideline. The estimated glomerular filtration rate (eGFR) was calculated using plasma creatinine, age and gender. Clinical failure was defined as a second antibiotic prescription for cystitis or pyelonephritis within 28 days post-prescription. We used mixed effects regression analysis, with patient and GP practice as random effects and demography, comorbidity, cystitis history as fixed effects.

Results: In 21,891 unique patients 42,473 episodes were included consisting of 31,014 uncomplicated cystitis, treated with 5 days nitrofurantoin (NF5,n=24,591), 1 dosage fosfomycin-trometamol (FT1,n=5,359) and 3 days trimethoprim (TMP3, n=1,064), and 11,459 complicated cystitis, treated with 7 days nitrofurantoin (NF7,n=10,628) and 7 days trimethoprim (TMP7,n=831). An eGFR below 60 mL/min was observed in 3,757 of 42,473 episodes (8.8%). Adjusted odds ratios (aOR) for clinical failure per 10 mL/min decrease in eGFR were 1.05 (95%CI:1.01-1.09) for NF5, 0.96 (95%CI:0.92-1.01) for FT1, 0.98 (95%CI:0.89-1.08) for TMP3, 1.05 (95%CI:1.02-1.09) for NF7 and 1.02 (95%CI:0.93-1.14) for TMP7. In patients with uncomplicated cystitis and normal renal function (eGFR ≥60 mL/min), FT1 or TMP3 resulted in more clinical failures than NF5, with aOR of 1.37 (95%CI:1.18-1.59) and 1.42 (95%CI:1.07-1.87), respectively. In patients with uncomplicated cystitis and impaired renal function (eGFR<60 mL/min), FT1 was associated with less clinical failures than NF5 (aOR 0.61,95%CI:0.39-0.95).

Conclusions: In patients with uncomplicated cystitis and impaired renal function treatment with nitrofurantoin was associated with more clinical failure than fosfomycin-trometamol. In patients with uncomplicated cystitis and normal renal function treatment with fosfomycin-trometamol or trimethoprim was associated with more clinical failure than nitrofurantoin.

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Abstract 1720

Current use of baseline chest CT in haematology patients at high risk for invasive fungal infection

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Background: Baseline chest computed tomography (BCT) in high-risk hematology patients appears to allow early diagnosis of invasive pulmonary aspergillosis (IPA) since recent studies found CT abnormalities close to admission in 36% and 31%, respectively. Distribution of BCT implementation in hematology units and the impact on patient outcome is unknown.

Materials/methods: : A web-based questionnaire was designed and disseminated via www.clinicalsurveys.net. Members of twelve international scientific bodies were invited. Estimated numbers of annually treated high-risk hematology patients, chest imaging timepoints and techniques, IPA rates, and follow-up imaging were assessed. BCT was defined as chest CT performed upon diagnosis of malignancy or hospital admission.

Results: Ninety-two of 142 participants (64%) from 43 countries answered all questions. Medical specialties included infectious diseases (n=69; 49%), hematology (n=68; 48%), microbiology (n=15; 11%), and other (n=26, 18%). Numbers of patients treated per year were estimated 5,505 acute myelogenous leukemia, 2,641 acute lymphoblastic leukemia, and 5,287 allogeneic hematopoietic stem cell transplantation.

Baseline CT was performed in 57% (n=54) of 92 hospitals. Upon diagnosis of malignancy or admission, 48% and 24% centers performed BCT, respectively. Overall, HSCT was the most frequent BCT indication (44.2%, n=42) and BCT was more frequently performed in relapsed than in *de novo* leukemia.

European centers performed BCT in 59%, whereas non-European centers did in 53%. CT was predominantly low-dose and contrast-enhanced in 38% of centers. Median estimated IPA rate was 8% and did not differ significantly between BCT centers (9%; IQR 5 - 15%) and non-BCT centers (7%; IQR 5 - 10%) (p=0.69). Follow-up CT after diagnosed IPA was performed in 98% (n=90), while only three (3.3%) centers did this at guideline-recommended timepoints.

Conclusions: In high-risk hematology patients baseline chest CT at diagnosis or admission became a standard-of-care. Randomized, controlled studies are needed to investigate its impact on patient outcome.

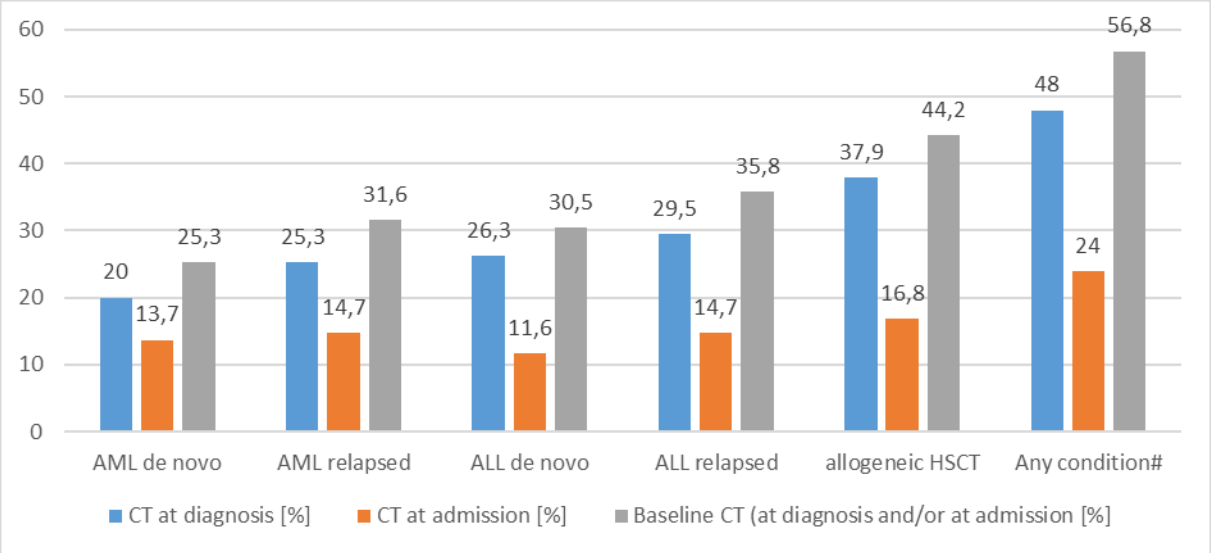

Figure 1. Baseline CT timepoints
#may be super-additive
CT=Computed Tomography; AML=Acute myelogenous leukemia; ALL=acute lymphoblastic leukemia; HSCT=hematopoietic stem cell transplantation.

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Abstract 1722

A rocky road: lessons learned from a case of disseminated *Rhodococcus hoagii* infection

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Background: *Rhodococcus* species are gram-positive bacilli that primarily infect immunocompromised patients. *Rhodococcus equi,* reclassified as *R. hoagii*, is the major pathogenic species that usually affects the pulmonary system, whereas bloodstream infections (BSI) are often catheter-related.
We describe a case of BSI where the source was a soft tissue infection mimicking Actinomycosis. The identification was established by 16S rRNA sequencing. This case underscores how *Rhodococcus* infections may be undiagnosed or misdiagnosed due to identification challenges in the routine laboratory.

Clinical presentation: A 46 year old HIV-infected man (CD4+count of 42 cell/mm^3; defaulted antiretrovirals) was admitted to hospital due to progressive dysphagia. CT scans revealed extensive necrosis of the mouth floor and neck lymphadenitis with abscesses draining via sinus tracts. *C. pseudotuberculosis* and unidentified gram-positive bacilli were initially isolated from the affected site. Follow-up culture revealed an unidentified gram-positive bacillus – confirmed by 16S rRNA sequencing as *Rhodococcus* species. TB cultures yielded *Mycobacterium intracellulare* and only anti-mycobacterial therapy was initiated at this stage.

On a subsequent admission for *C. neoformans* meningitis, a *Bacillus* species was cultured from blood.
Shortly afterwards, re-admission for pneumonia occurred. He developed a nosocomial BSI with *K. pneumoniae.* Other blood cultures during this admission showed *Bacillus* species and *Corynebacterium* species, respectively.
Dysphagia and failure of clinical improvement persisted. Multiple specimens from the neck and blood cultured *Turicella otitidis*. However, molecular methods identified them all as *R. hoagii.*

On the basis of in-vitro antibiotic susceptibility testing performed on the *R.hoagii*, the patient was commenced on imipenem, levofloxacin and rifampicin. He improved and was discharged on levofloxacin, rifampicin and other *M. intracellulare* treatment. Antiretroviral therapy was re-initiated.

Conclusions: Our case represents a disseminated infection with *R. hoagii*, with co-infection of *M. intracellulare*. Before molecular diagnostics, Rhodococcus was often misidentified as *Mycobacterium* species based on its acid-fast staining properties. The patient responded to combination therapy – recommended for at least nine months. *R. hoagii* was unidentified, misidentified or not identified to species level. This led to a significant delay in diagnosis and initiation of appropriate treatment.

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Abstract 1723

Risk factors and mortality in invasive Rasamsonia spp. infection: an analysis of cases in the FungiScope registry and from the literature

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Background: The *Rasamsonia* spp. complex comprises filamentous fungi causing pneumonia and occasionally disseminated disease in immunocompromised patients. To provide a knowledge base of risk factors and for therapeutic decisions in invasive *Rasamsonia* spp. complex infection.

Materials/methods: A literature search was performed in PubMed aiming at all reported cases of invasive infection due to *Rasamsonia* spp. (formerly *Geosmithia* spp./*Penicillium* spp.) since data base inception. These were complemented by cases from the FungiScope® registry. Cases of mere colonization were excluded.

Results: We identified 23 invasive infections due to *Rasamsonia* spp., six (26.1%) in the FungiScope® registry and 17 (73.9%) in the literature. Main risk factors were chronic granulomatous disease (n=12, 52.2%), immunosuppressive treatment (n=10, 43.5%), hematopoietic stem cell transplantation (n=7, 30.4%), graft-versus-host disease, and major surgery (n=4, 17.4%, each). Predominantly affected organs were the lungs (n=21, 91.3%), disease disseminated in seven cases (30.4%). Initial misidentification of the fungus occurred in 47.8% (n=11) and sequencing was used in 69.6% of patients (n=16) to establish definite diagnosis. Breakthrough infection occurred in 13 patients (56.5%). All patients received antifungal treatment, mostly with posaconazole (n=11), caspofungin (n=10) or voriconazole (n=9). Combination therapy was administered in 13 patients (56.5%). Susceptibility testing showed high minimum inhibitory concentrations for azoles and amphotericin B, but not for echinocandins. No preferable treatment influencing favorable outcome was identified. Overall mortality was 39% (n=9) at last patient contact while attributable mortality to *Rasamsonia* spp. was 17.4% (n=4.

Conclusions: *Rasamsonia* spp. are emerging fungi causing life-threatening infections, especially in immunocompromised and critically ill patients. Breakthrough infection occurs frequently and sequencing methods are necessary for diagnosis. Mortality is high. Treatment is challenging and clinicians dealing with this patient population should become aware of this infection.

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Abstract 1724

Emergence of novel recombinant Coxsackievirus A6 in Hong Kong

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Background: Coxsackievirus A6 (CV-A6), a member of enterovirus A in the genus Enterovirus of the family *Picornaviridae*, has recently emerged globally as serious public health threats. Since 2008, CV-A6 arose and replaced enterovirus A71 (EV-71) and CV-A16 as the main causative agents responsible for hand, foot and mouth disease (HFMD) outbreaks worldwide. Recombination is an important mechanism for genetic evolution in RNA viruses, and CV-A6 recombinant strains were reported in China, Thailand, United Kingdom and Spain. To determine whether recombination events play a role in the evolution of the emergence of CV-A6 strains in Hong Kong, CV-A6 strains isolated from hospitalized patients were sequenced. Potential recombinant CV-A6 strains were further proceed with complete genome sequencing and recombination analysis.

Materials/methods: Nasopharyngeal aspirates (NPAs) were collected from patients from regional hospitals in Hong Kong. All specimens were confirmed positive for CV-A6 by RT-PCR and partial 5' untranslated region (5' UTR) sequencing. The partial VP1, 2C and 3D regions were sequenced, and phylogenetic trees were constructed. Five CV-A6 were selected for complete genome sequencing and recombinant analysis.

Results: CV-A6 were detected positive in 40 NPAs collected from January 2010 to December 2018, and partial VP1 gene of 28 CV-A6 strains were amplified for genotyping. The phylogenetic analysis of VP1 gene revealed that CV-A6 strains circulating in Hong Kong were divided into two subgenotypes: D5 (n=24) and D4 (n=4). Subsequently, the phylogenetic analyses of 2C and 3D gene analysis showed that eight CV-A6 strains are potential recombinant strains. Complete genome sequencing was performed and four recombinant CV-A6 strains were identified. Recombination between CV-A6 and CV-A4, and recombination between CV-A6 and EV-A71 were observed in three and one recombinant CV-A6 strains, respectively. 3D gene was identified as the frequent recombination site for CV-A6 strains.

Conclusions: Recombination plays an important role in the emergence and evolution of CV-A6 strains in Hong Kong. Recombinant CV-A6 strains are generally recombinant with CV-A4 and EV-A71 strains at 3D gene.

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Abstract 1725

Interim analysis: a large-scale clinical evaluation of QMAC-DST for rapid drug susceptibility testing of *Mycobacterium tuberculosis*

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Background: The effective management of TB and MDR/XDR-TB relies upon rapid diagnosis and appropriate treatment of resistant infections. Culture-based phenotypic drug susceptibility testing (DST) methods are currently the gold standard for drug resistance detection. In the previous study, we examined the accuracy of QMAC-DST which is an automated rapid phenotypic DST system based on imaging technology. The results of the QMAC-DST for MDR/XDR-TB showed a high agreement rate compared to a conventional method, and the QMAC-DST could provide the fast result within around 1-week turnaround time. In the present study, we have been evaluating the accuracy and speed of the QMAC-DST system through a large number of clinical strains isolates collected from multi-centers. As an interim analysis, the result from 555 samples is presented.

Materials/methods: The Korean Institute of Tuberculosis (KIT, Osong, Republic of Korea) has provided laboratory services for public health centers. We conducted the conventional DST and the QMAC-DST for the 555 clinical strains which were sent to the KIT for DST from July 2019 to September 2019. Those strains were positive cultures in liquid or solid medium. The conventional DST was performed by the absolute concentration method with Lowenstein-Jensen (L-J) medium. And the QMAC-DST was performed by the automatic imaging and analyzing system with QMAC-DST panel. We compared the results of both methods and calculated the accuracy of QMAC-DST.

Results: Except for strains suspected of contamination or growth failure, The QMAC-DST for 480 clinical samples for 13 anti-tuberculosis drugs were showed a high agreement rate (98.73%) compared to conventional DST. The average time required for QMAC-DST was 7.9 days, which was much faster than conventional DST (21 days).

Conclusions: The QMAC-DST was evaluated with 555 samples out of 3000 targets. The interim results of QMAC-DST were reported 2ff3 weeks earlier than conventional DST and showed a high concordance rate. In this study, we confirmed that the QMAC-DST can provide a rapid and accurate diagnosis for effective TB treatment so that it can be an alternative DST method replacing slow conventional DST methods.

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Abstract 1726

Reactive hyperaemia measured by peripheral arterial tonometry correlates with glycocalyx degradation and the presence of sepsis in the critically ill patient

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Background: Sepsis is a life-threatening condition whose diagnose relies in markers of organic damage in the presence of infection. The endothelium is virtually present in every organ and is highly influenced by the circulating cytokines and may be responsible for the microvascular organic damage seen in sepsis. We investigated if reactive hyperaemia correlates with the presence of sepsis and whether it may be used to distinguish between septic and non-septic patients in the Intensive Care Unit (ICU).

Materials/methods: We performed a prospective study of a cohort of ICU admitted patients. Patients were accessed for endothelial dysfunction quantifying the Reactive Hyperaemia Index (RHI) using peripheral arterial tonometry and biomarkers of glycocalix degradation. Patients with infection were compared to a control group of patients without evidence of infection.

Results: Eighty-six patients were included in the study, 58 (67.4%) in the septic group and 28 (32.6%) in the control group. There were no significant clinical differences between groups except for age. The natural logarithm of RHI (Ln_RHI) was negatively correlated with cardiovascular comorbidities, disease severity and plasma levels of soluble E-selectin ($p=0.024$) and Syndecan-1 ($p<0.001$). Ln_RHI was lower in septic patients when compared with controls (0.53±0.48 vs 0.69±0.42, respectively) and multivariate analysis adjusted for age predicted that within each age group, each 0.1 unit decrease in the Ln_RHI increased the odds for infection by 14.6%.

Conclusions: Reactive hyperaemia measured by peripheral arterial tonometry seems to be closely related to endothelial glycocalix degradation and endothelial activation. Sepsis is associated with lower RHI in critically ill patients when compared to non-septic patients and RHI may be a useful tool for the diagnosis of infection in this setting, especially in an older population.

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Abstract 1728

Evaluation of the Aptima BV assay for detection of bacterial vaginosis by comParison with the BD MAX vaginal panel assay

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Background: Bacterial vaginosis (BV) is one of the most common lower genital tract conditions, of which the diagnosis is challenging due to its complex polymicrobial nature. To study the performance of the Aptima® BV assay (Hologic), 238 genital swabs were tested in parallel with the BD MAX™ Vaginal Panel (Beckton Dickinson). Both assays are nucleic acid target amplification-based, fully automated -sample in answer out- and include an internal control. Microbiome-based algorithms are used to determine BV test results.

Materials/methods: Two hundred thirty-eight swabs (97 cervical, 85 vaginal, 55 introitus, and 1 fluor) were from women ≥ 18 years (mean age 38, range 18-94) being seen by their general practitioner (symptomatic women, n=198) or for routine obstetric / gynaecological care (symptomatic and asymptomatic women n=40). Swabs were analysed by parallel testing on the same day. Two-hundred µl (BD Max) or 400 µl (Aptima) of Eswab medium were transferred to BD MAX™ UVE tubes or Aptima Specimen Transfer tubes, respectively, and tubes were placed directly on the BD MAX™ or the Panther system. At the same time, aliquots were frozen for discrepancy evaluation with the AmpliSens® Florocenosis / Bacterial vaginosis-FRT PCR kit (ATRiDA). If at least two tests were positive or negative for BV the sample was considered true positive or negative, respectively.

Results: Seventy-two samples tested positive in both assays, 133 samples negative, while 33 samples showed discordant test results. Further analysis of the discordant samples with the AmpliSens® kit yielded a BV-positive or BV-negative test result for 27 samples.

		Aptima® BV assay		
		Pos	Neg	
BD MAX™ Vaginal Panel	Pos	72	12**	84
	Neg	21*	133	154
		93	145	238

Discrepancies analysis	AmpliSens® assay				
	Pos	Neg	Intermediate	Unknown	
* Aptima® Pos BD MAX™ Neg	12	5	1	3	21
** Aptima® Neg BD MAX™ Pos	7	3	0	2	12
	19	8	1	5	33

For the Aptima assay for BV detection the number of true positives was 84, false positives 5, true negatives 136 and false negatives 7, yielding a sensitivity, specificity, PPV and NPV of 92,3%, 96,45%, 94,4% and 95,1%. For the BD MAX™ Vaginal Panel assay these values for BV were 86.8%, 97,9%, 96,3% and 92,0%, respectively. One sample yielded an invalid test result in the Aptima test, 10 samples in the BD test (6 indeterminate, 4 unresolved).

Conclusions: We conclude that the Aptima® BV assay is an easy to carry out test, suitable for the reliable detection of bacterial vaginosis.

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Abstract 1730

Effects of penicillin V on the intestinal microbiota in patients with pharyngo-tonsillitis

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Background: Increasing antimicrobial resistance is a growing threat to human health. The commensal microbiota, in particular the rich intestinal microbiota, may function as a reservoir of antibiotic resistance genes. Studies on the ecological impact of penicillin V with current dosage regimens are lacking. The objective of the present investigation was to evaluate potential impact on the faecal microbiota with focus on beta-lactam resistance.

Materials/methods: Thirty-one patients, a subset from a recent study, treated with penicillin V for 5 days (n= 14, daily dose 3.2g) or 10 days (n=17, daily dose 3.0g), contributed each with 3 faecal samples. The specimens were collected before penicillin V administration, directly after the last dose and 7-10 days after discontinuation of treatment. Samples were inoculated semi-quantitatively on non-selective and selective screening chromogenic agar plates, to study beta-lactam resistance, shift in Enterobacterales, overgrowth and shift among enterococci, colonisation with candida and Clostridoides difficile. Susceptibility testing was performed on resistant isolates. Results were analysed by Wilcoxon paired-rank sum test and Mann-Whitney U-test.

Results: The amount of Enterobacterales resistant to ampicillin and third generation cephalosporins, mainly Amp C producers, increased significantly from baseline (sample 1) to after the last dose of penicillin V (sample 2), $p<0.01$ and $p<0.05$, respectively. At follow-up (sample 3), the increase from baseline was no longer significant. There was a non-significant shift from E. coli to non-E. coli, between samples 1 and samples 2. Eight patients were newly colonised by unusual gram negative rods in sample 3. Three patients had new colonisation with Candida albicans in sample 2. One patient had moderate growth of toxin-positive C. difficile in sample 3 and symptoms consistent with C. difficile infection. No significant differences were seen between the two study groups (penicillin V for 5 or 10 days).

Conclusions: Treatment with penicillin V caused marked ecological impact on the faecal microbiota. The amount of beta-lactam resistant Enterobacterales increased significantly during the treatment period. Ecological disturbances in the microbiota were still seen 7-10 days after treatment discontinuation. These results challenges the general perception that penicillin V is an "ecological safe" agent that can be prescribed without inducing resistance.

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Abstract 1735

Genome-based surveillance of clinical vancomycin-resistant *Enterococcus faecium* reveals increased prevalence of vanB-type isolates of ST117/CT71 in German hospitals, 2010-2016

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Background: Enterococci are considered as common cause of nosocomial infections, where treatment options are limited due to intrinsic and acquired resistances. Particularly vancomycin- resistant *E. faecium* (VRE) represent a burden, since well-adapted lineages are widespread established in healthcare facilities. In recent years, the upcoming resistance to linezolid diminishes this last-line treatment option. For this study, microbiological and genome-based analyses of VRE clinical isolates were realized. VRE were collected as part of the tri-annual resistance studies of the Paul-Ehrlich-Society at 25 medical laboratories in Germany, Austria and Switzerland in 2010, 2013 and 2016.

Materials/methods: A total of 166 VRE isolates was collected. Susceptibility to 18 antibiotics was tested by applying the broth microdilution method. Resistance breakpoints were assessed according to EUCAST guidelines (v. 9.0). Whole genome sequencing was realized with Illumina technology. For high-resolution genotyping and to determine phylogenetic relations, cgMLST analyses were performed with the generated data.

Results: In 2010, 38 isolates were collected, in 2013 52 and in 2016 a total of 76. From 2010 to 2016, a change in vancomycin-resistance type from *vanA* to *vanB* was observed. 62 Different genotypes were identified and were assigned to distinct clusters in phylogenetic analysis, showing individual population composition for each study year. In total, the most abundant genotype was ST117 (45%). In 2016, the predominant lineage was genotype ST117/CT71 (n=23), showing the *vanB*-type; the predominant genotype detected in 2010 (ST192, *vanA*) was almost absent in 2016, while ST203 with *vanA*-type was present in all study years. Additionally for 2016, 8 linezolid-resistant isolates were identified, so in 2016 LVRE (*vanA* and *vanB*) had a prevalence of about 10%.

Conclusions: Structured surveys like the PEG resistance studies allow a snapshot of hospital pathogens' prevalence within a given time frame and geographical coverage. We observed the fluctuation of genetic lineages over time, like the rise of ST117 showing the *vanB*-type. cgMLST analyses determined various subtypes within ST117 such as CT71, which in turn ascertained a cross-hospital, regional or country-wide spread of distinct VRE strain types. At the same time, some lineages were present in all cohorts.

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Abstract 1743

Risk for antibiotic resistance in patients hospitalised with urinary tract infection: a matched case-control study using the French health insurance database

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Background: Antibiotic resistance rates are increasing among urinary pathogens, both in community and hospital infections, leading to increased therapeutic difficulties, and resulting in worse clinical and economic outcomes. Several risk factors of acquiring antibiotic-resistant urinary tract infections (UTIs) have been highlighted by previous studies, but few are universally accepted. This study aims to assess the risk factors for infection due to antibiotic-resistant bacteria (ARB) in patients hospitalized for an UTI, using the comprehensive French national health insurance database (SNDS).

Materials/methods: Incident hospitalizations for UTI diagnosis, due to an *Escherichia coli*, *Klebsiella pneumoniae*, *Staphylococcus aureus, Pseudomonas aeruginosa* or an Enterococcus were identified from Jan 1st 2015 to Dec 31 2017. Only stays for which bacteria could be determined were included. Cases (UTIs due to ARB) were matched to controls (UTIs without ARB) according to age (± 5 years), gender, infection code, year of admission, and bacterial species. Healthcare-associated (HCAI) and community (CAI) infections were studied separately, and conditional multivariate logistic regressions were stratified by gender.

Results: For all three years, 9759 cases were identified from which 6606 CAIs and 3001 HCAIs were matched with controls. For all infections, consumption of antibiotic in the last 3 months was a risk factor for ARB UTI, with an OR reaching 3.84 [3.04–4.85] for men with CAI who had received ≥ 3 antibiotics. The risk increased when the last antibiotic taken was broad spectrum, whether associated with a previous UTI or not (OR 2.59 [2.15–3.11] *vs*. 1.35 [1.18–1.53], respectively). Having undergone a surgical procedure on the urinary tract during the last 3 months increased the risk for men with CAIs (OR 1.39 [1.14–1.69]) and for women with HCAIs (OR 1.72 [1.37–2.17]). Staying in ICU > 7 days in the past 3 months increased slightly the risk for men with HCAIs (OR 1.44 [1.03–2.02]). Diabetes, immunosuppression, neurological disease, urinary tract diseases, and pregnancy had no impact on ARB infection.

Conclusions: This study confirms the importance of broad antibiotic consumption on the risk of UTI with ARB, and the importance of prevention during surgical procedure on the urinary tract, and long ICU stays.

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Abstract 1744

Characterisation of the microbial community in patients with pharyngeal gonorrhoea infection

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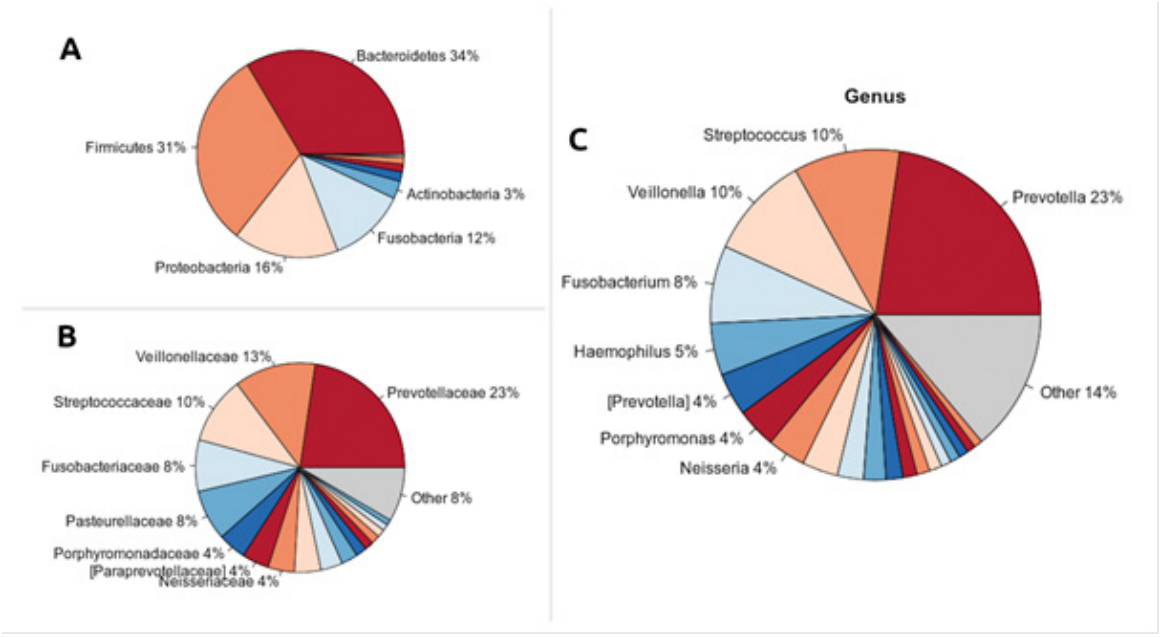
Background: Pharyngeal gonorrhea is a common sexually transmitted infection among 'men having sex with other men' (MSM). To appropriately survive and persist in the oro-pharynx, *Neisseria gonorrhoeae* (NG) has to compete with the local commensal bacteria. The aim of this study was to characterize the pharyngeal bacterial community profiles during an ongoing NG infection in a well-selected cohort of MSM.

Materials/methods: A total of 70 HIV-negative MSM reporting condomless oral intercourse were enrolled: in particular 45 non-infected subjects and 25 patients with pharyngeal gonorrhoea were considered. Starting from pharyngeal swabs, the pharyngeal microbiome composition was analysed through sequencing of hypervariable V3-V4 regions of the 16S rRNA gene. Bacterial biodiversity and distribution were characterized via alpha and beta diversity evaluations. A functional prediction of the bacterial metabolic pathways was performed using PICRUSt software and KEGG pathways database. Differences in abundances of bacterial taxa and functional pathways among experimental groups were analyzed by Mann-Whitney t-test, using MATLAB software (Natick, MA, USA). p-values < 0.05 were considered as significant for each statistical analysis.

Results: The pharyngeal microbiome of all subjects was dominated by *Prevotellaceae*, *Veillonellaceae* and *Streptococcaceae* families. Patients with pharyngeal gonorrhoea exhibited significantly higher levels of *Spirochaetaceae* (in particular, bacteria belonging to *Treponema* genus) compared to non-infected individuals. Considering low-abundance bacterial genera, an imbalance between aerobe and anaerobe microorganisms was observed: the pharyngeal microbiome of NG-positive patients was richer in several anaerobes (e.g. *Parvimonas*, *Peptococcus*, *Clostridiales*, *Prevotellaceae*) and poorer in various aerobe genera (i.e. *Pseudomonas*, *Escherichia*). The metabolic functional prediction indicated a more abundant involvement of D-glutamine and D-glutamate metabolism, carbohydrate metabolism, as well as a greater activation of the energy metabolism in patients with pharyngeal gonorrhea.



Conclusions: Information about the bacterial composition of the pharyngeal microbiome in case of gonorrhoea could shed light on the pathogenesis of the infection and open new perspectives for the prevention and control of this condition.

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Abstract 1745

Associations of HLA genotypes with adverse events of hepatitis and skin rash during treatment of latent tuberculosis infection

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Background: Treatment of latent tuberculosis infection (LTBI) is a cornerstone strategy for control of TB. Drug adverse events (AE) leading to treatment interruptions compromise treatment of LTBI. Considerable progress has been made in identifying genetic risk factors for idiosyncratic adverse drug reactions. This study aims to identify human leucocyte antigen (HLA) risk alleles associated with serious drug AE, hepatotoxicity and skin rash, which may be used as a tool to predict AE prior to treatment.

Materials/methods: We prospectively recruited patients who received LTBI treatment from Jan 2018 to Dec 2019, in Taiwan, across 7 hospitals. Whole blood was drawn for HLA typing using the HLAssure SE SBT Kit (TB Diagnostics Ltd) using DNA-based methods for determination of HLA alleles using PCR amplification with sequence based typing. Patients were followed up at baseline, week 2, 4, 8 and 12 for adverse events and liver function testing, while under 3 months isoniazid-rifapentine treatment (3HP) and followed monthly after 8 weeks while under 9 months of isoniazid (9H) or 4 months of rifampin (4R) treatment.

Results: 216 patients were enrolled, 106 women, 110 men, average age 54.3± 15.5 years. 131 were TB contacts, 36 were candidates for transplantation and 23 were candidates for anti-TNF alpha blocker treatment. Treatment regimens were 3HP in 166 (76.9%), 9H in 45 (20.8%) and 4R in 5 (2.3%). AE occurred in 134/216 (62.0%), of which 117 were on 3HP and 16 on 9H and 1 was on 4R. AE of at least grade 2 occurred in 37 (17.1%). The most common AE include fatigue (31.5%), dizziness (27.3%), nausea (17.6%), fever (13.0%), myalgia (11.1%), hepatitis (10.2%), anorexia (7.4%), pruritis (10.2%), skin rash (9.3%), gastrointestinal upset (5.1%), limb numbness (5.1%) and diarrhea (2.3%). Associated genotypes for hepatitis included HLA-*A*0101, A*0201, A*0203, B*4006*. Associated genotypes for skin rash included HLA-A**0101, A*3501*.

Conclusions: Several HLA genotypes are associated with serious adverse events of hepatitis and skin rash in patients undergoing treatment of LTBI. Further investigations are required to validate these risk alleles to predict AE in a larger population undergoing treatment for LTBI.

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Abstract 1750

Diversity and therapeutic potential of Klebisella pneumoniae bacteriophages and their depolymerases: genomics and enzymatic activity

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Background: *Klebsiella pneumoniae* has become a significant health threat in hospital settings. The rampant use of antibiotics has promoted the emergence of multidrug resistance(MDR) strains, particularly carbapenem-resistant and extended-spectrum-beta-lactamases(ESBL) producers. The unavailing use of current antibiotic treatments have prompted great interest in alternative treatments such as phage therapy. Lytic bacteriophages are considered an effective antidote against MDR pathogens for their ability to precisely adhere and degrade bacterial capsular polysaccharide, which acts as a protective layer to the bacterial cell and contributes to its pathogenicity. In this study, we have isolated and identified a large collection of obligately lytic *K.pneumoniae* phages that produce capsule depolymerases, enzymes that hydrolyse *Klebsiella* capsules. We conducted genotypic and phenotypic analyses to characterise these phages by studying their putative depolymerases genes against published homologues and over-expressing these enzymes to study their efficacy against MDR *K.pneumoniae,* respectively.

Materials/methods: The genomic DNA of *K.pneumoniae* phages(n=59) extracted by PCI/SDS extraction were sequenced by Illumina NexteraXT technology and assembled using various bioinformatics tools. The putative depolymerase genes were identified against published genomes of *K.pneumoniae* phages using a custom, in-house phage protein database. Homologues were identified using HHsearch which conducts a profile similarity searching based on protein function prediction. To examine the activity of these enzymes, the identified genes were cloned into pEXP5/TOPO vector and over-expressed using the Expressway cell-free *E.coli* expression system. The His-tagged proteins were analysed by SDS-PAGE and then purified using the HisPur-Ni-NTA purification kit.

Results: We successfully isolated and characterised 59 Caudovirales, obligately lytic *K.pneumoniae* phages consisting of the most common tailed phages *Siphoviridae*, *Podoviridae* and *Myoviridae*. We identified 33 putative depolymerase genes in 26 of our phages using stringent HHsearch criteria which showed similarity to several distinct capsular depolymerases such as hydrolases and lyases. Subsequently, eight putative structures were selected and five successfully cloned and over-expressed. SDS-PAGE analysis showed clear bands at expected sizes. The recombinant proteins were purified using nickel-affinity spin columns and the eluted fractions analysed by SDS-PAGE gel were pooled for further studies.

Conclusions: Characterization of novel depolymerases from our collection of *K.pneumoniae* phages may prove useful for effective treatment against MDR strains.

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Abstract 1755

Evaluation of a new commercial disc susceptibility kit for detection and differentiation of carbapenemases produced by Enterobacterales

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Background: The MASTDISCS® Avibactam Combi set for OXA-48 detection and carbapenemase screen is a kit comprising 3 discs. Disc A contains temocillin with KPC and MBL inhibitors; Disc B contains temocillin plus avibactam and Disc C contains a penem antibiotic. The kit is intended to allow detection of carbapenemase-producing Enterobacterales (CPE) and differentiation of isolates with OXA-48-like enzymes from those with KPC or metallo-ß-lactamase (MBL). We describe here the first evaluation of this assay using standard EUCAST / CLSI methodology.

Materials/methods: The kit was evaluated with a diverse collection of 208 well characterised Enterobacterales including carbapenemase-producers (CPE; *n* = 159), isolates with ESBL and/or AmpC ß-lactamase (*n* = 47) and two control strains. Susceptibility testing was performed using EUCAST methodology on Mueller-Hinton agar. After overnight incubation, inhibition zone diameters were measured and the presence of carbapenemases was inferred following the kit instructions.

Results: All of the CPE isolates (*n* = 159) were correctly assigned as being carbapenemase-producers (sensitivity: 100%; specificity: 92%). 4/49 other isolates were incorrectly assigned as carbapenemase-producers including isolates with TEM-10, LAT and two isolates with DHA-1. 61 out of 62 isolates with OXA-48-like enzymes were correctly assigned as OXA-48-like producers with one isolate inferred to be a producer of KPC or MBL. Of 97 isolates with KPC or MBL, all but one were correctly assigned as KPC/MBL producers. A single isolate with a combination of carbapenemases (VIM and OXA-48) was assigned as an OXA-48 producer. Finally, one isolate of CPE with NMC-A carbapenemase was falsely assigned as KPC/MBL.

Conclusions: The kit performed very well as a screening test with a challenging set of bacterial isolates. Most importantly, the presence of a carbapenemase was predicted with absolute sensitivity (100%) and high specificity (91.8%). Only 4 out of 49 non-CPE would require additional investigation as possible CPE – and the vast majority of these 49 isolates expressed ESBL or AmpC activity. This combination of 3 discs could be included with other antimicrobials for routine testing of Enterobacterales in clinical laboratories using EUCAST methodology.

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Abstract 1757

Impact of corticosteroids on alveolar macrophage interaction with mucorales

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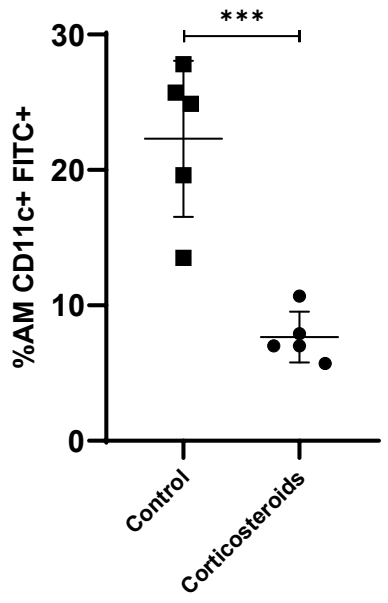
Background: Alveolar macrophages (AM) are lung first line of defence against moulds from the *Mucorales* order. They are able to control inhaled spore growth. Since corticosteroid use is a known risk factor for mucormycosis, the aim of this study was to decipher the role of corticosteroids on AM phagocytic and killing functions using a new *ex vivo* model.

Materials/methods: Male BALB/c mice were untreated or treated with 500 mg/kg of cortisone acetate at day 1 and 3 before AM collection through bronchoalveolar lavage. AM from untreated and corticosteroid-treated mice were then exposed to *Lichtheimia corymbifera* spores at a ratio of 1:5 in DMEM without phenol red in a 96-well plate at 37°C with 5% C02. Fungal growth was assessed using optical densities measured by spectrophotometer each hour for 48 hours at 800 nm. Flow cytometry was used for phagocytosis assay. After 1 hour of co-incubation, AM and spores were labelled with antibodies anti-CD11c+ and FITC, respectively. AM CD11c+FITC+ were consider having phagocytized spores. Statistical comParisons were performed using Mann-Whitney and Fisher tests.

Results: Absorbance of wells containing corticosteroid-treated AM was significantly higher than wells with untreated AM from 24h of coincubation with spores (0,219 ± 0,007 vs. 0,200 ± 0,003p=0.023). The difference in fungal growth persisted at 48h (p=0.001). Corticosteroid-treated AM showed a lower proportion of AM CD11c+FITC+ compared to that of untreated AM (7.6% vs 21.5%, p<0.001, figure 1.).

Conclusions: Corticosteroids enhanced fungal growth of *L. corymbifera* through AM phagocytosis alteration in our *ex vivo* model. Further studies are ongoing assessing killing functions of AM in this model.



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Abstract 1758

Is strongyloidiasis currently endemic in Croatia?

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Background: Due to its low prevalence and various clinical presentations, the *Strongyloides stercoralis* infection in temperate zones can be easily overlooked. As the majority of symptomatic cases are diagonosed during the stage of chronic infection reactivation in immunosuppressed hosts, with unknown time of primoinfection, current endemicity in European countries is difficult to assess. The epidemiological and clinical burden of the disease in Europe has not been well studied and there have been no such studies in Croatia yet. Knowing local epidemiological circumstancies is important in managing immunosuppressed persons and in transplant medicine. This study explored the epidemiological and clinical features of patients with strongyloidiasis, with particular aim to find elements for current endemicity of the disease.

Materials/methods: A retrospective descriptive study was performed that included patients of both genders and all ages treated for strongyloidiasis from January 2010 to May 2019 at the University Hospital for Infectious Diseases in Zagreb, Croatia. The diagnosis was made directly (by light microscopy of fecal samples after salinic provocation, three stool samples for parasites and ova, and/or tissue or duodenal aspirate samples), or indirectly by blood serology (in 83.1 and 16.9% of patients, respectively). Statistical analysis was done.

Results: Among 65 patients with strongyloidiasis, 60% were men, and 78.5% were aged 50-79 (range 17-82 y.; average: 62 y.). The number of patients significantly increased over the study period (p=0.013). Clinical presentations were: asymptomatic eosinophilia (41.5%), chronic symptomatic disease (33.9%), hyperinfection (6.1%) and acute primoinfection (18.5%). Altogether 20 patients (30.8%) were immunosuppressed (9 by corticosteroids, 4 cytostatic drugs, 7 immune-debilitating illness); four developed hyperinfection, with two lethal outcomes. The initial therapy was: albendazole in 71.7% of patients, 13.3% thiabendazole, 13.3% ivermectin, 1.7% mebendazole. Six patients (9.2%) received repeated treatment. The parasitologic cure rate between albendazole and ivermectin group was equal (p=0.0878) (lost to follow up: 48.8% in albendazole and 25% in ivermectin group).

Conclusions: Records of patients with acute primary infection confirm current endemicity for **s**trongyloidiasis in continental Croatia, and immunosuppressed travellers to this region should be advised to take precaution measures. Patients undergoing immunosuppression and organ donors from Croatia should be screened.

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Abstract 1764

Epidemiology of *Clostridioides difficile* infections among hospitalised community-acquired pneumonia patients who received empiric treatment with ceftriaxone plus a macrolide

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Background: *Clostridioides difficile* infection (CDI) among hospitalized community-acquired pneumonia (CAP) patients receiving ceftriaxone + macrolide (CTX+M), the most commonly prescribed CAP regimen, is under-researched.

Materials/methods: This is a retrospective study (2012–2015) of hospitalized patients (≥18 years) in the MedAssets database with primary discharge diagnosis of CAP; patients received CTX+M on Days 1–2, had no CDI admitting diagnosis, and had ≥1-year enrollment before index date. Patients with an ICD-9 code for CDI ≤60 days from index admission for CAP were identified and further stratified by Charlson Comorbidity Index (CCI)/Pneumonia Severity Index (PSI) risk scores from diagnosis codes. CDI incidence was tabulated across CCI/PSI categories.

Results: In total 278/33,173 (0.8%) identified patients had a CDI diagnosis ≤60 days after index admission. CDI incidence among CTX+M CAP patients was similar to CAP patients who received a fluoroquinolone on Days 1–2 of hospitalization (1.1%). Among CTX+M patients, CDI incidence in bivariate analyses was: age ≥65/<65 (1.0%/0.5%), prior/no prior CAP (1.3%/0.8%), cancer/no cancer (1.5%/0.7%), coronary heart disease (CHD)/no CHD (1.1%/0.6%), congestive heart failure (CHF)/no CHF (1.4%/0.7%), acute respiratory failure (ARF)/no ARF (1.5%/0.7%), dementia/no dementia (1.2%/0.8%), immunocompromising conditions (IC)/no IC (1.4%/0.9%), renal failure (RF)/no RF (1.4%/0.7%), and prior versus no hospitalization in past year (1.5% versus 0.8%). CDI incidence increased with increasing CCI (0 [0.4%], 1 [0.6%], 2 [0.9%], and ≥3 [1.2%]), and PSI class (≤2 [0.2%], 3 [0.9%], 4 [1.2%], and 5 [2.2%]). In multivariate analyses, PSI class, ARF, and CHD were independently associated with CDI; in a multivariate analysis that excluded PSI, age ≥65, ARF, and CHD, IC, and RF were independently associated with CDI (P<0.05, all analyses).

Conclusions: Certain CAP patient populations empirically receiving CTX+M may be at elevated risk for CDI. High-risk populations identified in this analysis are consistent with those identified in prior CDI risk-factor studies. Whether alternative antibiotics with a lower propensity to cause CDI than CTX-M can reduce this observed risk of CDI warrants further investigation.

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Abstract 1765

Clinical feasibility of simultaneous microdialysis of voriconazole and its N-oxide metabolite at target site demonstrated by *in vitro* investigations

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Background: Antifungal resistance is globally rising and the demand for rational and effective dosing regimens with antifungals such as voriconazole (VRC) thus intensifies. Currently, detailed knowledge of VRC pharmacokinetics (PK) is lacking, resulting in inadequate exposure or adverse events in patients. Application of microdialysis (μD), a minimally invasive sampling technique, in clinical studies, allows for determination of unbound drug concentrations at target site. However, metabolite concentrations are frequently of equal interest, as they contribute to efficacy, alter the PK of the parent drug or cause adverse events. Therefore, in this *in vitro* study, VRC and its *N*-oxide (NO) metabolite were chosen to investigate the feasibility of simultaneous μD of drug and drug metabolite prior to *in vivo* studies.

Materials/methods: CMA63 μD catheters (n=4) were placed in a static *in vitro* microdialysis system and perfused with Ringer's solution (RS). The medium consisted of RS containing (i) VRC, (ii) NO or (iii) VRC and NO combined at different concentrations ranging from 0.010 to 3.0 μg/mL. Relative recovery (RR) was determined as the ratio of the respective VRC or NO concentration in microdialysate and medium. Quantification was performed using a LC-MS/MS assay.

Results: Overall, mean RR of (i) VRC was 87.8% (95% CI: 87.0 – 88.7%, n=85) and did not change significantly when simultaneous μD with NO was performed ((iii) 88.4% (95% CI: 87.2 – 89.6%, n=82)). Non-significant were also the differences in the mean RR of NO with (ii) 91.7% (95% CI: 90.3 – 93.1%, n=85) in the absence and (iii) 89.8% (95% CI: 88.6 – 91.1%, n=82) in the presence of VRC.

Conclusions: The RR of VRC and NO were high, reproducible and independent of each other *in vitro*. Thus, the results provide a solid basis for unbiased measurements of target site concentrations *in vivo*. Since metabolites cannot be administered to humans, the substance-specific catheter calibration using retrodialysis must be replaced. In this regard the comparable RR of VRC and NO indicate the feasibility of VRC retrodialysis as surrogate to back-calculate the tissue fluid concentrations of NO. Ultimately, incorporating knowledge of target site PK into clinical decisions will contribute to the optimisation of dosing regimens.

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Abstract 1768

Prevalence and risk factors of inappropriate use of intravenous and urinary catheters in surgical and medical patients

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Background: Inappropriate use of catheters is common and associated with adverse patient outcomes, such as healthcare-associated infections. We previously conducted a successful project, entitled the RICAT-study, to reduce inappropriate use of intravenous and urinary catheters in medical wards. Broad-scale implementation should be started if inappropriate use is a hospital-wide problem. The current objective was to compare surgical and medical wards, and determine risk factors for inappropriate catheter use.

Materials/methods: We performed a prospective observational study from October, 2017 to May, 2018 in surgical wards of two university hospitals. We observed patients every other week for seven months, and assessed inappropriate use of intravenous and urinary catheters. Inappropriate use was compared with non-surgical wards of the RICAT-study. Primary outcomes were the percentages of inappropriate use of peripheral intravenous catheters (PIVCs) and urinary catheters on the days of data collection.

Results: We included 409 surgical patients (mean age 59.2 years; SD 15.3, 151 (37%) female) and compared this with 1781 medical patients (mean age 64.8 years; SD 17.6, 842 (47%) female). Inappropriate use occurred in 36 (8.5%) of 425 peripheral intravenous catheters in 373 surgical patients, compared to 400 (22.9%) of 1747 peripheral intravenous catheters in 1665 medical patients. This represents a difference of 14.4% (95% CI 11.1% to 17.8%; P < 0.001). Inappropriate use of urinary catheters occurred in 14 (10.4%) of 134 surgical patients, compared to 105 (32.4%) of 324 medical patients, a difference of 22.0% (95% CI 14.7% to 29.2%; P < 0.001). The main risk factor for inappropriate use of peripheral intravenous catheters was admission in medical wards; odds ratio 3.50 (95% CI 2.15 to 5.69), which was also one of the main risk factors for urinary catheters; odds ratio 2.75 (95% CI 1.36 to 5.55).

Conclusions: Inappropriate use of catheters is more common in medical wards compared to surgical wards. Prevention strategies to reduce healthcare-associated infections should primarily focus on sites with high prevalence of inappropriate use.

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Abstract 1772

Dalbavancin provides a second-line option for patients who fail conventional on outpatient parenteral antimicrobial therapy (OPAT): a case series in Aberdeen

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Abstract third-party references: Supported by NHS Grampian and NHS Scotland.

Background: Aberdeen Royal Infirmary's outpatient parenteral antimicrobial therapy (OPAT) service treats a variety of infections across specialties. Although OPAT is effective for many patients, some do fail on first-line therapy and so require further antibiotics. Dalbavancin, a second-generation lipoglycopeptide bactericidal antibiotic that is active against susceptible Gram-positive pathogens and can be administered as just two doses on days 1 and 8, provides a second-line option.

Materials/methods: The OPAT team report a cohort of 15 patients from a larger case series of 202 patients with skin and soft tissue infections, in whom dalbavancin was used as second-line therapy after previous antibiotic failure (Table 1).

Results: The 15 patients had failed on a variety of previous antibiotics, including teicoplanin (n=1), daptomycin/ceftazidime (n=1), flucloxacillin/tigecycline (n=1), daptomycin (n=4), clindamycin (n=2), ceftriaxone/teicoplanin (n=1), doxycycline (n=2), co-trimoxazole (n=2) and daptomycin/ciprofloxacin (n=1). Fourteen patients were given 1,500 mg dalbavancin as two doses – alone or in combination with clindamycin (n=2), ciprofloxacin (n=1) or doxycycline (n=1). One patient received 1,000 mg dalbavancin. In all 15 cases, the infection resolved, with three admissions prevented.

Conclusions: For patients with skin and soft tissue infections who fail on first-line antibiotics in the OPAT setting, dalbavancin provides an effective, convenient and potentially cost-saving second-line option.

Table 1 Case series: patient histories.

Patient	History
9	• Leg cellulitis
13	• Bilateral leg cellulitis
18	• Apron infection and leg cellulitis
54	• Enterococcal bacteraemia
55	• Staphylococcus aureus bacteraemia
83	• Skin and soft tissue infection (flare up of pyoderma gangrenosum)
85	• Right groin abscess
105	• Skin and soft tissue infection
108	• Skin and soft tissue infection
128	• Skin and soft tissue infection (left foot ulcer)
136	• Skin and soft tissue infection
148	• Skin and soft tissue infection (apron cellulitis)
156	• Skin and soft tissue infection (multiple infected pressure sores; Group C streptococci and *Pseudomonas*)
177	• Skin and soft tissue infection
196	• Skin and soft tissue infection

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Abstract 1773

Multiple evaluation of surgical antimicrobial prophylaxis in Japanese university hospitals

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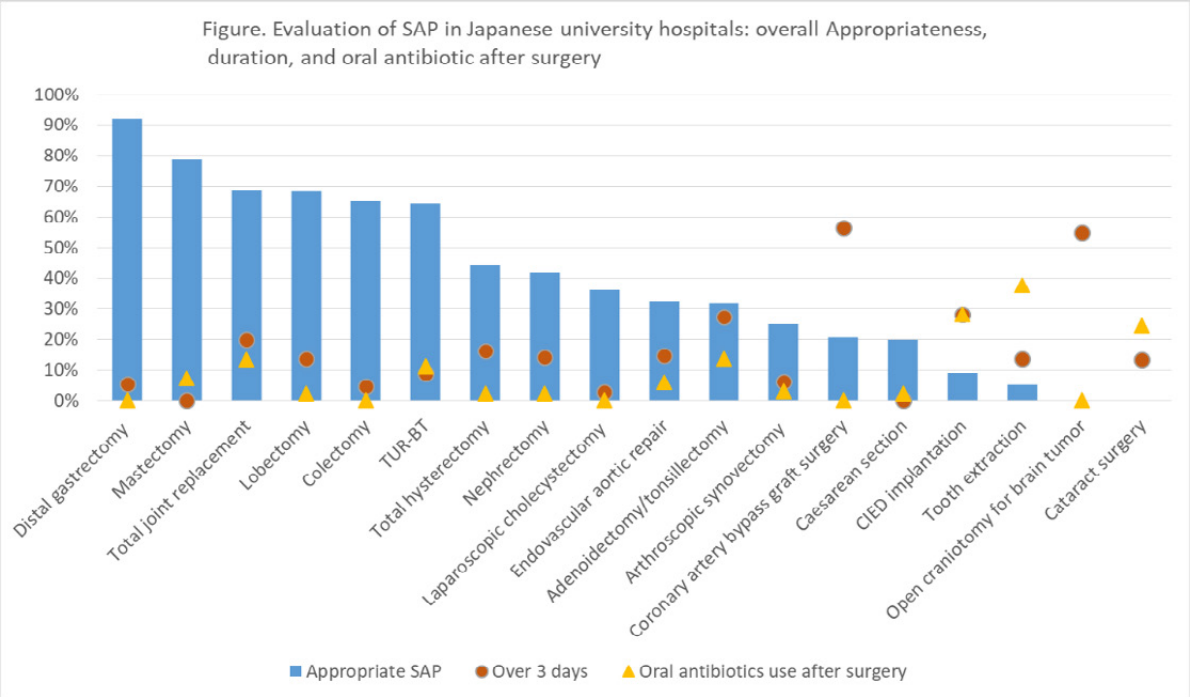
Abstract third-party references: On behalf of the Sectional Meeting of Clinical Research and Data Collection, Japan Infection Prevention and Control Conference for National and Public University Hospitals.

Background: Optimal surgical antimicrobial prophylaxis (SAP) can reduce surgical site infections, cost, and adverse events. In Japan, overall evaluation of SAP have not been performed. The purpose of this study was to reveal the adherence of Japanese Clinical Practice Guidelines for antimicrobial prophylaxis in surgery (JCPGL-AP), which was published in 2016, and to extract problems about SAP in Japanese university hospitals.

Materials/methods: This study was performed at 16 university hospitals (including 1 dental hospital). A total of 18 surgeries performed to over 18 year-old patients were selected to evaluate adherence of JCPGL-AP. Maximum 3 cases per each surgery within 4 weeks were collected from September to December 2018. To evaluate appropriateness of SAP, following items were surveyed: choice of antimicrobials during/after surgery, timing of administration before/during surgery, and duration of SAP. Surgeries were defined as appropriate SAP when all items were adhered to JCPGL-AP. Ophthalmologic- and neuro-surgeries were not listed in JCPGL-AP, thus open craniotomy and cataract surgery were excluded to evaluate the antibiotics choice and duration of SAP.

Results: A total of 688 cases were included in this study. Collected cases ranged from 22 to 45 (median 42) by the surgery, and 3 (dental hospital) to 54 (median 47) by the hospital, respectively. Percentage of appropriate items were as follows: choice of antimicrobials during surgery (467/601, 77.7%) / after surgery (475/601, 79.0%), timing of administration before surgery (632/664, 95.1%) / during surgery (612/665, 92.0%), and duration of SAP (375/601, 62.4%). Figure shows the percentage of appropriate SAP (281/601, 46.8%), duration of SAP over 3 days (115/688, 16.7%), and oral antimicrobial use after surgery (57/688, 8.3%). Percentage of appropriate SAP of general university hospitals ranged from 20.0% to 76.9% (median 48.8%).

Conclusions: Adherence rate of JCPGL-AP were significantly differed among surgeries and university hospitals. Oral Antimicrobial use after surgery and longer duration of SAP were seen in specific surgeries. Data of SAP about more surgeries and from community hospitals are necessary to reveal real-world SAP in Japanese hospitals.



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Abstract 1774

Contact effect of a Methylobacterium sp. extract on biofilm of a *Mycobacterium chimaera* strain isolated from a 3T heater-cooler system

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Abstract third-party references: Funded by a grant from the Instituto de Salud Carlos III (PI18/01068).

Background: *Mycobacterium chimaera* is an opportunistic, slowly growing, non-tuberculous mycobacterium currently gaining in importance due to the rise in mycobacteremia cases provoked by a strain that contaminates the 3T heater-cooler device (HCD) extracorporeal membrane oxygenator (ECMO). The aim of this study was to evaluate the effect of pretreating a surface with a *Methylobacterium sp.* CECT 7180 extract to inhibit the biofilm development of *M. chimaera* ECMO strain.

Materials/methods: The extract of the *Methylobacterium sp.* CECT 7180 was performed according to García-Coca *et al*. (*J Antibiot* (Tokyo). 2019 Sep 3.). The effect of this extract on biofilm development of *M. chimaera* ECMO was evaluated at 24, 48, 72, 96, and 120 h using hydrophobic uncoated sterile slide 24-well plates (Ibidi GmbH, Martinsried, Germany) according to the methodology described previously by Muñoz-Egea *et al*. (*Appl Environ Microbiol*. 2013 Feb; 79(3): 1065–1067). Pretreatment consisted of treating at room temperature for 15 min with 0.3 ml of PBS (control) or with 0.3 ml of *Methylobacterium sp.* CECT 7180 extract. After 15 min, the supernatant was removed and each well was washed once with PBS. Four parameters were studied: covered surface (%), thickness (µm), viability (%) and relative autofluorescence (%). Each condition was performed by triplicate.
The statistical data were analyzed by nonparametric pairwise comParisons using the nonparametric Mann-Whitney test with a level of statistical significance of $p<0.05$. The values are cited as median and interquartile range.

Results: The results obtained are represented in Figure 1.

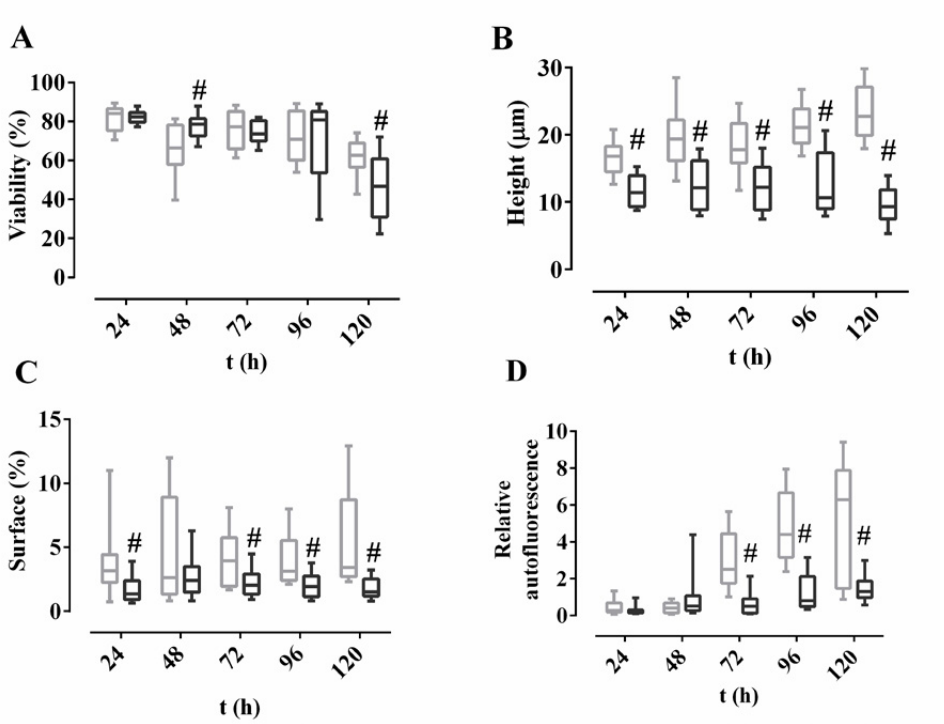

Figure 1. *M. chimaera* ECMO biofilm development over time on a control surface (gray) and on a surface treated with *Methylobacterium* extract (black). The four parameters evaluated were mycobacterial viability (A), biofilm height (B), biofilm covered surface (C), and relative autofluorescence (D). Bars indicate tenth and ninetieth percentiles. #: *P*-value < 0.001 for Wilcoxon test between control surfaces and surfaces treated with *Methylobacterium* extract. The bar represent 10th and 90th percentile.

Conclusions: In conclusion, exposing a surface to the *Methylobacterium sp.* Extract inhibits *M. chimaera* ECMO biofilm development. This extract could be used as a pre-treatment prior to disinfection protocols for equipment contaminated with mycobacteria

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Abstract 1775

NDT80 transcription factor acts as a repressor of *Candida parapsilosis* virulence attributes

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Background: *Candida parapsilosis* is a predominant species within non-albicans yeast responsible for invasive candidosis among immunocompromised patients. In fact, the prevalence of *C. parapsilosis* results from its notorious capacity to persist in the hospital environment for long periods. This ability is associated with its propensity to adhesion and form biofilm. In *C. albicans*, Ndt80 is one of the transcription factors that controls biofilm formation, hyphal growth and expression of genes related with cell wall organization. In *C. parapsilosis*, Ndt80 was associated with biofilm formation, however, its mechanistic role remain unveiled. This study aimed to understand the role of *NDT80* - CPAR2-213640 in *C. parapsilosis* virulence attributes.

Materials/methods: From *C. parapsilosis* BC014S strain two independent lineages lacking one (*ndt80Δ* – NG2 strain) or both (*ndt80ΔΔ* - EF16 strain) copies of CpNDT80 gene were generated using the *SAT1*-Flipper cassette. *ndt80Δ* and *ndt80ΔΔ* adherence to polystyrene microspheres (as a representative of abiotic surface) was quantified using a flow cytometric adhesion assay. Biofilm formation was also quantified by two independent methods: CV staining and dry weight. Gene expression of a set of transcription factors recognized as regulators of virulence factors (*ALS7*, *ALS3*, *CZF1*, *UME6*, *GZF3*, *CPH2*, *EFG1*, *BCR1, ACE2, STP3, CWH41, OCH1, RHR2* and *MKC1*) in *C. parapsilosis* were assessed by RT-qPCR. Using the murine macrophage cell line RAW264.7, the interaction of fungal-host immune system was characterized through macrophage fungal internalization and macrophage killing.

Results: Deleting *NDT80* substantially changed colony and cell morphologies from smooth and yeast-shaped to crepe and pseudohyphal elongated forms. Adherence to polystyrene microspheres and biofilm formation were enhanced in both *ndt80Δ* and *ndt80ΔΔ* mutants comparatively to wild type strain. Additionally, we identify *NDT80* as a repressor of *ALS7*, *UME6*, *CPH2*, *CWH41*, *ACE2* and *MKC1* transcription factors, being overexpressed in *ndt80ΔΔ* strain and associated with the trigger of virulence attributes exhibited by this strain. Ultimately, *ndt80ΔΔ* mutants, in their natural pseudohyphae phenotype, were more efficient in macrophage killing.

Conclusions: Our findings clearly demonstrate Ndt80 as a repressor of *Candida parapsilosis* virulence attributes (morphogenesis, adhesion and biofilm formation). Interestingly, phenotypes exhibited by *ndt80ΔΔ* mutants also confer enhanced ability to neutralize immune system response.

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Abstract 1779

Cross-platform comParison of one qPCR assay with four leading technologies and six master mixes for the detection of *Pneumocystis jirovecii*

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Background: *Pneumocystis jirovecii* is a fungus responsible for severe pneumonia in immunocompromised patients. Quantitative real-time PCR (qPCR) performed on respiratory samples is essential to detect and quantify this non-cultivable pathogen. Many molecular assays have been developed and lack of standardization results in significant differences among assays/centers. Studies initiated by the Fungal PCR Initiative evaluated 20 assays in 16 diagnostic centers pointing out the superiority in sensitivity of the mitochondrial small subunit (mtSSU) target[1]. To further promote standardization, we compared four thermocyclers and six master mixes for the detection of *P. jirovecii*.

Materials/methods: Whole nucleic acid (WNA) from three qPCR-positive and ten qPCR-negative broncho-alveolar lavages were extracted on QiaSymphony with the Virus Kit Pathogen (Qiagen). Positive and negative extracts were pooled to provide sufficient homogeneous material. The positive pool was extemporaneously diluted at 1:5, 1:10, 1:50, 1:100 and 1:1000 in the negative pool. Three master mixes were tested to detect DNA by qPCR and three to detect WNA by reverse transcriptase qPCR (Table 1). All tests targeted mtSSU using the same primers and probes. Experiments were performed on four thermocyclers (LightCycler 480, ABI7500, QuantStudio and Rotorgene).

Results: ComParison of quantitative cycle (Cq) values between the methods targeting WNA and the methods targeting DNA showed lower Cq values with WNA independently from thermocycler and mix. For high (pure extract) and low (1:1000 dilution) fungal loads, ΔCq values were 6.97 (± 2.95) and 5.81 (± 3.30) respectively ($p<0.0001$). Regarding DNA detection, lower Cqs were obtained with Mix1 compared to Mix2 and Mix3 with median ΔCq of 2.6 ($p=0.015$) and 2.9 ($p=0.039$) respectively. Regarding WNA detection, no mix was superior to the others. The mean efficiency of PCR reactions was similar. PCR efficiency was not significantly different according to the qPCR equipment ($p=0.14$).

Conclusions: This study confirms that amplifying WNA is more sensitive than DNA alone to detect *P. jirovecii* nucleic acids. Variability observed due to enzyme/kit and thermocycler is a hurdle to harmonizing PCR protocol and producing comparable data among centers. Further studies should focus on developing a calibration method for accurate assessment of fungal load.
[1]Gits-Muselli M. *et al. Medical Mycology* 2019.

	Mix	Manufacturer
1	Probes Master Mix	Roche
2	MasterMix Plus Low ROX	Eurogentec
3	Taqman Universal qPCR Master Mix	Applied Biosystem
4	Superscript III One step RT-PCR	Invitrogen
5	TaqMan™ Fast Virus 1-Step	Thermofischer Scientific
6	LightCycler Multiplex RNA Virus Master	Roche

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Abstract 1781

Association between susceptibility to quinolones in *Escherichia coli* and tetracycline use in the community: analysis of 9 communities with a single model

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Background: Tetracyclines are extensively used in the community. We previously found that tetracycline use was associated with resistance to quinolones in *E. coli* in a French community, but this association was not described in other communities. Pharmaco-epidemiological studies are usually conducted with arima models, that only apply to a single site. However, results of a model derived from a given site may not be extrapolated to another site. Our aim was to assess the association between tetracycline use and quinolone susceptibility in *E. coli* isolates of several communities, using a single model.

Materials/methods: Monthly time series of proportions of quinolone susceptible *E. coli* and uses of quinolones and tetracyclines (in DDD/1000 inhabitants/month) were obtained from 9 communities (France, n=1; Israel, n=7; Spain, n=1), between 2009 and 2018. A single linear mixed effects model was used to assess the relationship between antimicrobial use and resistance in different sites, with site as a random effect, including a 1st order auto-correlation. Results were provided as estimate (95% confidence interval) of fixed effect (FE) and range of random effects (RE).

Results: Median (range) population was 434,000 (190,000 to 1,346,000). The proportion of susceptible isolates increased significantly with time (time FE, +0.032 (+0.012 to +0.052); RE range, -0.041 to +0.036). Quinolone use significantly decreased (time FE, -0.21 (-0.30 to -0.11); RE range, -0.30 to +0.15), but tetracycline use showed no significant temporal trend (time FE, 0.01 (-0.06 to +0.07); RE range, -0.12 to +0.18). In multivariate analysis, quinolone susceptibility was associated with both quinolone use (lag, 7 months; FE,-0.040(-0.074 to -0.004); RE range, -0.022 to +0.006) and tetracycline use (lag, 8 months; FE, -0.073 (-0.140 to -0.007); RE range, -0.198 to +0.094).

Conclusions: A single linear mixed effects model with autocorrelation can be used to assess the relationship between antimicrobial use and resistance in several communities. Both community uses of tetracycline and quinolones were associated with decreased susceptibility to quinolones in *E. coli*, with high variability across communities. These results suggest that decreasing tetracycline use in the community may decrease quinolone resistance in community isolates of *E. coli*.

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Abstract 1782

A mortality prediction model for adult intensive care unit patients infected with *Klebsiella pneumoniae* in a tertiary hospital: a retrospective cohort study

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Background: *Klebsiella pneumoniae* (*K. pneumoniae*) infections, especially infections with multidrug-resistant strains, can be life-threatening and are a critical public health concern. *K. pneumoniae* infections are even more critical and the antibiotic resistance rate is much higher in intensive care unit (ICU) patients. This study aimed to develop and evaluate the accuracy of a prediction model and risk score to predict 14-day mortality in adult ICU patients infected with *K. pneumoniae* in a tertiary hospital.

Materials/methods: For this retrospective cohort study, data were extracted from the medical records of adult patients admitted to the ICU of a 1900-bed tertiary hospital in Vietnam in 2016-2018 and in whom *K. pneumoniae* was isolated. We used univariable and multivariable logistic regression analyses to develop a valid prediction model and a simplified risk score for 14-day mortality. We assessed their discriminative ability by optimism-corrected area under a receiver operating characteristic curve (AUC) and their calibration by calibration plots and Hosmer-Lemeshow test statistics.

Results: In total, 249 patients were included in the analysis. Their 14-day mortality was 28.9%. Out of 18 prognostic determinants, the final prediction model comprised of route of referral, Sequential Organ Failure Assessment score and Charlson comorbidity index at infection onset, presence of central venous catheter, intracerebral haemorrhage operation within 72 hours before infection onset, and the absence of adjunctive treatment to remove the probable focus of infection [see Table 1; AUC (95% CI): 0.80 (0.76-0.82); Hosmer-Lemeshow test: p=0.165, after bootstrapping]. The simplified risk score corresponded to a very low (0%), low (7.8%), moderate (18.2%), high (50.6%) and very high (100%) risk of mortality for scores 0-1, 2-3, 4-5, 6-8 and 9-13, respectively.

Table 1. Independent predictors of 14-day mortality, the corresponding odds ratios and contribution to risk score

	Regression coefficients (95% CI)	OR (95% CI)	Contribution to risk score#
Intercept	-4.75 (-6.27, -3.45)		
Route of referral	0.97 (0.19, 1.83)	2.65 (1.21, 6.21)	1
SOFA score 4-11	1.30 (0.39, 2.36)	3.68 (1.47, 10.63)	2
SOFA score ≥12	2.20 (0.95, 3.54)	8.99 (2.58, 34.80)	3
Charlson index =1	0.72 (-0.28, 1.74)	2.06 (0.75, 5.67)	1
Charlson index ≥ 2	0.84 (0.05, 1.68)	2.32 (1.05, 5.37)	1
Central venous catheter	1.45 (0.68, 2.30)	4.28 (1.98, 10.01)	2
Intracerebral haemorrhage operation	1.39 (0.19, 2.64)	4.03 (1.21, 14.05)	2
Absence of adjunctive treatment	2.75 (1.67, 3.97)	15.65 (5.33, 52.86)	4

OR = Odds Ratio; 95% CI = 95% Confidence Interval; SOFA = Sequential Organ Failure Assessment

Simplified risk score: Total score = 1*Intra-hospital referral + 2*SOFA score 4-11 + 3*SOFA score ≥12 + 1*Charlson index ≥ 1 + 2*Presence of Central venous catheter + 2*Intracerebral haemorrhage operation + 4*Absence of adjunctive treatment

Conclusions: We constructed a prediction model and risk score for 14-day mortality in adult ICU patients with *K. pneumoniae* infection in a tertiary hospital which could support patient risk stratification and clinical decision making in this setting.

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Abstract 1786

Temporal and regional prevalence of carbapenemase-producing Enterobacterales in Switzerland from 2013 to 2018

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Background: Increasing rates of carbapenemase-producing Enterobacterales (CPE) have been observed in Europe and all over the world. CPE represent a great concern since they are frequently associated to resistance to multiple antibiotics thus reducing therapeutic options.

Materials/methods: Data on human CPE isolates from 2013 to 2018 were collected by the Swiss Centre for Antibiotic Resistance (ANRESIS) and analysed for temporal and regional trends. A statistical detection of regional clusters was performed with the SaTScan software embedded in WHONET.

Results: From 2013 to 2018, yearly detection of CPE isolates has increased considerably from 65 to 212. The most frequently isolated species were *Klebsiella pneumoniae* (54% of the cases), followed by *Escherichia coli* (28%). The most frequent carbapenemase genotypes were OXA-48-types (43%), KPC (21%), and NDM (14%). At the regional level, highest numbers of CPE isolates per 100'000 inhabitants were identified in the Geneva and the Ticino regions. Multivariable analyses of regional and temporal trends of CPE cases confirmed an increase in total number, higher prevalence in the Geneva region and in male patients. In contrast to the French speaking parts (Western and Geneva regions) where OXA-48-types were the predominant genotypes (55% and 60%, respectively), KPC was the most frequently detected genotype in the Italian speaking region of Ticino (62%). SaTScan outbreak detection analysis identified a total of seven clusters in five different regions of Switzerland.

Conclusions: In a first continuous surveillance of CPE in Switzerland it was shown that the epidemiological situation aggravated nationwide and that regional patterns of CPE genotypes mirror the situations in neighbouring European countries.

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Abstract 1788

Characterisation of immune response of patients with rheumatic disorders and latent tuberculosis infection

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Background: The use of antitumor necrosis factor agents (anti-TNF) (biologics) for the treatment of inflammatory rheumatic disorders has reopened the tuberculosis (TB) problem also in countries with low TB incidence, due to the increased risk of TB reactivation in subjects with latent tuberculosis infection (LTBI). This study aims to evaluate the effect of biologics on acquired immunity to Mtb, at enrolment and at the end of preventive treatment

Materials/methods: We enrolled 11 RD-LTBI at the baseline and at the end of preventive treatment. LTBI subjects started the biological agent after the first month of TB-therapy. As controls, we enrolled 11 LTBI subjects without RD. Cells were stimulated with antigens contained in TB1 and TB2 tubes of QFT-Plus. We characterized the cytokine (IFNγ, TNFα, IL2) and phenotypic profile (CD45RA, CD27) of Mtb-specific T-cells by cytometry. Wilcoxon signed rank test was performed.

Results: We found that the use of biological drugs does not reduce the ability of CD4 and CD8 T-cells to respond to Mtb stimulation. Moreover, we found an increased CD8 T-cell response at the end of TB preventive therapy in both LTBI groups.

Regarding the CD4 T-cell response, LTBI subjects had higher proportion of $IFN\gamma^{+}TNF\alpha^{+}IL2^{+}CD4^{+}$ T-cells (p=0.04) and $IFN\gamma^{-}TNF\alpha^{+}IL2^{+}CD4^{+}$ T-cells (p=0.01) at the baseline compared to end of therapy. Differently, RD-LTBI subjects had a similar cytokine profile of CD4 T-cells before and after TB- therapy.

Regarding the CD8 T-cell response, this response was characterized by a high proportion of IFNγ producing T-cells both before and after TB-therapy, independently of the RD status.

Regarding the phenotype, the Mtb-specific CD4 T-cells showed predominantly a central memory phenotype before and after therapy in both RD-LTBI and LTBI. The Mtb-specific CD8-response showed mainly an effector phenotype

Conclusions: The increased risk to develop active-TB disease is an emerging aspect in the use of biological drugs of patients with rheumatic disorders. These preliminary data show that the use of biological agents does not reduce the ability of CD4 and CD8 T-cells to respond to Mtb-stimulation. This study is helpful to understand the immunological safety of the biological drugs and to identify new candidate biomarkers of Mtb-infection.

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Abstract 1789

Results of a screening programme for Strongyloidiasis in HIV-positive immigrants

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Background: Distinctive characteristics of *Strongyloides stercoralis* are its ability to persist and replicate within a host for life and its potential to cause life-threatening infection in an immunocompromised host as HIV patients. The aims of this cross-sectional study were to describe the results of a systematic serological screening program for strongyloidiasis in HIV positive patients.

Materials/methods: Between 2009 and 2018, a prospective serological screening program for strongyloidiasis in all immigrant patients diagnosed of HIV infection with infection confirmed by Western-Blot, in Asturias, a region in the north of Spain was conducted. Three formalin-ether concentrated stool samples and an enzyme-linked immunosorbent assay for anti-*S. stercoralis* antibodies were used as screening tools. We considered that infection exits if the microscopic visualization of larvae in stool sample and/or the ELISA was positive. In positive patients was discarded the presence of other nematodes or filarias.

Results: Of the 83 screened patients (average age 39 [10] years, 61.8% of them female, average time in Spain 760 days). Twelve patients (13.5%) had a positive serological test for *S. stercoralis* and in only four of them was the microscopic visualization of larvae of *S. stercoralis* by formalin-ether concentration of faeces positive. The areas of origin were Central Africa (61.4%), South America (26.5%), West Africa (7.2%), North Africa and Mexico and Central America (2.2% respectively).Fifty percent of *Strongyloides* positive patients come from Central Africa (6/51,; prevalence 11.7%) and the rest from South America (6/22; prevalence 27.2%; P= 0.0550; OR 3.4375 [0.9739 -12.1325]). Infection was significantly more frequent in patients from Paraguay (P = 0.0042 OR 81 [4.0066 – 1637]). There is not differences in CD4+ count, viral load, sex, age or time in Spain between infected and no infected patients. No patients had HTLV-I coinfection. Fifty-two percent of patients were asymptomatic at the moment of diagnostic. *Strongyloides* positive patients had higher levels of eosinophilia (842,42±724,989 cells/mm^3 versus 280,91 ± 428,765 cells/mm^3;p=0.003)

Conclusions: Strongyloidiasis is frequent in immigrant HIV positive patients, specially proceeding from Equatorial Guinea and Paraguay. Screening for Strongyloidiasis, even in asymptomatic patients should be taken fully into account. Serological test are useful in screening programs.

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Abstract 1795

Anidulafungin-loaded hybrid organo-inorganic sol-gel coating can prevent the prosthetic joint infections provoked by *Candida albicans*

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Abstract third-party references: Funded by a grant from the Mutua Madrileña Foundation

Background: Prosthetic joint infections occur infrequently, but they represent the most devastating complication. Nowadays, yeast belonging to *Candida* genus, mainly *C. albicans*,are gaining relevance. These PJI are infrequent, they use to show high recurrence rates. Local antibiotic therapy is a desired featured which would allow locally preventing or treating these infections. In order to overcome prosthetic joint infection, sol-gel technology allows loading the coating with antifungical and osteointegrative molecules such us organophophite compounds. The aim of this work was to evaluate the prophylatic effect of coatings loaded with anidulafungin using an *in vivo* murine model of candidal prosthetic joint infection.

Materials/methods: Sol-gel coating was produced using a molar ratio of 1:2 (MAPTMS:TMOS) and an organophosphite dispersed in ethanol. The unloaded coating was loaded with 20 mg of anidulafungin per 20,3 mL and was used to coat chemical polished Ti6Al4V samples (CP+A). Chemical polished Ti6Al4V samples without coating were used as control (CP).
The surgical procedure was performed as described previously by Lovati *et al.* (PLoS One. 2013 Jun 20;8(6):e67628) using only one of two femurs of each mouse treated ad libitum with 4 mg/mL of dexametasone and 100 mg/mL of enrofloxacin from a week before surgery and upwards and infected with a *C. albicans* isolated from a hip PJI (Cal 35). During five weeks, weight, limping and piloerection of animals were monitored. After five weeks, the animals were sacrificed and the bacterial load was estimated and confirmed in the peri-implant bone tissue and the implant using the methodology described by Esteban *et al.* (*J. Clin. Microbiol*. 2008 vol. 46 no. 2 488-492). Each treatment was performed five times

Results: The results are shown in the Figure 1. Fifty percent (3/6) of Cal 35-infected CP group were positive culture and 100% percent Cal 35-infected CP+A group were negative culture (0/6) (p-value=0.0228).

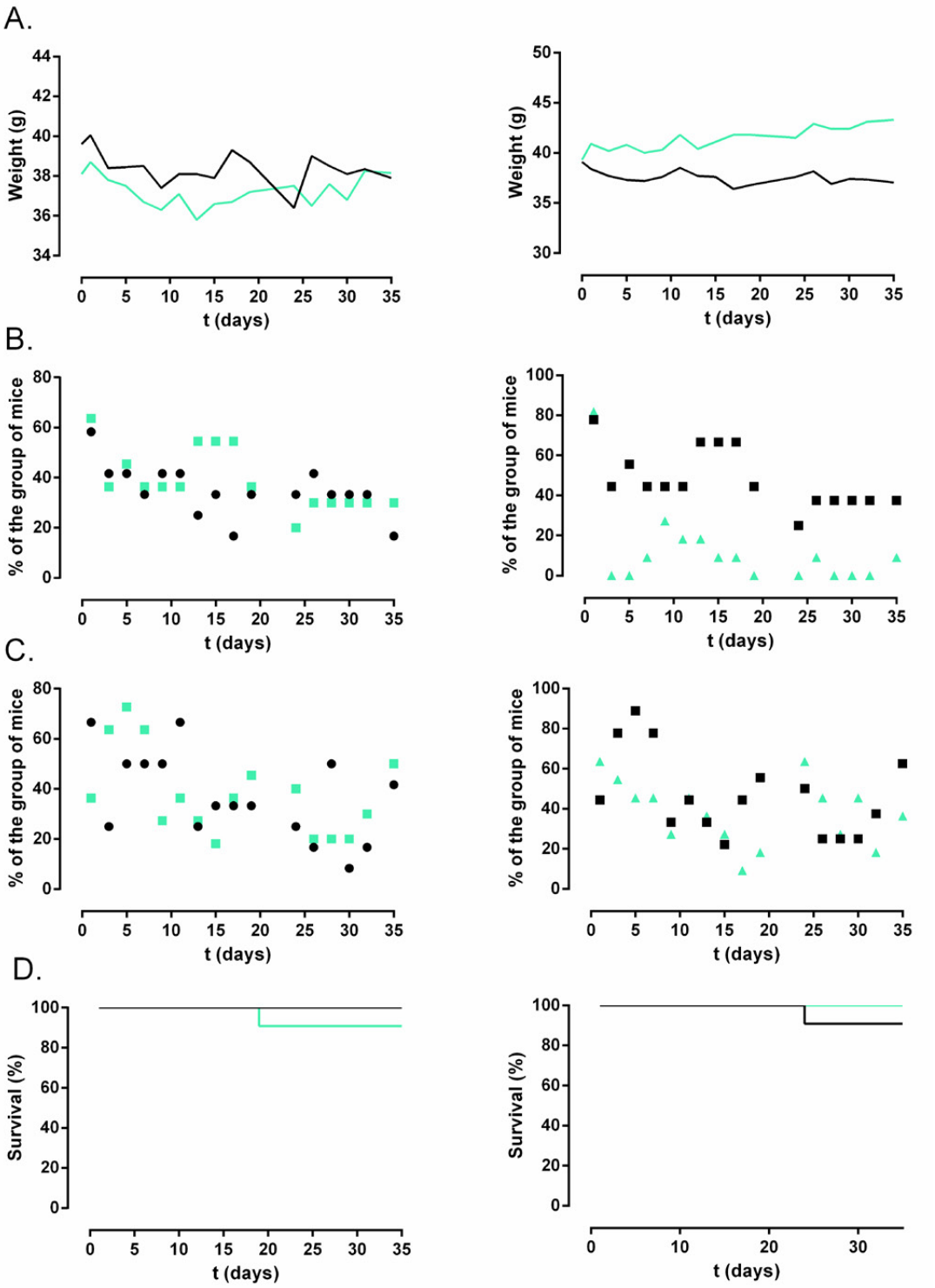

Figure 1. Median weight (A), limping (B), piloerection (C), and survival (D) in different noninfected group (black), and Cal 35-infected group (green) with CP (left column) and CP+A (right column) over time.

Conclusions: Anidulafungin-loaded hybrid organo-inorganic sol-gel coating can prevent at local level PJI provoked by *C. albicans*.

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Abstract 1798

Serodiagnosis of Lyme borreliosis: is IgM in serum more harmful than helpful?

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Background: Interpretation of serological findings in suspected Lyme borreliosis (LB) may be challenging in endemic areas and IgM antibodies in serum are often associated with false positive reactivities. There is a risk for over-diagnosis of LB, inadequate use of antibiotics and potential delay of proper diagnosis. The clinical value of IgM analysis in serum in LB diagnosis is therefore questioned. The aims of this study were to investigate how well the clinical recommendations for the diagnosis of LB and when to test for borrelia-specific antibodies were followed in Jönköping County, Sweden, and to evaluate the clinical value of IgM antibodies in serum.

Materials/methods: In total, 4428 borrelia-specific antibody tests in serum were analyzed in Jönköping County during 2017. Of these, 643 individual patients had positive results (IgM and/or IgG), of which we had to exclude 33 patients due to inaccessible medical records. The remaining patients (n=610) with positive test results were then divided into separate groups of either IgM and/or IgG-positivity. Based on current European recommendations, we defined the criteria for correct indication for serological testing and how to evaluate the diagnosis made by the clinician. Medical records and laboratory test results for each patient were then assessed according to these criteria.

Results: Only 183/610 (30%) of patients were tested according to the European recommendations. The groups positive for either isolated IgG or both IgM and IgG antibodies showed a similar pattern with high number of diagnoses assessed as being confident or doubtful. Isolated detection of IgM (without concomitant IgG) was only helpful in 50% of the diagnoses assessed as being confident or doubtful. Thus, 50% of the LB diagnoses in patients with isolated IgM reactivity in serum were assessed as incorrect (LB unlikely).

Conclusions: Isolated IgM positivity in serum shows limited clinical value in LB diagnostics and needs further assessment before being reported by the laboratory.

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Abstract 1800

Application of a new molecular biology method for carbapenem-resistant *Enterobacteriaceae* detection in rectal swabs

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Background: The extreme ease with which the CPEs (Carbapenemase Producing Enterobacteriaceae) spread, requires the implementation of an effective screening program that allows the rapid identification of resistant strains. In this study we evaluated the diagnostic utility of an innovative molecular biology method for CPE detection in rectal swabs. Furthermore, we verified the percentage of rectal colonization as a predictive event for CPE bacteremia in the patients.

Materials/methods: In February-March 2019, 153 rectal swabs from intensive care unit (36%), hematology (19%), cardiology (17%), and other departments (28%) were examined. All the samples were analyzed by phenotypic method on McConkey with Ertapenem disk and E-test on MH for Meropenem (Biomerieux) and examined by Real-time PCR multiplex, using Allplex Entero-DR Assay kit (Allplex, Seegene, Republic of Korea) on automatic system Nimbus IVD (Seegene) which allows to identify simultaneously 8 resistance genes: KPC, VIM, NDM, IMP, OXA-48; van-A, vanB; CTX-M. Blood cultures were analyzed with automatic Bactec FX (BD) system, subcultures from positive vials and identification by mass spectrometry (MALDI-TOF Bruker). Antibiograms were performed with Phoenix instrument (BD) and interpreted according to EUCAST criteria.

Results: The results obtained by phenotypic method and molecular screening indicate a perfect agreement between the two tests for 135 samples (88%). In particular, 20 (13%) were positive for the molecular method only, for CPE resistance genes, 115 samples (75%) agreed on negativity and positivity to resistance genes for ESBL and VRE genes, 59% (10 of 17) of patients with positive molecular analysis and negative culture had already been positive before. We also evaluated how many of the examined patients, positive for CPE rectal colonization, subsequently developed bacteremia: 25% (39 patients) of patients tested were affected by bacteremia caused by the same micro-organism.

Conclusions: The application of new molecular biology techniques in surveillance allows the rapid detection of CPE and given the extreme sensitivity of the method, is able to detect the presence of resistance genes early even in conditions of low bacterial load. This approach offers the clinician useful information for patient management and the possibility of promptly administering the most appropriate antibiotic therapy to counteract a possible bacteraemia.

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Abstract 1801

Impact of ribotype on *Clostridioides difficile* diagnostics

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Background: *Clostridioides difficile* infection (CDI) is one of the most common health-care associated infections worldwide. The ability of a strain to produce toxins is crucial for clinical disease. An accurate diagnosis of CDI remains a challenge, and underdiagnosis is an issue in Europe. A wide variety of diagnostic tests are available and the choice of reference method or gold standard is crucial in order to assess the accuracy of a test. One drawback of many studies comparing diagnostic techniques is that the local epidemiology is not taken into consideration, and several studies have been carried out in high prevalence or outbreak settings. This prospective study investigates the performance of diagnostic methods for detection of *C. difficile* infection in Sweden, including impact of PCR ribotype on diagnostic performance.

Materials/methods: Between 2011 and 2016, a total of 17878 stool samples from 26 laboratories were tested by either well-type enzyme immunoassays (EIAs), membrane bound EIAs, cell cytotoxicity neutralization assay (CTA) or nucleic acid amplification tests (NAATs) and subsequently cultured for *C. difficile*. Roughly half of the samples (9454/17878) were subjected to diagnostic testing both on the fecal sample and on the 1323 isolated *C. difficile* strains. All *C. difficile* isolates were typed by PCR ribotyping, and classified as toxigenic or non-toxigenic based on the empirical knowledge of the association between toxin-positivity and ribotype.

Results: The overall sensitivity, specificity, and positive and negative predictive values were highest for NAATs and membrane EIAs. Ribotype specific sensitivity varied greatly between methods and ribotypes. All methods had 100% sensitivity against ribotype 027 and 013. For other types the sensitivity ranged from 33% to 85% in fecal samples and from 78% to 100% on isolates. For the most prevalent ribotypes (014, 020 and 001) the sensitivity varied between 38% and 100% in the fecal samples, with the lowest sensitivity observed for well-type EIAs and CTA.

Conclusions: The large variation in diagnostic sensitivity implies that type distribution significantly affects the outcome when evaluating diagnostic performance. Furthermore, performing comparative studies of diagnostic tests in settings with high prevalence of ribotype 027 will overestimate the general performance of diagnostic tests.

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Abstract 1802

Changes in the gut microbiota due to smoking in patients with inflammatory bowel disease

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Abstract third-party references: Smoking Research Foundation

Background: Smoking is one of the important factors affecting the onset and pathogenesis of inflammatory bowel disease (IBD). The effects of smoking are different depending on the disease types, and it is thought to promote the aggravation and relapse of Crohn's disease (CD), but to suppress those of ulcerative colitis (UC). However, the underlying mechanisms by which smoking affects IBD has not been fully studied. In this study, we investigated the effects of smoking on the composition of oral and intestinal microbiota.

Materials/methods: Saliva, feces, and colonoscopy aspirates from 77 UC (smokers 10, ex-smokers 28, non-smokers 39) and 12 CD (smoker 3, ex-smoker 3, non-smoker 6) patients. The gut microbiota was analyzed by 16S rRNA gene sequencing.

Results: The subjects were classified into 4 clusters (Cluster A to D) from the microbial composition of colonoscopy aspirates rich in mucoadhesive bacteria. Smokers were predominantly classified (8 out of 13), whereas non-smokers were not (19 out of 76), in Cluster D. Co-abundance groups analysis revealed that patients clustered in Cluster D had increased abundance of oral bacteria, including *Streptococcus*, in the colonic aspirates. *Streptococcus* and *Megasphaera* were also increased in the saliva of smokers.

Conclusions: Smoking seems to facilitate the colonization of oral bacteria in the colonic mucosa. This might affect the mucosal immune system and the pathology of IBD.

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Abstract 1804

ComParison of Cutibacterium acnes biofilm formation between strains isolated from prosthetic join infection and healthy skin microbiota

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Background: *Cutibacterium acnes* is a Gram-positive facultative anaerobe rod. It colonizes human skin and can causes invasive infections such as periprosthetic joint infection (PJI). *C. acnes* causes disease through a number of virulence factors, such as biofilm formation during implant infection. In this study, we compared the biofilm formation of C. acnes isolates recovered from healthy skin with isolates recovered from deep tissue in PJI patients.

Materials/methods: We used the modified in-vitro biofilm test by Stepanovic et al. (APMIS 2007, 115 (8): 891-9) as a static biofilm assay, using BHI+ 2% glucose with a bacterial inoculum of 10^7 CFU/mL. at 37ºC for 48h in anaerobic conditions and crystal violet for staining. One hundred and twenty-five C. acnes isolates recovered from PJI (n=89) from eight European centers, and healthy skin from face (HS) volunteers (n=36) were used. Biofilm formation of isolates was based on the optical density (OD) of each strain and the optical density control (ODc) measured at 570 nm, and classified into weak (ODc<OD<2xODc), moderate (2xODc<OD<4xODc), and strong (OD>4xODc) biofilm-former. The statistical data were analyzed by using a comParison test of proportions with a level of statistical significance of $p<0.05$.

Results: All isolates were biofilm-former types (Table 1). There was no statistical significant difference in between the biofilm-forming ability of strains isolated from these different sources.

Biofilm-former type (%)	PJI (n)	HS (n)	p-value
Weak	28.09 (25)	13.89 (5)	0.092
Moderate	57.30 (51)	72.22 (26)	0.120
Strong	14.61 (13)	13.89(5)	0.917

Table 1.

Conclusions: Although some reports suggest that *C. acnes* strains isolated from PJI produce more biofilm *in vitro* (Holmberg et al. Clin Microbiol Infect. 2009; 15 (8): 787-95), according with our data, both infection-associated and skin commensal isolates of *C. acnes* have the potential to form a static biofilm *in vitro* independently of the source of isolation.

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Abstract 1805

Prevalence of non-tuberculous mycobacteria in a tertiary hospital in Beijing, China, January 2013 to December 2018

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Background: In China, patients diagnosed with tuberculosis (TB) or suspected of having TB, are referred to a thoracic specialist hospital for further treatment. However, clinical manifestations of non-tuberculous mycobacteria (NTM) diseases and TB are quite similar. A considerable number of patients TB or suspected TB, are lost in tertiary hospitals. This study retrospectively analyzed the identification data of NTM samples to provide a general outline of the prevalence of NTM in a tertiary hospital in China.

Materials/methods: Clinical data of patients who tested positive/negative for *Mycobacterium tuberculosis* (MTB) or NTM using a screening test (Real-time fluorescent PCR detection) from January 2013 to December 2018 at Peking Union Medical College Hospital (Beijing), were collected. Data on Mycobacteria species identification, which was carried out by DNA microarray chip, was also collected. Trend analysis of annual constituent ratio was carried out by trend Chi-square tests using SPSS 22.0 and a P value < 0.01 was considered statistically significant.

Results: Mycobacterial species were detected in 1514 specimens from 1508 patients, among which NTM accounted for 37.3% (565/1514), increasing from a prevalence of 15.6% in 2013 to 46.1% in 2018 (P<0.001). Among the 565 NTM positive specimens, the majority (55.2%) were from female patients. Furthermore, patients aged 45-65 years accounted for 49.6% of the total patients tested. Among 223 NTM positive specimens characterized further, the majority (86.2%) were from respiratory tract, whilst 3.6% and 3.1% were from lymph nodes and pus, respectively. *Mycobacterium intracellulare* (31.8%) and *Mycobacterium chelonae / Mycobacterium abscessus* (21.5%) were the most frequently detected species, followed by *M. avium* (13.5%), *M. gordonae* (11.7%), *M. kansasii* (7.6%), and others.

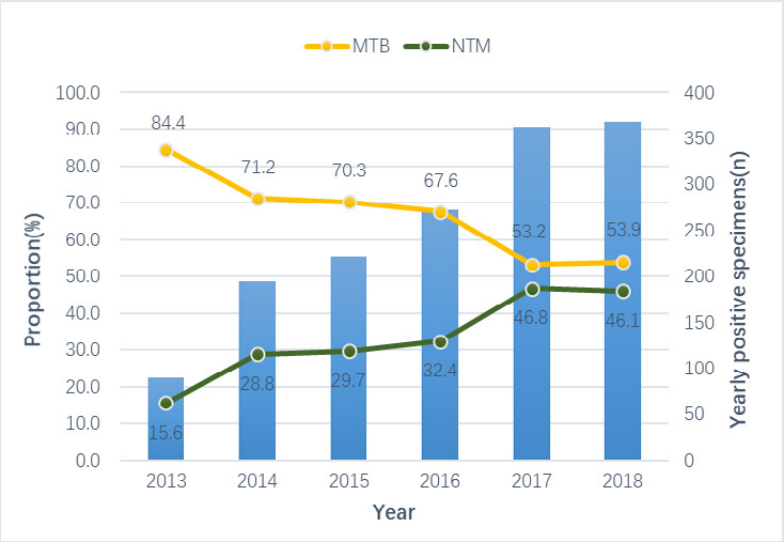

Figure. Distribution of Positive specimens in *Mycobacterium* nucleic acid detection during 2013 - 2018.

Conclusions: The proportion of NTM among mycobacterial species detected in a tertiary hospital in Beijing, China, increased rapidly from year 2013 to 2018. Middle-aged patients are more likely to be infected with NTM, especially females. *Mycobacterium intracellulare* and *Mycobacterium chelonae/ Mycobacterium abscessus* were the most frequently detected NTM pathogens. Accurate and timely identification of NTM is important for diagnosis and treatment.

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Abstract 1806

Novel organism verification and analysis (NOVA) study: identification of potentially novel bacterial species from a diverse spectrum of clinical isolates

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Background: During routine diagnostic work, a small number of bacterial isolates may not be identified reliably using the conventional identification method MALDI-TOF MS, due to insufficient reference data or the presence of a novel organism. We have established an algorithm to identify and characterize such strains using 16S rRNA gene sequence analysis and whole genome sequencing (WGS) in a prospective and systematic manner. Here we present preliminary data.

Materials/methods: Bacterial isolates from diverse clinical specimens which could not be identified definitely by MALDI-TOF MS (Bruker Daltonics, database version 4.1) were subject to partial 16S rRNA gene sequencing (approx. 800bp). All strains with 16S rRNA sequence identities ≤99.0% compared to validly described species were analyzed by WGS (MiSeq/ NextSeq, Illumina) in our institution, for full 16S rRNA gene, rMLST, and digital DNA-DNA-hybridization (dDDH) analysis. Isolates are stored to enable further characterization.

Results: Since 2016, 28 novel clinical isolates were collected (19 Gram-positive, nine Gram-negative). Twenty represent aerobic or facultatively anaerobic organisms and eight are anaerobic strains. Among the aerobic bacteria 12 are Gram-positive rods, four Gram-negative rods, three Gram-negative cocci, and one a Gram-positive coccus. The anaerobic bacteria include four Gram-positive cocci, two Gram-positive rods, and two Gram-negative rods. The strains were isolated from 11 biopsies and 11 swabs with localization of extremities (8), ear (6), miscellaneous (10) as well as three blood cultures, one urine and two with unknown source. Identities of the 28 corresponding 16S rRNA gene sequences ranged from 90-98.5% and 24/28 have a dDDH of <70%, as determined by WGS data. Two novel species were detected repeatedly: three independent isolates belonging to the *Microbacteriaceae* family; and an unknown *Corynebacterium* sp. was detected in two patients. Clinical relevance of the isolates has not yet been investigated.

Conclusions: Our preliminary data indicate a diverse spectrum of hitherto undescribed cultured bacterial organisms from various body sites. We have defined an algorithm for rapid characterization of these isolates, within a well-equipped clinical microbiological laboratory. Publications arising to date include an emendation of *Auritidibacter ignavus* (Bernard K et al. IJSEM, 2019) and description of *Mycobacterium basiliense* (Seth-Smith, Frontiers in Microbiology, 2019).

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Abstract 1812

Once-daily dose ceftriaxone plus ampicillin: an alternative for *Enterococcus faecalis* infective endocarditis OPAT treatment

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Abstract third-party references: on behalf of the Grupo Andaluz para el estudio de las infecciones Cardiovasculares de la Sociedad Andaluza de Enfermedades Infecciosas (GAEICV-SAEI)

Background: Ceftriaxone 2g/12 hours plus ampicillin 2g/4 hours is a safe and effective strategy for the treatment *Enterococcus faecalis* infectious endocarditis. Ceftriaxone administration as 4g once-daily short infusion allows its inclusion in outpatient parenteral antibiotic therapy programs (OPAT), avoiding the use of two infusion pumps simultaneously. Given the importance of ceftriaxone exposure to obtain the synergistic effect with ampicillin, an examination of ceftriaxone high once-daily dose pharmacokinetic profile is warranted.

Materials/methods: This Phase II, open-label, crossover, pharmacokinetic study, enrolled healthy adult volunteers, wo underwent two sequential treatment phases. During Phase A all volunteers received 2g of ceftriaxone each 12 hours during 24 hours followed by 7-day washout. Then, all the participants received Phase B medication, which consisted on 4g single dose of ceftriaxone. Throughout both phases each volunteers underwent intensive PK sampling over 24 hours. For concentrations lower than 100 mg/L, ceftriaxone unbound plasma concentrations were estimated assuming 10% of total drug. Ceftriaxone total concentrations were measured using validated LC-MS/MS methods, following FDA criteria.

Results: Twelve participants were enrolled and completed both phases. Five were female and median age and BMI were 28 years and 26.1 kg/m2. Mean concentration (GM±SD) 24 hours after the first dose (C24h) and estimated unbound C24h (uC24h) were 83.39±25.90 mg/L (range 47.98-135.73) and 8.34±2.59 mg/L (range 4.80-13.57) in phase A and 34.60±11.16 mg/L (range 18.50-51.07) and 3.46±1.12 mg/L (range 1.85-5.11) in phase B, respectively. In both cases mean uC24h were superior to 2 mg/L, the concentration required to maintain ceftriaxone synergistic activity. All patients achieved estimated unbound plasma concentrations superior to the concentration suggested to maintain ceftriaxone synergistic activity at least 20 hours, and most of them (>80%) 24 hours. Ceftriaxone total exposure, measure by AUC0-24, was similar in both phases and mean values were (GM±SD) 3319.6±614.3 mg.h/L in phase A vs 3035.4±573.3 mg.h/L in phase B (p=0.266). No grade 3 or 4 adverse events or laboratory abnormalities were observed.

Conclusions: Ceftriaxone plasma concentrations 24 hours after 4g single-dose administration are adequate to maintain the synergistic activity with ampicillin during 24 hours, allowing patient inclusion in OPAT programs without risk of inadequate exposure.

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Abstract 1813

Does automated susceptibility testing overcall temocillin resistance?

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Background: Temocillin is a semi-synthetic penicillin with narrow spectrum activity against *Enterobacteriaceae,* including AmpC and extended spectrum beta-lactamase (ESBL) producing organisms. Temocillin has the potential to be an important tool in clinical practice to treat serious infections caused by multi-resistant organisms and for antimicrobial stewardship purposes, including reducing use of critical antibiotics such as carbapenems. Common current clinical microbiology laboratory practice involves use of automated susceptibility testing methods such as the Becton-Dickinson (BD) Phoenix™. However, reported resistance rates to temocillin for *Enterobacteriaceae* isolates at our clinical microbiology laboratory far exceeds that expected by our knowledge of temocillin's stability in the presence of beta-lactamase enzymes, leading to a hypothesis that Phoenix is overcalling temocillin resistance. This potentially poor quality data may lead to greater reluctance to utilise the antibiotic in clinical practice and give incorrect antimicrobial resistance epidemiology data.

Materials/methods: Prospective data was collected on *Enterobacteriaceae* blood culture isolates at our clinical microbiology laboratory from July 2017 to October 2018. Isolates were routinely tested for susceptibility on Phoenix and results recorded. Isolates that were deemed temocillin resistant on Phoenix had the temocillin susceptibility test repeated using an alternative method, for example a temocillin E-test and the concordance of the results was investigated.

Results: 87% (117/134 isolates) of *Enterobacteriaceae* blood culture isolates initially reported to be temocillin resistant, were found to be susceptible when re-tested using an alternative method. This reduced the overall reported temocillin resistance rate from 26% (209/805 isolates) to 2% (17/730 isolates).

Conclusions: Temocillin resistance in *Enterobacteriaceae* blood cultures isolates reported using automated susceptibility testing on BD Phoenix was only confirmed to be true using a second susceptibility testing method in 13% of cases. Phoenix overcalls temocillin resistance. All laboratories relying on BD Phoenix for temocillin susceptibility testing should confirm initial resistant results using a 2nd susceptibility testing method, such as a temocillin Etest. Becton-Dickinson should consider withdrawing temocillin from their Phoenix automated susceptibility testing panels until more reliable resistance results can be obtained.

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Abstract 1816

Burden of surgical site infections after solid organ transplantation in the Swiss transplant cohort study

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Background: Surgical site infections (SSI) after solid organ transplantation (SOT) result in increased morbidity due to antibiotic therapy and surgical revision, and have been associated with a negative impact on graft function and patient survival. Studies addressing this important hospital-acquired infection after SOT are very limited and mostly derived from retrospective studies.

Materials/methods: The Swiss Transplant Cohort Study prospectively collects clinical data of lung, heart, kidney, liver, pancreas, and combined (e.g. kidney-pancreas, kidney-liver) transplant recipients. We analyzed SSIs occurring within 90 days post-transplant that were related to all transplant surgical procedures in Switzerland between June 2008 and October 2018. We excluded patients that received serial transplants.

Results: A total of 193 SSIs were observed in 4794 transplantations (378 heart, 449 lung, 1052 liver, 2564 kidney, 7 pancreas, 195 kidney-pancreas, 149 other combined transplants), corresponding to an incidence of 4.0%. Median time from surgery to SSI was 18 days (interquartile range [IQR] 10-32 days). The incidences of SSIs were 6.9%, 4.7%, 4.9%, 2.2%, 14.3%, 17.4%, 2.7% after heart, lung, liver, kidney, pancreas, combined kidney pancreas and other simultaneous transplantations, respectively. In 161 (83.4%) SSIs a causative pathogen was identified, whereas in 16.5% diagnosis was established based solely on clinical findings. The majority of SSIs was caused by bacteria (n= 131, 67.9%) and presented in 19 cases with concomitant bacteremia. SSIs were most frequently caused by gram-positive bacteria (n= 105, 80.2%), with enterococcal infections being most common (n= 54, 41.2%, 12 polymicrobial infections) (Figure). Fungal SSIs were identified in 15.5% of transplant recipients. *Candida* spp. were the main cause of fungal SSIs (n= 30, 6 SSIs with detection of more than on fungal pathogen) with a predominance of *Candida albicans* (n= 21, 70.0%).

Conclusions: In our cohort of SOT recipients we found a SSI rate of 4.0%. The highest SSI rate was observed after combined kidney pancreas transplantations and the lowest SSI rate after kidney transplantation. Most SSIs were caused by gram-positive bacteria, with enterococci being most frequent.

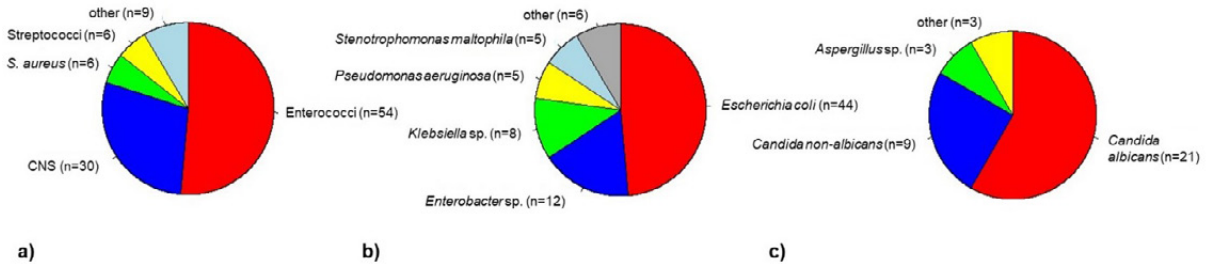

Figure: Frequency of detected pathogens in surgical site infections

a) Gram-positive pathogens
b) Gram-negative pathogens
c) Fungal pathogens

Abbreviation: CNS coagulase-negative *Staphylococcus* spp.

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Abstract 1817

Epidemiological investigation of newly detected highly lethal Borna disease virus 1 cases reinforcing indirect shrew contact as possible source of infection: results from in-depth interviews, Germany, 2019

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Background: In 2018, Borna disease virus 1 (BoDV-1) was first confirmed as a zoonotic pathogen causing severe human encephalopathy in Germany with an extremely high case fatality (15/16). Bicoloured white-toothed shrews (*Crocidura leucodon*) have been identified as reservoir hosts shedding virus in urine, saliva and faeces in endemic areas. Clinical presentation, risk factors and transmission routes for human infection are unknown. We aimed to generate hypotheses about transmission routes and provide evidence to guide prevention.

Materials/methods: We defined cases as BoDV-1-confirmed by pro- or retrospective nucleic acid detection. Viruses were sequenced. We conducted interviews with family members at patients´ homes in 2019 using a standardized semiqualitative questionnaire covering a broad spectrum of clinical presentation and pre-existing conditions. Queried exposures included housing environment, profession, animal contacts, outdoor activities, travel, and nutrition.

Results: We identified family members of five patients deceased 1996 through 2019 (4/5 female, median age 25 years, range 13-56). Immunosuppression was known for none. Four had presented with fulminant encephalitis starting with headache and fever, the fifth had initially shown signs of Guillain-Barré-syndrome. All had developed confusion, deep coma and had died within a median of 2.5 (range 1-11) months after symptom onset. All had lived their whole life in rural areas of Germany. Other than private gardening no communalities were identified. Three families kept domestic or farm animals (cat, dog, hare, duck, chicken). Family members did not know of any direct contact to shrews, but all had observed irregular peridomestic presence of shrews. Three families reported domestic cats bringing home shrews. All human BoDV-1 sequences clustered with animal BoDV-1 sequences from the respective regions.

Conclusions: Rural residence is a common denominator of all five patients but transmission routes remain poorly understood. Phylogenetic analysis and shrew presence suggest peridomestic infection from the local reservoir. In the absence of direct shrew contact, most likely transmission may be via indirect contact. Interviews with other patients´ families are ongoing. To prevent cases of this fatal zoonosis, we recommend against avoidable contact to shrews and their secretions and published an online-handout on prevention measures targeting the public in endemic areas.

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Abstract 1822

T2 magnetic resonance technology in the diagnosis of sepsis and clinical impact in patient management

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Background: Rapid and effective antimicrobial therapy is crucial to improve septic patient outcome, while inappropriate empirical therapy is a well-known, strong, independent predictor of mortality. Multidrug resistant organisms (MDRO) have reached to a pandemic level during the last two decades. A delay of 3-5 days has been found for effective therapy of systemic infections by MDRO. Thus, a rapid identification of pathogens, especially of bacterial species known to be multi-drug resistant, is a major goal in the diagnosis of sepsis.

Differently from technologies applicable on positive blood culture, dependent on the time of positivization of the sample, molecular tests performed directly on whole blood samples allow rapid identification of the etiological agents and are supposed to dramatically impact on patient outcome. Recently, the T2 Magnetic Resonance technology (T2Dx®) has been approved by FDA for laboratory diagnosis of sepsis by ESKAPEc organisms, with high sensitivity and specificity.

Materials/methods: The aim of this study was to evaluate the accuracy and the clinical impact of T2Bacteria Panel of T2Dx® system in comParison with the standard blood culture protocol in the early detection of ESKAPEc pathogens in patients with sepsis. Blood samples for culture and T2 testing were collected from 61 patients and diagnostic accuracy was evaluated. Duration of empirical therapy, and switch to target therapy were compared in patient with positive or negative T2 results.

Results: T2Bacteria Panel sensitivity and specificity were 100% (panel targets) and 94.6%, respectively. Time to report of positive T2Bacteria results was significantly lower than that of positive blood cultures (4.24 h ± 3.4 h *vs* 24.2 h ± 33.4 h, $p < 0.001$). The percentage of patients in which antibiotic therapy was switched to target therapy the same day of sample collection was significantly higher in patients with positive T2 results (37.5% *vs* 11.4%, $p = 0.0312$). Duration of empirical therapy was shorter in these patients (34.11 h ± 23.87 h *vs* 80.48 h ± 73.40 h).

Conclusions: T2Bacteria Panel, allowing rapid detection of ESKAPEc pathogens, significantly impacts on the switch from empiric to target therapy, and represents a novel, valuable tool to improve the management of septic patients.

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Abstract 1823

Marine organisms from Yucatán Peninsula (México) as a potential natural source of new antimicrobial compounds against multidrug-resistant pathogens

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Background: Antibiotic resistance has become a global health emergency and new therapeutic options to treat multidrug-resistant pathogen infections are indisputably needed. Oceans constitute an important natural source of bioactive molecules mainly due to their high biological diversity. Porifera (sponges) and Cnidaria (soft coral) are the most productive phyla regarding this aspect. Here we report the antimicrobial activity found in organic extracts of marine invertebrate species collected along the coasts of the Yucatan Peninsula and selected according to chemotaxonomical criteria.

Materials/methods: Samples were collected in different coastal zones of the Yucatan Peninsula, during three different periods of time (2016-2018). Taxonomic identification of sponges was performed and the organic extracts were prepared. *In vitro* antimicrobial screening of sixty-three marine organisms (50 sponges and 13 ascidians) against four bacterial species of multidrug-resistant pathogens, three gram-negative (*Acinetobacter baumannii*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*) and the gram-positive *Staphylococcus aureus,* was conducted in this study. MICs were evaluated through microdilution assay.

Results: Eight out of sixty-three species displayed activity against the bacteria tested (TABLE 1), being the organic extracts of *Agelas citrina* and *Haliclona curacaoensis* the most active, and reflecting respectively MICs of 0.5-8 and 32 mg/L. Four extracts (*A. dilatata*, *A. citrina*, *H. curacaoensis* and *A. compressa*) showed antibacterial activity against all pathogenic species tested, while the rest exhibited a narrow-spectrum antibiotic activity. Other extracts of marine organisms did not present antimicrobial activity (MICs ≥512 mg/L).

Conclusions: This work constitutes the first wide antimicrobial screening report of the marine sponges and ascidians collected from the Yucatán Peninsula, México. Extracts of some marine species showed a relevant antimicrobial activity. Purification and identification assays of the active compounds are currently being developed.

Species	MIC (mg/L)			
	Acinetobacter baumannii ATCC 17978	*Klebsiella pneumoniae* ATCC 700603	*Pseudomonas aeruginosa* ATCC 27823	*Staphylococcus aureus* ATCC 29213
Agelas citrina	**8**	**8**	**8**	**0,5**
Agelas dilatata	128	64- 128	**32**	64
Agelas sceptrum	≥512	256	64	>512
Amphimedon compressa	**32**	**32**	**32**	**32**
Monanchora arbuscula	≥512	≥512	≥512	16
Haliclona curacaoensis	**4**	**16**	**32**	**4**
Dysidea sp.	**16**	≥512	≥512	32
Aiolochroia crassa	**32**	128	128	64

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Abstract 1824

Influence of empirical piperacillin-tazobactam on 30-day mortality in bacteraemia due to ESBL-producing versus non-ESBL-producing non-AmpC *Enterobacteriaceae*

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Background: The comparative efficacy of piperacillin-tazobactam (PTZ) against non-ampC Enterobacteriaceae depending on the production of ESBL is unclear. The aim of the study was to assess the possible influence of empirical therapy with piperacillin-tazobactam (PTZ) on 30-day mortality in patients with bacteraemia due to susceptible non-ampC ESBL-producing compared with non-ESBL-producing *Escherichia coli*, *Klebsiella* spp. and *Proteus mirabilis* (EKP).

Materials/methods: Retrospective analysis of a prospectively collected database of patients with bacteraemia diagnosed at a 750-bed university hospital in Barcelona (Spain) from January 2003 to December 2018. Monomicrobial episodes due to EKP susceptible to PTZ (MIC≤ 8 mg/L) and empirically treated with PTZ were selected. Multivariate analysis was performed by a step backward logistic regression procedure.

Results: A total of 1323 EKP bacteraemia episodes were included of which 109 (14.7%) were due to ESBL-producers. In univariate analysis, 30-day mortality was associated with ESBL-producers in episodes with a urinary tract infection source (7/42 [16.7%] *vs.* 26/412 [6.3%]; OR 2.9, 95%CI 1.2-7.3, p=0.02) but not in those with other sources (9/67 [13.4%] *vs.* 89/802 [11.1%]; OR 1.2, 95%CI 0.5-2.5, p=0.5). In episodes with a urinary source, ESBL-producers remained an independent predictor of 30-day mortality (OR 3.1, 95%CI 1.1-9.1) along with age over 65 (OR 3.8, 95%CI 1.3-10.5), an ultimately/rapidly fatal prognosis of underlying disease (OR 3.6, 95%CI 1.5-8.4), chronic corticosteroid therapy (OR 6.8, 95%CI 2.7-16.9), neutropenia (OR 5.3, 95%CI 1.4-19.1) and shock (OR 5.2, 95%CI 2.2-12.3)..

Conclusions: In patients with PTZ-susceptible *E.coli, Klebsiella* spp. or *P.mirabilis* bacteraemia receiving empirical therapy with PTZ, a very good outcome (30-day mortality below 10%) seems to be a reasonable expectation only for those with a urinary tract infection due to non-ESBL producers.

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Abstract 1826

Respiratory ß-2-microglobulin exerts direct antimicrobial activity

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Background: The respiratory tract is a major entry site for pathogens into the human body. To combat bacterial infections, the immune system has a large variety of host defence mechanisms at its disposal. Part of the innate immune system and a first line of defence are antimicrobial peptides (AMPs). To search for novel AMPs from the human respiratory tract, a peptide library established from human broncho-alveolar-lavage (BAL) fluid was screened for antimicrobial activity against Gram-positive and Gram-negative bacterial pathogens.

Materials/methods: The peptide library was prepared from 20 liter of pooled human BAL. Peptides and small proteins were extracted by acetic acid and separated through ultrafiltration (cut-off 20 kDa). Employing reversed phase chromatography 76 different peptide fractions were generated from the BAL pool. Antimicrobial activity was determined by agar diffusion assays allowing the efficient detection of antibacterial activity within a small sample size. Bacterial membrane integrity was measured by sytox green uptake and bacterial cells were visualized by transmission electron microscopy (TEM).

Results: After three testing-cycles and subsequent purification of active BAL fractions we identified ß-2-microglobulin (B2M) for its antimicrobial activity. B2M is a subunit of the MHC-1 receptor complex present at the surface of every nucleated cell. It is known to inhibit the growth of *Listeria monocytogenes* and *Escherichia coli* and to facilitate phagocytosis of *Staphylococcus aureus*. Using commercially available B2M we could confirm a dose-dependent inhibition of *Pseudomonas aeruginosa* as well as *L. monocytogenes*. To localize AMP activity within the B2M sequence, peptide fragments of the molecule were tested for antimicrobial activity. Sytox green uptake into bacterial cells following the exposure to B2M was determined and revealed a dose-dependent loss of bacterial membrane integrity. TEM analysis showed areas of disrupted bacterial membranes in *L. monocytogenes* incubated with B2M and high amounts of lysed bacterial cells.

Conclusions: In conclusion B2M as part of an ubiquitous cell surface complex may represent a potent antimicrobial agent by interfering with bacterial membrane integrity.

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Abstract 1828

Improved detection of van-B bearing *E. faecium* isolates in a German hospital laboratory by a modified routine workflow for antimicrobial susceptibility testing

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Background: Vancomycin-resistant *E. faecium* (VRE) are an emerging problem in the German health care system. Various factors are under discussion to enhance VRE-spread. One factor that may contribute to the spread of VRE is the low expression of Vancomycin-resistance. Facing a significant increase of VRE in the past two years, our hospital laboratory started to improve the detection of Vancomycin-susceptible Van-B positive isolates in developing a new workflow for antimicrobial susceptibility testing (AST) adding a Van-A/Van-B-PCR and chrome agar plates to the routinely performed AST.

Materials/methods: ***Routine workflow:*** AST was performed with VitekII AST-611 (biomerieux) alternatively with agar diffusion (biorad) following EUCAST standard procedures and breakpoint interpretation guidelines. First time isolated VRE in a patient underwent Van-A/Van-B-PCR (TiBMol). ***Modified workflow:*** Every Vancomycin susceptible *E. faecium* isolate underwent Van-A/Van-B-PCR-Testing (TiBMol). *E. faecium* isolates from material other than VRE-screening material were streaked on chromagar (bioMerieux) in parallel to the purity control. Data analysis was performed with hybase®-system to eliminate copy-strain counts of isolates.

Results: From 01.03. to 31.08.19 a total amount of 686 E. faecium AST from 361 patient was carried out. 186 isolates were tested Vancomycin resistant, 175 Vancomycin susceptible. From the Vancomycin susceptible strains 35 (20%) beared the Van-B-Gene detected by PCR, none show a Van-A gene. The parallel to AST streaked chromagar showed a positive VRE result in 32 cases.

AST result for Vancomycin

	resistant	susceptible
Total Number of patient isolates	186	175
Van-A positive isolates	n.e.	0
Van-B positive isolates	n.e.	35 (20,0%)
Chromagar (modified workflow)	n.e.	32 (2 negative, one not evaluable)

Conclusions: We found a remarkable 20% proportion of phenotypically Vancomycin-susceptible and Van-B-positive E. faecium -isolates after modification of the AST-workflow. Those isolates would normally be undetected by routine AST and therefor escape surveillance and further hygiene measures. VRE chromagar additionally streaked out to the purity control may help to detect these strains. Further investigation has to be done on the performance on other automated or manual AST systems. Of further interest would be the genomic analysis of these strains in comParison to phenotypically vancomycin resistant strains to understand their role in VRE-epidemiology.

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Abstract 1829

Human endogenous retroviruses as markers of severity in sepsis

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Abstract third-party references: bioMerieux, Hospices Civils de Lyon

Background: Sepsis is defined as a life-threatening organ dysfunction caused by a dysregulated host response to infection. The heterogeneity of the disease present a major clinical challenge with regard to the therapeutic coverage, and this day the proposed markers are not enough to stratify patients. The human endogenous retroviruses (HERVs) could be relevant markers, due to their expression in inflammatory and autoimmune diseases and their emerging immunological properties (envelopes and non-coding sequences).

Materials/methods: In order to determine to what extent the HERVs are expressed and modulated in the blood compartment, in inflammatory and immunocompromised contexts *in vitro* and *in vivo*, we used a custom high density DNA chip allowing the transcription analysis of 360,689 HERVs. The HERVs expression was objectified in endotoxin tolerance (ET) *ex vivo* model in peripheral blood mononuclear cells (PBMCs) of healthy volunteers and in whole blood of healthy volunteers and 120 septic shock patients, stratified or not according to the immune status determined by mHLA-DR level.

Results: About 7 % of HERVs are expressed in the blood compartment including notably hundreds of identified HERV-H and PRIMA-41 loci. The HERV transcriptome is modulated in *ex vivo* ET model, letting appear two major transcriptional phenotypes. Major differences in HERVs expression was observed between septic patients and healthy volunteers. More, the HERVs transcriptome was modulated between septic patients, according to their immune status. Using a signature of modulated elements, we have been able to stratify an independent validation cohort with a clear difference in severity between two clusters of patients.

Conclusions: We illustrated the importance of addressing both the exome and repetitive DNA repertoires to increase our understanding of sepsis pathophysiology. The added value of these newly identified HERVs markers should be evaluated in a larger cohort of septic patients. If they prove to be robust, they could further serve as a stratification tool prior to immunostimulatory treatment and to monitor drug efficacy, which could contribute to the reduction of mortality in sepsis patients.

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Abstract 1831

Detection of rifampin and isoniazid resistance using molecular testing to initiate an ethambutol-free 3-drug regimen in pulmonary tuberculosis: a French non-inferiority multi-centre randomised clinical trial

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Background: Current guidelines recommend initiation of a 4-drug regimen (rifampin RIF, isoniazid INH, pyrazinamide PZA and ethambutol EMB) for drug- susceptible tuberculosis (TB). The rationale behind the use of EMB is to prevent the emergence of resistance to RIF in case of primary resistance to INH (5% prevalence in France in 2018). Early detection of INH resistance using molecular testing may allow to initiate treatment with an EMB-free 3-drug regimen. This strategy has not been evaluated in settings with low incidence INH resistance.

Materials/methods: FAST-TB, a phase 4 French multicenter, open-label non-inferiority trial, compared two strategies: (i) PCR-based detection of INH and RIF resistance at baseline using Genotype MTBDR *Plus* v2.0® and then start a 3-drug containing TB regimen without EMB if no resistance detected (PCR arm), vs. (ii) standard 4-drug combination and treatment initiation, pending phenotypic drug-susceptibility testing results (C arm). Adult patients with acid-fast bacilli (AFB+) on respiratory samples were enrolled; patients with previous TB treatment were excluded from the study. The primary endpoint was the proportion of patients with treatment success defined as bacteriological and clinical cure within the first year after enrollment. A non-inferiority margin of 10% was used.

Results: 201 patients were randomized, 104 in the PCR arm and 99 in the C arm: 27% were female, median age was 37 [IQR: 27-51] years, 72% were born in Africa, and 5.4% were HIV-infected. Chest X-ray showed excavations in 64% of the cases and half of the participants had bilateral abnormalities. We detected 7 (3.5%) patients with INH phenotypic resistance, 2 in the PCR arm and 5 in the C arm. Overall, 167 patients met criteria of treatment success: 86/104 (82.7%) in the PCR arm and 81/99 (81.8%) in the C arm with a difference of +0.87% (95%IC: -9.64; 11.39), meeting non-inferiority criteria.

Conclusions: In a setting with low incidence of TB and INH resistance, the use of a 3-drug combination with RIF, INH and PZA based on early detection of INH and RIF resistance using MTBDR *Plus*® test on AFB+ sputum samples was non-inferior to a 4-drug containing regimen.

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Abstract 1832

Bacterial profile associated with oral cancer: metagenomic analysis in oral micro-niches

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Background: Oral microbiota is associated with Oral Squamous Cell Carcinoma (OSCC), mainly by persistent inflammatory processes and production of acetaldehyde. Variation of bacterial communities within the oral cavity depending on anatomical location (niches) is well established. Studies with high-throughput sequencing describe the composition and abundance total bacteria in the oral micro-niches. However, at present no studies have characterized different oral micro-niches in OSCC. The objective of this study was to determine and compare tumoral tissue, saliva and dental plaque bacterial profiles, in patients with OSCC.

Materials/methods: A total of nine OSCC patients were included. Samples included saliva, dental plaque and tumor tissue. DNA was extracted from all samples. Subsequently, libraries were prepared using Illumina Nextera XT®. For sequencing paired-end MiSeq of Illumina® was used. Trimmomatic software was used to evaluate quality. Moreover, identification of bacteria in each sample was performed with Kraken Aligner V1.0. Initially, bacteria associated with tumoral tissue was identified. Subsequently, intra and inter-patient samples where bacteria in saliva and dental plaque samples were statistically significant (p-value < 0.05) were compared.

Results: In tumoral tissue of patients with OSCC, eighteen species of bacteria were identified. The more characteristic bacteria in OSCC were a profile of nine species of bacteria *Riemerella anatipestifer, Chlorobium phaeobacteroides, Yersinia enterocolitica, Proteus mirabilis, Mycoplasma hyorhinis, Flavobacterium psychrophilum, Streptococcus pyogenes,* and *Mycoplasma hyopneumoniae* in a sub-group of patients, and *Alteromonas mediterranea* in other sub-group of patients. After saliva and dental plaque comParison high similarity was observed, where the more abundant bacteria were *Prevotella melaninogenica, Capnocytophaga ochracea, Fusobacterium nucleatum* and *Haemophilus influenzae,* nevertheless no sub-groups were observed. Last, bacterial profile associated which OSCC in saliva and dental plaque was scarce or absent representing less than 3% of the total bacteria in those samples.

Conclusions: A profile of nine species of bacteria were predominant in tumoral tissue. Saliva and dental plaque samples do not contain bacteria associated with OSCC.

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Abstract 1834

Vancomycin pharmacokinetics in patients undergoing extracorporeal membrane oxygenation after 48 hours of treatment

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Background: Extracorporeal membrane oxygenation (ECMO) could affect drug pharmacokinetics (PK), which is critical for antimicrobial effectiveness. Vancomycin PK during ECMO has been previously studied, but only in the first 48 hours of treatment (Initial-48h). The aim of this study was to assess vancomycin PK during ECMO after 48 hours of treatment (After-28h) and compare with those estimated from the complete cohort and initial-48h.

Materials/methods: A retrospective observational study was carried out in patients under simultaneous treatment with vancomycin and ECMO between January 2016 and January 2019 whose vancomycin serum concentrations were measured. The variables recorded were: ECMO type and indications, renal replacement therapy, dose, creatinine, exitus, vancomycin serum concentration and day of the analysis. The PK analysis was performed using Abbottbase Pharmacokinetics Systems software (Abbott Diagnostics Division, Irving, TX, USA), adjusting experimental data according to a compartmental linear model using Bayesian estimates. Two-sided t-student test was used for comparing vancomycin PK parameters (PKp) obtain from i48h, a48h and the complete cohort.

Results: Six patients were excluded for lack of data and 13 patients were analyzed. Most patients 84.6%(11) underwent venoarterial ECMO. ECMO indications were 7(53.8%) cardiogenic shock, 3(23%) ventricular dysfunction and others 3(23%). Exitus occurred in 6(46.2%) patients, and 3(23%) underwent concomitant renal replacement therapy. Vancomycin was measured in 38 samples, 28(73.7%) after 48 hours of treatment.

Vancomycin PK-p estimated from a48h, i48h and the complete cohort are depicted in table 1. No significant differences were observed in any case ($p>0.05$), but a48h, a tendency towards higher Vd, Cl and $T_{1/2}$ and lower AUC were detected.

Table 1

PKp	After-48h	Initial-48h	Complete cohort
Vd (L/kg)	0.864±0.304	0.799±0.1	0.847±0.267
Cl (L/h/kg)	0.039±0.017	0.036±0.010	0.039 ± 0.015
AUC (mg*h/L)	605.6±165.6	831.4 ± 402.3	671.1 ± 270.6
$T_{1/2}$ (h)	18.38±11.64	17.86±6.9	18.24 ± 10.5

Vd: Volume of distribution, Cl: Vancomycin clearance, AUC: Area under the curve, $T_{1/2}$: Half-life

Conclusions: Vancomycin PKp estimated from our population are similar to those previously described, including high variability. Vancomycin PKp after-48h were not previously described, and despite being similar to other populations, the tendencies observed warranted further studies in bigger populations to detect finest variations.

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Abstract 1835

Tuberculosis impacts immune-metabolic pathways resulting in perturbed cytokine responses

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Background: Tuberculosis (TB) is a major public health problem for which host-directed therapeutics are proposed as novel treatment strategies. However, their successful development still requires a more comprehensive understanding of how *Mycobacterium tuberculosis* (*M.tb*) infection impacts immune and metabolic host responses.

Materials/methods: To address this challenge we applied standardised immunomonitoring tools to compare induced immune responses between individuals with latent *M.tb* infection (LTBI) and active TB disease (n=50). Whole blood was collected and stimulated with TB antigens (TB Ag), Bacillus Calmette-Guérin (BCG), IL-1b, and a Null control. Immune responses were analyzed at proteomic, transcriptomic, metabolomic and cellular levels. The TB patients were analyzed both prior to, and after, successful antibiotic treatment.

Results: This approach revealed multiple differential immune responses in active TB disease at transcriptomic, proteomic, metabolomic and cellular levels. These immune differences were absent after successful antibiotic treatment highlighting their disease-specific nature. Integrative analysis of these different datasets permitted a detailed characterisation of the perturbed IFNγ response in TB disease. Specifically TB patients had different IFNγ responses as compared to LTBI controls, at the proteomic, but not transcriptomic level. We also identified dysregulated IL-1 responses to BCG stimulation in TB patients, for both agonist (IL-1a/b) and antagonist (IL-1RA) responses. Furthermore, the combination of novel digital ELISA readouts with Mass Spectometry identified novel immune-metabolic drivers of IL-1RA secretion.

Conclusions: This study improves our knowledge of how *M.tb* alters key immune responses, and will support the design of improved diagnostic, prophylactic and therapeutic tools.

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Abstract 1839

Actinotignum schaalii in breast abscesses, an emerging pathology? Report on five cases

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Background: *Actinotignum schaalii* are Gram-positive rod-shaped bacteria known to be responsible for urinary tract infection in elderly and patient with urological conditions. Breast abscesses caused by *A. schaalii* are rare (only two cases previously described), so few clinical or microbiological data were available. This review of five cases describes the clinical profile of patients with breast abscesses caused by *A. schaalii*, as well as the antimicrobial susceptibility.

Materials/methods: From 2017 to 2019, clinical isolates of *A. schaalii,* isolated from breast abscesses from patients hospitalized in the University Hospital of Poitiers were included. Culture identification was performed by MALDI-ToF (Vitek-MS, bioMérieux). Antimicrobial susceptibility was assessed by the E-test method (bioMérieux), on Brucella Blood Agar media plates (bioMérieux). MICs were interpreted using the EUCAST 2019 v9.0 breakpoint table. In order to determine the analytical performance of culture to identify *A. schaalii*, 20 breast abscess samples with similar clinical presentation were tested. The presence of *A. schaalii* DNA was challenged using a specific qPCR assay targeting the *gyrB* gene, as previously described [1].

Results: Among the five patients, the median age was 46 years (from 37 to 50 years). All patients had a polymicrobial infection, 80% were active smokers, 60% had an underlying immunodepressive condition (diabetes, cancer, immunodepressive therapy) and 40% had a chronic abscess. Evolution was favorable in every case, without recurrence at six months. Treatment was based in all cases on surgical drainage of the abscess. Three out of five patients also received a short course of antibiotics. Antimicrobial susceptibility is detailed in Table 1. *A. schaalii* DNA was detected in all samples with positive *A. schaalii* culture. The qPCR assay was negative for all *A. schaalii* negative breast abscess samples (n=20). These latter included negative and positive bacterial cultures.

Table 1: In vitro activity of 11 antimicrobial agents against 5 clinical isolates of *A. schaalii* recovered from breast abscesses.

Antibiotics	MIC (mg/L)				
	Case 1	Case 2	Case 3	Case 4	Case 5
Penicillin G	0.012	0.016	0.016	0.012	<0.002
Amoxicillin	0.094	0.064	0.094	0.094	<0.016
Gentamicin	2	3	2	4	0.38
Vancomycin	0.125	0.19	0.094	0.094	0.047
Linezolid	0.25	0.19	0.25	0.25	0.125
Moxifloxacin	0.5	0.38	0.5	0.5	0.25
Ciprofloxacin	1.5	1.5	4	3	4
Tetracycline	0.125	0.064	0.125	0.094	0.094
Cotrimoxazole	>32	0.047	>32	0.25	0.064
Clindamycin	0.023	>256	>256	0.032	24
Quinupristin-Dalfopristin	0.19	0.19	0.125	0.094	0.125

Conclusions: *Actinotignum schaalii* breast abscesses occur mainly in young patients with a smoking history. Infection can be diagnosed with standard culture methods and are frequently polymicrobial. Resistance to clindamycin, ciprofloxacin and cotrimoxazole were frequent.

[1] Bank et al. Actinobaculum schaalii, a Common Uropathogen in Elderly Patients, Denmark. Emerg Infect Dis 2010;16:76–80. https://doi.org/10.3201/eid1601.090761.

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Abstract 1840

ComParison of early effects of *Streptococcus pneumoniae* vaccination policies on nasopharyngeal carriage in a Palestinian population

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Abstract third-party references: my abstract supported by Al Quds university

Background:*Streptococcus pneumoniae* can asymptomatically colonize the nasopharynx and cause a various range of illnesses. Pneumococcal conjugate vaccines (PCVs) are at present used in different countries. The aim of the study is to determine the effect of different vaccination policies PCV7/13 to that PCV10 on the carriage rates and comparing the impact of different vaccination policies in East Jerusalem and West Bank region.

Materials/methods: Five cross-sectional surveillances *of S.pneumoniae* were carried out in East Jerusalem and Palestinian authority (PA), where two Palestinian populations with different vaccination policies were screened, with an annual average of 348 and 616 children., respectively, were performed during 2009-2016. Nasopharyngeal swabs and data were collected from children less than 5 years old. In East-Jerusalem (EJ), PCV7 was implemented in 2009 and replaced by PCV13 in late 2010, while in Palestine (PA), PCV10 was implemented in 2011.

Results:A total of 4686 children were screened in EJ (n=1615) and PA (n=3070), the overall rate of *S.pneumoniae* carriage did not change significantly during the 5 first years of the study, in either population. The pediatric subjects from EJ were determined to carry *S.pneumoniae* during the 5 years study, 2009, 2010, 2011, 2014, and 2016 as 28.9%, 29.3%,26.9%,30.7% and 16.9%, respectively. In addition 35.9%, 33.6%, 28.8%, 28.6% and 32.9% of the pediatric subjects from PA were shown to carry *S.pneumoniae in 2009-2016*, respectively. By year 2016,*S.pneumoniae* carriage was reduced significantly in EJ from ff29% on average to ff17%,following seven years application of PCV7/13. In PA, where follow-up included only 5 years after PCV10 application, *S.pneumoniae* carriage remained ff30%.

Interestingly, VT7 strains gradually decreased following PCV implementation. Following vaccine implementation, during the study period, there was a significant decrease in carriage of *S.pneumoniae* in the EJ between 2009 and 2016. No significant variation was seen in the overall carriage of *S.pneumoniae* between 2009 to 2016 in PA. PCV10 was introduced to PA late in 2011, but *S.pneumoniae* carriage was approximately (160/566) 28% in2011, prior to vaccine introduction, and (216/656), 32.9% in 2016, five years following vaccine implementation.

Conclusions: Following PCV implementation, adecrease in the prevalence of VT strains was observed in EJ, and PA.

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Abstract 1842

A selective culture medium for screening ceftazidime/avibactam resistant Gram-negative isolates

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Background: The emergence of carbapenemases in Enterobacterales, in particular of the Klebsiella pneumoniae carbapenemases (KPCs) that are associated to multidrug resistance, represent a high priority for the development of novel antibacterials. Avibactam, a non-β-lactam inhibitor, is able to restore the efficacy of ceftazidime against KPC producers. However, resistance to the novel ceftazidime-avibactam (CAZ-AVI) association is increasingly reported among clinical strains expressing KPC variants. Taking in account the increasing isolation of those CAZ/AVI-resistant enterobacterales, a selective culture medium for screening CAZ-AVI-resistance in Gram-negative bacteria (*Enterobacterales*, *Pseudomonas aeruginosa)* was developed.

Materials/methods: This medium (SuperCAZ/AVI) contains ceftazidime, avibactam, zinc sulfate, daptomycin, and amphotericin B. It was evaluated with 50 CAZ/AVI-susceptible (40 *Enterobacterales* including *Enterobacter cloacae*, *Klebsiella pneumoniae, and Escherichia coli*, 10 *Pseudomonas aeruginosa), and* 42 CAZ/AVI-resistant (20 *Enterobacterales* including *Enterobacter cloacae*, *Klebsiella pneumoniae, and Escherichia coli, 22 Pseudomonas aeruginosa*) Gram-negative isolates. In addition, testing was performed by spiking stools with a series of resistant isolates, at different concentrations.

Results: Sensitivity and specificity of detection of the SuperCAZ/AVI medium were ca. 100%. By testing stools spiked with CAZ/AVI-resistant or -susceptible Gram-negative bacteria (92 isolates), an excellent performance of the medium was observed, with a lowest detection limit ranging from 10^1 to 10^2 CFU/ml.

Conclusions: The Super CAZ/AVI medium constitutes a screening medium aimed to detect CAZ/AVI-resistant bacteria regardless of their resistance mechanism. This Super CAZ/AVI medium may be used for prospective screening, and epidemiological surveys that may contribute to rapidly detect carriers of CAZ/AVI resistant isolates, and consequently to rapidly implement infection control measures in order to limit their spread.

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Abstract 1843

Is it realistic to offer an antibiotic susceptibility bonus to developers?

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Background: Return on investment for antibiotic development needs to be amended, without jeopardizing the future efficacy of novel compounds through high volume sales. This study explores the feasibility of a financial bonus that depends on levels of antibiotic susceptibility over time after approval. This bonus is intended to align pharmaceutical industry interests with public health interests through prolongation of efficacy through time. But how could such a bonus scheme work, with regards to magnitude and eligibility?

Materials/methods: This multidisciplinary (business, economics and microbiology) study utilized literature study, market analyses, Delphi consultation, informal interviews, and investment analysis.

Results: Findings from this (public-sector funded) project show that a suitable bonus magnitude should be sufficiently high to deter profit-driven mass marketing, low value or riskier sales, but not so high that the company would prevent access to their product where there is justified need. To be effective it must be clear that it is not intended as a traditional R&D incentive (indeed a large-scale monetary reward is needed independently from this scheme). What is proposed here is a proper bonus paid for strong product performance -- i.e. proven ability to stave off resistance. Since not all factors contributing to resistance will be under company control, falling below the susceptibility threshold does not imply being penalized – it is simply that the product did not perform to this higher standard. With regard to the susceptibility criterion, there are advantages in utilizing epidemiological cut-offs to determine bonus eligibility rather than MIC break points to avoid gaming strategies. Linear eligibility thresholds could run from 100% wild type (weight=1) to ≤50% (weight=0). Additional binary weights can be applied to ensure that only useful and accessible products are eligible.

Conclusions: The theory underlying an Antibiotic Susceptibility Bonus and its different components is backed by market dynamics and experts in the field, and can be facilitated by on-going efforts in microbiology and lab quality standardization and widespread AMR surveillance initiatives. The bonus could be considered alongside -- or as a performance-related component of -- a pull-based R&D reward such as a market entry reward or an insurance/supply contract.

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Abstract 1844

Clinical and laboratory features of mixed invasive mycoses in adult haematologic patients with invasive aspergillosis

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Background: We investigated the features of mixed invasive mycoses (IM) in hematologic patients.

Materials/methods: Retrospective study in 1998-2019 yy. Diagnostic criteria EORTS/MSG, 2008 were used.

Results: In group I we included 72 adult hematologic patients with combination of invasive aspergillosis (IA) and non-*Aspergillus* caused mycoses, median age – 41 years (18 - 75), males – 71%. The comParison group consisted of 519 hematologic patients with IA, median age – 46.5 years (18 – 79), males – 56%.

The predominant underlying diseases were acute leukemia (51% vs 44%) and lymphomas (35% vs 34%). Mixed IM less often developed in patients with chronic leukemia (6% vs 9%) and multiple myeloma (3% vs 8%). The main risk factors were severe neutropenia (79% vs 73%), and steroid therapy (72% vs 69%). Mixed IM occurred significantly more frequently in patients with lymphocytopenia (63% vs 52%, p = 0.01), immunosuppressive therapy (33% vs 23%, p = 0.04), ICU stay (29% vs 7%, p = 0.0001), and after allo-HSCT (33% vs 23%, p = 0.04).

In patients with mixed IM ≥ 2 organs (29% vs 5%, p = 0.001), CNS (15% vs 2%, p = 0.03), and paranasal sinus involvement (10% vs 4%) were more often observed; respiratory failure (51% vs 34%, p = 0.0001), hemoptysis (13% vs 5%, p = 0.005), and hydrothorax (9% vs 3%) were more often noted. The main causative agents of IA were *A. fumigatus* (40% vs 43%) and *A. niger* (34% vs 33%). Non-*Aspergillus* pathogens were: mucormycetes – 35%, *Pneumocystis jirovecii* – 25%, *Candida* spp. – 22%, hyalohyphomycetes - 9%, *Cryptococcus neoformans* – 4%, rare yeasts – 4%, and pheohyphomycetes – 1%. Overall 12-week survival in the mixed-infection group was significantly lower (52% vs 84%, p = 0.0001).

Conclusions: Mixed invasive mycoses occurred in patients with persistent lymphocytopenia (63%), long-term immunosuppressive therapy (33%), ICU stay (29%), and after allo-HSCT (33%). Non-*Aspergillus* etiological agents were mucormycetes – 35%, *Pneumocystis jirovecii* – 25%, and *Candida* spp. – 22%. In patients with mixed invasive mycoses, ≥ 2 organs (29% vs 5%, p = 0.001) and CNS involvement (15% vs 2%, p = 0.03) were more often observed. Overall 12-week survival: 52% vs 84%, p = 0.0001.

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Abstract 1848

Investigation and control of measles outbreak in Balkh province, Afghanistan, Dec 2016- 2017

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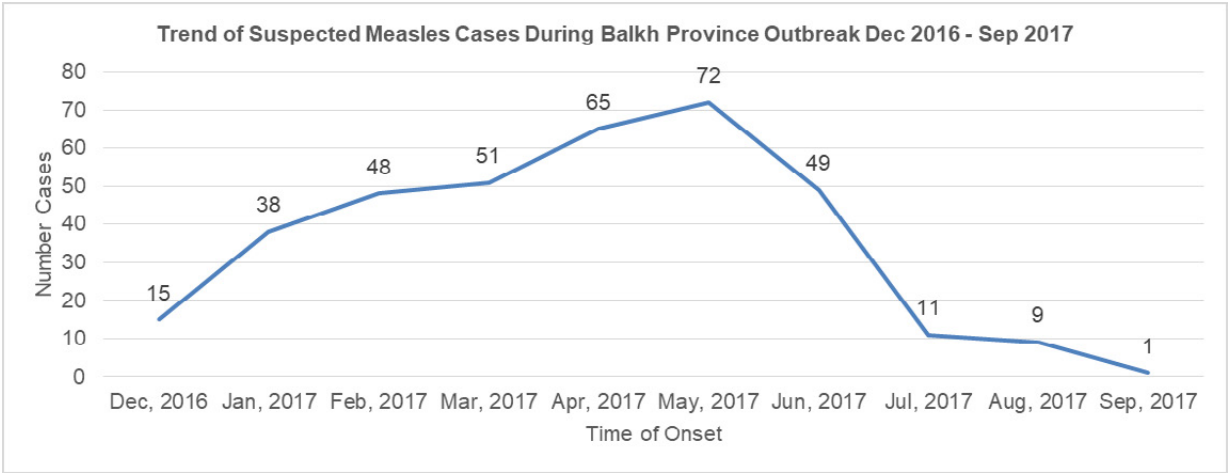
Background: Measles is a most contagious infection known to humans, and ranks among the top four childhood killers worldwide. Despite immunization progression, unfortunately Afghanistan is still an endemic country for measles outbreaks. Over 20 of the 34 provinces in Afghanistan, of the 25,000 reported cases in 2017, 1235 cases reported by Balkh province

Materials/methods: On December 2016 the index suspected measles case reported by surveillance focal point from an internally displaced people (IDP) encampment in Dehdadi District of Balkh province. Outbreak investigation conducted, a measles case defined as any person with fever, maculopapular rash, conjunctivitis and cough or coryza in the affected area since 3rd Dec 2016. Rapid assessment conducted in the area for vaccine coverage and active case finding. Blood serum specimen collected and shipped to Central Public Health Laboratory in Kabul and confirmed by ELISA-IgM test.

Results: Of the 546155 population 359 suspected measles cases identified attack rate AR = 6.6/10000 and male to female ratio 1.3:1. Of the173 cases tested for measles IgM, 131(75.7%) (95% CI 68.6, 81.9) confirmed. There were 17 deaths that indicated case fatality rate (CFR) (4.7%) (95% CI 2.5, 6.9). The mean age of cases was 30.6 months and ranged 1 month -29 years. One dose of vaccination coverage among the IDP population was 18%, while only 6 (1.67%) of all cases had received one dose of measles vaccine. We conducted two rounds village-wide immunization campaign and vaccinated 61084 children, subsequently, cases ceased.

Conclusions: To eradicate measles, high vaccination coverage must be maintained, and this must be the focus of local and national authorities. Low vaccination coverage looks likely caused of the outbreak. The high contagiousness of measles requires initial widespread supplemental vaccination to stop a large epidemic; small efforts will not be successful.



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Abstract 1851

An ultrasensitive test for the detection of Clostridiodes difficile toxins in stool samples using a single-molecule counting method

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Background: *Clostridiodes difficile* infection is considered an urgent antibiotic resistance threat by the CDC, accounting for ff225,000 hospitalizations, 12,800 deaths, and ff$1B in healthcare costs in the US in 2017. The presence of the secreted toxins A and B, that cause the devastating symptoms of this gastrointestinal infection are diagnostic of *C. difficile* infection (CDI). However, the rapid testing methods currently used to detect CDI lack accuracy: Enzyme immunoassays are specific but lack sensitivity and nucleic acid amplification tests (NAAT) are sensitive but lack specificity. This has resulted in the adoption of complex algorithms for *C. difficile* diagnosis. We present results for a new toxin test that demonstrate both high sensitivity and specificity for *C. difficile* toxins A and B on a fully automated benchtop platform.

Materials/methods: The detection technology uses non-magnified digital imaging to count single toxin molecules that are tether together target-specific magnetic and fluorescent particles. The 30 minute method includes the use of a dye-cushion to eliminate wash steps and the need for time consuming specimen preparation steps. We determined analytical performance characteristics of the test using negative clinical stool samples spiked with purified toxin. To assess clinical performance, we tested 787 stool samples from 5 clinical sites and compared the results with the cellular cytotoxicity neutralization assay (CCNA).

Results: The test's LoD for toxin B was 60 pg/mL. ComParison of the new test to the CCNA reference method gave 95% positive percent agreement (PPA) (83/87 samples) and 95% negative percent agreement (NPA) (667/700 samples).

Conclusions: The results presented demonstrate the potential of the *C. difficile* toxin test to aid in the diagnosis of CDI and reduce the need for testing algorithms that require multiple assays.

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Abstract 1853

Activity of the β-lactamase inhibitor LN-1-255 against plasmid-mediated Class C cephalosporinases enzymes from *Enterobacteriaceae*

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Background: Class C β-lactamases are clinically relevant cephalosporinases encoded on the chromosomes or plasmids of many *Enterobacteriaceae.* Overexpression can confer resistance to broad-spectrum cephalosporins, such as cefotaxime or ceftazidime. Classical inhibitors such as clavulanic acid, sulbactam, and tazobactam have a very limited effect on AmpC β-lactamases. Avibactam, approved in 2015, was the first β-lactamase inhibitor that provide activity against these enzymes. The aim of the study was to evaluate the inhibition ability of the experimental inhibitor LN-1-255 against plasmid-mediated AmpC enzymes.

Materials/methods: bla_{DHA-1}, bla_{DHA-7}, bla_{CMY-2}, bla_{CMY-54}, bla_{FOX-3} and bla_{FOX-4} genes encoding plasmid-mediated class C enzymes were cloned to pBGS18 and transformed into *Escherichia coli* TG1. MICs were performed to cefoxitin (FOX), ceftazidime (CAZ) and the combinations cefoxitin/LN-1-255 and ceftazidime/LN-1-255. bla_{CMY-2} and bla_{CMY-54} genes were cloned into the p-GEX-6P-1 plasmid, electropored into *E. coli* BL21 and encoded proteins were then purified. For inhibition kinetics, IC_{50} for tazobactam, avibactam and LN-1-255 was calculated.

Results: The inhibitor LN-1-255 displayed a relevant ability to decrease the MICs to cephalosporins, decreasing 2-32 and 8-2056-fold the MICs to FOX and CAZ, respectively. The IC_{50} of LN-1-255 was in the nanomolar range, 24 and 17 nM for the CMY-2 and CMY-54 β-lactamases, showing excellent hydrolysis efficiency. Avibactam showed a similar efficacy inhibiting CMY-2, being less efficient against CMY-54. Tazobactam displayed an inhibition efficacy 68 and 22-fold lower than LN-1-255 against CMY-2 and CMY-54, respectively.

Conclusions: We describe the inhibitory activity of LN-1-255 against the plasmid-mediated AmpC of *Enterobacteriaceae*. Cephalosporins in combination with LN-1-255 were effective against cephalosporins-resistant strains. LN-1-255 displayed better IC_{50} than tazobactam or avibactam. Therefore, LN-1-255 represents a potential new therapeutic option in combination with cephalosporins against plasmid-mediated AmpC *Enterobacteriaceae*. A complete analysis of kinetic and microbiological assays for all enzymes and inhibitors are currently being developed.

	MICs (mg/L)				IC_{50} (mM)		
***E. coli*+ pBGS18/β-lactamase**	**FOX**	**FOX+LN-1-255 (16 mg/L)**	**CAZ**	**CAZ+LN-1-255 (16 mg/L)**	**β-lactamase inhibitor**	**CMY-2**	**CMY-54**
DHA-1	32	4	64	<0,12	Tazobactam	1.646±0.81	0.370±0.070
DHA-7	32	2	256	<0,12	Avibactam	0.016±0.002	0.091±0.017
CMY-2	128	4	64	0,25	LN-1-255	0.024±0.006	0.017±0.007
CMY-54	64	2	256	0,25			
FOX-3	≥512	256	256	32			
FOX-4	64	16	128	2			

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Abstract 1854

Infection and mortality rates due to carbapenem-resistant organisms in infants admitted to the neonatal unit

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Background: Healthcare-associated multidrug resistant bacterial infections, particularly due to carbapenem resistant organisms (CRO), has been on the rise globally. Most studies on CRO prevalence are from high-income countries, with very few from low-middle income countries (LMIC). Although limited, the reported prevalence of infections and mortality due to CRO in LMIC has been alarmingly high. This study evaluated the rates of infection and all-cause mortality due to CRO in infants admitted in a hospital from a low-middle income country.

Materials/methods: Positive bacterial cultures from sterile sites in infants admitted to the neonatal unit at Chris Hani Baragwanath Academic Hospital, Johannesburg, South Africa, in 2018, was retrieved from the microbiology laboratory and reviewed retrospectively. Type of organism, susceptibility results and outcomes were recorded. Among these, the Gram-negative isolates, including the CRO, were extracted. Rates and outcomes were analysed.

Results: There were 804 positive cultures (excluding coagulase-negative Staphylococci) from sterile sites, giving an infection rate of 12.6/1000 patient days. Of these 539 (67%) were Gram-negative isolates. The common Gram-negatives were *Acinetobacter baumannii* (225/539; 42%) and *Klebsiella pneumoniae* (229/539; 42%). 176 (78%) of the *Acinetobacter baumannii* isolates and 75 (33%) of the *Klebsiella pneumoniae* isolates were CRO, accounting for 47% of all Gram-negatives. The rate of carbapenem resistant *Acinetobacter baumannii* (CRAB) was 2.8/1000 patient days and carbapenem resistant *Klebsiella pneumoniae* (CRE) was 1.2/1000 patient days. The rates of CRAB varied from a trough of 0.8/1000 patient days to a peak of 5.8/1000 patient days per month, and those of CRE varied from 0.2/1000 patient days to 2.5/1000 patient days per month. The all-cause mortality rate in infants with Gram-negative isolates was 20%. The mortality was 26% in infants with CRAB and 40% in infants with CRE. The all-cause mortality rate in infants with CRO was 30%. The mortality rate in infants with CRO was higher than those with non-CRO (30% vs 11%; $p < 0.05$).

Conclusions: There was a high rate of positive cultures from sterile sites in 2018. Gram-negative organisms predominated, and among these carbapenem resistance was high. Rates of CRO varied over the months, suggesting outbreaks. CRO were associated with high mortality rate.

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Abstract 1855

Colonisation and infection with ESBL-producing and carbapenem-resistant *Enterobacteriaceae* in kidney transplant recipients: risk factors, impact on renal graft function and use of hospital resources

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Background: ESBL-producing and carbapenem resistant (CR) Enterobacteriaceae are a common cause of severe infection, morbidity and mortality in kidney transplant recipients (KTR). Few studies have investigated the risk factors for ESBL-producing/CR Enterobacteriaceae colonization and infection in this group of patients, the effect of colonization and infection on KTR's renal graft function, and the use of hospital resources.

Materials/methods: Retrospective follow-up study on a consecutive series of patients undergoing kidney transplantation at Parma University Hospital (Italy) between January-2016 and December-2018. We examined the difference in risk factors by two-sample Mann-Whitney test, and Fisher's exact test for continuous and categorical variables. Crude and adjusted (donor's/recipient's age, recipient's gender) renal function (eGFR) decline was compared by mixed-effects random-coefficients models, hospital resources by negative binomial regression.

Results: We enrolled 180 KTR (mean recipient's age: 52,42 [SD 12,40]; males 65%; mean donor's age: 54,59 [SD 15,57]) and followed them up for 2-years post transplantation. Cumulative prevalence of colonization 3-months post-transplantation and cumulative incidence of infection were 26,1% and 9,4% for ESBL, and 4,4% and 1,6% for CR. ESBL colonization was associated with hemodialysis vs peritoneal dialysis (93% vs 70% non-colonized), dialysis vintage (mean months: 65,00 vs 41,93) and retention of ureteral stent for more than one month after transplant (28% vs 12%) ($p<0.05$ for all); ESBL infection was associated with retention of ureteral stent (47% vs 13%; p=0,002) whereas CR colonization was associated with surgical complication during transplant admission (50% vs 15% p=0,027). Two patients (both with CR) died over the study follow-up, whereas none of the patients lost the graft. There was a non-statistically significant trend of eGFR yearly decline, being sharper (up to -5mL/min/year) in patients with CR colonization compared to non-colonized. In comParison with non-colonized patients, adjusted mean days of carbapenem treatment in ESBL/CR colonized/infected was 5,6 vs 0,7 (p= 0,002); length-of-hospital stay 5,6 vs 0,7 (p= 0,002); days on drug-resistant-infection intravenous-outpatient-therapy 1,6 vs 0,07 (p= 0,005).

Conclusions: The study shows that ESBL and CR colonization and infection in KTR are associated with longer hemodialysis vintage, urological procedures, and surgical complications, and that they cause an increase in the hospital resources use.

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Abstract 1865

Risk score for non-ventilator-associated hospital-acquired pneumonia (nvHAP)

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Background: Pneumonia is one of the most common healthcare-associated infections, and the burden of disease is higher in non-ventilated than in ventilated patients. Identifying patients at high risk for non-ventilator-associated hospital-acquired pneumonia (nvHAP) allows targeting prevention measures to high-risk patients. We derived and validated a risk score to predict nvHAP in a broad patient collective.

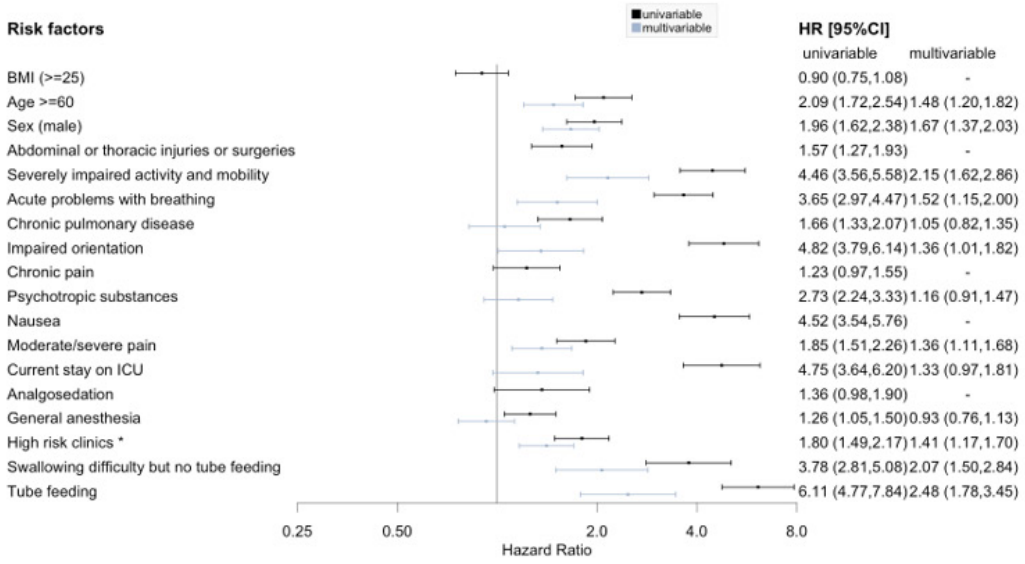
Materials/methods: We included all inpatients ≥18 years of age, discharged during a 2.5-year period from the University Hospital Zurich, Switzerland. The derivation cohort consisted of patients from the first two years; the remainder of patients was included in the validation cohort. The derivation cohort was used to identify distinct and easily available risk factors for nvHAP by applying uni- and multivariable Cox proportional hazards models. These risk factors were used to compute a risk score. Receiver operator characteristics (ROC) analyses were performed in the derivation and validation cohort to evaluate the nvHAP risk score's ability to predict pneumonia incidence ≥2days, ≥4days, and ≥6days after the assessment of risk factors.

Results: The derivation and validation cohort comprised 69'608 and 17'642 patients with an nvHAP rate of 0.69% (n=483) and 0.61% (n=107), respectively. After assessing 18 risk factor candidates, eight risk factors were incorporated in a simple 'nvHAP risk score' ranging from 0 to 11 points (age ≥60 = 1 point; male sex = 1 point; severely impaired activity and mobility = 2 points; acute problems with breathing = 1 point; impaired orientation = 1 point; moderate/severe pain = 1 point; affiliation to high risk clinic = 1 point; swallowing difficulties or tube feeding = 3 points). The areas under the ROC in the derivation and validation cohort were 0.78 and 0.72 to predict nvHAP ≥2 days in advance, 0.77 and 0.70 ≥4 days in advance, and 0.76 and 0.69 ≥6 days in advance.

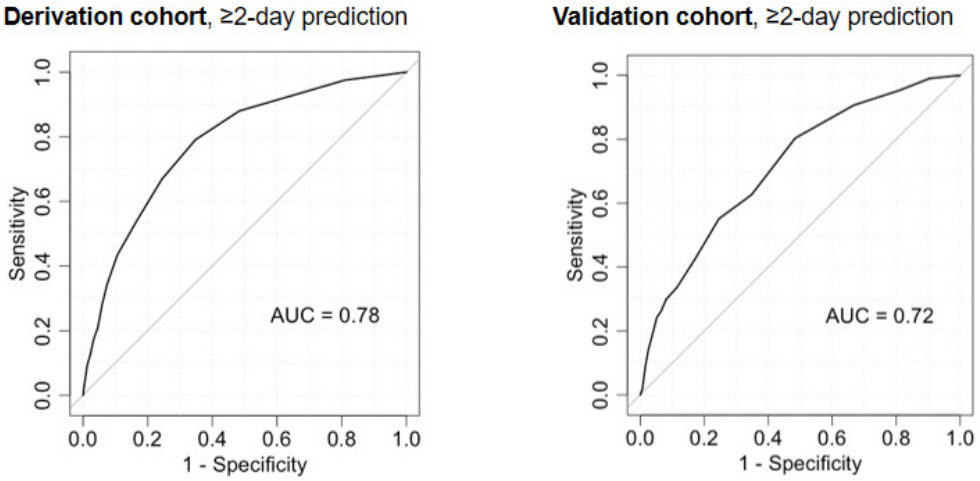
Conclusions: We developed a simple risk score for nvHAP that is applicable on a very broad acute care patient population. It allows identification of patients at high risk for nvHAP ≥6 days in advance with a fairly good predictive accuracy.

Figure 1

a) Forest plot of hazard ratios of potential risk factors for nvHAP



b) ROC curves for nvHAP risk score to predict nvHAP ≥ 2 days in advance



Abbreviations: AUC, area under the curve; BMI, body mass index; CI, confidence interval; HR, hazard ratio; ICU, intensive care unit; nvHAP, non-ventilator-associated hospital-acquired pneumonia; ROC, receiver operator characteristics

* High risk clinics: Internal medicine and all subspecialties, clinics performing major surgical procedures on chest, abdomen, or extremities.

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Abstract 1873

Spatiotemporal mapping of Bartonella bacilliformis in Peru and qualitative analysis of local perceptions and understanding of the disease

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Background: Carrion's disease is a biphasic illness caused by *Bartonella bacilliformis* and is endemic to parts of Peru. Understanding its spatiotemporal behavior is a key factor to improve pre-emptive measures. This study aims to identify spatiotemporal clusters of disease in Peru and elucidate local perceptions about the disease, to provide the basis for further research to guide elimination strategies.

Materials/methods: Spatial autocorrelation, hotspot and spatiotemporal analysis were carried out using ArcGIS and SatScan software to identify disease clusters over time. Data from the department of Ancash (Peru), showing absolute number of cases of Carrion's disease was analysed to look for trends in the data between January 2000 and June 2019. Focus group discussions took place among health workers and community members in Ancash and core themes were identified.

Results: The departments of Ancash and Cajamarca contained significant hotspots of disease and were part of the eight clusters identified by spatiotemporal analysis. Clusters were also identified in previously non-endemic departments, with one significant secondary spatiotemporal cluster identified in the department of Puno from 2006 to 2007. In general, within Ancash, males and females were similarly affected (most commonly in the youngest age group), with similar number of cases of acute and chronic forms of the disease reported each year. Five core themes emerged from the focus groups – presentation, aetiology, prevention, diagnosis, treatment. Community members were aware of the disease and most would visit the clinic if unwell. Health workers discussed preventive interventions and the influence of experience and antibiotic availability on treatment.

Conclusions: This study provides evidence supporting the theory that Carrion's disease is spreading into previously non-endemic areas and highlights the beliefs of local health workers and communities regarding this disease. Carrion's disease could still be targeted for elimination, but further research is needed for this to occur, before the window of opportunity closes.

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Abstract 1876

Reduced production of bacterial membrane vesicles predicts mortality in ST45/USA600 methicillin-resistant *Staphylococcus aureus* bacteraemia

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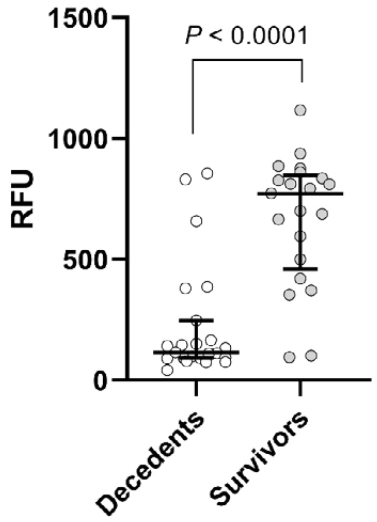
Background: *Staphylococcus aureus* is one of the major cause of infection related morbidity and mortality in humans. Prognostic biomarkers such as IL-10 and TNFα produced after manifestation of symptoms are not routinely orderable tests in standard clinical microbiology.Therefore Identification of a prognostic microbial factor may pave ways for early identification. We hypothesize that membrane vesicles (MV), detached portions of the staphylococcal membrane enriched with multiple immunomodulatory effectors, may represent a microbial factor that can be detected early in infection and predict clinical outcome. In the present study we establish that clinical isolates from survivors of endovascular ST45/USA600 staphylococcal infection produce significantly more MV than from decedents.

Materials/methods: Forty-four well-characterized sequential ST45/USA600 isolates were selected for this study. Of these 44 isolates, 21 were isolated from patients who survived the infection and 23 were isolated from decedents. Isolates were confirmed to be ST45 by multi-locus sequence typing. Pertinent clinical data along with calculated clinical risk scores were recorded. Phenotypic and genomic strain characterization was performed. MV were isolated by three different methodsand detected using a vesicle membrane-specific styryl dye (FM1-43,) Descriptive data was expressed as mean and standard deviation, median and interquartile range, or frequencies and percentage. Univariable analysis was performed using Student's t-test, Wilcoxon rank sum, or Fisher's exact. Classification and Regression Trees (CART) were used to determine an RFU breakpoint for mortality.

Results: In ST45/USA600 clade, low MV production *ex vivo* is strongly associated with 30-day mortality. Preliminary targeted genome sequence analysis does not identify any significant differences between isolates in *agrABDC, sigAB, sle1* or *psmα1-4* sequence suggesting some other, unknown factor is responsible for differences in MV production. Therefore, the genetic differences between strains that results in differential MV production remain unclear.

Conclusions: Low production of MV is associated with an increased risk of mortality in staphylococcal bacteremia caused by ST45/USA600 MRSA. MV can be rapidly quantified allowing for facile integration into existing clinical microbiology workflows.



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Abstract 1879

Prevention of pneumocystis pneumonia by Ibrexafungerp in a murine prophylaxis model

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Abstract third-party references: Supported by SCYNEXIS, Inc.

Background: *Pneumocystis* pneumonia (PCP) is an opportunistic fungal infection that affects immunocompromised patients. Ibrexafungerp (IBX) is an oral and intravenous antifungal from a novel class of glucan synthase inhibitors, triterpenoids, and has shown activity against *Candida*, *Aspergillus*, and PCP in a murine therapy model. We evaluated the ability of IBX to prevent PCP in a prophylaxis model of murine PCP.

Materials/methods: **Experiment 1:** Balb/c mice (10 mice/group) were infected by intranasal inoculation with *Pneumocystis murina*, immune-suppressed with dexamethasone in acidified drinking water and treated with 30-, 15- and 7.5 mg/kg, IBX/BID. Control groups treatment included TMP-SMX (50/250 mg/kg QD) and vehicle. After 6 weeks, mice were sacrificed and prevention was determined by organism burdens (asci and total nuclei). **Experiment 2**: Balb/c mice were immune-suppressed and infected as in Exp. 1. Treatment groups included: 1) 30 mg/kg BID x 6wk; 2) 30 mg/kg/BID x 6wk followed by cessation of treatment with IBX but with immune-suppression for 3 additional weeks; 3) 15 mg/kg BID 1 week prior and 6 wks after infection and immune suppression; 4) 15mg/kg BID for 8 wks; 5) 15 mg/kg BID for 6 wks then IBX was discontinued but with immune suppression; 6) untreated, vehicle control.

Results: **Experiment 1:** No *P. murina* nuclei or asci were observed after 6 weeks of treatment at a dose of 30 mg/kg/BID in the prophylaxis mouse model of PCP, similar to positive control, TMP/SMX. Some nuclei and asci were observed in the lower dose IBX groups. **Experiment 2:** To investigate whether any *P. murina* remained after different regimens of prophylaxis, treatment of IBX was withdrawn at both doses for an additional 3 wks of immune suppression to provoke the growth of any remaining fungi. Group 1 showed reduction in total nuclei and asci to undetectable. Group 2 did not result in any recrudescence of infection. Group 3 and 4 showed similar reduction in organism burden. Group 5 was similar to untreated control.

Conclusions: These results demonstrate that 30 mg/kg BID IBX prevented PCP in a murine model. We suggest that IBX could be a viable option for preventing PCP in immunocompromised patients.

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Abstract 1881

Impact of chemoprophylaxis on the outcomes of Plasmodium vivax and Plasmodium ovale imported malaria cases among civilian travellers

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Background: Malaria prophylaxis aims at reducing infection with *Plasmodium*. In those infected with *Plasmodium vivax* or *Plasmodium ovale,* it may alter the clinical course since it does not target hepatic forms. This study aimed at describing the clinical course of *P. vivax* or *P. ovale* malaria in travelers, based on chemoprophylaxis use.

Materials/methods: We conducted a case-control analysis of the outcomes of *P. vivax and P. ovale* infections nested in the cohort of imported malaria cases in civilian travelers reported to the French National Reference Center for Malaria from January 2006 to December 2017. We assessed the effect of chemoprophylaxis on the incubation period, delay between symptoms and diagnosis, type of medical care, biological findings at admission, type of symptoms and duration of hospitalization using adjusted logistic regression. As only infected travelers were observed, we assessed prophylaxis effect on post-infection outcomes using a counterfactual approach.

Results: Among 360 *P. vivax* and 756 *P. ovale* civilian travelers cases, 33% and 48%, respectively, reported a chemoprophylaxis use. There were 16 and 7 severe cases respectively, one patient died. Eighty percent of patients had symptoms less than 6 months after return. Chemoprophylaxis users had a greater risk to present symptoms more than 2 months after returning for both species (*P. vivax* OR: 3.40, 95% CI: [1.76-6.56], p<0.001, *P. ovale* OR: 2.42, 95% CI: [1.74-3.36], p<0.001), and those infected by *P. ovale* had a greater risk of having diagnosis more than 3 days after onset of symptoms (OR: 1.52, 95% CI: [1.07-2.17], p<0.05). Attributing these changes to prophylaxis was possible as long as the proportion of overall travelers to endemic areas under prophylaxis, was less than 50%. There was no impact on the other studied characteristics.

Conclusions: Civilian travelers infected by *P. vivax* or *P. ovale* reporting chemoprophylaxis use had a greater risk of delayed onset illness after infection (probably first relapse). The full impact of chemoprophylaxis on infection with relapse-causing species should consider both reduction in infection and delay onset of symptoms, hence the need of new recommendations of chemoprophylaxis for travelers exposed to these species, acting against both erythrocytic and liver stages.

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Abstract 1882

Murine typhus, a step beyond the clinic: how does it affect us in the 21st century? Epidemiology in Spain (1997-2015)

Beatriz Rodríguez-Alonso[1], Hugo Almeida[2], Montserrat Alonso Sardón[3], Virginia Velasco-Tirado[1], Ángela Romero-Alegría[1], Amparo López Bernús*[1], Cristina Carranza-Rodríguez[4], Marta Del-Río-García[1], Nerea-María Casado-Espada[1], Alba García-Pérez[1], Jana Chelea[1], Patricia Colina-Azofra[1], Jose Luis Perez Arellano[4], Moncef Belhassen-García[1]

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Background: Murine typhus (MT) is a zoonosis caused by Rickettsia typhi. Its main host is the rat and its vector to the human is the rat flea. The clinical picture is characterized by headache, fever, skin rash and liver function alteration. The severe pattern affects up to 10% of patients with pulmonary or renal involvement and even admission to Intensive Care Units. The prevalence of MT is considered underestimated since most cases are mild and self-limited. The aim of our study is to analyze the epidemiological impact of MT in patients who required hospitalization in the Spanish National Health System (NHS) between 1997 and 2015.

Materials/methods: Retrospective longitudinal descriptive study of in-patients diagnosed with Rickettsia typhi in Spanish public hospitals between 1997 to 2015. We obtained the data from the Minimum Basic Data Set of patients admitted to the NHS with a diagnosis of Rickettsia typhi: International Classification of Diseases, Ninth Revision, Clinical Modification (ICD-9-CM), 081.0, provided by the Health Information Institute of the Ministry of Health and Equality.

Results: A total of 99 cases were registered. Most cases were men (63, 63.6%). Mean age (±SD) was 46.4 years (±19.0). 85 (85.9%) cases were an urgent hospital admission. The period incidence rate (IR) was 0.12 (95% CI, 0.09-0.14) cases per million person-years. An irregular distribution was observed throughout the study period, although there was a slight upward trend between 2013 and 2015. Canary Islands had the highest IR (2.17), followed by Andalusia (IR: 0.07). Esporadic cases were evenly distributed without other clear geographical aggregates. The average (±SD) hospital stay was 11 days (±9.9). Only 1 (1%) case died.

Conclusions: Despite of the small sample, our data suggests that MT is an emerging disease in Spain, as literature reflects. Regardless of its low incidence, all the authors agree with the huge underestimation of this zoonosis, due to the self-limited nature of most cases and the low clinical suspicion. In our study, the highest number of cases is recorded in the Canary Islands and Andalusia. The mortality rate remains very low. The control of MT should focus on primary prevention.

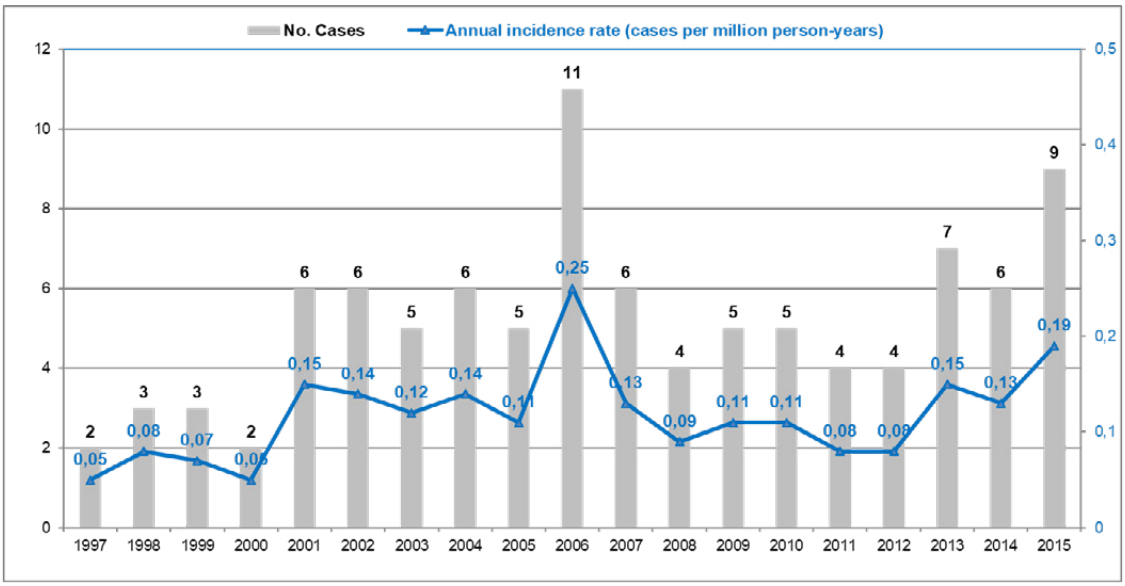

Figure 1. Temporal distribution of cohort (1997-2015) total population of Spain: cases and annual incidence rate *(cases per million person-years)*.

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Abstract 1883

Post-transplant lymphoproliferative disorders and association of antiviral prophylaxis in a nationwide cohort study

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Background: Post-transplant lymphoproliferative disorder (PTLD) is a serious complication of transplantation. Most PTLD in solid organ transplant recipients (SOT) are induced by Epstein-Barr virus (EBV) infection. However, the role of antiviral prophylaxis in the prevention of EBV-associated PTLD is controversial.

Materials/methods: SOT recipients enrolled in the Swiss Transplant Cohort Study (STCS) transplanted from 2008 to 2018 were included. We assessed incidence, presentation and outcome of histologically proven PTLD. In addition, we assessed the impact of anti-viral prophylaxis ((Val-)Acyclovir), (Val-)Ganciclovir) on the incidence of PTLD using adjusted stratified Cox regression models.

Results: We included 4'811 patients with a follow-up duration of 24'455 patient-years (py) (median follow-up time 4.68y/patient, IQR 2.35-7.74). 54 histology proven PTLD-cases were identified, 36 were EBV positive (EBV-PTLD). Median age at transplantation was 54 years overall (IQR 42 -62), 61y (IQR 54-63) for non-EBV-PTLD cases and 41y (IQR 24-60) for EBV-PTLD. Histopathological-classification revealed early lesions in 6 (11%), polymorphic in 15 (28%) and monomorphic PTLDs in 33 (61%) of cases. Extra-nodal sites were common (74%), CNS involvement was present in 7 cases (13%). PTLD incidence rate was 2.21/1000py and 1.47/1000py for EBV-PTLD. Highest incidence was found among lung transplant recipients with 4.47/1000py (4.19/1000py for EBV-PTLD). Incidence for EBV-PTLD at 1, 2 and 3 years post-transplantation were 2.81;1.94;1.71/1000py respectively vs. 0.43;0.35;0.28/1000py for non-EBV-PTLD (Figure1), median time post-transplantation to EBV-PTLD was 14.5 months vs. 61 months to non EBV-PTLD (p <0.001). We did not find a significant effect of antiviral prophylaxis ((Val-)Acyclovir or Val-)Ganciclovir)) on EBV-PTLD incidence, however some evidence towards lower risk for early EBV-PTLD (<2y post-transplantation) was seen for patients with ganciclovir prophylaxis (HR 0.34 (95%CI: 0.12-1.02, p=0.054). Overall mortality during follow-up was 14.45%, in patients with PTLD, related mortality was 31% for EBV-PTLDs, and 33% for non-EBV-PTLDs.

Conclusions: PTLD incidence in our cohort was low, although associated with high mortality. Incidence of EBV-PTLD declined over time and was highest in the first 2 years post-transplantation, while non-EBV-PTLD incidence did not decline. Antiviral prophylaxis had no significant effect on EBV-PTLD occurrence.

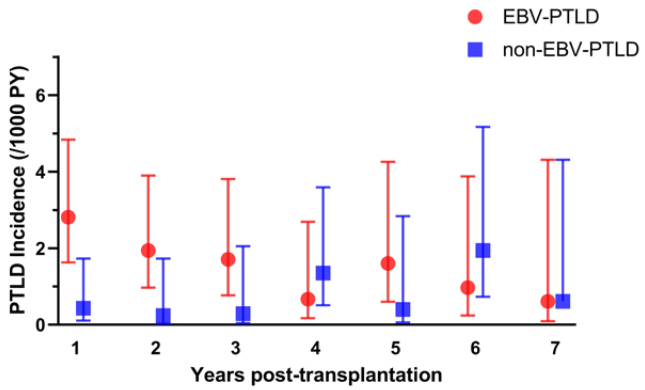

Figure 1. EBV- and non-EBV-PTLD Incidence per 1000 patient-years
Symbols represent point-estimates, whiskers 95% confidence intervalls.
EBV, Ebstein-Barr Virus. PTLD, Post Transplant Lymphoproliferative Disorder. PY, patient-years.

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Abstract 1884

Viral meningitis in adults: what are we missing? The use of viral capture sequencing to detect pathogens in the cerebrospinal fluid of adults with meningitis

Fiona Mcgill*[1;2;3], Rafal Tokarz[4], Emma Thomson[5], Anna Da Silva Filipe[5], Stephen Sameroff[4], Shirin Ashraf[5], Ian Lipkin[4], Caroline Corless[6], Chitra Pattabiraman[2;7], Michael Griffiths[1;2;8], Anna Maria Geretti[2;9], Benedict Michael[1;2;10], Nick Beeching[9], David Mckee[11], Ian Hart[6], Ken Mutton[12], Agam Jung[3], Alastair Miller[2], Tom Solomon[1;2;10]

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Background: Many patients with meningitis never have an aetiology identified, leading to unnecessary courses of antibiotics and antivirals, prolonged hospitalisation, and uncertainty for patients. Viruses are the most common cause of meningitis where a pathogen is found. Therefore, we used new viral capture sequencing methods to identify any viruses present in cerebrospinal fluid (CSF) from patients with meningitis and no pathogen identified.

Materials/methods: CSF from 76 adults was tested by VirCapSeq-VERT, an oligonucleotide probe set designed to capture viral targets using high throughput sequencing. Patients were categorised as either a) suspected viral meningitis – CSF pleocytosis and no pathogen found on routine molecular testing with a suspicion of viral aetiology based on validated clinical scores and/or negative 16s rRNA PCR testing (n=38), b) proven viral meningitis – CSF pleocytosis and virus identified on routine molecular testing (n=17), or c) not meningitis – symptoms and signs of meningitis but no CSF pleocytosis (n=21).

Results: VirCapSeq-VERT detected twelve individual viruses in 16/38 (42%) CSF samples from patients with suspected viral meningitis. Most viruses detected [58% (7/12)] were clinically relevant and included - *Herpes simplex virus* type 2, *Enteroviruses*, *Varicella zoster virus*, HIV, *Toscana virus*, *Rotavirus* and *Saffold virus*. Other viruses detected, unlikely to be clinically relevant, were *Epstein barr virus, Human herpes virus 6, Human pegivirus, Merkel cell polyomavirus* and *Human papillomavirus*. In the proven viral meningitis group one virus, additional to what had previously been found, was detected in one sample – *Human pegivirus* – not thought to be clinically relevant. 14% (3/21) of samples from patients without meningitis had a virus detected. The only viruses detected in this group were *Human pegivirus* (x2) and *Merkel cell polyomavirus*, neither of which are clinically relevant.

Conclusions: Sequencing methods enable the detection of a wide variety of pathogens. VirCapSeq-VERT increases the chances of detecting a virus due to its agnostic approach. This study shows that new diagnostic methods can allow more patients with meningitis to have an aetiological cause identified. Further work is needed to determine the prevalence of atypical viral candidates in meningitis and the clinical impact of using sequencing methods in real time.

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Abstract 1885

Optimising the combination of ceftazidime/avibactam and gentamicin against KPC-producing *Klebsiella pneumoniae* (KPC-Kp) with aminoglycoside-modifying enzymes

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Background: Although the β-lactam/β-lactamase inhibitor ceftazidime/avibactam is active against KPC-Kp, treatment failure rates up to 45% have been reported. Combinations with ceftazidime/avibactam and an aminoglycoside may be synergistic, however, ff90% of KPC-Kp harbor the aminoglycoside-modifying enzyme *aac(6')-Ib,* which partially inactivates gentamicin. An alternate allele, *aac(6')-Ib',* is also harbored by some KPC-Kp and fully inactivates gentamicin. The purpose of this study was to evaluate bacterial killing by combinations of ceftazidime/avibactam with gentamicin against KPC-Kp with *aac(6')-Ib* or *aac(6')-Ib'*.

Materials/methods: Clinical KPC-Kp isolates containing *aac(6')-Ib* (KPC-Kp-085 and -213) and *aac(6')-Ib'* (KPC-Kp-061 and -078) were used in all experiments. Ceftazidime/avibactam and gentamicin MICs were determined using broth microdilution. Time-kills were performed using a starting inoculum of ff10^8CFU/mL and viable bacterial counts were quantified at 0, 1, 2, 4, 6, 8, and 24 hours, to examine clinically relevant concentrations of ceftazidime/avibactam (5/0.94, 20/3.75, and 80/15mg/L) and gentamicin (0.625, 1.25, 2.5, 5, and 10mg/L) alone and in combination. Synergy was defined as a ≥2$\log_{10}$CFU/mL reduction by the combination compared to each agent alone.

Results: Each isolate was susceptible to ceftazidime/avibactam and gentamicin according to CLSI. KPC-Kp-085,-213, -061, and -078 ceftazidime/avibactam MICs were 0.5, 0.03, 0.25, and 0.5mg/L and gentamicin MICs were 0.25, 0.25, 4, and 4mg/L, respectively. Ceftazidime/avibactam concentrations of 5/0.94, 20/3.75, and 80/15mg/L achieved ≤1, 1-3, and >3$\log_{10}$CFU/mL reductions at 24 hours, respectively against all isolates. For *aac(6')-Ib* containing isolates, gentamicin concentrations ≥2.5mg/L were bactericidal (≥3$\log_{10}$CFU/mL reduction) whereas no gentamicin concentration was bactericidal for *aac(6')-Ib'* containing isolates. For *aac(6')-Ib* containing isolates, ceftazidime/avibactam 20/3.75mg/L combined with gentamicin ≥2.5mg/L achieved ≥7$\log_{10}$CFU/mL reductions, whereas gentamicin ≥10mg/L was needed for *aac(6')-Ib'* containing KPC-Kp. Gentamicin combined with ceftazidime/avibactam was synergistic for all isolates. However, lower gentamicin concentrations were required to achieve synergy against *aac(6')-Ib* containing KPC-Kp.

Conclusions: Ceftazidime/avibactam failed to eradicate susceptible KPC-Kp as monotherapy. Combinations of gentamicin and ceftazidime/avibactam were synergistic but displayed more activity against isolates with *aac(6')-Ib* than *aac(6')-Ib'*. Using rapid diagnostics to differentiate between *aac(6')-Ib* and *aac(6')-Ib'* may be useful to quickly optimize combination therapy for KPC-Kp infections.

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Abstract 1886

Longitudinal (2011-2018) activity of oritavancin against Gram-positive isolates causing bacteraemia and endocarditis in Europe, including enterococcal infections requiring adjusted daptomycin dosing

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Abstract third-party references: This study was performed by JMI Laboratories and supported by A. Menarini Farmaceutica Internazionale s.r.l (AMFI), which included funding for services related to preparing this abstract.

Background: Oritavancin is a long-acting lipoglycopeptide antibiotic with rapid bactericidal activity. This study assessed oritavancin activity against *Staphylococcus aureus* (SA), *Enterococcus faecalis* (EF), and *E. faecium* (EFM) causing bloodstream infection (BSI), including infective endocarditis (IE) and vancomycin-resistant enterococci (VRE) displaying elevated-daptomycin (EDAP) MIC values (≥2 mg/L). The longitudinal activity of oritavancin was also evaluated.

Materials/methods: A total of 4,198 SA, 1,211 EF, and 953 EFM were recovered from BSI in 44 European medical centres (2011-2018), including 146 SA isolates causing IE and 111 EDAP-VRE isolates. Species identification was confirmed by MALDI-TOF MS, when necessary, and susceptibility testing were performed by broth microdilution method following CLSI/EUCAST guidelines.

Results: Overall, oritavancin showed similar MIC_{50} (0.03 mg/L) and MIC_{90} results (0.06 mg/L) against MRSA, MSSA, and SA isolates causing IE (28.1% MRSA). Oritavancin displayed potent activity against EF regardless of susceptibility to daptomycin ($MIC_{50/90}$, 0.015/0.03-0.06 mg/L; Table). Only 15 (1.2%) EF isolates were resistant to vancomycin, and 84.7% of those displayed VanA phenotypic profile. In contrast, VRE were observed in 19.8% of EFM isolates, among which VanA was also the predominant phenotype (84.7%). Although, EFM isolates displaying VRE and EDAP MIC phenotypes showed slightly higher oritavancin MIC values ($MIC_{50/90}$, 0.015/0.06 mg/L) than VSE-EFM with daptomycin MIC ≤1 mg/L ($MIC_{50/90}$, ≤0.008/≤0.008 mg/L), all isolates but one (oritavancin MIC, 0.25 mg/L) were inhibited by oritavancin at MIC of ≤0.12 mg/L. MRSA rates were 27.0% in 2011, 22.8% in 2018 and varied from 20.9% to 29.4% during the 8-year period. Yearly oritavancin MIC_{50} results were 0.015 mg/L or 0.03 mg/L and MIC_{90} results varied from 0.03 mg/L to 0.12 mg/L against MRSA. Against EF, yearly oritavancin MIC_{50} results remain at 0.015 mg/L and MIC_{90} results were 0.03-0.06 mg/L. No variation was observed on oritavancin MIC_{50} results (≤0.008 mg/L) against EFM isolates and MIC_{90} were 0.015-0.03 mg/L.

Conclusions: Oritavancin showed potent activity against this collection of isolates causing BSI and IE in Europe, including enterococci with decreased susceptibility to daptomycin. In addition, oritavancin maintained stable *in vitro* potency throughout the 8-year study period with no apparent temporal trends.

Organism / Phenotype (No. of isolates)	Cumulative % inhibited by oritavancin at (mg/L):							$MIC_{50/90}$
	≤0.008	0.015	0.03	0.06	0.12	0.25	0.5	
S. aureus (4,198)	3.0	37.4	80.2	95.1	99.9	100.0		0.03/0.06
MSSA (3,124)	3.0	36.9	80.0	95.1	100			0.03/0.06
MRSA (1,074)	2.7	38.7	80.9	95.2	99.7	100		0.03/0.06
SA-IE (146)	3.4	36.3	76.7	93.8	99.3	100		0.03/0.06
E. faecalis (1,211)	32.4	72.5	90.0	96.1	99.3	99.9	100	0.015/0.03
Non-EDAP (1,142)	33.3	73.0	90.3	96.2	99.3	99.9	100	0.015/0.03
EDAP (69)	17.4	63.8	85.5	94.2	98.6	100		0.015/0.06
E. faecium (953)	82.9	91.9	96.6	99.0	99.9	100		≤0.008/0.015
Non-EDAP / VSE (316)	93.7	99.1	100					≤0.008/≤0.008
EDAP / VRE (110)	36.4	61.8	77.3	91.8	99.1	100		0.015/0.06

MSSA, methicillin-susceptible *S. aureus*; MRSA, methicillin-resistant *S. aureus*; EDAP, elevated daptomycin MIC (≥ 2 mg/L); non-EDAP, non-elevated daptomycin MIC (≤1 mg/L); VSE, vancomycin-susceptible enterococci; VRE, vancomycin-resistant enterococci.

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Abstract 1887

Delafloxacin activity against drug-resistant *Streptococcus pneumoniae*, *Haemophilus influenzae*, Haemophilus parainfluenzae, and Moraxella catarrhalis from European medical centres (2014-2018)

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Abstract third-party references: This study was performed by JMI Laboratories and supported by A. Menarini Farmaceutica Internazionale s.r.l (AMFI), which included funding for services related to preparing this abstract.

Background: Delafloxacin (DLX) is an anionic fluoroquinolone (FQ) that has been approved in the United States and in Europe for the treatment of acute bacterial skin and skin structure infections and was recently approved in the US for treatment of community-acquired bacterial pneumonia (CABP). In the present study, *in vitro* susceptibility (S) results for DLX and comparator agents were determined for CABP pathogens including *Streptococcus pneumoniae* (SPN), *Haemophilus influenzae* (HI), *H. parainfluenzae* (HP) and *Moraxella catarrhalis (*MC) clinical isolates from European hospitals participating in the SENTRY Program during 2014-2018.

Materials/methods: A total of 2,111 SPN, 1,087 HI, 701 MC, and 17 HP isolates were collected from community-acquired respiratory tract infections (CARTI) during 2014-2018 from European hospitals. Sites included only 1 isolate/patient/infection episode. Isolate identifications were confirmed at JMI Laboratories. Susceptibility testing was performed according to CLSI broth microdilution methodology, and EUCAST (2019) breakpoints were applied where applicable. Other antimicrobials tested included levofloxacin (LEV) and moxifloxacin (MOX; not tested in 2015). Multidrug-resistant (MDR) SPN isolates were categorized as being nonsusceptible (NS) to amoxicillin-clavulanate, erythromycin (ERY), and tetracycline; other SPN phenotypes were ERY-NS, or penicillin (PEN)-NS. β-lactamase (BL) presence was determined for HI, HP, and MC.

Results: The activities of the 3 FQs are shown in the table. The most active agent against SPN was DLX, with the lowest $MIC_{50/90}$ values of 0.015/0.03 mg/L. DLX activities were similar when tested against the MDR or PEN-NS for SPN phenotypes. ERY-NS isolates had DLX $MIC_{50/90}$ results of 0.015/0.03 mg/L. DLX was the most active FQ against HI, HP, and MC. BL presence did not affect FQ MIC values for HI or MC; only 1 HP isolate was BL-positive.

Conclusions: DLX demonstrated potent *in vitro* antibacterial activity against SPN, HI, HP, and MC. DLX was active against MDR SPN that were NS to the agents commonly used as treatments for CABP. These data support the utility of DLX in CABP including when caused by antibiotic resistant strains.

Organism/Phenotype (n)	Delafloxacin $MIC_{50/90}$ (mg/L)	Levofloxacin $MIC_{50/90}$ (mg/L)	Moxifloxacin $MIC_{50/90}$ (mg/L, n[a])
S. pneumoniae (2,111)	0.015/0.03	1/2	≤0.12/0.25 (1,991)
MDR (177)	0.015/0.06	1/2	≤0.12/0.25 (164)
PEN-NS (591)	0.015/0.03	1/2	≤0.12/0.25 (554)
ERY-NS (476)	0.015/0.03	1/2	≤0.12/0.25 (445)
H influenzae (1,087)	≤0.001/0.002	≤0.015/0.03	0.03/0.06 (1,003)
BL-positive (200)	≤0.001/0.002	≤0.015/0.03	0.03/0.03 (186)
H. parainfluenzae (17)	0.008/>0.06	0.03/0.5	0.06/0.25 (11)
M. catarrhalis (701)	0.004/0.008	0.03/0.06	0.06/0.06 (610)
BL-positive (591)	0.004/0.008	0.06/0.06	0.06/0.06 (591)

[a]Number of isolates tested for moxifloxacin, not tested in 2015.

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Abstract 1891

Typing of emm1 Group A streptococci using MALDI-TOF MS

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Background: In recent years, invasive infections caused by group A streptococcus (GAS) are increasing. Among them, *emm1*-type GAS are highly pathogenic, and it is said that the invasive infections are significantly more cases of fulminant type, and the mortality rate and the persistence survival rate are high. Here, we propose a new technique which is able to discriminate highly pathogenic *emm1* type and other types using MALDI-TOF MS and statistical analysis software.

Materials/methods: We searched biomarkers that were able to discriminate *emm* types using frequently isolated types of the invasive infectious disease-derived GAS strain, *emm 1* strain, *emm 12* strain, *emm 28* strain, and *emm 89* strain. The above four types of *emm* strains were cultured on sheep blood agar plate for 24 hours. MALDI mass spectra were observed by positive linear mode for *m/z* 4000-20000. Biomarkers were selected by using eMSTAT Solution statistical analysis software (Shimadzu, Japan). To evaluate the selected biomarker, a blind test was conducted using 379 strains derived from pharyngitis / tonsillitis, including B, C, and G hemolytic streptococci.

Results: We used eMSTAT Solution to search marker peaks that contribute to discriminate *emm1* from other types. As a result of the search, it can be confirmed that the peak of *m/z* 10932 was detected in all samples of *emm1* while the peak was not detected in other types. Next, a blind test of 379 clinical isolates was performed using the peak of *m/z* 10932 as a biomarker. In the gene analysis of the conventional method, 97 out of 379 strains were typed to *emm1*. Similarly, 92 (94.8%) of the 97 strains were typed to be *emm1* using the biomarker. Both methods showed a high positive concordance rate. In this method, three *emm1* strains were typed to be non-*emm1* strains (*emm11* strain (n = 1) and *emm28* strain (n = 2)), and the negative concordance rate was 98.9%.

Conclusions: This is the first result that discriminates *emm1* type of GAS by MALDI-TOF MS. This new MALDI-based method is easier and faster than conventional methods like DNA sequencing.

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Abstract 1892

Tuberculosis remains a threat in Portuguese patients treated with anti-TNFα

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Background: universal screening for tuberculosis (TB) before anti-TNFα therapy and treatment of those who have latent TB (LTB) resulted in a significant reduction of active TB. However, we still diagnose TB in this population. We aimed to review severe TB cases in patients treated with anti-TNFα admitted to a tertiary hospital ID department between 2013-19.

Materials/methods: clinical records from patients with active TB were reviewed with data pertaining the inflammatory immunomediated disease, anti-TNFα treatment, TB screening and TB episode collected.

Results: ten cases of TB were documented (mean age 42.6 years, 7 men), 5 were under adalimumab, 3 under infliximab and 1 under golimumab and certolizumab pegol each. Five patients had a diagnosis of Inflammatory Bowel Diseases, 5 rheumatologic immune disease (2 psoriatic arthritis, 2 ankylosing spondylitis, 1 rheumatoid arthritis). All underwent LTB screening prior to anti-TNFα therapy with average time between screening and therapy of 4.8 months (range: 1-15). Eight were negative and TB screening during anti-TNFα therapy was not repeated. LTB diagnosis was made in the remaining: one was treated with rifampicin (6 months), the other with isoniazid (9 months). In these two cases, active TB was diagnosed, respectively, 4 and 3 years after LTB screening and treatment. Time between anti-TNFα therapy onset and TB diagnosis was 55 months (range: 3-138) and between TB symptoms and its diagnosis 1.6 months (range: 1-5). Six patients had disseminated TB (involvement of central nervous system 2, lymphatic 5, hepatic 4, pleural 2), 2 pulmonary tuberculosis (PTB) with hepatic and pleural involvement each, and 2 PTB. Multisensitive *Mycobacterium tuberculosis* was recovered from biological samples in 9 patients, the remaining case being a presumptive diagnosis. All patients were treated with a 4-drug regimen with average treatment duration of 10.1 months (range: 9-15) and overall favorable evolution. Immunosuppressive therapy was resumed without anti-TNFα.

Conclusions: TB under anti TNFα therapy remains an important diagnosis despite TB screening. As before, 60% of our cases comprise disseminated forms. A high level of TB suspicion should be maintained, regular screening of TB under anti-TNFα therapy is probably worth being done and better tests for TB screening are welcomed.

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Abstract 1893

ComParison of the microbiological efficacy of disinfection using ultraviolet and aerosolised hydrogen peroxide system for carbapenemase-producing *Enterobacteriaceae* in a healthcare setting

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Background: Carbapenemase-producing *Enterobacteriaceae* (CPE) are a growing problem in the worldwide. Environmental cleaning is important strategy to prevent CPE transmission and "no-touch" methods including ultraviolet C (UV-C) and aerosolized hydrogen peroxide (aHP) system have been evaluated to overcome the shortcomings of manual cleaning. However, data regarding efficacy of UV-C and HP system against CPE are limited. We thus compared the microbiological efficacy of disinfection using UV-C and aHP as area decontamination in a healthcare setting.

Materials/methods: This study was conducted in empty single patient rooms with dimension of 48.3 m3 at a tertiary hospital, Seoul, South Korea from May to October, 2019. We ran 4 rooms with 2 UV-C and 2 aHP, respectively and 30 formica sheets contaminated with KPC-producing *Klebsiella pneumoniae* (10^6 CFU) were placed in the room, both direct and indirect sites. After intervention, median log reduction and decontamination rate were assessed using Rodac plates.

Results: We observed median 5.52 log reduction after UV-C (n=60) and median 5.37 log reduction after aHP (n=60) (P=0.86), and 50% decontamination rate after UV-C and 45% decontamination rate after aHP (P=0.71) (Table 1). At direct sites, UV-C showed higher median log reduction (5.91 vs. 5.61, P=0.002) and decontamination rates (83% vs. 53%, P=0.03) than aHP. Conversely, at indirect sites, aHP showed higher median log reduction (4.63 vs. 5.07, P=0.02) and decontamination rate (17% vs. 37%, P=0.01) than UV-C.

Conclusions: Both UV-C and aHP reduced bacterial contamination in a single room. aHP was significantly more effective at indirect sites, and UV-C was significantly more effective at UV direct sites. Depending on the shadow area, healthcare facilities might choose between UV-C and aHP.

Table 1. Microbial efficacy of UV-C and aHP

		UV-C	aHP	P-value
Median log reduction (IQR)	Total (n=60)	5.52 (4.65-5.91)	5.37 (4.78-5.91)	0.86
	Direct (n=30)	5.91 (5.91-5.91)	5.61 (4.97-5.91)	0.002
	Indirect (n=30)	4.63 (4.20-5.19)	5.07 (4.55-5.91)	0.02
Decontamination rate*	Total (n=60)	30 (50%)	27 (45%)	0.71
	Direct (n=30)	25 (83%)	16 (53%)	0.03
	Indirect (n=30)	5 (17%)	11 (37%)	0.01

*It was defined as the ratio of the number of less than 2.5 CFUs per plate to the total number of plates

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Abstract 1894

Identification of novel mobile colistin resistance gene mcr-10

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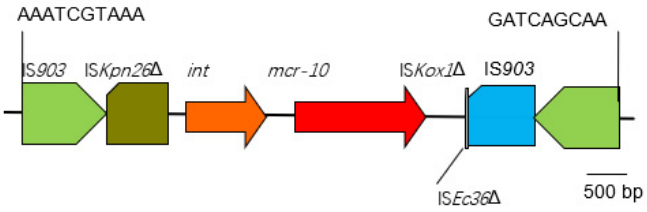
Background: Mobile colistin resistance (*mcr*) genes represent an emerging challenge. We found and characterized a gene that is likely a new variant of *mcr*.

Materials/methods: An *Enterobacter roggenkampii* (a member of *Enterobacter cloacae* complex) clinical strain with a *mcr*-like gene encoding a new phosphoethanolamine transferase was subjected to whole genome sequencing using both Illumina short-read and MinION long-read platforms. This gene was cloned on pBC SK and then transferred into a colistin-susceptible *E. roggenkampii* strain. Conjugation and electroporation experiments were performed to examine the location of the *mcr*-like gene. The prevalence of *mcr-10* was screened for depositions of GenBank. The 3D and secondary structures of this MCR-like protein were predicted using Phyre2 and ESPript 3 and were compared with known MCR proteins (MCR-1 to 9) and chromosomally encoded MCR-like phosphoethanolamine transferases (designated MCR-B here) of various *Buttiauxella* species.

Results: Here we describe a novel *mcr* gene, *mcr-10*, on an non-self-transmissible IncFIA plasmid of an *E. roggenkampii* clinical strain. *mcr-10* has the highest nucleotide identity (79.69%) with *mcr-9* and encodes MCR-10 with 82.93% amino acids identical to MCR-9. *mcr-10* confers 4-fold increase of colistin MIC (from 1 to 4 mg/L) when cloned into a colistin-susceptible *E. roggenkampii* strain. By screening GenBank, *mcr-10* was found in various *Enterobacteriaceae* species of countries in four continents, suggesting that this gene has widely spread. MCR-10 shows 79.04% to 83.67% amino acid identity and highly conserved predicted protein structures with MCR-Bs. MCR-10, MCR-9 and MCR-B proteins may therefore originate from a common ancestor. *mcr-10* was adjacent to a site-specific recombinase-encoding gene and was bracketed by IS*903* and may be mobilized by site-specific recombination or composite transposon (Fig).

Conclusions: Our results indicate that *mcr-10* is a novel plasmid-borne colistin resistance gene and warrants immediate monitoring and further studies.

Figure. Genetic context of mcr-10 on pMCR10_090065. Gene *int* encodes a XerC-type tyrosine recombinase, which may mediate mobilization of adjacent genetic components via site-specific recombination. Δ represents truncated insertion sequences. Two copies of IS*903* are located at upstream and downstream of *int-mcr-10* and the 9-bp abutting sequences are indicate.



500 bp

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Abstract 1895

Dalbavancin as definitive therapy for Gram-positive infections in patients with haematologic malignancies and haematopoietic cell transplant recipients

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Background: Patients with hematalogic malignancies and hematopoietic cell transplants (HCT) are at an increased risk of infection due to the use of immunosuppressive agents, neutropenia, and central venous catheters. These infections are frequently caused by Gram-positive bacteria and are often complicated requiring extended courses of intravenous (IV) antibiotics. Dalbavancin is an IV lipoglycopeptide antibiotic with unique pharmacokinetics allowing for once weekly dosing. The aim of this study was to assess the efficacy of dalbavancin for definitive treatment of Gram-positive infections in patients with hematologic malignancies and HCT recipients at an academic medical center.

Materials/methods: This was a retrospective, single-center observational study from January 2016 – May 2019 of patients receiving dalbavancin at West Virginia University Hospitals. Patients were included if they were greater than 18 years of age, active hematologic malignancy or HCT recipient, and received at least one dose of dalbavancin for a Gram-positive blood stream infection (BSI) or skin and soft tissue infection (SSTI). The primary outcome was to evaluate clinical resolution of infection. Secondary outcomes were to determine infection recurrence within 30 days after dalbavancin completion, difference in efficacy for indication, and length of inpatient stay prior to outpatient dalbavancin.

Results: Fifty-seven patients met inclusion criteria, 24 (42%) were HCT recipients. Most patients were male (65%) with a median age of 60 years and weight of 87.4 kg. Acute myeloid leukemia was the most common malignancy (28.3%). BSIs were the most common dalbavancin indication, (52.6%).Overall, the clinical resolution rate was 78.9% (95% CI 0.6656 – 0.8767). Resolution was observed in 80% of BSIs versus 77.8% of SSTIs (P = 0.8372). In patients without resolution, failure occurred in 10% of BSIs versus 7.4% of SSTIs (P = 0.7297) and recurrence was observed in 10% of BSIs versus 14.8% of SSTIs (P = 0.7014). The most frequent dosing regimens were 1,000 mg weekly and one 1,500 mg dose for BSIs and SSTIs, respectively. The median length of stay was seven days.

Conclusions: Dalbavancin appears to be an adequate treatment option for Gram-positive BSIs and SSTIs in this population. Using dalbavancin allows for outpatient treatment and may allow for earlier hospital discharge.

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Abstract 1897

Excess length of acute inpatient stay attributable to acquisition of hospital-onset *Enterobacteriaceae* bloodstream infection with and without antimicrobial resistance: a multistate model analysis

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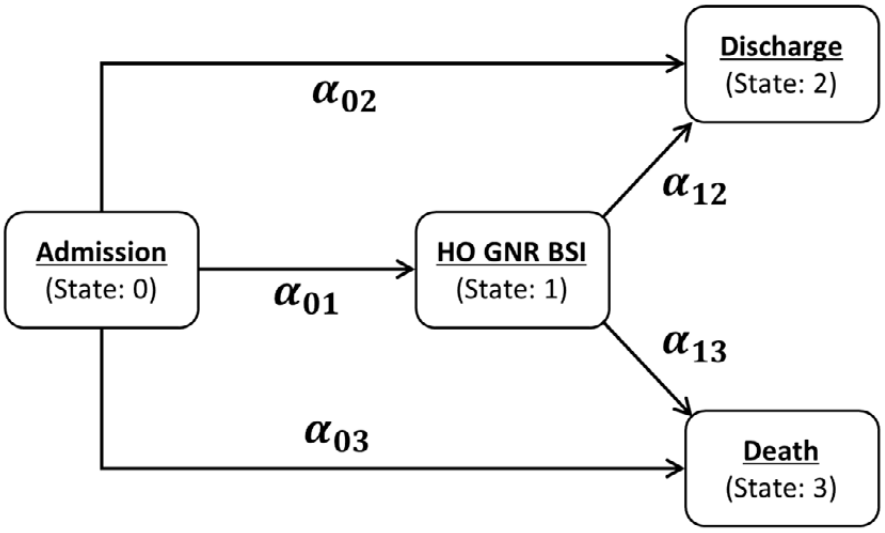
Background: Hospital length of stay (LOS) is an important outcome impacted by healthcare-associated infections (HAIs) and antimicrobial resistance (AMR). However, measurement of excess LOS can be subject to survival bias when considering death as a censoring event due to variable timing of HAI onset and high mortality. We aimed to estimate unbiased change in LOS attributable to hospital-onset (HO) Enterobacteriaceae bloodstream infections (BSI) using multistate models without considering death as a censoring event.

Materials/methods: We analyzed a retrospective matched-cohort that included all case patients who developed HO BSI due to *Escherichia coli* or *Klebsiella* spp. (BSI onset >48 hours after the admission) during the period 2003 to 2013 at 130 hospitals within the US Veterans Health Administration System. Up to three uninfected control patients per case were identified and matched at patient-level based on gender, hospital and LOS before the onset of BSI. Case patients were further categorized by the resistance profile to fluoroquinolones (FQ) and extended-spectrum cephalosporins (ESC). A multistate model (Figure) was utilized, and change in LOS was estimated as an effect of the intermediate state (HO BSI: State 1 in Figure). We stratified analyses by isolate susceptibilities to FQ (FQ-S and FQ-R) and ESC (ESC-S and ESC-R) and assessed extra LOS for each category.

Results: 5,964 patients who had HO BSI due to *E. coli* (2,663/44.7%) or *Klebsiella* spp. (3,301/55.3%) and 15,213 uninfected patients were analyzed. 957 patients (16.9%) and 1,638 patients (28.9%) had organisms resistant to FQ and ESC, respectively. AMR was associated with larger change in LOS for both FQ (FQ-S: 12.13 days (95% CI: 6.25-17.88) vs. FQ-R: 12.94 days (95% CI: 2.35-24.31), difference: 0.81 days (95%CI: 0.56-1.05), p<.001) and ESC (ESC-S: 11.57 days (95%CI: 6.25-17.42) vs. ESC-R: 16.56 days (95%CI: 3.63-30.38), difference: 4.99 days (95%CI: 4.75-5.24), p<.001).

Conclusions: In this large matched cohort study, HO Enterobacteriaceae BSI with or without resistance to FQ or ESC was associated with attributable excess LOS. Resistance to FQ or ESC was associated with longer increases in LOS than seen in cases infected with susceptible isolates, and the impact was greater in ESC resistance compared to FQ.



α_{ij}: Hazard Rate for Transition from Status i to Status j

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Abstract 1899

De-escalation of carbapenems to ciprofloxacin in the treatment of bacteraemia caused by extended spectrum beta-lactamase-producing *Enterobacteriaceae*

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Background: Carbapenems are recommended for the treatment of bacteremia caused by extended spectrum beta-lactamase (ESBL)-producing Enterobacteriaceae. However, increased use also selects for carbapenem resistance. Alternatives to carbapenem have yielded conflicting results in recent studies, with limited data evaluating fluoroquinolones (FQ) as carbapenem-sparing options. This study aimed to evaluate the use of ciprofloxacin as step-down from carbapenems in the treatment of bacteremia due to ESBL-producing Enterobacteriaceae.

Materials/methods: Patients with ESBL-producing Enterobacteriaceae bacteremia were evaluated in a retrospective cohort study. We compared patients who received definitive carbapenem therapy throughout (carbapenem group) versus those who were switched from carbapenem to ciprofloxacin (ciprofloxacin group) within 8 days of definitive therapy. The primary outcome evaluated was 30-day all-cause mortality. Secondary outcomes included re-infection and readmission rates, incidences of Clostridioides difficile and carbapenem-resistant infections, and length of hospitalisation. Factors influencing mortality were analysed via logistic regression.

Results: A total of 179 patients were included. There were 148 patients in the carbapenem group and 31 patients in the ciprofloxacin group. Median age was 74 years old and 52% were males. Patient demographics and treatment-related characteristics were similar between groups. Duration of carbapenem use prior to ciprofloxacin switch was 5 days (interquartile range [IQR] 3-6 days). The 30-day mortality were not statistically different between groups (0/31 [0%] vs. 16/148 [10.8%%]; p=0.07). The median total duration of antibiotic treatment was longer in the ciprofloxacin group (16 vs.15 days; p=0.01). However, the median duration of hospitalisation was significantly shorter for the ciprofloxacin group [8 (IQR 8-13) vs. 15 days (IQR 9-19); p=0.01]. Other secondary outcomes were not statistically different between both groups. Failure to reach clinical stabilisation by day 5 was associated with mortality (adjusted odds ratio 7, 95% confidence interval 1.66-29.4).

Conclusions: Ciprofloxacin can be an effective carbapenem-sparing therapy for the treatment of bacteremia caused by ESBL-producing Enterobacteriaceae. Switching from carbapenem to ciprofloxacin can be considered when the patient achieved clinical stabilisation, and may result in shorter hospital stay.

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Abstract 1901

Evaluation of rapid extraction methods coupled with recombinase polymerase amplification assay for point-of-need diagnosis of post-kala-azar dermal leishmaniasis

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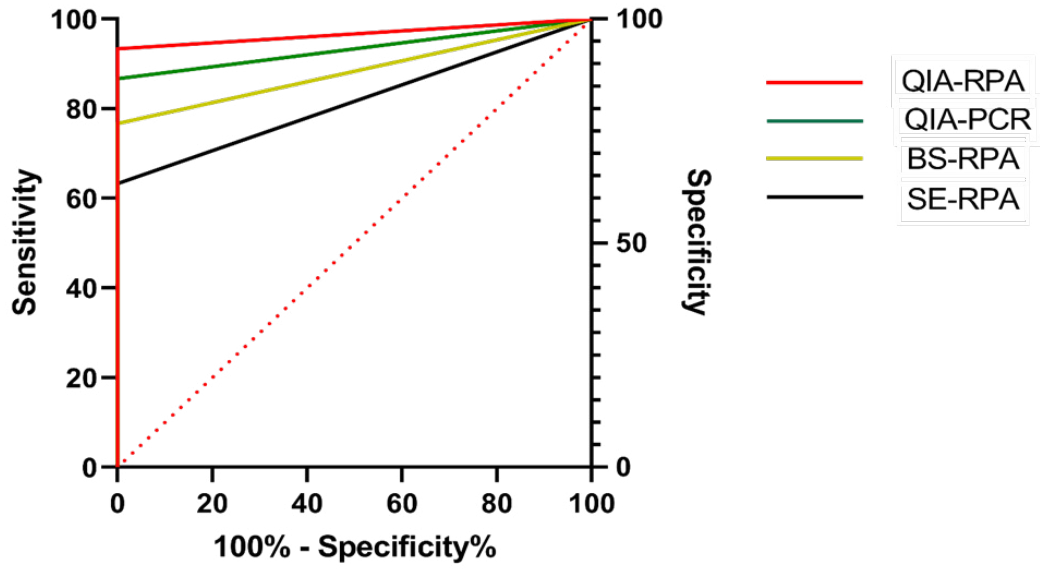
Background: Post kala-azar dermal leishmaniasis (PKDL) usually develops as sequelae of visceral leishmaniasis (VL) and can manifest in multiple dermatological forms. Since PKDL patients harbor Leishmania donovani parasites and can potentially trigger inter-epidemic transmission of the disease, the success of kala-azar elimination programme could be jeopardized by these cases. Although several molecular methods with promising diagnostic efficacy have been developed to detect PKDL cases, albeit complicated and expensive DNA extraction methods limit their application in resource poor settings. To address this, in comParison to a reference DNA extraction method (Qiagen), we evaluated two rapid DNA extraction methods and determined their impact on the detection of the parasite DNA using our newly developed recombinase polymerase amplification (RPA) assay.

Materials/methods: Thirty suspected PKDL cases were enrolled after diagnosis by clinical examination and a positive rk39 strip test. DNA was extracted from three skin biopsy samples using either a spin column-based method (Qiagen) or one of two rapid DNA extraction methods, (Boil & Spin (B&S) and SpeedXtract (SE)). RPA and qPCR were subsequently performed with the extracted samples to detect L. donovani DNA.

Results: Using DNA extracted by Qiagen method, the qPCR and RPA assays exhibited sensitivities of 86.7% and 93.3% respectively. In contrast, the sensitivity of RPA assay dropped to 76.7% and 63.3%, respectively, when the B&S and SE rapid extraction methods were performed. Despite this compromised sensitivity, B&S-RPA technique yielded an excellent agreement with both Q-qPCR (k = 0.828) and Q-RPA (k =0.831) techniques. Moreover, SE-RPA showed good agreement with Q-qPCR (k = 0.755), Q-RPA (k =0.692) and B&S-RPA (k =0.635) assays. As expected, with all of the three DNA extraction methods, both qPCR and RPA assay showed absolute specificity.

Conclusions: This study finding substantiates the superior diagnostic efficacy of Qiagen DNA extraction method over B&S and SE method in detecting LD DNA through RPA assay from skin biopsy of PKDL patients. To apply these rapid DNA extraction methods in resource-constrained settings, further methodological refinement is warranted to improve DNA yield and purity through rigorous experiments.



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