

Fungal Genetics Conference

March 15-20, 2022



Table of Contents

Gen	etics Society of America
Fun	gal Policy Committee and Conference Organizers5
-	nsors
Gen	eral Information
	Registration Desk and Badges
	Registration Desk Schedule
	Conference App
	Oral Presenters
	Poster Presentations
	Viewing Sessions Online
	Exhibitor and Sponsor Information
	Event Sponsors
	Safety Protocols
	COVID-19 Testing
	Meals
	Internet Access
	Job and Meeting Postings
	Presenting Author Index
	Slack Chat Channels
	Security/Lost and Found
	Quiet Space
	Parking
Con	ference Policies
	Code of Conduct
	Accessibility
	Diversity and Inclusion
	Social Media/Photo/Video Policy
Sche	edule of Events20
	Presentation and Workshop Session Listings
Post	er Session Listings
Spoi	nsor Ads
Asilo	omar Map

Genetics Society of America



Genetics Society of America



GSA is an international scientific society representing more than 5,000 researchers and educators around the world. As well as connecting researchers through conferences and career programs, we publish two peeredited scholarly journals, GENETICS and G3: Genes | Genomes | Genetics. We encourage you to join GSA so you can make use of exclusive member benefits and get involved in the Society's many programs, including professional development training, awards, advocacy, and more. Join us as we work to advance the field and serve our community. Visit genetics-gsa.org for more information.



GENETICS has been innovating since 1916, publishing high quality original research across the breadth of the field.

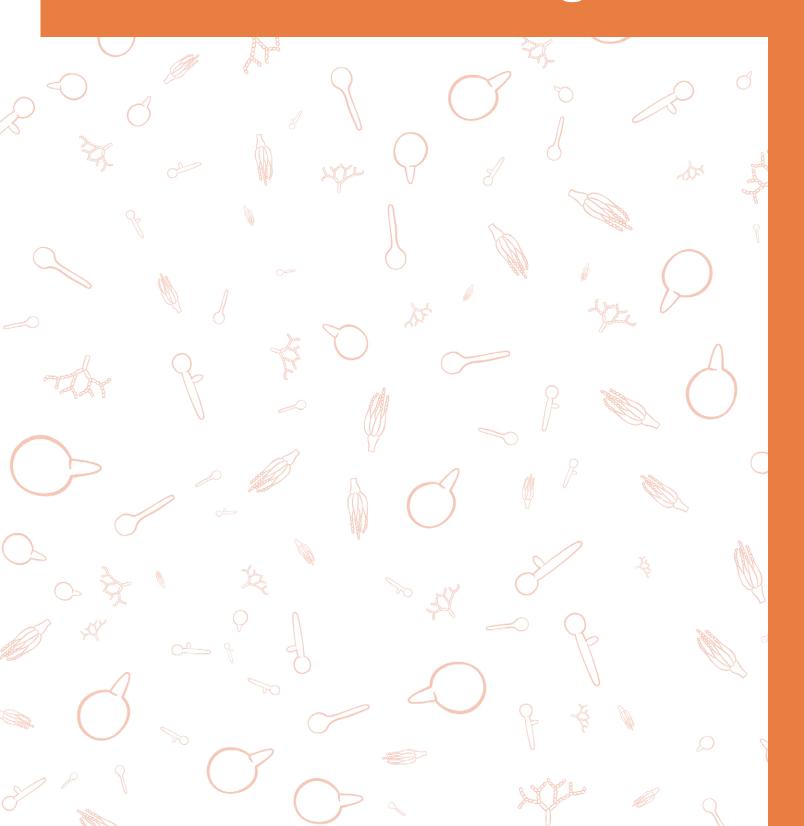


G3: Genes | Genomes | Genetics is an open access journal that publishes high quality, useful results regardless of perceived impact.

2022 GSA Board of Directors

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Fungal Policy Committee and Conference Organizers



Fungal Policy Committee and Conference Organizers

Fungal Policy Committee and Conference Organizers

Natalia Requena, Karlsruhe Institute of Technology – KIT, FPC Chair (2019–2022)

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John Leslie, Fungal Genetics Stock Center

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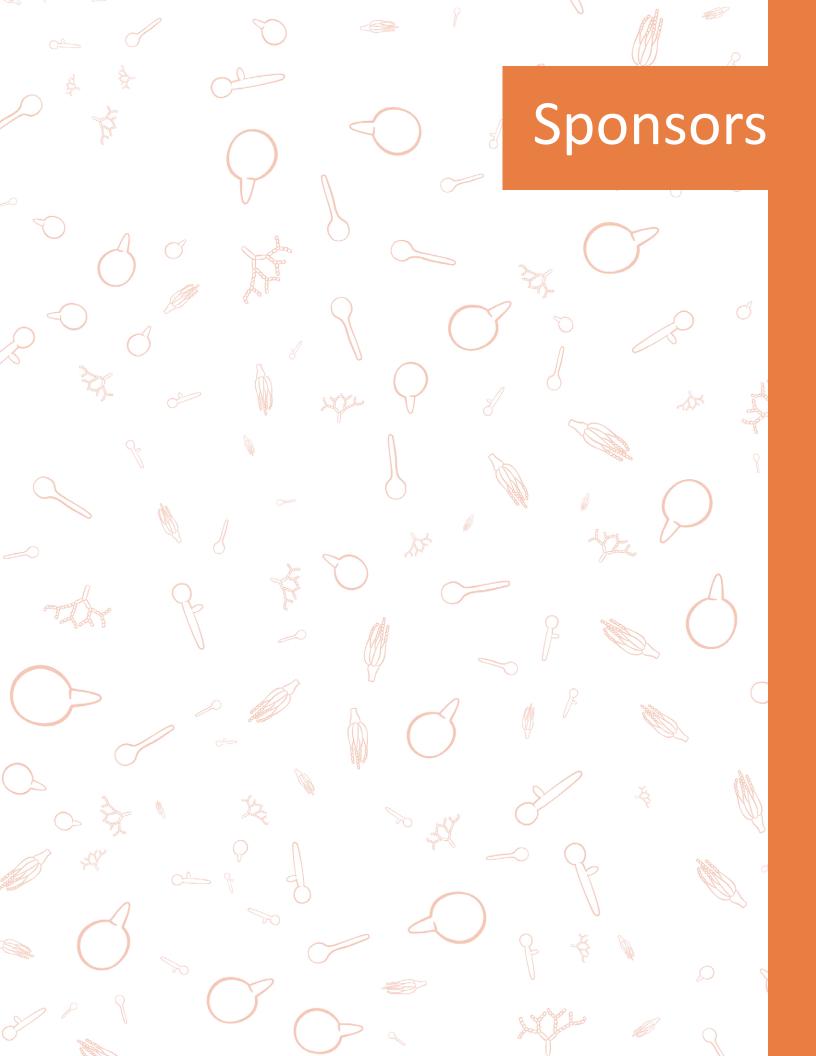
Scientific Organizers

Jennifer Lodge, Duke University

Oded Yarden, Hebrew University

GSA Fungal Conference Poster Award Organizer

Deborah Bell-Pedersen, Texas A&M University



Conference Sponsors

Genetics Society of America and the organizers gratefully acknowledge the following sponsors:

Gold Sponsors

















Silver Sponsors











Bronze Sponsors





Supporters





General Information

Registration Desk and Badges

You should have received your registration badge in advance via email and printed it out. Badges will not be printed onsite. In the registration area in Surf and Sand, you will need to show your green check mark obtained from 42Chat (indicating you uploaded your vaccination verification and negative test results) and you will be given a badge cover and lanyard. For admission to the sessions, posters, exhibits, and receptions, you must have your official conference badge.

You can download the Program and Abstract Books on the conference website or access all the information in the Conference App. Certificates of Attendance and Participation are available online.

Registration Desk Schedule

Tuesday, March 15	4:30 p.m. – 9:30 p.m.
Wednesday, March 16	8:00 a.m. – 5:00 p.m.
Thursday, March 17	8:30 a.m. – 2:00 p.m.
Friday, March 18	8:30 a.m. – 1:00 p.m.
Saturday, March 19	8:30 a.m. – 11:00 a.m.

Conference App

In-person participants: Download the GSA Meetings app to your smartphone (available on both iOS and Android platforms) to have meeting information at your fingertips. Once you download the App, you will not need an internet connection to access previously downloaded information. You will only need an internet connection to download updates. Blackberry users and Windows Mobile Device users can access the App through the web version available on the conference website.

Virtual participants: Virtual attendees will use the App to participate in the conference. Sign into the App using your registration badge ID number and last name. The App is available in two formats: Desktop App (for desktop and laptop computers), or Mobile App (for Apple iOS and Android mobile devices).

You can find your registration badge ID in your conference registration confirmation email, which was sent from the address NoReply@Convention-Mail.com.

Oral Presenters

NEW PROCEDURES THIS YEAR - All speakers must go to the Speaker Check-In located in Triton 24 hours before the start of your session to upload and review your presentation and become familiar with the equipment that will be in the session room. You will NOT be able to use your own computer or upload your presentation in the session room. The day of your presentation, arrive 30 minutes before the start of your session (not your talk) and let the session chair know that you are there.

Poster Presentations

All posters are available from March 14 to April 8 as a PDF with an (optional) 2-minute audio overview in the Conference App. Be sure to view all the posters in the app and leave feedback. To view a poster, look for the "Virtual Poster" link near the bottom of each poster's entry in the App.

Poster presenters who are attending the conference in person have been assigned a presentation time according to the schedule below. All three poster sessions will be in the Fireside Pavillion, which is located under Fred Farr Forum. Two posters will share a 4' high x 8' wide poster board. Each author will have a net usable space of 3' 10" (111.8 cm) high x 3' 10" (111.8 cm) wide.

All in-person posters will be up for one day. Presenters should remove their posters at the end of their poster session. If you do not remove your poster, it may be lost or thrown away. The meeting does not take responsibility for posters that are not removed on time. Set up your poster after 8:00 a.m. the day of your presentation.

Tuesday, March 15	View all the virtual posters while traveling to the meeting		
Wednesday, March 16	All "W"ednesday posters must be displayed 7:00 p.m. – 10:30 p.m.		
	7:30 p.m. – 8:30 p.m.	Odd-numbered posters	
	8:30 p.m. – 9:30 p.m.	Even-numbered posters	
	9:30 p.m. – 10:30 p.m. Open Viewing		
Thursday, March 17	All "T"hursday posters must be displayed 7:00 p.m. – 10:30 p.m.		
	7:30 p.m. – 8:30 p.m. Odd-numbered posters		
	8:30 p.m. – 9:30 p.m. Even-numbered posters		
	9:30 p.m. – 10:30 p.m. Open Viewing		
Friday, March 18	All "F"riday posters must be displayed 7:00 p.m. – 10:30 p.m.		
	7:30 p.m. – 8:30 p.m. Odd-numbered posters		
	8:30 p.m. – 9:30 p.m. Even-numbered posters		
	9:30 p.m. – 10:30 p.m. Open Viewing		

Viewing Sessions Online

Remote attendees can view sessions via the App:

Plenary Sessions - Registrants access live plenary sessions through the App. Five minutes before a plenary session starts, log in using your registration badge ID number and last name. Tap the "Join Webinar" button on the session. The Join Webinar button will be visible 10 minutes before the start of the session.

Concurrent Sessions - A recording of each session will be available in the session listings on the App within 24 hours after the session ends. The recordings will be available until April 8.

Poster Sessions - PDFs and audio overviews of all of the posters will be available via the App March 14 through April 8.

Exhibitor and Sponsor Information

Please be sure to visit with the company representatives during the poster sessions.



M N N

www.biosensesolutions.dk

oCelloScope™ Live-Cell Imaging – Automated Microbial Growth Kinetics and Morphology Analysis The oCelloScope™ platform is used by microbiologists all over the world to study growth and morphology. We use image analysis and machine learning to provide a time-lapse technology 250 times more sensitive than using OD (plate readers).

www.mycoworks.com

In 2013, co-founders Philip Ross and Sophia Wang formed MycoWorks, a San Francisco-based biomaterials company dedicated to bringing new mycelium materials to the world. MycoWorks' patented Fine Mycelium technology, an advanced manufacturing platform and breakthrough in materials science, engineers mycelium during growth to form proprietary, interlocking cellular structures for unparalleled strength and durability.



SDI SCIENTIFIC BIOPROCESSING

ww.fungidb.org

FungiDB integrates whole genome sequence and annotation, experimental and environmental isolate sequence data and includes comparative genomics, analysis of gene expression, bioinformatics tools and automated analysis, user comment system capturing community expertise, the genome annotation editor Apollo, Galaxy platform for private data analysis, and a web interface for data mining. In addition, we will be available Wednesday through Friday, 7:30 a.m. – 8:45 a.m. via a recurring zoom meeting. Please log in to ask us any questions:

www.scientifcbio.com

SBI is a collective of scientists, engineers and business people committed to making intelligent, dynamic sensors and instruments that monitor biomass, pH, and dissolved oxygen easily accessible and available to the thousands of cell scientists and bioprocessing engineers who are on the cutting edge of scientific and medical breakthroughs. Our job is to power your scientific audacity. For every experiment, every day.

https://liverpool-ac-uk.zoom.us/j/99758022770

Meeting ID: 997 5802 2770, Passcode: fLr=@x%6



www.unionbio.com

Union Biometrica provides flow cytometry for objects that are too large for traditional cytometers, such as fungal pellets, and offers an alternative to manual sorting. These instruments analyze and dispense objects based on size and fluorescent parameters. Automating this process offers increased speed, sensitivity, quantification, and repeatability of experiments.

www.ginkgobioworks.com

Headquartered in Boston, Ginkgo Bioworks uses the most advanced technology on the planet – biology – to grow products instead of manufacturing them. We design custom microbes for customers across multiple markets, and build our foundries to scale the process of organism engineering using software and hardware automation.

Event Sponsors

Ginkgo BioWorks is sponsoring the Opening Mixer, Tuesday, March 15, 7:30 p.m. – 9:00 p.m. PST Please be sure to visit their table during the poster sessions Wednesday through Friday.

The Better Meat Co. is sponsoring the Career Exploration Workshop, Thursday, March 10, 2:00 p.m. – 3:00 p.m. PST

This event will showcase the broad options available to those with a PhD by hosting a panel of individuals from multiple career paths. Career sectors highlighted may include academic research, industry research, biotech, science writing, science teaching, and academic administration.

Publishing Workshop, Wednesday, March 9, 8:30 a.m. – 10:00 a.m. PST

Curious about the peer review process? Join us for an overview of peer review presented by the Executive Editor of the GSA Journals GENETICS and G3: Genes | Genomes | Genetics. Editors from Fungal Biology and Biotechnology and Fungal Genetics and Biology along with other journal editors will participate in a panel discussion answering attendee questions about the entire process—from submission to review to publication. Students and postdocs are invited to attend. All guestions welcome!

Safety Protocols

In-person attendees are required to wear the most protective masks they can access, ideally N95s or KN95s, while attending the conference. If you do not have access to a high-quality mask, a limited supply of complimentary masks are available in Surf and Sand.

All rooms will be set with maximum seating so that attendees can sit at the spacing with which they are comfortable.

Hand sanitizers will be available in all the meeting rooms and public space.

Coffee breaks will be available outside each meeting room. Please keep your mask on while in line and only remove to drink your coffee.

Daily self monitoring: If you experience any of the listed symptoms, do not enter the meeting space. Contact Asilomar Guest Services and gsaconferences@genetics-gsa.org to have a rapid test brought to you. Symptoms requiring a rapid test: fever or chills, cough, shortness of breath, fatigue, muscle or body aches, headache, new loss of taste or smell, sore throat, congestion or runny nose, nausea or vomiting or diarrhea.

COVID-19 Testing

Onsite rapid antigen and PCR COVID tests are available for a fee and by appointment for attendees who need or want to be tested (e.g. to comply with international travel regulations). The testing site will be in Marlin and open during the times listed below. Registrants are responsible for signing up and paying for any testing they require. Please make appointments for a test using the QR code below:



Thursday, March 17	1:00 p.m. – 3:00 p.m.
Friday, March 18	10:30 a.m. – 2:30 p.m.
Saturday, March 19	10:30 a.m. – 2:30 p.m.

Complimentary rapid antigen tests will be available to attendees who feel unwell or experience symptoms outside of the hours posted above.

Meals

Meals are not included in the conference registration fee. Guests staying at Asilomar and those who purchased a meal plan are invited to eat at Crocker Dining Hall. If you prefer to not to eat inside the Dining Hall, you can pick up a to-go meal in Crocker Dining Hall and then sit at the picnic tables available in the Meadow outside or bring your meal back to your room. Meals are offered at the following times:

Breakfast	7:30 a.m. – 8:30 a.m.
Lunch	12:00 p.m. – 1:00 p.m.
Dinner	6:00 p.m. – 7:30 p.m.

Unfortunately, due to COVID restrictions, Asilomar is not selling individual meal tickets for purchase at the front desk as they have done in the past.

Internet Access

Complimentary Wi-Fi is available in the meeting rooms and Fireside Pavillion.

Network: Asilomar Conference

Password: conference (all lower case).

Job and Meeting Postings

Individuals and institutions offering or seeking employment and organizers of meetings may post notices and resumes on the "Community Notices" bulletin board in the Poster Sessions. Employers are also welcome to post listings in the #jobs channel in the #Fungal22 Slack workspace.

Presenting Author Index

To search for specific oral and poster presenters, use the search function in the Conference App.

Slack Chat Channels

The #Fungal22 Slack workspace is the place to meet other attendees online during the conference. You can join and create chat channels based on your interests. There are channels for getting technical help, discussing new papers and preprints, sharing job ads, and connecting with other attendees around shared interests.

Security/Lost and Found

For all emergencies and lost and found items, contact Asilomar security by dialing 0 from any house phone. The conference registration desk will be able to assist you as well.

Quiet Space

There are living rooms available in Lodge, Afterglow, Pirates Den, and Stuck Up Inn if you want to disconnect for a few minutes during a session.

Parking

Parking is complimentary on the Asilomar grounds.



Code of Conduct

The Genetics Society of America Conferences foster an international community of geneticists and provide an opportunity to discuss scientific advances and form new collaborations.

GSA values your attendance and wants to make your experience productive and inspiring by fostering an open exchange of ideas in a professional setting. Our Code of Conduct was established to communicate a transparent set of standards and guidelines for acceptable behavior at GSA Conferences and to provide a positive, safe, and welcoming environment for all attendees, vendors, volunteers, and staff.

All conference participants (regardless of their role) are expected to follow the Code of Conduct while attending any portion of the meeting, including but not limited to meeting rooms, the exhibit/poster hall, meeting areas in the official conference venue, and social events provided by the meeting or vendors.

Unacceptable Behaviors

Unacceptable behaviors include, but are not limited to:

- Intimidating, harassing, abusive, discriminatory, derogatory, or demeaning speech or actions by any participant and at all related events
- Harmful or prejudicial verbal or written comments or visual images related to gender, gender expression, gender identity, marital status, sexual orientation, race, religion, political orientation, socioeconomic, disability or ability status, or other personal characteristics, including those protected by law
- Inappropriate use of nudity and/or sexual images in public spaces (including presentation slides and posters)
- Deliberate intimidation, stalking, or following
- Violating the rules and regulations of the conference hotel
- Sustained disruption of scientific sessions or other events
- Unwelcome and uninvited attention or contact
- Physical assault (including unwelcome touching or groping)
- Real or implied threat of physical harm
- Real or implied threat of professional or financial damage or harm
- Harassing or unwanted photography
- Photographing slides of oral presentations and posters without permission
- Recording of scientific and other sessions without permission

Taking action or making a report

Need to file a complaint? For instructions on how to confidentially report a Code of Conduct violation, please visit genetics-gsa.ethicspoint.com. In addition, GSA staff is available to assist participants in contacting our Ethics Committee to make a report. Please email Tracey DePellegrin, GSA Executive Director, at tracey.depellegrin@genetics-gsa.org.

Consequences of non-compliance

Anyone asked by GSA staff, a Session Chair, Workshop Leader, Moderator, Presenter, or Zoom representative to stop unacceptable behavior is expected to comply immediately. Retaliation toward GSA or toward someone reporting an incident or after experiencing any of the following consequences will not be tolerated and may result in additional sanctions.

The consequences of non-compliance with GSA's Code of Conduct may include:

- Immediate removal from accessing the online meeting and Slack channels without warning
- Restrictions from future GSA meeting attendance
- Termination of GSA membership or positions on GSA Boards or Committees
- Incidents may be reported to the proper authorities

Accessibility

GSA is committed to assisting attendees with special needs. If you have accessibility questions or requests, please email gsaconferences@genetics-gsa.org.

Diversity and Inclusion

GSA is committed to promoting equality, diversity, and inclusion to create greater opportunity for any individual to fulfill their scientific potential, irrespective of their background, gender, or circumstances. This diversity leads to innovation by attracting the widest possible talent to the community and fostering a greater diversity of ideas, approaches, and perspectives. The Organizing Committee aims to select speakers and session chairs that represent the breadth and diversity of the discipline and conference participants. GSA especially encourages the Committee to select excellent speakers from groups traditionally underrepresented in science.

Social Media/Photo/Video Policy

Live tweeting of presentations is allowed unless the speaker explicitly opts out by stating so at the start of their talk. Taking or sharing photos or videos of posters is permitted only with the presenter's consent during the assigned poster session. Taking photos of posters while the presenter is not present is strictly prohibited. By attending a GSA conference, you grant GSA the right to use your photograph, name, and likeness for use in GSA educational, news, or promotional materials.



All times are listed in Pacific Standard Time (PST).

THURSDAY, March 10		
11:00 a.m. – 11:30 a.m.	Getting Involved in GSA's Early Career Professional Development	Virtual
12:00 p.m. – 1:00 p.m.	Conference Success Tips and Welcome from the Early Career Leadership Program	Virtual
2:00 p.m. – 3:00 p.m.	Career Exploration Panel	Virtual
3:30 p.m. – 4:30 p.m.	Multilingual Networking	Virtual
MONDAY, March 14		
3:00 p.m. – 11:00 p.m.	Asperfest 18 In-person only	Chapel
5:00 p.m. – 7:00 p.m.	Workshop Registration	Surf and Sand
6:00 p.m. – 7:00 p.m.	Dinner (for those staying at Asilomar)	Crocker Hall
TUESDAY, March 15		
8:30 p.m. – 3:00 p.m.	Asperfest 18 In-person only	Chapel
	Fusarium Workshop In-person only	Fred Farr Forum
9:00 p.m. – 5:00 p.m.	Magnafest In-person only	Kiln
4:00 p.m. – 7:00 p.m.	Speaker Check-In Speakers must check in 24 hours before their session to upload their presentation and review the equipment.	Triton
4:30 p.m. – 9:30 p.m.	Registration Be sure and have your green check mark ready, showing your vaccination verification and negative test results have been uploaded.	Surf and Sand
5:00 p.m. – 7:00 p.m.	Review Virtual Posters PDF and audio overview of posters	
6:00 p.m. – 7:00 p.m.	Dinner	Crocker Hall
7:30 p.m. – 9:00 p.m.	Opening Welcome Social Sponsored by Ginkgo BioWorks	Merrill Hall
8:00 p.m. – 9:00 p.m.	Networking Hotspots	Merrill Hall

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WEDNESDAY, March 16				
7:30 p.m. – 8:30 p.m.	Breakfast	Crocker Hall		
7:30 p.m. – 8:45 p.m.	FungiDB Help Desk (see Conference app for zoom link)	Virtual		
7:30 p.m. – 5:00 p.m.	Speaker Check-In Speakers must check in 24 hours before their session to upload their presentation and review the equipment.	Triton		
8:00 p.m. – 5:00 p.m.	Registration Be sure and have your green check mark ready showing your vaccination verification and negative test results have been uploaded.	Surf and Sand		
8:45 p.m. – 9:00 p.m.	Welcome and Opening Remarks	Merrill Hall and Chapel		
9:00 p.m. – 12:00 p.m.	Plenary Session I: Cell Biology and Morphology	Merrill Hall and Chapel		
12:00 p.m. – 1:00 p.m.	Lunch For those staying at Asilomar, or those who have bought meal tickets	Crocker Hall		
12:30 p.m. – 1:45 p.m.	JGI Workshop	Merrill Hall		
12:30 p.m. – 1:45 p.m.	Multilingual Networking	Fireside Pavilion		
12:30 p.m. – 1:45 p.m.	Oomycete Community Discussion Forum	Scripps		
	Concurrent Platform Sessions			
	Circadian Rhythms and photobiology	Kiln		
	Extreme environments	Scripps		
	Human fungal pathogens	Merrill Hall		
3:00 p.m. – 6:00 p.m.	Interactions with prokaryotes and viruses	Nautilus		
	Morphological transitions and cell walls	Chapel		
	RNA and RNAi biology	Fred Farr Forum		
	Symbionts and endophytes	Heather		

WEDNESDAY, March 16 (continued)		
3:00 p.m. – 4:00 p.m.	Virtual Networking Meet Ups	Virtual
6:00 p.m. – 7:30 p.m.	Dinner	Crocker Hall
7:30 p.m. – 9:00 p.m.	North Central Coordinating Committee, Genetics and Biochemistry of Plant-Fungal Interactions	Kiln
7:30 p.m. – 10:30 p.m.	Poster Session I and Exhibits Odd number W posters 7:30 p.m. – 8:30 p.m. Even numbered W posters 8:30 p.m. – 9:30 p.m. Open Viewing W posters 9:30 p.m. – 10:30 p.m.	Fireside Pavilion
9:30 p.m. – 10:30 p.m.	Networking Hotspots	Fireside Pavilion
THURSDAY, March 17		
7:30 p.m. – 8:30 p.m.	Breakfast	Crocker Hall
7:30 p.m. – 8:45 p.m.	FungiDB Help Desk (see Conference app for Zoom link)	Virtual
7:30 p.m. – 5:00 p.m.	Speaker Check-In Speakers must check in 24 hours before their session to upload their presentation and review the equipment.	Triton
8:00 p.m. – 9:00 p.m.	Virtual Networking Meet Ups	Virtual
8:30 p.m. – 2:00 p.m.	Registration	Surf and Sand
9:00 p.m. – 12:00 p.m.	Plenary Session II: Cross species interactions	Merrill Hall and Chapel
12:00 p.m. – 1:00 p.m.	Lunch For those staying at Asilomar and those who bought meal tickets	Crocker Hall
1:00 p.m. – 3:00 p.m.	Covid Test Site	Marlin

THURSDAY, March 17 (continued)

	Concurrent Platform Sessions	
	Chromatin, heterochromatin, and epigenetics	Fred Farr Forum
	Lipid metabolism and signaling	Scripps
3:00 p.m. – 6:00 p.m.	Natural and experimental diversity, evolution and populations	Kiln
	Plant pathogens	Merrill Hall
	Secondary metabolism and production of useful metabolites	Chapel
	Spore development, dormancy and germination	Heather
	Stress	Nautilus
6:00 p.m. – 7:00 p.m.	Dinner	Crocker Hall
7:30 p.m. – 10:30 p.m.	Poster Session II and Exhibits Odd number T posters 7:30 p.m. – 8:30 p.m. Even numbered T posters 8:30 p.m. – 9:30 p.m. Open Viewing of T posters 9:30 p.m. – 10:30 p.m.	Fireside Pavilion
9:30 p.m. – 10:30 p.m.	Networking Hotspots	Fireside Pavilion
FRIDAY, March 18		
7:30 p.m. – 8:30 p.m.	Breakfast	Crocker Hall
7:30 p.m. – 8:45 p.m.	FungiDB Help Desk (see Conference app for zoom link)	Virtual
7:30 p.m. – 5:00 p.m.	Speaker Check-In Speakers must check in 24 hours before their session to upload their presentation and review the equipment.	Triton
8:30 p.m. – 2:00 p.m.	Registration	Surf and Sand
9:00 p.m. – 12:00 p.m.	Plenary Session III: Evolution and Development	Merrill Hall and Chapel
10:30 p.m. – 2:30 p.m.	Covid Test Site	Marlin

FRIDAY, March 18 (continued)		
12:00 p.m. – 1:00 p.m.	Lunch For those staying at Asilomar and those that bought meal tickets, lunch is available in Crocker Hall and box lunches are available on the Main Lodge deck.	Crocker Hall
12:45 p.m. – 1:45 p.m.	Careers in Academia	Virtual
	Concurrent Platform Sessions	
	Interactions with other non-human/plant eukaryotic species	Fred Farr Forum
	Mating and sexual development	Merrill Hall
3:00 p.m. – 6:00 p.m.	Molecular basis of biotrophy	Heather
	Mycobiomes and their implications	Nautilus
	Natural and applied bioconversion and biodegradation	Kiln
	Small molecules in communication	Scripps
	Speciation, diversity and evolution	Chapel
6:00 p.m. – 7:00 p.m.	Dinner	Crocker Hall
7:30 p.m. – 10:30 p.m.	Poster Session III and Exhibits Odd numbered F posters 7:30 p.m. – 8:30 p.m. Even numbered F posters 8:30 p.m. – 9:30 p.m. Open Viewing of F posters 9:30 p.m. – 10:30 p.m.	Fireside Pavilion
9:30 p.m. – 10:30 p.m.	Networking Hotspots	Fireside Pavilion
SATURDAY, March 19		
7:30 p.m. – 8:30 p.m.	Breakfast	Crocker Hall
7:30 p.m. – 5:00 p.m.	Speaker Check-In Speakers must check in 24 hours before their session to upload their presentation and review the equipment.	Triton
8:30 p.m. – 2:30 p.m.	Covid Test Site	Marlin
8:30 p.m. – 11:00 p.m.	Registration	Surf and Sand

SATURDAY, March 19 (continued)			
8:45 p.m. – 9:00 p.m.	Fungal Community Meeting and election of FGPC members	Merrill Hall and Chapel	
9:00 p.m. – 12:00 p.m.	Plenary Session IV: Signaling and Metabolism	Merrill Hall and Chapel	
12:00 p.m. – 1:00 p.m.	Lunch For those staying at Asilomar and those who bought meal tickets	Crocker Hall	
12:15 p.m. – 1:45 p.m.	Fungal Genetics Policy Committee Meeting	Surf and Sand	
	Concurrent Platform Sessions		
	Coolest tools for fungal biology	Chapel	
	Emerging and re-emerging fungi in a changing world	Heather	
	From genome to pangenome	Kiln	
2:00 p.m. – 5:00 p.m.	Fungal determinants of host response	Fred Farr Forum	
	Fungal recognition (self and non-self)	Scripps	
	Fungicides and antifungals	Merrill Hall	
	Systems biology and biomaterials	Nautilus	
5:30 p.m. – 5:45 p.m.	Fungal Conference and GSA Poster Award Presentations	Merrill Hall and Chapel	
5:45 p.m. – 6:30 p.m.	Perkins/Metzenberg Lecture presented by B. Gillian Turgeon, Cornell University, USA	Merrill Hall and Chapel	
6:30 p.m. – 7:30 p.m.	Dinner	Crocker Hall	
8:30 p.m. – 11:00 p.m.	Closing Party Refreshments will be served outside so be sure and bring a jacket	Merrill Hall	
SUNDAY, March 20			
7:30 p.m. – 8:30 p.m.	Breakfast	Crocker Hall	
WEDNESDAY, March 30			
8:30 p.m. – 10:00 p.m.	Publishing Workshop	Virtual	

Wednesday, March 16 8:45 a.m. - 9:00 a.m. Merrill Hall and Chapel

Welcome and Opening Remarks

Conference Organizers Jennifer Lodge and Oded Yarden,

Jessica Velez, GSA Welcome

Wednesday, March 16 9:00 a.m. - 12:00 p.m. Merrill Hall and Chapel

Plenary Session I: Cell Biology and Morphology

Session Chairs:

Louise Glass, University of California, Berkeley **Steve Harris**, University of Manitoba, Canada

1 9:00 am Trade-off between Plasticity and Velocity in Mycelial Growth. Norio Takeshita, University of Tsukuba

2 9:30 The exocytic RAB11 pathway. Miguel Penalva, CSIC Centro de Investigaciones Biológicas 'Margarita Salas'

3 10:00 A little key will open a large door: unexpected pleiotropic roles of fungal surface-active proteins in fungal cells. Irina Druzhinina, Nanjing Agricultural University

10:30 Break

4 11:00 Role of the fission yeast NDR kinase Orb6 in the response to environmental stress. Fulvia Verde, University of Miami Miller School of Medicine

5 11:30 Temperature adaptation of biological phase separation. Amy Gladfelter, UNC Chapel Hill

Wednesday, March 16 12:30 p.m. – 1:45 p.m.

Workshops

Multilingual Networking, Fireside Pavilion Oomycete Community Discussion Forum, Scripps JGI Workshop, Merrill Hall

Wednesday, March 16 3:00 p.m. – 6:00 p.m. Merrill Hall

Human fungal pathogens

Session Chairs:

Neil Gow, University of Exeter, UK Xiaorong Lin, University of Georgia, USA

- **6** 3:00 Immune recognition of fungi: deciphering the writing on the wall. **Neil Gow**, University of Exeter
- 7 3:20 Unmasking chitin in C. neoformans: Panic or protection? Rajendra Upadhya, Washington University, St. Louis
- 8 3:40 Candida albicans and IL-17A stimulate cytokine production by oral epithelial cells via different mechanisms. Jianfeng LIN, The Lundquist Institute
- 9 4:00 The ephrin tyrosine kinase receptor, EphA2, serves as a gateway for Cryptococcus neoformans into the central nervous system. Amelia Bennett, University of California
- 4:20 Break
- 10 4:40 A ricin-like toxin derives tissue necrosis during invasive mucormycosis. Ashraf Ibrahim, The Lundquist Institute at Harbor-UCLA Medical Center
- 11 5:00 Roles of Candida albicans chromosome instability in the host. Huijuan Yan, UCSF
- 12 5:20 Roles for microglia in Cryptococcus meningoencephalitis. J Muse Davis, University of Iowa
- **13** 5:40 Leveraging machine learning essentiality predictions and chemogenomic interactions to identify antifungal targets. Ci Fu, University of Toronto

Wednesday, March 16 3:00 p.m. – 6:00 p.m. Fred Farr Forum

RNA and RNAi biology

Session Chairs:

Michael Feldbrugge, Heinrich Heine University, Germany

Jin-Rong Xu, Purdue University, USA

14 3:00 Alternative Transcription start sites in *Cryptococcus*. **Guilhem Janbon**, Institut Pasteur

15 3:20 Endosomal mRNA transport. **Michael Feldbrugge**, Heinrich-Heine University

16 3:40 The ribonucleoprotein complex components JSN-1 and GUL-1 are involved in asexual development in *Neurospora crassa*. **Anne Yenewodage**, Hebrew University of Jerusalem

17 4:00 An RNA-binding protein that evolved a change in function to control fungal growth: the surprising history, structure, and function of Ssd1. **Edward W. J. Wallace**, The University of Edinburgh

4:20 Break

18 4:40 Extracellular vesicle-mediated cross-kingdom transport of plant mRNAs into fungal cells to suppress pathogenicity. **Hailing Jin**, University of California

19 5:00 Exclusively RNAi-based antimicrobial drug resistance is inherited after meiosis in the mucormycosis pathogen *Mucor circinelloides*. **Carlos Pérez-Arques**, Duke University School of Medicine

20 5:20 How important is cross-kingdom RNA interference in nature? **Arne Weiberg**, Ludwig-Maximilians University - LMU

21 5:40 Identification of a stage-specific co-factor required for A-to-I mRNA editing during sexual reproduction in fungi. **Huiquan Liu**, Northwest A&F University

Wednesday, March 16 3:00 p.m. – 6:00 p.m. Heather

Symbionts and endophytes

Session Chairs:

Natalia Requena, Karlsruhe Institute of Technology, Germany

Carolyn Young, Oklahoma State University, USA

22 3:00 Endohyphal bacteria modulate tissue colonization, saprotrophy, and thermotolerance by endophytic fungi *in vitro* and under field conditions. **A. Elizabeth Arnold**, The University of Arizona

23 3:20 How do plants deploy smRNAs to engage with beneficial microorganisms while fighting pathogens? **Maitree Pradhan**, Karlsruhe Institute of Technology - KIT

24 3:40 Mycangial colonization in the laurel wilt (*Raffealea lauricola*)-Ambrosia beetle symbiosis. **Ross Joseph**, University of Florida

25 4:00 Testing the role of the transcription factor TvSom1 in adhesion of *Trichoderma* virens germlings. **Benjamin Horwitz**, Technion - IIT

4:20 Break

26 4:40 The combined activity of two secreted fungal enzymes is implicated in fungal accommodation in the roots and triggers cell death in different host species. **Alga Zuccaro**, University of Cologne

27 5:00 Deciphering the potential niche of novel black yeast fungal isolates in a biological soil crust based on genomes, phenotyping, and melanin regulation. **Erin Carr**, University of Nebraska-Lincoln

28 5:20 Establishment of functional symbioses between *Epichloë* endophytes and the modern cereals rye (*Secale cereale*) and hexaploid wheat (*Triticum aestivum*). **Richard Johnson**, Agresearch Grasslands

29 5:40 Genetic determinants of endophytism in the *Arabidopsis* root mycobiome. **Fantin Mesny**, Max Planck Institute for Plant Breeding Research

Wednesday, March 16 3:00 p.m. – 6:00 p.m. Chapel

Morphological transitions and cell walls

Session Chairs:

Steve Free, SUNY University at Buffalo, USA **Anita Sil**, University of California San Francisco, USA

30 3:00 *Candida* biofilms: importance, regulation, and evolution. **Clarissa Nobile**, University of California, Merced

31 3:20 Targeting the fungal cell wall. **Carol Munro**, University of Aberdeen

32 3:40 Multi-omics Profiling Reveals New Pathways Regulating Hyphal Morphogenesis in *Candida albicans*. **Kyunghun Min**, Stony Brook University

33 4:00 Nanoscale imaging of dynamic cell wall formation in fission yeast. **Fred Chang**, UCSF

4:20 Break

34 4:40 A myosin light chain, linking fungal morphology and filament extension, is critical for *Candida albicans* growth robustness. **Robert Arkowitz**, University Cote d'Azur/CNRS/INSERM

35 5:00 Structural base of the cell wall diversity of *Candida glabrata*. **Lars-Oliver Essen**, Philipps University

36 5:20 Study of the physiological role of amyloid structures in the pathogenic yeast *Candida albicans*. **Thierry Mourer**, Institut Pasteur

37 5:40 Defining the septin interactome and its role in appressorium-mediated plant infection by the rice blast fungus *Magnaporthe oryzae*. **Iris Eisermann**, The Sainsbury Laboratory

Wednesday, March 16 3:00 p.m. – 6:00 p.m. Scripps

Extreme environments

Session Chairs:

Nina Gunde-Cimerman, University of Ljubljana, Slovenia

Julia Schumacher, Federal Institute for Materials Research and Testing, Germany

38 3:00 Stable parasexuality – a novel fungal reproductive strategy uncovered by population genomics. **Cene Gostinčar**, University of Ljubljana, Biotechnical Faculty

39 3:20 A cystic fibrosis patient lung environment allowed for coexistence of multiple *Exophiala dermatitidis* clades over time. **Tania Kurbessoian**, University of California, Riverside

40 3:40 Surviving in the brine: a multi-omics approach for understanding the physiology of the halophile fungus *Aspergillus sydowii*. **Ramon Alberto Batista Garcia**, Universidad Autónoma del Estado de Morelos (RFC UAE671122G49)

41 4:00 The Ess1 prolyl isomerase and its target, the CTD of RNA polymerase II, in cold-adapted fungi. **Steven Hanes**, SUNY-Upstate Medical University

4:20 Break

42 4:40 Developing genetic tools to unlock the biotechnological potential of anaerobic gut fungi. **Radwa Hanafy**, University of Delaware

43 5:00 *Knufia petricola* – a model for exploring the biology of black rock-inhabiting fungi. **Julia Schumacher**, BAM

44 5:20 Diversity of genomic adaptations to post-fire environment in higher fungi points to a crosstalk between charcoal tolerance and sexual development. **Andrei Stecca Steindorff**, Lawrence Berkeley National Laboratory

45 5:40 Resistance and adaptation of the melanized yeast *Exophiala dermatitidis* to ionizing radiation exposure. **Zheng Wang**, US Naval Research Laboratory

Wednesday, March 16 3:00 p.m. – 6:00 p.m. **Nautilus**

Interactions with prokaryotes and viruses

Session Chairs:

Nancy Keller, University of Wisconsin-Madison, USA Ioly Kotta-Loizou, Imperial College London, UK

46 3:00 Antifungal Potential of the Skin Microbiome. Lindsay Kalan, University of Wisconsin-Madison

47 3:20 Horizontal transmission and loss-driven evolution in Mycoavidus, a Mortierella-associated endohyphal bacterium. Kevin Amses, Oregon State University

48 3:40 A shelter from the elements: understanding requirements for fungal chlamydospore formation and bacterial invasion. Isabelle Ludwikoski, University of Wisconsin - Madison

49 4:00 From iron to antibiotics: Bacterial-fungal interactions revealed by genome-wide mutational analyses. Emily Pierce, University of California San Diego

4:20 Break

50 4:40 Elucidating Fungal Immune Receptors and Testing the Potential Role of Nucleotide-binding Domain Leucine-rich Repeat-like Proteins (NLRlike) Against Bacterial Antagonists. Frances Stark, University of California, Berkeley

51 5:00 Characterization of internal ribosomal entry sites in fungal RNA viruses and their potential use in multiple gene expression in filamentous fungi. Sotaro Chiba, Nagoya University

52 5:20 A GPI-anchored protein gene from the chestnut blight fungus Cryphonectria parasitica is a hypovirus-specific virulence factor and a tolerance factor against hypovirus infection. Dae-Hyuk Kim, **Chonbuk National University**

53 5:40 Deciphering the mycovirome of *Botrytis* cinerea. Ana Ruiz-Padilla, Universidad Politécnica de Madrid. CBGP (UPM-INIA)

Wednesday, March 16 3:00 p.m. - 6:00 p.m. Kiln

Circadian Rhythms and photobiology

Session Chairs:

Luis Corrochano, University of Seville, Spain Jennifer Hurley, Rensselaer Polytechnic Institute, USA

54 3:00 Circadian Clock Control of mRNA Translation. Deborah Bell-Pedersen, Texas A&M University

55 3:20 Insights into biological responses to light from baker's yeast S. cerevisiae, an organism lacking established photoreceptors. Mikael Molin, Chalmers University of Technology

56 3:40 A role for gene expression and mRNA stability in the mechanism underlying circadian nutritional compensation in Neurospora crassa. Christina Kelliher, Geisel School of Medicine at Dartmouth

57 4:00 Dark stipe mutants in fruiting body development of Coprinopsis cinerea. Shanta Subba, University of Goettingen

4:20 Break

58 4:40 Conformational Changes in the Circadian Negative Arm Correlate with Dynamic Interactomes Involved in Diverse Biological Processes. Jacqueline Pelham, Rensselaer Polytechnic Institue

59 5:00 Casein kinase 1 and disordered clock proteins form functionally equivalent phospho-based circadian modules in fungi and mammals. Axel Diernfellner, Heidelberg University Biochemistry Center

60 5:20 Genome wide insights into signal integration by the G-protein pathway for regulation of carbonand secondary metabolism. Miriam Schalamun, Austrian Institute of Technology

61 5:40 The evolution of DNA repair: how a cryptochrome photoreceptor became a CPD photolyase in mucoral fungi. Luis Corrochano, Universidad de Sevilla

Thursday, March 17 9:00 a.m. – 12:00 p.m. Merrill Hall and Chapel

Plenary Session II: Cross species interactions

Session Chairs:

Elaine Bignell, University of Exeter, UK Frances Trail, Michigan State University, USA

62 9:00 am Cross-kingdom interactions in arbuscular mycorrhizal symbiosis. Maria Harrison, Boyce Thompson Institute

63 9:30 Metarhizium: jack of all trades, master of many. Raymond St. Leger, University of Maryland

64 10:00 Chemical interactions between fungi and nematodes. Reinhard Fischer, Karlsruhe Institute of Technology (KIT)

10:30 Break

65 11:00 A structure for effector delivery in smut fungi? Regine Kahmann, Max Planck Institute for Terrestrial Microbiology

66 11:30 A Ralstonia pickettii endosymbiont allows Rhizopus microsporus to evade amoeba and cause opportunistic virulence in animals. Elizabeth Ballou, University of Exeter, Centre for Medical Mycology

Thursday, March 17 3:00 p.m. - 6:00 p.m. Merrill Hall

Plant Pathogens

Session Chairs:

Matthias Hahn, University of Kaiserslautern, Germany Barbara Valent, Kansas State University, USA

67 3:00 Functional diversification of effectors in smut fungi. Gunther Doehlemann, University of Cologne

68 3:20 Fungal Pathogens Utilize Extracellular Vesicles for Transport of Effector Proteins into Plant Host Cells. Claire Whitaker, UC Riverside

69 3:40 Multiple mutagenesis of *Botrytis cinerea* by an improved CRISPR/Cas9 protocol reveals high redundancy of phytotoxic proteins for necrotrophic infection. Matthias Hahn, Kaiserslautern Univ

70 4:00 Pyricularia HAG effector family interactions with rice candidate target proteins. Nicholas Farmer, Texas A&M University

4:20 Break

71 4:40 Appressorium-mediated plant infection by Magnaporthe oryzae is regulated by a Pmk1-dependent hierarchical transcriptional network. Miriam Oses-Ruiz, Public University of Navarre

72 5:00 Alternative sulfur scavenging and host colonization by the plant pathogen Raffaelea lauricola. Joshua Konkol, University of Florida

73 5:20 Oomycete RXLR effectors enter plant cells by clathrin-mediated endocytosis. Paul Birch, University of Dundee

74 5:40 Pathotypes of Fusarium oxysporum f. sp. fragariae express discrete repertoires of accessory genes and induce distinct host transcriptional responses during root infection. Peter Henry, United States Department of Agriculture

Thursday, March 17 3:00 p.m. – 6:00 p.m. Chapel

Secondary metabolism and production of useful metabolites

Session Chairs:

Jens Frisvad, Technical University of Denmark, Denmark

Jae-Hyuk Yu, University of Wisconsin-Madison, USA

75 3:00 Honor by association, leveraging global gene co-expression networks for specialized metabolic pathway discovery. Jennifer Wisecaver, Purdue University

76 3:20 Lichen-like consortia and multicellular structures protect algae against bacterial toxins. Mario Krespach, Leibniz Institute for Natural Product Research and Infection Biology - Hans Knöll Institute

77 3:40 CRISPR-based transcriptional activation tool for silent genes in filamentous fungi. Laszlo Mozsik, University Leiden

78 4:00 The fungal battery: A redox flow battery containing the biosynthesised quinone phoenicin from Penicillium astrosanguineum. Jens Laurids Sørensen, Aalborg University

4:20 Break

79 4:40 No genes left behind: Associating phenotypes with genes in Neurospora crassa. Scott Baker, Pacific Northwest National Laboratory

80 5:00 Culturing *Aspergillus nidulans* in soil microcosm elucidates its ecological behavior and interaction with soil microbiota. Daisuke Hagiwara, University of Tsukuba

81 5:20 Deciphering lichen secondary metabolism by genetic dereplication, transcriptome analysis, and heterologous expression. Wonyong Kim, Sunchon **National University**

82 5:40 Novel secondary metabolites and their biosynthesis from new Aspergilli of Australia. Yit-Heng Chooi, University of Western Australia

Thursday, March 17 3:00 p.m. - 6:00 p.m. **Nautilus**

Stress

Session Chairs:

Jesús Aguirre, Universidad Nacional Autónoma de México, Mexico

Deborah Bell-Pedersen, Texas A&M University, USA

83 3:00 Pathogenic fungi at the crossroads of metal starvation and oxidative stress. Valeria Culotta, Johns Hopkins University Bloomberg School of Public Health

84 3:20 ROS regulate mitochondrial dynamics in Aspergillus nidulans. Jesus Aguirre, Instituto de Fisiologia Celular-UNAM

85 3:40 Phosphorylation/dephosphorylation of the Cochliobolus heterostrophus stress-activated MAPK Hog1 in response to plant phenolic acids. Rina **Zuchman**, Technion

86 4:00 Signaling Pathway Loss-of-Function Alleles and Evolutionary Hotspots in the Fungi. Paul Magwene, Duke University

4:20 Break

87 4:40 Regulation of cell shape and virulence factor expression in response to temperature in the fungal pathogen Histoplasma capsulatum. Anita Sil, Univ California, San Francisco

88 5:00 Circadian Clock-Controlled Translation of Specific *Neurospora crassa* mRNAs Requires Rhythmic eIF2α Activity and P-bodies. **Kathrina Castillo**, Texas **A&M University**

89 5:20 Ccr4 and Gcn2 contribute differentially to stress-specific translational repression in C. neoformans. Corey Knowles, SUNY Buffalo

90 5:40 A Tor1 N-terminal region required for Candida albicans anabolic- and stress regulation. Wanjun Qi, Boston Children's Hospital/Harvard Medical School

Thursday, March 17 3:00 p.m. – 6:00 p.m. Fred Farr Forum

Chromatin, heterochromatin, and epigenetics

Session Chairs:

Alessia Buscaino, University of Kent, UK David Cook, Kansas State University, USA

91 3:00 Control and function of facultative heterochromatin in Neurospora crassa. Zachary Lewis, University of Georgia

92 3:20 Heterochromatin marks perturb transcriptional robustness and underpin dispensability of genes across evolutionary timescales in fungi. Sabina Tralamazza, University of Neuchâtel

93 3:40 Methylation of H4 controls gene expression in facultative heterochromatin. Mareike Moeller, **Oregon State University**

94 4:00 RNAi and heterochromatin independently control gene expression and transposable elements in Mucorales. María Isabel Navarro-Mendoza, Duke University

4:20 Break

95 4:40 A prion accelerates proliferation at the expense of lifespan. David Garcia, University of Oregon, Institute of Molecular Biology

96 5:00 Probing the role of N6-methyladenine DNA modification within the Rhizopus microsporus and Mycetohabitans symbiosis. Margaret Branine, Cornell University

97 5:20 Periodic DNA patterns associated with chromatin regulation in Fungi. Stephen Mondo, DOE Joint Genome Institute

98 5:40 Chromatin remodeling is required for the expression of small interfering RNAs from repetitive DNA loci in *Neurospora crassa*. Eugene Gladyshev, Institut Pasteur

Thursday, March 17 3:00 p.m. – 6:00 p.m. Heather

Spore development, dormancy and germination

Session Chairs:

Michelle Momany, University of Georgia, USA Chris Koon Ho Wong, University of Macau, China

99 3:00 The conidial coin toss: asymmetric spore adhesion in Colletotrichum graminicola. Brian Shaw, Texas A&M University

100 3:20 Differences in spore size and atmospheric survival shape stark contrasts in the dispersal dynamics of two closely related fungal pathogens. Anne Pringle, UWisconsin-Madison

101 3:40 RNA Editing Controls Toxicity of a Neurospora Spore Killer. Nicholas Rhoades, Illinois State University

102 4:00 The HMG Domain-Containing Transcription Factors Hgr1 and Hgr2 are Putative Dormancy Factors of Cryptococcus Spores. Megan McKeon, University of Wisconsin-Madison

4:20 Break

103 4:40 Aspergillus niger conidial germination: 3D live cell exploration. Susanne Fritsche, Austrian Centre of Industrial Biotechnology (ACIB GmbH), Technical University of Vienna

104 5:00 Developmental genetics of host invasion initiated by fungal conidia. Soumya Moonjely, Michigan State University

105 5:20 Sporulation environment drives variation in genetically-identical conidia. Michelle Momany, Univ Georgia

106 5:40 Transcription activity before dormancy in fungal conidia modulates phenotypic variation and affects the fitness and capabilities of fungal cells after germination. Koon Ho Wong, University of Macau

Thursday, March 17 3:00 p.m. – 6:00 p.m. Scripps

Lipid metabolism and signaling

Session Chairs:

James Konopka, University of California, Los Angeles, **USA**

Naweed Naqvi, Temasek Life Sciences Laboratory, Singapore

107 3:00 Two distinct lipid transporters together regulate invasive filamentous growth in Candida albicans. Martine Bassilana, University Cote d'Azur/ CNRS/INSERM

108 3:20 Lipid flippase mediated Cryptococcus-host interaction during pulmonary cryptococcosis. Siddhi Pawar, Rutgers University

109 3:40 Role of Arv1 protein in sterol metabolism and pathogenicity of the chestnut blight fungus Cryphonectria parasitica. Soumyadip Kundu, Mississippi State University

110 4:00 Sterol homeostasis is critical for surface structure organization and virulence in Cryptococcus neoformans. Hau Lam Choy, Washington University in St. Louis

4:20 Break

111 4:40 Oxylipin Signals Affecting Host and Pathogen Interactions. Nancy Keller, Univ Wisconsin, Madison

112 5:00 Eisosomes mediate a novel pathway for regulating PI(4,5)P, in Candida albicans that is critical for cell wall morphogenesis and virulence. Carla Lanze, Stony Brook University

113 5:20 Role of the *Malassezia* lipidome in human skin health. Thomas Dawson, Agency for Science, Technology and Research

114 5:40 Lipid peroxidation and mitochondrial metabolism enable regulated cell death in Rice Blast. Qing Shen, Temasek Life Sciences Laboratory Thursday, March 17 3:00 p.m. – 6:00 p.m. Kiln

Natural and experimental diversity, evolution and populations

Session Chairs:

Christina Cuomo, Broad Institute, USA Jianping Xu, McMaster University, Canada

115 3:00 Metal tolerance in the mycorrhizal fungus Suillus luteus. Sara Branco, University of Colorado Denver

116 3:20 Using machine learning to gain insight on how environment and diet influence the evolution of galactose metabolism across the budding yeast subphylum. Marie-Claire Harrison, Pomona College

117 3:40 The extrachromosomal circular DNAs of the rice blast pathogen Magnaporthe oryzae contain a wide variety of LTR retrotransposons, genes, and effectors. Pierre M Joubert, University of California, Berkeley

118 4:00 Clonality and recombination in natural populations of Candida auris. Jianping Xu, McMaster University

4:20 Break

119 4:40 Genomic variation across a clinical Cryptococcus population linked to disease outcome. Poppy Sephton-Clark, Broad Institute of MIT and Harvard

120 5:00 Genetic and epigenetic variants underpinning within-species transcriptional polymorphism in a major fungal pathogen. Leen Abraham, University of Neuchatel

121 5:20 Giant *Starship* elements mobilize accessory genes in fungal genomes. Emile Gluck-Thaler, University of Neuchatel

122 5:40 Evolution of Aspergillus fumigatus Biofilm Morphotypes in Host Microenvironments, Robert **Cramer**, Dartmouth University

Plenary Session III: Evolution and Development

Session Chairs:

Joe Heitman, Duke University, USA Eva Stukenbrock, Kiel Evolution Center, Germany

123 9:00 am Evolution repeats itself in fungal morphogenetic transitions - in search of mechanisms of convergent evolution. **Laszlo Nagy**, Biological Research Center, HAS

124 10:00 The genetics and genome biology of multinucleate arbuscular mycorrhizal fungi. **Nicolas Corradi**, University of Ottawa

10:30 Break

125 11:00 Genomics, species limits, and evolution of the shiitake genus *Lentinula*. **David Hibbett**, Clark University

126 11:30 Deep tissue infection by an invasive human fungal pathogen requires novel lipid-based suppression of the IL-17 response. **Suzanne Noble**, UCSF School of Medicine

127 9:30 Rise and fate of mutations in the fairy ring mushroom Marasmius oreades. **Hanna Johannesson**, Uppsala University

Friday, March 18 3:00 p.m. – 6:00 p.m. Fred Farr Forum

Interactions with other non-human/ plant eukaryotic species

Session Chairs:

Monika Schmoll, Austrian Institute of Technology, Austria

Chengshu Wang, Chinese Academy of Sciences, China

128 3:00 Talking to your inner self – on the interaction between *Trichoderma reesei* QM6a and its endohyphal *Methylobacterium*. **Monika Schmoll**, University of Vienna

129 3:20 Human mediated contact between amphibian-killing chytrid variants results in repeated recombination. **Thomas Jenkinson**, California State University, East Bay

130 3:40 Characterizing variation within the European *Batrachochytrium* salamandrivorans epidemic. **Moira Kelly**, Ghent University

131 4:00 Deciphering the molecular mechanisms involved with plant-insect-fungal interactions. **Marcio Silva-Filho**, University of São Paulo

4:20 Break

132 4:40 Genes for an extended phenotype: Biosynthesis of volatile sesquiterpenes in a pathogenic fungus is used to entice male flies into fatal mating's with infected female cadavers. **Henrik De Fine Licht**, University of Copenhagen

133 5:00 Repeat-driven genome expansion and twospeed genome architecture of amphibian-infecting chytrids. **Theresa Wacker**, University of Exeter

134 5:20 Regulation of infection of insects by the fungus *Metarhizium robertsii*. **Weiguo Fang**, Zhejiang University

135 5:40 Unraveling the biology of Nematophagy During a Fungal-Nematode Predator-Prey Interaction Using Time-Course Transcriptomic analysis. **Hung-Che Lin**, Institute of Molecular Biology, Academia Sinica

Friday, March 18 3:00 p.m. - 6:00 p.m. Kiln

Natural and applied bioconversion and biodegradation

Session Chairs:

Yitzhak Hadar, The Hebrew University of Jerusalem, Israel

Taina Lundell, University of Helsinki, Finland

136 3:00 Integrating multifaceted genetic tools to gear up the discovery of fungal mechanisms of wood decay. Jiwei Zhang, University of Minnesota

137 3:20 Characterization and engineering of non-model microorganisms for biotechnological applications. Hugh Purdy, University of California, Santa Barbara

138 3:40 Chance favours the prepared spore – how to jumpstart cellulase production. Wolfgang Hinterdobler, AIT Austrian Institute Of Technology

139 4:00 The active microbial communities of oil degradation – exploring bioremediation of mine waste water, Petter Madsen

4:20 Break

140 4:40 The transcription factor Roc1 is a regulator of cellulose degradation in the wood-decaying mushroom Schizophyllum commune. Peter Jan Vonk, **Utrecht University**

141 5:00 Prevalence of aromatic lignin monomer metabolism phenotypes in a collection of woodinhabiting fungi and characterization of putative metabolic pathways, Leon Rogers

142 5:20 Lignocelluloses and solid waste substrates transformed by wood-decay fungi for production of natural compounds. Taina Lundell, University of Helsinki

143 5:40 Degradation strategy of wood extractives by conifer-degrading wood decay fungus. Chiaki Hori, **Hokkaido University**

Friday, March 18 3:00 p.m. – 6:00 p.m. **Nautilus**

Mycobiomes and their implications

Session Chairs:

Teresa E. Pawlowska, Cornell University, USA Julia Segre, National Human Genome Research Institute, USA

144 3:00 Human skin microbiome: trans-kingdom characterization and investigating an emerging fungal pathogen. Julia Segre, National Human Genome Research Institute, NIH

145 3:20 Intestinal mycobiome in allogeneic hematopoietic cell transplantation. Bing Zhai, Shenzhen Institute of Advanced Technology

146 3:40 Adaptive immunity induces mutually beneficial interactions with gut fungi. Kyla Ost, University of Utah

147 4:00 Characterizing the role of anaerobic fungi in lignocellulolytic microbial communities and the gut mycobiome of herbivorous non-human primates. Katharine Dickson, University of California, Santa Barbara

4:20 Break

148 4:40 When and how do fungi impact the evolution of bacteria? Benjamin Wolfe, Tufts University - Biology

149 5:00 Interrogating the poplar fungal microbiome interactions using meta-transcriptomics and constructed communities. Jake Nash, Duke University

150 5:20 Metabarcoding as a tool for investigating the influence of endosymbiotic bacteria on Mucoromycota fungal host community structure in the Sonoran Desert. Nicole Reynolds, Cornell University

151 5:40 Global evolutionary patterns and drug resistance acquisition in the human pathogen Aspergillus fumigatus. Johanna Rhodes, Imperial College London

Friday, March 18 3:00 p.m. – 6:00 p.m. Merrill Hall

Mating and sexual development

Session Chairs:

Fabienne Malagnac, University Paris Saclay **Brenda Wingfield**, University of Pretoria, South Africa

152 3:00 Identifying novel sexual reproduction defects by TN-seq in *Schizosaccharomyces pombe*. **Caroline Craig**, Stowers Institute for Medical Research

153 3:20 Obligate sexual reproduction of a homothallic fungus closely related to the *Cryptococcus* pathogenic species complex. **Marco A. Coelho**, Duke University Medical Center

154 3:40 Agaricomycete multicellular development and biomolecule formation with focus on the model system *Cyclocybe aegerita* and its relatives. **Florian Hennicke**, Ruhr-Universität Bochum (RUB)

155 4:00 Role of A-to-I RNA editing in *Sordaria macrospora* sexual development. **Ines Teichert**, Allgemeine und Molekulare Botanik

4:20 Break

156 4:40 Systematic deletions of histone methyltransferase and demethylase genes reveal their role in RIP and sexual development. **Pierre Grognet**, Universite Paris-Saclay, CNRS

157 5:00 Live-Cell Imaging of Sexual Reproduction in *Podospora anserina*: the foreplay. **Sylvain Brun**, Universite de Paris

158 5:20 Diverse sexual strategies underpinned by the mating-type locus in the non-model fungal family *Ceratocystidaceae*. **Markus Wilken**, University of Pretoria

159 5:40 Functional analyses of putative target genes of Argonaute-like protein (FgAGO2) required for sexual development in *Fusarium graminearum*. **Sung-Hwan Yun**, Soonchunhyang Univ

Friday, March 18 3:00 p.m. – 6:00 p.m. Heather

Molecular basis of biotrophy

Session Chairs:

Armin Djamei, University of Bonn, Germany **Alga Zuccaro**, University of Cologne, Germany

160 3:00 A common FOLD among plant symbiotic and pathogenic fungi. **Sebastian Schornack**, University of Cambridge

161 3:20 Conserved secreted effectors determine endophytic growth and multi-host plant compatibility in a vascular wilt fungus. **Antonio Di Pietro**, Universidad de Cordoba

162 3:40 *Blumeria graminis* effector proteins target a conserved host cell polarity pathway for establishment of biotrophic infection structures. **Ralph Hückelhoven**, Technical University of Munich

163 4:00 Co-repressor Topless, a central effector hub for the *Ustilago maydis*/maize interaction. **Armin Djamei**, University of Bonn, INRES

4:20 Break

164 4:40 Cytoplasmic effector translocation during early biotrophic invasion by the rice blast fungus. **Ely Oliveira-Garcia**, Louisiana State University

165 5:00 Deletion of the killer kinase *KIL1* abolishes penetration peg formation in the predator yeast *Saccharomycopsis schoenii*. **Mareike Rij**, Hochschule Geisenheim University

166 5:20 Conditional role of a signal peptidase component in the establishment of biotrophy by the maize anthracnose pathogen *Colletotrichum graminicola*. **Renata Belisario**, University of Kentucky

167 5:40 Impairment of the cellulose degradation machinery enhances *Fusarium oxysporum* virulence but limits its reproductive fitness. **Clara Sanchez-Rodriguez**, Department of Biology, ETH Zurich

Friday, March 18 3:00 p.m. – 6:00 p.m. Chapel

Speciation, diversity and evolution

Session Chairs:

A. Elizabeth Arnold, University of Arizona, USA **Toni Gabaldón**, Catalan Institution for Research and Advanced Studies, Spain

168 3:00 Ecological generalism drives hyperdiversity of secondary metabolite gene clusters in xylarialean endophytes. **Jana M. U'Ren**, University of Arizona

169 3:20 Fungal digestive enzyme profile: Essential for fitness and integrated part of speciation and evolution. **Lene Lange**, BioEconomy, Research & Advisory

170 3:40 Genomic diversity across 17 clinical isolates of *Candida auris* shapes *in vitro* evolution and rapid development of fluconazole resistance. **Laura Burrack**, Gustavus Adolphus College

171 4:00 Genome-scale phylogeny of the fungal order Sordariales. **Noah Lisa Hensen**, Uppsala University

4:20 Break

172 4:40 Allele specific expression during fruiting body formation in *Pleurotus ostreatus*. **Zsolt Merényi**, Biological Research Centre

173 5:00 Understanding the nature of the reproductive barriers within the wood decay species *Trichaptum abietinum*. **Dabao Sun Lu**, University of Oslo

174 5:20 Host specificity determines a new fungal plant pathogen population. Wagner Calegari Fagundes, Max Planck Institute for Evolutionary Biology & Christian-Albrechts University Kiel

175 5:40 Three-dimensional chromatin organization determines the evolution of adaptive genomic regions in the plant pathogen *Verticillium dahliae*. **David E Torres**, Wageningen University and Research

Friday, March 18 3:00 p.m. – 6:00 p.m. Scripps

Small molecules in communication

Session Chairs:

Francine Govers, Wageningen University, The Netherlands

Benjamin Horwitz, Israel Institute of Technology, Israel

176 3:00 The diversity in fungal volatile organic compound profiles. **Maaria Rosenkranz**, Helmholtz Zentrum Munich

177 3:20 Using random barcoded transposonsite sequencing (Rb-TnSeq) bacterial libraries to explore the effects of volatiles from *Trichoderma atroviride*. **Catharine Adams**, UC Berkeley

178 3:40 MERLIN unlocks the secrets to chitin signaling: Using gene-network inference to predict mediators of fungal response to lipochitooligosaccharides. **Cristobal Carrera Carriel**, University of Wisconsin-Madison

179 4:00 Copper homeostasis and *Cryptococcus neoformans* cell surface architecture. **Corinna Probst**, Duke University

4:20 Break

180 4:40 Connecting fungal genomes with the behavioral phenomes of ants, manipulated by *Ophiocordyceps*. **Charissa de Bekker**, University of Central Florida

181 5:00 *Phytophthora* zoospores display klinokinetic behaviour in response to a chemoattractant. **Michiel Kasteel**, Wageningen University

182 5:20 RNA interference affects fungus-fungus interactions in the biocontrol agent *Clonostachys rosea*. **Edoardo Piombo**, Swedish University of Agricultural Sciences

183 5:40 *Lactobacillus*-secreted Yak1 inhibitor, 1-acetyl-beta-carboline, blocks *Candida albicans* morphogenesis and biofilm formation. **Jessie MacAlpine**, University of Toronto

Saturday, March 19 8:45 a.m. – 9:00 a.m. Merrill Hall and Chapel

Fungal Community Meeting and election of FGPC members

Saturday, March 19 9:00 a.m. – 12:00 p.m. Merrill Hall and Chapel

Plenary Session IV: Signaling and Metabolism

Session Chairs:

Axel Brakhage, International Leibniz Research School, Germany

Vera Meyer, Technical University of Berlin, Germany

184 9:00 am Unlocking the biotech potential of the anaerobic fungi (Neocallimastigomycetes). Michelle O'Malley, University of California, Santa Barbara

185 9:30 The complexity of Sweet - Competing carbon perception pathways in filamentous fungi. J. Philipp Benz, Technical University of Munich

186 10:00 The diets of biotrophs and opportunists in unhealthy hosts. James Kronstad, Univ British Columbia

10:30 Break

187 11:00 Materialize fungi. Han Wosten, Utrecht University

188 11:30 How a fungus protects itself when producing a secondary toxic metabolite. Gustavo H. Goldman, FCFRP, Universidade de Sao Paulo

Saturday, March 19 2:00 p.m. – 5:00 p.m. Fred Farr Forum

Fungal determinants of host response

Session Chairs:

Andy Alspaugh, Duke University, USA Bart P. H. J. Thomma, Wageningen University, The Netherlands

189 2:00 Fungal pathogen effector-mediated dysbiosis to stimulate disease development in plant hosts. Bart Thomma, University of Cologne

190 2:20 *Cryptococcus neoformans* Chitin Synthase 3 (Chs3) Plays a Critical Role in Dampening Host Inflammatory Responses. Camaron Hole, University of Tennessee Health Science Center

191 2:40 Botrytis cinerea secretes small RNA containing extracellular vesicles that enter plant cells through clathrin-dependent endocytosis. Baoye He, **UCR**

192 3:00 Roles of candidalysin of *Candida albicans* in the gut permeability and brain pathology. Courtney Smith, UTSA

3:20 Break

193 3:40 Unravelling the gene networks coordinating core and host-specific infection programs in the polyphagous plant pathogenic fungus Sclerotinia sclerotiorum. Sylvain Raffaele, INRAE - LIPME

194 4:00 Analysis of commensal *Candida* albicans strains reveals genomic variability but conserved pathogenic potential. Teresa O'Meara, University of Michigan

195 4:20 Metabolomic profiling of behaviorally manipulated insects infected by "zombie ant fungus" (Ophiocordyceps). Ian Will, University of Central Florida

196 4:40 The Venturia inaequalis effectorome is expressed in waves, and is dominated by expanded families with predicted structural similarity to avirulence effector proteins. Mercedes Rocafort, **Massey University**

Saturday, March 19 2:00 p.m. - 5:00 p.m. Heather

Emerging and re-emerging fungi in a changing world

Session Chairs:

Sarah Gurr, University of Exeter, UK Nick J. Talbot, The Sainsbury Laboratory, UK

197 2:00 The global movement of fungal and oomycete crop pathogens: mechanistic models, predictions and perils. Sarah Gurr, University of Exeter

198 2:20 Evolutionary Morphogenesis, Chytrids and the rise of The Fungi. Edgar Medina, UMass Amherst

199 2:40 A pandemic clonal lineage of the wheat blast fungus. Hernán A Burbano, University College London

200 3:00 Convergent recognition of the *Magnaporthe* oryzae host specificity determinant PWL2 in divergent grass species. Diana Gómez De La Cruz, The Sainsbury Laboratory

3:20 Break

201 3:40 Emerging tree pathogen *Phellinus noxius* has a long evolutionary history in eastern Asia, Australia, and the Pacific Islands. Olga Kozhar, Colorado State University

202 4:00 Genomic diversification of the specialized parasite of the fungus-growing ant symbiosis. Kirsten Gotting, University of Wisconsin Madison

203 4:20 The maize mycobiome and implication on mycotoxin contamination in relation to climatic patterns. Bwalya Katati, Wageningen University and Research

204 4:40 Metagenomics approaches to understanding the synergistic roles of environment and chytrid infection in host extinction. Matthew Fisher, Imperial Col London

Saturday, March 19 2:00 p.m. – 5:00 p.m. Merrill Hall

Fungicides and antifungals

Session Chairs:

Judith Berman, Tel-Aviv University, Israel Gabriel Scalliet, Syngenta, UK

205 2:00 Pararesistance: a non-genetic mechanism of antifungal drug resistance. Jinglin Lucy Xie, Stanford University School of Medicine

206 2:20 Targeting Aspergillus fumigatus hypoxia response pathways to potentiate contemporary antifungal therapies. Cecilia Gutierrez Perez, **Dartmouth College**

207 2:40 Exploiting synergistic and antagonistic drug interactions to improve treatment of systemic fungal infections. Jessica Brown, University of Utah

208 3:00 Live cell imaging to understand fungicide mode of action. Gero Steinberg, Univ Exeter

3:20 Break

209 3:40 Predicting predictability of fungicide resistance evolution. Nichola Hawkins, NIAB

210 4:00 Methionine synthase as a target for antifungal drug development. Jennifer Scott, The University of Manchester

211 4:20 Unanticipated drug-fungal interactions and their potential to impact the outcome of infection. Glen Palmer, University of Tennessee Health Sciences Center

212 4:40 Inhibitor targeting the Prp8 intein splicing of Cryptococcus neoformans, Hongmin Li

Saturday, March 19 2:00 p.m. - 5:00 p.m. Chapel

Coolest tools for fungal biology

Session Chairs:

Alexandra Brand, University of Exeter, UK Matthew S. Sachs, Texas A&M University, USA

213 2:00 DIVERSIFY - A flexible multispecies approach for construction of efficient heterologous fungal cell factories. **Uffe Mortensen**, Technical University of Denmark

214 2:20 4-color live-cell imaging and other novel microscopy tools reveal dynamic sub-cellular distributions of core clock components in Neurospora crassa. Ziyan Wang, Geisel School of Medicine at Dartmouth

215 2:40 A platform for functional analysis for Candida albicans strain variation. Yinhe Mao, University of Georgia

216 3:00 FungiDB: Free online informatic tools for fungal and oomycete biologists. Omar Harb, University of Pennsylvania

3:20 Break

217 3:40 Fungal Bioreporters to Monitor Outcomes of Host-Cell Interactions. Neta Shlezinger, The Hebrew University

218 4:00 Development of a rapid and reversible system for targeted protein depletion in the filamentous fungus, Fusarium graminearum. John Ridenour, Oregon State University

219 4:20 Genes of unknown function conserved across fungi: a call for action. Igor Grigoriev, US DOE Joint Genome Institute

220 4:40 Novel GCaMP6 imaging of cytosolic free calcium dynamics reveals stress-specific signalling responses in the fungal pathogen, Candida albicans. Callum J Parkin, University of Exeter

Saturday, March 19 2:00 p.m. – 5:00 p.m. Kiln

From genome to pangenome

Session Chairs:

Li-Jun Ma, University of Massachusetts, Amherst, USA **Jason Stajich**, University of California, Riverside, USA

221 2:00 Combined Pan-, Population-, and Phylo-Genomic Analysis of *Aspergillus fumigatus* Reveals Population Structure and Lineage-Specific Diversity. **Lotus Lofgren**, Duke University

222 2:20 Fusarium effectome analysis reveals high diversity of effectors and direct relationship with the fungus lifestyle and their strategies for host colonization/infection. **Domingo Martínez-Soto**, University of Massachusetts

223 2:40 An orthologous gene coevolution network provides insight into eukaryotic cellular and genomic structure and function. **Jacob Steenwyk**, Vanderbilt University

224 3:00 Births, deaths and survival of a retrotransposon family in the face of repeat induced point mutations (RIP). **Ivar Westerberg**, Uppsala University

3:20 Break

225 3:40 The distributed genome of *Fusarium* oxysporum: mix and match of core and accessory chromosomes. **Like Fokkens**, Wageningen University

226 4:00 A Pangenomic assessment of a Cercospora beticola global population. **Nathan Wyatt**, USDA-ARS

227 4:20 Complete Genome Sequences and Genome-Wide Characterization of *Trichoderma* Biocontrol Agents Provide New Insights into their Evolution and Variation in Genome Organization, Sexual Development and Fungal-Plant Interactions. **Ting-Fang Wang**, Academia Sinica

228 4:40 A global pangenome analysis of tan spot (*Pyrenophora tritici-repentis*) reveals an open genome and virulence factors nested in mobile elements. **Reem Aboukhaddour**, Agriculture and Agri-Food Canada

Saturday, March 19 2:00 p.m. – 5:00 p.m. Scripps

Fungal recognition (self and non-self)

Session Chairs:

Paul Dyer, The University of Nottingham, UK **André Fleissner**, Technische Universität Braunschweig, Germany

229 2:00 Allorecognition genes drive reproductive isolation in *Podospora anserina*. **Aaron A. Vogan**, Uppsala University

230 2:20 An NLR-like system delimits individuals in the basidiomycete *Coprinopsis cinerea*. **Ben Auxier**, Wageningen University

231 2:40 Self- and non-self-recognition for cell fusion and heterokaryon incompatibility in the industrial filamentous fungus *Aspergillus oryzae*. **Jun-ichi Maruyama**, The University of Tokyo

232 3:00 Functional Amyloids Are Widespread in Fungal Biofilm Adhesins. **Peter Lipke**, CUNY Brooklyn College

3:20 Break

233 3:40 A chitin polysaccharide monooxygenase functions in trans with a plasma transmembrane protein to trigger allorecognition upon cell contact. **Adriana Rico Ramirez**, UC BERKELEY CAMPUS

234 4:00 Interspecies interactions of *Neurospora crassa* and *Botrytis cinerea* are mediated by a conserved cell-cell communication mechanism. **Andre Fleissner**, TU Braunschweig

235 4:20 Competing for cheating escalates the deleterious effects of reproductive parasitism. **Duur Aanen**, Wageningen University

236 4:40 Fungal Chemical Warfare: How Secondary Metabolites Influence Relationships in Maize Associated Fungi. **Tim Satterlee**, USDA/ARS

Saturday, March 19 2:00 p.m. – 5:00 p.m. **Nautilus**

Systems biology and biomaterials

Session Chairs:

Luis F. Larrondo, Pontifical Catholic University of Chile, Chile

Kevin McCluskey, Bolt Threads, USA

237 2:00 Laccase expression in the dung fungus Coprinopsis cinerea with 17 natural laccase genes. Ursula Kües, University of Goettingen

238 2:20 Production of Organic Acids in Engineered Aspergillus. Jon Magnuson, Pacific Northwest **National Laboratory**

239 2:40 MY-CO SPACE: An artistic-scientific vision on how to build with fungi. Vera Meyer, TU Berlin

240 3:00 Use of a cell-free expression (CFE) to fast characterize fungal enzymes in the wood decomposer Rhodonia placenta. Jesus Castano Uruena, University of Minnesota

3:20 Break

241 3:40 Sustainable protein production for food applications from a microbe, Fusarium strain flavolapis, isolated from Yellowstone National Park. Debbie Yaver, Nature's Fynd

242 4:00 Understanding DNA Uptake by Anaerobic Fungi. Tejas Navaratna, UC Santa Barbara

243 4:20 Growing the future of biomaterials: learning from fungal genetics to tune Fine Mycelium™. Rachel **Linzer**, MycoWorks

244 4:40 Mycotecture off planet: fungi as a building material on the Moon and Mars. Lynn Rothschild, NASA Ames Research Center

Saturday, March 19 5:30 p.m. – 5:45 p.m. Merrill Hall and Chapel

Fungal Conference and GSA Poster Award Presentations

Saturday, March 19 5:45 p.m. - 6:30 p.m. Merrill Hall and Chapel

Perkins/Metzenberg Lecture presented by Gillian Turgeon, Cornell University, **USA**

Session Chair:

Marc Orbach, University of Arizona, USA

Gillian Turgeon is a Professor and Chair of the Section of Plant Pathology and Plant-Microbe Biology in the School of Integrative Plant Science at Cornell University. Her research concerns molecular mechanisms of fungal virulence to plant hosts (inter-organismal recognition) and filamentous ascomycete mating (intra-organismal recognition), both with a particular focus on secondary metabolite determinants.

Biochemistry and Metabolism	245-292
2. Biotechnology	293-335
3. Cell Biology and Development	336-442
4. Comparative and Functional Genomics	443-551
5. Fungal Diversity	552-586
6. Gene Regulation	587-676
7. Pathogenic and Mutalistic Interactions	677-817
8. Population and Evolutionary Genetics	818-872
9. Synthetic Biology	873-885
11. Other	886-905

1. Biochemistry and Metabolism

245W Casein kinase 1 and disordered clock proteins form functionally equivalent phospho-based circadian modules in fungi and mammals **Axel Diernfellner** Heidelberg University Biochemistry Center

246T Conformational Changes in the Circadian Negative Arm Correlate with Dynamic Interactomes Involved in Diverse Biological Processes **Jacqueline Pelham** Rensselaer Polytechnic Institue

247F Quantitative phosphoproteomic analysis of appressorium development by the rice blast fungus *Magnaporthe oryzae* **Frank L.H. Menke** The Sainsbury laboratory

248W Anaerobic fungi are an untapped source of biotechnologically relevant membrane proteins **Susanna Seppala** University of California, Santa Barbara

249T Pyrolyzed substrates induce aromatic compound metabolism in the post-fire fungus, *Pyronema domesticum* **Monika S. Fischer** UC Berkeley

250F Inhibitor targeting the Prp8 intein splicing of *Cryptococcus neoformans* **Hongmin Li** University of Arizona, Tucson

251W Characterization of *Phanerochaete* chrysosporium mutants resistant to *Bagassa* guianensis wood extractives **Delphine Noël** Université de Lorraine

252T Isolation of mutants *resistant to itraconazole* in the white-rot fungus *Phanerochaete chrysosporium* RP78 leads to identification of alleles in *CYP51/ERG11* **Rodnay Sormani** LORRAINE UNIVERSITY

253F Methionine synthase as a target for antifungal drug development **Jennifer Scott** The University of Manchester

254W Mutation in the ribosomal protein gene eL42 results inCycloheximide resistance in the Ophiostomatales **Brenda Wingfield** University of Pretoria

255T Structure of the

translating *Neurospora* ribosome arrested by cycloheximide **Matthew Sachs** Texas A&M University

256F Sre1, a transcription factor controlling ergosterol biosynthesis, stimulates response to nickel, an important micronutrient for fungi **Amber Matha** The University of Georgia

257W Oxygen mediated cell-cell heterogeneity and antifungal drug susceptibility in *Aspergillus fumigatus* biofilms **Kaesi Morelli** Dartmouth College

258T Manganese Transporters and Virulence in *Candida albicans* **Asia Wildeman** Johns Hopkins School of Public Health

259F Temperature-specialized function of glycogenins in *Cryptococcus neoformans* **Liza Loza** Washington University in St. Louis

260W Capsule glycosylation in *Cryptococcus neoformans* **Thomas Hurtaux** Washington University in St. Louis

261T Analysis of Roles for CPC-2 in Degrading the Plant Cell Wall Carbohydrate Cellulose **Anthony Silva** UC Riverside

262F Lipid flippase mediated Cryptococcus-host interaction during pulmonary cryptococcosis **Siddhi Pawar** Rutgers University

263W Lipid flippase regulation of antifungal drug resistance and virulence in *Cryptococcus neoformans* **Chaoyang Xue** Rutgers University

264T Role of Arv1 protein in sterol metabolism and pathogenicity of the chestnut blight fungus *Cryphonectria parasitica* **Soumyadip Kundu** Mississippi State University

265F Differential effects of G-protein subunits on multiple cellulase enzymes in *Neurospora crassa* **Abel Vargas** University of California, Riverside

266W Lignocelluloses and solid waste substrates transformed by wood-decay fungi for production of natural compounds **Taina Lundell** University of Helsinki

267T A RiPPing time: Exploring a novel peptide from *Zymoseptoria tritici* **Rosie Ford** University of Bristol

268F Identifying unique metabolite patterns during wood decay by brown rot fungi using metabolomics **Jesus Castano Uruena** University of Minnesota

269W Functional characterization of the GATA-type transcription factor PaNsdD in the filamentous fungus *Podospora anserina* and its interplay with the sterigmatocystin pathway **Florence Chapeland-Leclerc** Universite de Paris

270T *cexA* and its regulatory processes – a closer look into the citric acid production mechanism of *Aspergillus niger* **Aline Reinfurt** Austrian Centre of Industrial Biotechnology (ACIB GmbH)

271F Elucidating the biosynthesis of ribosomally synthesized backbone N-methylated macrocyclic peptides **Lukas Sonderegger** ETH Zürich

272W Effect of *LaeA* on the secondary metabolism in the filamentous fungus *Podospora anserina* **Huijuan WANG** Universite de Paris

273T Primary, secondary and tertiary metabolites, proteins and carbohydrates **Jens Frisvad** Technical University of Denmark

274F Evolution-driven combinatorial chemistry by genetics using fungal natural product gene clusters **Pablo Cruz-Morales** Technological University of Denmark

275W Pathogenic fungi at the crossroads of metal starvation and oxidative stress **Valeria Culotta** Johns Hopkins University Bloomberg School of Public Health

276T Interaction of the bZIP-type transcription factors NapA and RsmA in the regulation of oxidative stress defence and sterigmatocystin production of *Aspergillus nidulans* **István Pócsi** University of Debrecen

277F Heterotrimeric G-Protein Signaling and Carbon Catabolite Repression in *Neurospora crassa* **Yagna Anandkumar Oza** University of California, Riverside

278W Tryptophan biosynthesis genes in the mushroom *Coprinopsis cinerea* **Ursula Kües** University of Goettingen

279V The Crz1 transcription factor of *Fusarium verticillioides* is required for lipid metabolism regulation and fumonisin production. **Andrea Cacciotti** Sapienza Università di Roma

280V Beyond the symbiosis: Novel modulating roles of lipochitooligosaccharides and chitooligosaccharides in the development of fungi and nearby microbes. **Tomas Rush** Oak Ridge National Laboratory

281V Electrophysiological characterization of a diverse group of sugar transporters from *Trichoderma reesei* **Sami Havukainen** VTT Technical Research Center of Finland Ltd

282V Functional characterization of a highly specific L-arabinose transporter from *Trichoderma reesei* **Sami Havukainen** VTT Technical Research Center of Finland Ltd

283V Sirtuins are involved in cell wall integrity, secondary metabolites production and virulence in Aspergillus fumigatus **André Damasio** Institute of Biology, University of Campinas (UNICAMP)

284V Four cell surface phosphate transporters in *Candida albicans* contribute to homeostasis at distinct ambient pH and phosphate concentrations **Maikel Acosta Zaldivar** Boston Children's Hospital

285V Endocytosis of the tetraspan eisosome-resident proteins, a developmentally regulated membrane-remodeling mechanism **Ada Biratsi** NCSR Demokritos

286V Functional analysis of the Cwh43p ortholog CwhA of *Fusarium fujikuroi*. **Marta Franco-Losilla** University of Seville

287V The emerging role of a cyclase gene in the biosynthesis of ochratoxin A: The case study of *Aspergillus carbonarius* **Massimo Ferrara** Pacific Northwest National Laboratory

288V A novel trichothecene toxin phenotype associated with horizontal transfer and altered gene function in the *Fusarium buharicum* species complex **Robert Proctor** USDA ARS NCAUR

289V Evolution of secondary metabolite gene clusters: what is the role of fungal interactions in driving metabolic diversification? **Mario Franco** The University of Arizona

290V The genetic basis of oligopeptide biosynthesis in the early diverging fungus *Mortierella alpina* **Jacob Martin Wurlitzer** Friedrich-Schiller-University Jena

291V New approaches to understand the regulation of neurosporaxanthin biosynthesis in *Fusarium fujikuroi* and its relationship with other biological processes. **Julia Marente** University of Sevilla

292V Unprecedented polyketide synthase genes are associated with (pre-)anthraquinone biosynthesis in *Cortinarius* mushrooms **Nikolai Löhr** Friedrich Schiller University, Department Pharmaceutical Microbiology at the Hans-Knöll-Institute

2. Biotechnology

293W Heterochromatin protein 1 (HP1) knockout mutants exhibit cellulolytic enzyme cocktail alterations in *Trichoderma reesei* **Frederique Bidard** IFP Energies nouvelles

294T Quantifying fungal pellets during submerged cultivation: from 3D X-ray microtomography imaging to diffusive mass transport **Lars Barthel** Technische Universität Berlin

295F Synthetic tools to regulate unconventional secretion for production of heterologous proteins in *Ustilago maydis* **Kai Hussnaetter** Heinrich Heine University

296W Novel Technologies For Investigating Biological Rhythms In Budding Yeast **Tom Mickleburgh** North Carolina State University

297T Insertional mutagenesis using *TC1-mariner* transposon *impala* in the wheat fungal pathogen *Zymoseptoria tritici* **Yohann Petit** French National Institute for Agronomical Research

298F Identification and characterization of an intergenic "safe haven" region in human fungal pathogen *Cryptococcus gattii* **Yeqi Li** University of Georgia

299W Repair of CRISPR-Cas12a induced DNA doublestrand breaks in *Magnaporthe oryzae* generates locus-dependent mutation profiles **Jun Huang** Kansas state University

300T Use of a cell-free expression (CFE) to fast characterize fungal enzymes in the wood decomposer *Rhodonia placenta* **Jesus Castano Uruena** University of Minnesota

301F Understanding DNA Uptake by Anaerobic Fungi **Tejas Navaratna** UC Santa Barbara

302W Fungi to the rescue – revolutionizing food production through biotechnology **Bastian Joehnk** Formo Bio GmbH

303T Development of fungal-based biomaterials using the tinder fungus *Fomes fomentarius* **Bertram Schmidt** Technische Universität Berlin

304F Targeting Aspergillus fumigatus hypoxia response pathways to potentiate contemporary antifungal therapies **Cecilia Gutierrez Perez** Dartmouth College

305W Discovery and characterization of a potent antifungal peptide through OBOC combinatorial library screening. **Kiem Vu** University of California

306T Copper bioleaching from treated wood waste and biosorption by *Phanerochaete* chrysosporium **Kevin Claudien** Université de Lorraine

307F Development of Broad-Spectrum Natural Antimicrobials using *Aspergillus oryzae* **Dasol Choi** University of Wisconsin-Madison

308W High-Throughput Screening Platform for Novel Antifungals to Address Antimicrobial Resistance **S. Earl Kang Jr** Ginkgo Bioworks

309T Fungal Degradation Behavior of a High-biomass Content, Mixed Pressure-Sensitive Adhesive **Jesus D. Castano** University of Minnesota

310F Heterologous expression of a *Trichoderma longibrachiatum* xyloglucanase GH74 in *Aspergillus nidulans* with potential applications in biotechnology **Alex Contato** Oklahoma State University

311W Filamentous fungal cell factory for producing 7-aminocephalosporanic acid by engineering cephalosporin C producing fungus *Acremonium chrysogenum* **Xuemei Lin** Ruhr-University Bochum

312T Characterization and engineering of non-model microorganisms for biotechnological applications **Hugh Purdy** University of California, Santa Barbara

313F Chance favours the prepared spore – how to jumpstart cellulase production **Wolfgang Hinterdobler** AIT Austrian Institute Of Technology

314W Heterologous expression of biosynthetic gene clusters from lichen-forming fungi **Riccardo lacovelli** University of Groningen

315T The fungal battery: A redox flow battery containing the biosynthesised quinone phoenicin from *Penicillium astrosanguineum* **Jens Laurids Sørensen** Aalborg University

316F Computer-Aided, Resistance-Gene-Assisted Genome Mining for Proteasome and HMG-CoA Reductase Inhibitors **Berl Oakley** University of Kansas **317W** The *Aspergillus oryzae* Fermentate D-Tox Effectively Degrades Aflatoxins and Patulin **Dasol Choi** University of Wisconsin-Madison

318T Heterologous expression of pheichrome, a photosensitizer used for photo dynamic therapy using the co-expression system of *Saccharomyces cerevisiae* **Dae-Hyuk Kim** Chonbuk National University

319F MY-CO SPACE: An artistic-scientific vision on how to build with fungi **Vera Meyer** TU Berlin

320W Laccase expression in the dung fungus *Coprinopsis cinerea* with 17 natural laccase genes **Ursula Kües** University of Goettingen

321T Expression of an immunocomplex for dengue virus in *Saccharomyces cerevisiae* **Dae-Hyuk Kim** Chonbuk National University

322V Deciphering new compound pathways in non-engineered *Aspergilli* using a CRISPR toolbox: *Aspergillus californicus* as a starting point **Fabiano Contesini** Technical University of Denmark

323V Identification of transcription factors involved in *Aspergillus nidulans* adaptation to recombinant protein production **Everton Paschoal Antoniel** University of Campinas (Unicamp)

324V Agrobacterium tumefaciens-mediated transformation of Aspergillus nidulans: an efficient tool for targeted gene recombination using selectable nutritional markers **Virginia Casado del Castillo** University of Salamanca

325V Editing the *Trichoderma reesei* genome using *in-vitro* assembled MAD7/gRNA ribonucleoprotein **Sandra Merino** Archer Daniels Midland Co.

326V A library of *Aspergillus niger* chassis strains for morphology engineering connects strain fitness and filamentous growth with submerged macromorphology **Timothy Cairns** Technische Universität Berlin

327V Decaying hardwood associated lignolytic enzyme producing fungi as mediators in low density polyethylene deterioration and the draft genome sequence of Phlebiopsis flavidolba Prameesha Perera University of Kelaniya

328V *In vitro* polyethylene degradation ability of Schizophyllum commune is supported by the presence of the laccases with polyethylene binding sites as reveled by in silico molecular docking analysis Hasni Dharmasiri University of Kelaniya

329V Sexual crossing, chromosome-level genome sequences, and comparative genomic analyses for the medicinal mushroom Antrodia cinnamomea Ting-Fang Wang Academia Sinica

330V Fungal Batteries: Production Of Fungal Quinones To Be Used As Electrolytes In Redox Flow Batteries Johan Christiansen Technical University of Denmark

331V Predicting production of known, putative, and unknown microbial metabolites through network analysis Muralikrishnan Gopalakrishnan Meena Oak **Ridge National Laboratory**

332V A genetic platform to produce secondary metabolites of non-Dikarya fungi Markus **Gressler** Friedrich Schiller University Jena

333V Enhanced production of Taxol® by elicitorinduced transcription factors: Two endophytic fungi from Taxus wallichiana Zucc. Kamalraj Subban Christian-Albrechts-Universität zu Kiel

334V Aspergillus niger customized enzymatic cocktail for cello-oligosaccharide production Fernanda Lopes de Figueiredo University of Campinas (UNICAMP)

335V Polygalacturonases from Aspergillus japonicus and Thermoascus aurantiacus: Enzyme production using low-cost carbon source, biochemical properties and applications in clarification of fruit juices Nelciele Cavalieri de Alencar Guimarães Oliveira Oklahoma State University

3. Cell Biology and Development

336T Structural Insights of the Blue-Light Photosensor BcLOV4 from the Plant Pathogenic Fungi Botrytis cinerea Matthew Cleere CUNY

337F FBAR proteins anchor the fission yeast contractile ring Blake Commer North Carolina State University

338W Protein Secretion Requires Extracellular Vesicles Rebekkah Friske Oklahoma State Univeristy

339T Phosphorylation-mediated Ccp1-Ndc80 switch at the N-terminus of CENP-T regulates kinetochore assembly in fission yeast **Fei Li** New York University

340F Investigating heterochromatin-mediated antifungal resistance in Cryptococcus neoformans isolated from HIV patients in Tanzania Becky Yeboah University of Edinburgh

341W Localization of frequency mRNA by PERIOD-2 contributes to period length determination in the Neurospora crassa circadian clock. Bradley Bartholomai Geisel School of Medicine at Dartmouth

342T Circadian Oscillations in Trichoderma atroviride and the Role of Core Clock Components in Secondary Metabolism, Development, and Mycoparasitism Against the Phytopathogen Botrytis cinerea Luis Larrondo Pontificia Universidad Catolica de Chile

343F A versatile set of protein tags to improve purification of nuclei Shan Hays Western Colorado University

344W 4-color live-cell imaging and other novel microscopy tools reveal dynamic sub-cellular distributions of core clock components in Neurospora crassa Ziyan Wang Geisel School of Medicine at Dartmouth

345T Novel GCaMP6 imaging of cytosolic free calcium dynamics reveals stress-specific signalling responses in the fungal pathogen, Candida albicans Callum J Parkin University of Exeter

346F Hyphal growth rate correlates to the spatial distribution of the endocytic collar in three ascomycete species Joseph Vasselli Texas A&M University

347W Interspecies interactions of *Neurospora* crassa and Botrytis cinerea are mediated by a conserved cell-cell communication mechanism Andre Fleissner TU Braunschweig

348T Functional Amyloids Are Widespread in Fungal Biofilm Adhesins Peter Lipke CUNY Brooklyn College

349F Nuclear Competition and Coordination in Neurospora crassa Syncytia Alexander Mela The University of California, Berkeley Campus

350W Live cell imaging to understand fungicide mode of action Gero Steinberg Univ Exeter

351T Antifungal Screening of 54 Single Plant Essential Oils Against Aspergillus fumigatus Yainitza Hernandez-Rodriguez Florida Gulf Coast University

352F Identification of a protein-protein interaction site essential for mitotic entry to guide antifungal drug design in Aspergillus fumigatus Isabelle **Storer** University of Manchester

353W Membrane integrity contributes to resistance of Cryptococcus neoformans to the cell wall inhibitor caspofungin Maureen Donlin Saint Louis University

354T The Aspergillus fumigatus morphogenesisrelated kinase, CotA, orchestrates hyphal growth in response to carbon source quality Adela Martin-Vicente University of Tennessee Health Science Center

355F The phosphatase Sac1 mediates capsule secretion in Cryptococcus neoformans Elizabeth **Gaylord** Washington University in St. Louis

356W Investigating temperature-induced transcriptional changes that underlie fungal morphogenesis in Histoplasma capsulatum Anna **Morrison** UCSF

357T Hyphal branch formation in the opportunistic human pathogen Candida albicans Antonio Serrano University Cote d'Azur/CNRS/INSERM

358F The RAM signaling pathway links morphology, thermotolerance, and CO, tolerance in human fungal pathogen Cryptococcus neoformans Benjamin **Chadwick** University of Georgia

359W A role for the Rsp5 ubiquitin ligase and its interactome in the pathogenesis of Cryptococcus neoformans Lukas du Plooy Duke University

360T The role of cytochrome c in leukocyte induced Aspergillus fumigatus cell death. Matthew James Geisel School of Medicine at Dartmouth College

361F The *Cryptococcus neoformans* Flc1 homologue controls calcium homeostasis and survival in the infected host Lukasz Kozubowski Clemson University

362W Elucidating a Novel Role for Septins During High Temperature Stress Response in *Cryptococcus* neoformans Stephani Martinez Barrera Clemson University

363T Determining the role of the spore-enriched protein Isp2 in the maintenance of dormancy Anna Frerichs University of Wisconsin Madison

364F Sterol homeostasis is critical for surface structure organization and virulence in Cryptococcus neoformans Hau Lam Choy Washington University in St. Louis

365W Two distinct lipid transporters together regulate invasive filamentous growth in Candida albicans Martine Bassilana University Cote d'Azur/ CNRS/INSERM

366T Live-Cell Imaging of Sexual Reproduction in *Podospora anserina*: the foreplay **Sylvain Brun** Universite de Paris

367F Regulatory role of VE-1 in transcription during sexual development in the fungus Neurospora crassa Sara Cea-Sánchez University of Seville

368W The fungal sexual revolution continues: indications of sexuality in the citric acid producing fungus Aspergillus niger. Valeria Ellena TU Wien

369T The Mating Transcriptome of *Phycomyces* blakesleeanus Jesús F. Peña University of California, Riverside

370F Diverse sexual strategies underpinned by the mating-type locus in the non-model fungal family Ceratocystidaceae Markus Wilken University of Pretoria

371W MATch Maker: A curated web-portal and database for fungal mating-type sequences Markus Wilken University of Pretoria

372T Identifying novel sexual reproduction defects by TN-seq in Schizosaccharomyces pombe Caroline **Craig** Stowers Institute for Medical Research

373F Epistatic genetic interactions govern morphogenesis during sexual reproduction and infection in a global human fungal pathogen Sheng Sun Duke University Medical Center

374W Widespread tissue-specific gene expression during fruiting body development of Coprinopsis cinerea revealed by laser-capture microscopy coupled single-cell RNA sequencing Torda Varga Biological Research Center, Eötvös Loránd Research Network (ELKH)

375T Role of a septin duplication in fruiting body development of a complex multicellular model fungus Máté Virágh Biological Research Center, Szeged, Hungary

376F Funtional characterization of regulatory genes in Schizophyllum commune identifies nine new genes related to mushroom development Peter Jan **Vonk** Utrecht University

377W Characterisation of sexual reproduction mechanisms of *Pyricularia oryzae* to determine genetic bases of male and female fertility. Alexandre **Lassagne** Cirad

378T The *ndrC* gene, which is regulated by *nsdD*, controls sexual development in Aspergillus nidulans Yu Kyung Kim Woosuk University

379F Dark stipe mutants in fruiting body development of Coprinopsis cinerea Shanta Subba University of Goettingen

380W DFG-5 plays a key role in the extracellular targeting of Neurospora crassa glycoproteins for incorporation into the cell wall and secretion into the growth medium **Stephen Free** University at Buffalo

381T Defects on endocytosis cause alterations in actin and produce aberrant hyphal morphology of Neurospora crassa Marisela Garduño-**Rosales CICESE**

382F Functional characterization of DENN domain proteins in Aspergillus nidulans Steven Harris Iowa **State University**

383W Trade-off between Plasticity and Velocity in Mycelial Growth Norio Takeshita University of Tsukuba

384T Evidence that the Vesicle Supply Center function of the Spitzenkörper resides in the Actin Cytoskeleton Salomon Bartnicki-Garcia CICESE

385F Nanoscale imaging of dynamic cell wall formation in fission yeast Fred Chang UCSF

386W Aspergillus niger conidial germination: 3D live cell exploration **Susanne Fritsche** Austrian Centre of Industrial Biotechnology (ACIB GmbH), Technical University of Vienna

387T Investigating molecular mechanisms that underlie thermal dimorphism and pathogenesis of Histoplasma capsulatum Sarah Heater University of California, San Francisco

388F Study of the physiological role of amyloid structures in the pathogenic yeast Candida albicans. Thierry Mourer Institut Pasteur

389W Putative oxidoreductase Cip1 is critical for pheromone-independent unisexual development in Cryptococcus neoformans Nathan Glueck University of Georgia

390T Temperature adaptation of biological phase separation Amy Gladfelter UNC Chapel Hill

391F Investigating the role of Hsp90 in the regulation of Histoplasma capsulatum morphology and transcriptional response Jillian Freese J. Craig Venter Institute

392W Multi-omics Profiling Reveals New Pathways Regulating Hyphal Morphogenesis in Candida albicans Kyunghun Min Stony Brook University

393T Investigating How the Septin Cytoskeleton Controls Morphogenesis in Marine Fungi Ellysa Vogt University of North Carolina at Chapel Hill

394F Probing the unconvetional lifestyle of the multibudding yeast, Aureobasidium pullulans Claudia **Petrucco** Duke University

395W The Nma1 protein promotes long distance transport mediated by early endosomes in *Ustilago* maydis Jörg Kämper Karlsruhe Institute of Technology

396T Live cell imaging and changes to effector composition elucidate adaptations of Magnaporthe oryzae pathotypes to different plant genera Tyler **Suelter** Kansas State University

397F Molecular characterization of Pex5b-dependent import of soluble cargo into peroxisomes of *Ustilago* maydis Michael Bölker Univ Marburg

398W Biofilm formation in the filamentous fungus Fusarium graminearum Rebecca **Shay** Michigan State University

399T Plant ATG8 as a Possible Extracellular Vesicle Marker Huaitong Wu University of California at Riverside

400F Role of the plasma membrane H⁺-ATPase Pma1 in pH homeostasis, development and virulence of the fungal pathogen Fusarium oxysporum Melani Mariscal UNIVERSIDAD DE CORDOBA

401W The ribonucleoprotein complex components JSN-1 and GUL-1 are involved in asexual development in Neurospora crassa Anne Yenewodage Hebrew University of Jerusalem

402T Transcriptome investigation of *mpkB*mkkB mutants related to secondary metabolism and sexual development of Aspergillus nidulans Kap-Hoon **Han** Woosuk University

403F Local Translation and Nuclear Autonomy in a Multinucleate Fungus Ashbya qossypii Ameya Jalihal UNC Chapel Hill

404W Evolutionary Morphogenesis, Chytrids and the rise of The Fungi Edgar Medina UMass Amherst

405T Distribution of non-canonical septins in fungi Brent Shuman University of Georgia

406F Phosphorylation / dephosphorylation of the Cochliobolus heterostrophus stress-activated MAPK Hog1 in response to plant phenolic acids Rina **Zuchman** Technion

407W Assessing the impact of regulator of G protein signaling proteins in Neurospora crassa using conventional phenotypic assays and a quantitative image analysis algorithm Katherine **Borkovich** University of California

408T Aspergillus nidulans septa appear to be indispensable for surviving cell-wall stress Mark Marten Univ Maryland, Baltimore County

409F Investigating germination initiation in the pathogenic fungus Aspergillus fumigatus Justina Stanislaw University of Georgia

410W The conidial coin toss: asymmetric spore adhesion in Colletotrichum graminicola Brian **Shaw** Texas A&M University

411T Aspergillus fumigatus hexameric septin complex is involved in spore cell wall organization and immune evasion José Vargas-Muñiz Southern Illinois University at Carbondale

412F Developmental genetics of host invasion initiated by fungal conidia Soumya **Moonjely** Michigan State University

413W Developmental genetics of spore germination in Epichloë festucae Esteban Valverde **Bogantes** Michigan State University

414V The 14-3-3 homologs (Bmh1 and Bmh2) individually contribute to the proper integrity of the budding yeast kinetochore **Guhan kaliyaperumal** Anbalagan Indian Institute of Technology Bombay

415V Cell wall dynamics in fast growing fungal hyphal cells Louis Chevalier Institut Jacques Monod, CNRS, Paris, France

416V Trehalose metabolism is differentially modulated during cold stress response of postharvest pathogenic fungi Carmit Ziv Agricultural Research Organisation

417V Centromere Evolution during Fungal Pathogens Pneumocystis Adaption to Mammals **Ousmane H. Cisse** National Institutes of Health

418V Investigating Gene-dependent cell death in Cryptococcus neoformans Madhura Kulkarni Johns Hopkins University, Bloomberg School of Public Health

419V Novel putative seven-transmembrane receptors may underlie complex multicellularity in mushroomforming fungi Csenge Földi Biological Research Centre

420V The annexin ANXC4 plays a substituting role for ANX14 during Ca²⁺-mediated membrane damage responses in Neurospora crassa Linda Matz Technische Universität Braunschweig

421V Characterization of Bud3 domains sufficient for bud neck targeting in S. cerevisiae Yao Yan Kansas State University

422V Tools for *Knufia petricola*: new techniques for CRISPR/Cas9-based genome editing Eileen Erdmann Federal Institute for Materials Research and Testing (BAM)

423V *Schizophyllum commune* in radioactive/metal contaminated environments Erika Kothe FSU

424V BRO1 localizes to a specific subpopulation of vesicular structures which mediate cell-cell fusion in N. crassa. Hamzeh Haj Hammadeh Technische Universität Braunschweig

425V COT-1 kinase activity is required for proper conidial germination and directed hyphal growth in Neurospora crassa Lucas Well Technische Universitaet Braunschweig

426V The dual roles of Pef1, a penta-EF-hand protein, in plasma membrane integrity and polarized growth in Candida albicans Martin Weichert University of Braunschweig

427V The role of the *A. niger* antimicrobial peptide AnAFP in the cell's homeostasis of life and death Stephan Starke TU Berlin

428V Swe1 homologs in *Cryptococcus neoformans*: Roles in stress response, virulence, and the G₂/M Checkpoint Rodney Colón-Reyes Clemson University

429V Unraveling the Essential Transcription Factors in Cryptococcus neoformans Seung-Heon Lee Yonsei University

430V GAG, a polysaccharide cytotoxin? **Caitlin** Zacharias Research Institute of the McGill University Health Centre

431V Understanding the impact of the combination of hapE and hmg1 mutations in A. fumigatus clinical triazole drug resistance Ana C O Souza St Jude Children's Research Hospital

432V Establishing minimal conditions sufficient for titanization in Cryptococcus neoformans/gattii species complex Mariusz Dylag Clemson University

433V Unraveling the biology of Nematophagy During a Fungal-Nematode Predator-Prey Interaction Using Time-Course Transcriptomic analysis Hung-Che Lin Institute of Molecular Biology, Academia Sinica

434V A model of the bud emergence 46 (BEM46) protein mode of action based on transcriptomics data in Neurospora crassa Krisztina Kollath-Leiss Christian-Albrechts-Universität zu Kiel

435V Uniparental nuclear inheritance following bisexual mating in fungi Vikas Yadav Duke University Medical Center

436V Role of microtubules and actin in the intracellular organization in the entomopathogenic fungus Metarhizium brunneum Olga A. Callejas-**Negrete CICESE**

437V From a Cap to a Collar, ontogeny of the subapical endocytic collar in filamentous fungi Rosa R. Mouriño-Pérez CICESE

438V Investigating the cell biology of plant infection by the rice blast fungus Magnaporthe oryzae Berlaine **Quime** The Sainsbury Laboratory

439V Chemical inhibition of nuclear division and migration during appressorium development in the rice blast fungus, Magnaporthe oryzae Brandon Mangum University of Georgia

440V Identification and functional characterization of the putative cyclin FlpA as a regulator of the metula-to-phialide transition during conidiophore development of Aspergillus nidulans Oier Etxebeste Faculty of Chemistry, University of the **Basque Country**

441V A Tor1 N-terminal region required for *Candida* albicans anabolic- and stress regulation Wanjun Qi Boston Children's Hospital/Harvard Medical School

442V Cell wall and turgor pressure affect the release of extracellular membrane vesicles in filamentous fungi Shyun-ichi Urayama University of Tsukuba

4. Comparative and Functional **Genomics**

443W Karyotype evolution via chromosome fusion-inversion in Kwoniella, the sister genus to Cryptococcus Marcia David-Palma Duke University

444T Periodic DNA patterns associated with chromatin regulation in Fungi Stephen Mondo DOE Joint Genome Institute

445F Long transposon-rich regional centromeres in the oomycete Phytophthora sojae reveal divergence of centromere features in the Stramenopila-Alveolata-Rhizaria (SAR) lineages Yufeng "Francis" Fang GreenLight Biosciences

446W Stable genome transformation via zoospore electroporation in the Chytridomycota Andrea Vu North Carolina State University

447T Genes of unknown function conserved across fungi: a call for action **Igor Grigoriev** US DOE Joint Genome Institute

448F Diversity of genomic adaptations to postfire environment in higher fungi points to a crosstalk between charcoal tolerance and sexual development Andrei Stecca Steindorff Lawrence Berkeley National Laboratory

449W A Pangenomic assessment of a Cercospora beticola global population Nathan Wyatt USDA-ARS

450T Analysing the Pangenome of Aspergillus fumigatus to Uncover Accessory Genes Involved in Azole Resistance Harry Chown University of Manchester

451F Aspergillus fumigatus pan-genome analysis identifies genetic variants associated with human infection Amelia Barber Leibniz-HKI

452W Giant Starship elements mobilize accessory genes in fungal genomes Emile Gluck-**Thaler** University of Neuchatel

453T Within-species variability of the insectpathogenic fungus Metarhizium acridum revealed by pangenomic analysis **Dinah Parker** University of Copenhagen

454F Comparison of long-read sequencing platforms for de novo genome assemblies of the fungal cereal pathogen Bipolaris sorokiniana Shaobin Zhong North Dakota State University

455W Pangenome analyses of *Fusarium* isolates infecting banana reveals evolutionary dynamics of the adaptive genome Anouk van Westerhoven Wageningen University and Research

456T Seeing red: investigations of spatial expression in hyphae indicate horizontally acquired bikaverin production in *Monosporascus* limits fungal-fungal interactions Aaron Robinson Los Alamos National Laboratory

457F Comparative genomics in *Coccidioides* **Kelsey** Aadland University of California, Riverside

458W Domestication history and its relation to clonal heterogeneity and microevolution of Saccharomyces cerevisiae in the human host Walter Pfliegler University of Debrecen

459T High-throughput genetics and essential gene discovery in Cryptococcus neoformans Blake **Billmyre** Stowers Institute for Medical Research

460F Genetic interaction mapping via pooled CRISPR-Cas9 insertional mutagenesis in the human fungal meningitis pathogen Cryptococcus neoformans Manning Huang University of California, San Francisco

461W A versatile selection free CRISPR-Cas9 transformation system for A. fumigatus Norman van Rhijn University of Manchester

462T The narrow footprint of ancient balancing selection surrounding nonself recognition genes in Aspergillus fumigatus Ben Auxier Wageningen University

463F Meiosis in the human pathogenic fungus Aspergillus fumigatus produces the highest known number of crossovers Eveline **Snelders** Wageningen University

464W Global analysis of circuitry governing Candida albicans morphogenesis within host immune cells Nicola Case University of Toronto

465T Systematic genetic analysis of *Candida* albicans filamentation in response to elevated temperature **Emma Lash** University of Toronto

466F A New Genetic Toolset Reveals Regulators of Candida auris Morphogenesis Darian Santana University of Michigan

467W tRNA-ome of the human fungal pathogen Aspergillus fumigatus: high-throughput functional analysis reveals a valine tRNA isodecoder involved in Azole sensitivity Lauren Dineen University of Manchester

468T Characterizing genomic and phenotypic traits of the human pathogen Aspergillus flavus and its non-pathogenic close relatives E. Anne **Hatmaker** Vanderbilt University

469F COFUN: Final report on the construction of the genome wide-knockout library in A. fumigatus Michael Bromley The University of Manchester

470W QTL Mapping and Bulk Segregant Analysis to determine natural polymorphisms associated with CO₃ tolerance in Cryptococcus neoformans Benjamin Chadwick University of Georgia

471T Transcriptome Analysis of the Entomopathogenic Fungus Culicinomyces clavisporus Dana Foresman Nova Southeastern University

472F Conservation, expansion and functional adaptation of Transcriptional Factor Repertoire in the Fusarium oxysporum Species Complex Houlin Yu University of Massachusetts Amherst

473W Comparative QTL Mapping of Predation Resistance in a Microbial Predator-Prey System Thomas Sauters Duke University

474T Genome-wide identification of sexualreproduction genes in fission yeast via transposoninsertion sequencing Blake Billmyre Stowers Institute for Medical Research

475F Segmental duplication, repeat-induced point mutation, and chromosome relocation in Neurospora crassa: non-coding regions are junkyards for de novo elements and factories for evolution Rudy Diaz Yale School of Public Health

476W The C₂H₃ transcription factor SltA is involved in conidial germination and hyphal elongation in Aspergillus fumigatus Tim Baltussen Radboudumc

477T Characterizing the role of anaerobic fungi in lignocellulolytic microbial communities and the gut mycobiome of herbivorous non-human primates Katharine Dickson University of California, Santa Barbara

478F Transcriptomic analysis of *Schizophyllum* commune in response to the lignin treatment Jaehyuk **Choi** Incheon National University

479W The active microbial communities of oil degradation – exploring bioremediation of mine waste water **Petter Madsen** Uppsala University

480T Integrating multifaceted genetic tools to gear up the discovery of fungal mechanisms of wood decay Jiwei Zhang University of Minnesota

481F Prevalence of aromatic lignin monomer metabolism phenotypes in a collection of wood-inhabiting fungi and characterization of putative metabolic pathways **Leon Rogers** Oregon State University

482W The extrachromosomal circular DNAs of the rice blast pathogen *Magnaporthe oryzae* contain a wide variety of LTR retrotransposons, genes, and effectors **Pierre M Joubert** University of California, Berkeley

483T Heat adaptation in *Fusarium oxysporum* **Dilay Hazal Ayhan** University of Massachusetts Amherst

484F Exploring the genomes of *Phyllosticta*, a genus with multiple lifestyles **Valerie Buijs** Westerdijk Fungal Biodiversity Institute

485W Factors driving genome evolution of *Anisogramma anomala*, the Eastern Filbert Blight fungus, reveal lifestyle and pathogen biology **Alanna Cohen** Rutgers The State University of New Jersey

486T Has *Cercospora kikuchii* vanished in the U.S.? Comparative genomics provides new clues **Burton Bluhm** University of Arkansas System Division of Agriculture

487F Complete Genome Sequence of Newly Reported *Fusarium solani* Sugarbeet Pathogen **Abbeah Mae Navasca** North Dakota State University

488W Mini-chromosomes as drivers of genetic diversity and host-adaptation in the blast fungus *Magnaporthe oryzae* **Thorsten Langner** The Sainsbury Laboratory

489T A putative transcriptional activator from the *PEP* cluster in *Fusarium vanettenii* contributes to virulence on pea **Ambika Pokhrel** Auburn University

490F Transcriptome analysis of *ras2* knockout mutant and wild type *Fusarium circinatum* strains: molecular insights into growth, development and virulence **Emma Steenkamp** University of Pretoria

491W Elucidating the obligate biotroph lifestyle of *Phyllachora maydis* **Emily Roggenkamp** Michigan State University

492T Comparative analyses of effector and CAZyme profiles in *Rhizoctonia* species **Juanita Gil** University of Arkansas

493F Signatures of necrotrophy in genomes of the Eurotiales **Tristan Wang** Cornell University

494W A near-complete genome assembly of the tomato pathogen *Cladosporium fulvum* reveals a compartmentalized genome architecture and the presence of a dispensable chromosome **Alex Zaccaron** University of California, Davis

495T Assembly and annotation of the mitochondrial genomes of four powdery mildew pathogens reveals remarkable variation in size and nucleotide composition **Alex Zaccaron** University of California, Davis

496F Exploring the Carbohydrate-active enzyme profiles of Ophiostomatoid fungi **Kamaldeep Bansal** UNIVERSITY OF FLORIDA

497W The latent pine pathogen *Diplodia* sapinea contains two dispensable chromosomes with distinct genomic characteristics **Tuan A. Duong** University of Pretoria

498T Study of the transcriptional regulation of the host-pathogen interaction between *Ulmus americana* and *Ophiostoma* spp **Thais Campos de Oliveira** Université Laval

499F Decoding wood decay mechanisms in *Armillaria* species using new genomes **Neha Sahu** Biological Research Centre

500W Uncovering long non-coding RNA associated with drug response in *Aspergillus fumigatus* **Harry Chown** University of Manchester

501T Sifting noncanonical Basidiomycete biosynthetic gene clusters from shared genomic regions **Zachary Konkel** The Ohio State University

502F Telomere-to-telomere genome assemblies for *Fusarium circinatum* **Lieschen De Vos** Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria

503W A reciprocal chromosome translocation within the American clade of the *Fusarium fujikuroi* species complex (FFSC) **Lieschen De Vos** Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria

504T Aspergillus as model for analyzing the fungal digestive enzyme profile -to be included in species description and classification? **Lene Lange** BioEconomy, Research & Advisory

505F Fungal digestive enzyme profile: Essential for fitness and integrated part of speciation and evolution **Lene Lange** BioEconomy, Research & Advisory

506W A diversified metabolic toolkit in budding yeasts linked to ecological adaptation **Carla Gonçalves** Vanderbilt University

507T Three-dimensional chromatin organization determines the evolution of adaptive genomic regions in the plant pathogen *Verticillium dahliae* **David E Torres** Wageningen University and Research

508F The GATA transcription factor NsdD governs development and metabolism via species-specific gene regulatory networks in *Aspergillus nidulans* and *Aspergillus flavus* **Heungyun Moon** University of Wisconsin-Madison

509W Comparative transcriptomics to study stress induced morphological changes in fungi **Arpad Csernetics** Biological Research Centre, Szeged

510T Chromosomal responses to telomere dysfunction in *Pyricularia oryzae* are determined by subterminal sequence composition **Mostafa Rahnama** University of Kentucky

511F High-throughput functional profiling of *Trichoderma atroviride* by RbTDNA-seq **Jose Manuel Villalobos Escobedo** University of California, Berkeley

512W Functional analysis of the bZIP transcription factors AtfA and AtfB in *Aspergillus nidulans* **Istvan Pocsi** University of Debrecen

513T Genome-wide analysis of AtfA/AtfB-mediated menadione stress response in *Aspergillus nidulans* **István Pócsi** University of Debrecen

514V Characterizing Genetic Mechanisms for Measuring Day-Length in *Neurospora crassa* **Sienna Casciato** Rutgers University

515V Derivative Profiling to Determine Differential Analysis in -omic Datasets **Harley Edwards** University of Maryland, Baltimore County

516V Generation of Synthetic Time-Course Omics Data using Long Short Term Memory Networks **Joseph Zavorskas** University of Connecticut

517V Revealing the effector repertoire of the sweetpotato black rot fungal pathogen *Ceratocystis fimbriata* **Camilo H. Parada-Rojas** NC State University

518V Fungal mitochondrial genomics - insights and challenges **Steven Ahrendt** DOE Joint Genome Institute

519V Identification of structurral protein orthologs using predicted protein structures **Fred Dietrich** Duke University

520V No genes left behind: Associating phenotypes with genes in *Neurospora crassa* **Scott Baker** Pacific Northwest National Laboratory

521V REPAINT – an artificial intelligence algorithm for the comprehensive phenotyping of conidial fungi **Irina S. Druzhinina** Nanjing Agricultural University

522V Uncovering the fungal pangenome of *Penicillium* **Celine Petersen** Aalborg University

523V Comprehensive high-throughput phenotypic microarrays analysis of clinical diversity in *Aspergillus fumigatus* **Renad Aljohani** Imperial College London

524V Exploring Pan-Genomes At MycoCosm **Richard D. Hayes** DOE Joint Genome Institute, Lawrence
Berkeley National Laboratory

525V Complete Genome Sequences and Genome-Wide Characterization of *Trichoderma* Biocontrol Agents Provide New Insights into their Evolution and Variation in Genome Organization, Sexual Development and Fungal-Plant Interactions **Ting-Fang Wang** Academia Sinica

526V *Metarhizium robertsii* is a multifunctional insect pathogen and plant growth promoter **Huiyu Sheng** University of Maryland, College Park

527V Genomic and transcriptomic differences between maize- and sorghum-specific *Exserohilum turcicum* isolates **Santiago Mideros** University of Illinois at Urbana-Champaign

528V Asymmetrical dose-responses shape the evolutionary trade-off between antifungal resistance and nutrient use **Philippe C Després** Institut de biologie intégrative et des systèmes, Université Laval

529V Quantifying the path to resistance to one of the oldest antifungal drugs **Romain Durand** Université Laval

530V Genome-wide Functional Analysis of WD40 Repeat-containing Proteins in *Cryptococcus neoformans* **Jin-Tae Choi** Yonsei University

531V Balancing positive and negative selection: metabolic consequences of antifungal resistance via constitutive Mrr1 activity in *Candida lusitaniae* **Elora Demers** Geisel School of Medicine at Dartmouth

532V Evolution of mycorrhizal symbiosis in Inocybaceae **Faheema Khan** Uppsala University

533V Biocontrol activity and genomic analyses of the antagonistic, yeast-like fungus *Aureobasidium pullulans* **Florian Freimoser** Agroscope

534V Identification of key genes of the defense response of the mushroom-forming fungus *Schizophyllum commune* against fungal and bacterial antagonists **Erik Beijen** Utrecht University

535V Revisiting Meiotic Mutants in *Coprinopsis cinerea* using a Genomic Approach **Abigail Burke** Roanoke College

536V *Trichoderma reesei* Rad51 tolerates mismatches in hybrid meiosis with diverse genome

sequences Ting-Fang Wang Academia Sinica

537V Kingdom-wide analysis of fungal transcriptomes and tRNAs reveals conserved patterns of adaptive evolution **Rhondene Wint** University of California - Merced

538V Comparative genome analysis of *Fusarium* culmorum and *F. graminearum* reveals a different type of chromosomal organization but a common gene repertoire linked to virulence on wheat **Martin Urban** Rothamsted Research

539V Genome of the ginger pathogen *Pythium myriotylum* uncovers the most extensive arsenal of virulence-related genes amongst *Pythium* plant pathogens **Paul Daly** Jiangsu Academy of Agricultural Sciences

540V Comparative pathogen-host interaction phenotype analysis in human and plant microbial pathogens using PHI-base **Martin Urban** Rothamsted Research

541V Full genome sequence of onion black mold causing *Aspergillus welwitschiae* reveals the presence of putative mycotoxin gene clusters **Jagath Ranasinghe** University of Kelaniya

542V Genome Wide Association Mapping to characterize a virulent sexual population of wheat stem rust (*Puccinia graminis* f. sp. *tritici*) from the Pacific Northwest using barley and wheat differentials **Arjun Upadhaya** Washington State University

543V A Pyrenophora resource to identify protein structural homologues **Paula Moolhuijzen** Curtin University

544V Genus-wide analysis of *Fusarium* polyketide synthases reveals broad chemical potential **Daren Brown** USDA

545V Analysis of 22 *Apiospora* genome assemblies uncovers a great biosynthetic potential for secondary metabolites **Trine Sørensen** Aalborg University

546V Evolution-driven discovery of new bioactive fungal molecules **Olga Mosunova** Westerdijk Fungal Biodiversity Institute

547V Nonribosomal peptide synthetase gene clusters and characteristics of NRPS-dependent siderophore synthetases in Armillaria and other species in the Physalacriaceae Martin Coetzee University of Pretoria

548V Transposons activate during monokaryosis in a mushroom-forming fungus Markus Hiltunen Uppsala University

549V Comparative genomics highlights the importance of drug efflux transporters during evolution of mycoparasitism in Clonostachys subgenus Bionectria Magnus **Karlsson** Swedish University of Agricultural Sciences

550V Loss of *SAF1* and *RRM3* together leads to Growth Defects and Compromise in Genome Stability in Saccharomyces cerevisiae NARENDRA BAIRWA Shri Mata Vaishno Devi University

551V Genome comparison of 45 fungal endophytes from Rubiaceae Kelsev Scott The Ohio State University

5. Fungal Diversity

552T Regulation of fungal gene expression in ectomycorrhizal roots underlying heavy metal soil stress Haihua Wang University of Florida

553F Pathogenic fungi in Norwegian barns - first survey of Aspergillus fumigatus azole resistance in Norway Erik Magnus Nedland Henriksen Norwegian Veterinary Institute

554W Analysis of Wood-Decay Fungal Communities Associated with Contrasting Zones of the American Wood Protection Association Decay Hazard Map Jed Cappellazzi Oregon State University

555T Genetic determinants of azole stress in Aspergillus fumigatus Shivani Ror University of Iowa

556F Categorizing Filamentation Phenotypes Across Divergent C. albicans Strains in vitro and in vivo Nichole Brandquist University of Nebraska at Omaha

557W RNAseq analysis identifying a core gene set of Linnemannia elongata involved in the chitin process Kaile Zhang University of Florida

558T The impact of dietary *Debaryomyces* hansenii yeast on the human gut mycobiome Justin **Tran** University of Nebraska-Lincoln

559F The air mycobiome is decoupled from the soil mycobiome in the California San Joaquin Valley John **Taylor** University of California, Berkeley

560W Metabarcoding as a tool for investigating the influence of endosymbiotic bacteria on Mucoromycota fungal host community structure in the Sonoran Desert Nicole Reynolds Cornell University

561T Impact of fungal pigment from *Chlorociboria* spp. on community composition and decay Ray Van Court Oregon State University

562F Fungi adaptation to actinide contamination : accumulation of europium in the filamentous fungus Podospora anserina Eva Cabet Université de Paris/ Unite LIED/Equipe B2C

563W Septins in the unconventional cell divisions of the extremophilic black fungus Knufia petricola. Grace Hamilton University of North Carolina

564T Small-spored *Alternaria* species associated with potato leaf spot across the US for nearly two decades Ipsita Mallik North Dakota State University

565F *Fusarium* in Nebraska Corn **Yuchu Ma** University of Nebraska-Lincoln

566W Genetic diversity of *Fusarium oxysporum* f. sp. vasinfectum California race 4 isolates and Alabama field isolates Miranda Otero Auburn University

567T Genetic diversity and pathogenicity of Botryosphaeriaceae and Diaporthaceae causing defects of hazelnut nuts from Italy. Muhammad Waqas University of Turin

568F The Systematics of North American Rhizopogon Using Modern Molecular Techniques Thelmalyn Montenegro California State University, Fresno

569W Genomic diversification of the specialized parasite of the fungus-growing ant symbiosis Kirsten **Gotting** University of Wisconsin Madison

570T Interrogating the poplar fungal microbiome interactions using meta-transcriptomics and constructed communities Jake Nash Duke University

571V Program number not assigned.

572V Dissecting Ascochyta blight disease of Field pea using genomics and population genetics approaches Yvonne Ogaji Department of Jobs, Precincts and Regions. AgriBio, Centre for AgriBioscience

573V Genome diversity in *F. musae* isolated from banana and human host. Luca Degradi University of Milan

574V Interspecies interactions between a mycoparasite and its prey are mediated by a conserved cell-cell communication mechanism. Natascha Stomberg Institut fuer Genetik

575V Measuring the mutagenic properties of antifungal drugs within Aspergillus fumigatus Michael **Bottery** University of Manchester

576V The maize mycobiome and implication on mycotoxin contamination in relation to climatic patterns Bwalya Katati Wageningen University and Research

577V Fusarium spp. associated with wheat nodes and grain in representative sites across the western Canadian Prairies Mohamed Hafez Agriculture and Agri-Food Canada

578V Pyrenophora tritici-repentis in Japan: first report on race structure and a novel *ToxA* haplotype **Mohamed Hafez** Agriculture and Agri-Food Canada

579V An updated checklist of wood decay fungi in the Maltese Islands. Marco lannaccone University of Malta

580V The novel 15-keto NX-2 and 15-keto NX-3 Fusarium trichothecenes: pathway, phytotoxicity, and pathogenicity Imane Laraba ARS, USDA, NCAUR, MPM

581V Genetic diversity of banana infecting Fusarium spp. strains in Cuba Einar Martinez de la Parte Wageningen University and Research

582V Fusarium musae diversity from a mitochondrial comparative perspective Valeria Tava University of Milan

583V Tandem-approach of direct-infusion HRMS and LC-QTOF-MS for the evaluation of food safety and useful secondary metabolites in Aspergillus oryzae Sharon Marie Bahena-Garrido National Research Institute of Brewing

584V Can the quality of ITS regions in genome assemblies be trusted? Barbara Robbertse NCBI

585V Selection controls genetic diversity among nuclei populating strains of arbuscular mycorrhizal fungi **David Manyara** Uppsala University

586V 1000 lichen MAGs: a reference-free census of lichen symbionts Gulnara Tagirdzhanova University of Alberta

6. Gene Regulation

587W Investigating heterologous expression in N. crassa James Mierendorf Illinois State University

588T Complex and critical roles for the AtrR transcription factor in control of *cyp51A* expression in Aspergillus fumigatus Sanjoy Paul The University of Iowa

589F Duplication, Redundancy, and Divergence: roles of the Aspergillus nidulans paralogous transcription factors LeuR and LeuB in leucine biosynthesis, nitrogen assimilation, and transcriptome regulation Joel T. Steyer Kansas State University

590W Analysis of *defective in silencing* (*dis*) mutants of Fusarium graminearum to understand the formation and maintenance of facultative heterochromatin Michael Freitag Oregon State University

591T A reverse genetics approach to identify genes affecting H3K27 methylation levels in Fusarium graminearum Elizabeth Milford Oregon State University

592F Methylation of H4 controls gene expression in facultative heterochromatin Mareike Moeller Oregon State University

593W Development of genetics and molecular tools to study DNA N⁶-adenine methylation in earlydiverging fungi Carlos Lax Universidad de Murcia (Q3018001B)

594T Systematic deletions of histone methyltransferase and demethylase genes reveal their role in RIP and sexual development. Pierre **Grognet** Universite Paris-Saclay, CNRS

595F Loss of EZH2-like or SU(VAR)3-9-like proteins causes simultaneous perturbations in H3K27 and H3K9 tri-methylation and associated developmental defects in the fungus Podospora anserina Fabienne **MALAGNAC** University Paris Saclay

596W The histone variant H2A.Z in *Fusarium* graminearum, its genomic location and its environment Aurelie Etier MycSA

597T The ATP-dependent chromatin remodeling factor, Isw1, governs development in Fusarium graminearum, partially through regulation of facultative heterochromatin John Ridenour Oregon State University

598F Gene expression divergence correlates with histone modifications in the fungal plant pathogen Verticillium dahliae David E Torres Sanchez Wageningen University and Research

599W A prion accelerates proliferation at the expense of lifespan David Garcia University of Oregon, Institute of Molecular Biology

600T RNAi and heterochromatin independently control gene expression and transposable elements in Mucorales María Isabel Navarro-Mendoza Duke University

601F Regulation and product identification of FmPKS8, a so far cryptic PKS in F. mangiferae Anna Atanasoff-Kardjalieff University of Natural Resources and Life Sciences, Vienna

602W Heterochromatin marks perturb transcriptional robustness and underpin dispensability of genes across evolutionary timescales in fungi Sabina Tralamazza University of Neuchâtel

603T A new role in G2-M control revealed by a reciprocal translocation involving the snxA shuttling mRNA-binding protein and a GYF-domain protein in Aspergillus nidulans Steven James Gettysburg College

604F Data-driven modelling captures dynamics of the circadian clock of *Neurospora crassa* **Michael Brunner** Heidelberg University Biochemistry Center

605W FREQUENCY Phosphosite Mutations Perturb Temperature Compensation of the Neurospora Circadian Clock Elizabeth-Lauren Stevenson Geisel School of Medicine at Dartmouth

606T Novel NuA4 subunits reveal a crucial role of dynamic expression of the negative arm of the circadian clock Bin Wang Geisel School at Dartmouth

607F carP, a long non-coding RNA with broad effects on Fusarium fujikuroi transcriptome. Javier Pardo-Medina Universidad de Sevilla

608W Circadian Clock-Controlled Translation of Specific Neurospora crassa mRNAs Requires Rhythmic eIF2α Activity and P-bodies **Kathrina Castillo** Texas A&M University

609T A platform for functional analysis for *Candida* albicans strain variation Yinhe Mao University of Georgia

610F *In vivo* analysis of hyphal morphogenesis in *C*. albicans. Rohan Wakade University of Iowa

611W The Ess1 prolyl isomerase and its target, the CTD of RNA polymerase II, in cold-adapted fungi. **Steven Hanes** SUNY-Upstate Medical University

612T Regulatory conservation of *EFG1* indirect target genes by WOR3 Max Cravener University of Georgia

613F Characterization of a *Candida albicans* transcription factor family **Amelia White** University of Georgia

614W The effect of Hxk1 and Hxk2 on open chromatin regions and gene expression in *Candida albicans* **Stefanie Wijnants** KULeuven

615T Dss1 and Cap60 are required for capsule formation, stress response, and virulence in *Cryptococcus neoformans* **Olumuyiwa Igbalajobi** University of British Columbia

616F Analysis of pre-filamentous *Candida* albicans cells identifies differing requirements for filamentation in *in vitro* models and defines the pre-filamentation transcriptome Jill Blankenship University of Nebraska at Omaha

617W The HMG Domain-Containing Transcription Factors Hgr1 and Hgr2 are Putative Dormancy Factors of *Cryptococcus* Spores **Megan McKeon** University of Wisconsin-Madison

618T Natural variation by collaboration between antagonistic morphotype master regulators **Eunsoo Do** University of Georgia

619F Natural variation in *Candida albicans* glycolytic regulator activities **Minju Kim** University of Georgia

620W Reaching across the aisle: Sculpting of *C. albicans* biofilm/hyphal gene expression network through collaboration among antagonistic cell type regulators **Aaron Mitchell** University of Georgia

621T The role of *C. neoformans* casein kinase Yck2 in translational reprogramming during host temperature adaptation **Amanda Bloom** SUNY University at Buffalo

622F Gcn2 compensates for the absence of Hog1 in *Cryptococcus neoformans* **David Goich** University at Buffalo

623W Translational suppression by ribonuclear protein (RNP) granules: a mechanism for post-transcriptional regulation of *Candida albicans* filamentation **Melissa Tosiano** Carnegie Mellon University

624T Functional characterization of basic helix-loophelix transcription factor family in *Cryptococcus neoformans* **Mona Pokharel** Rutgers University

625F Truncation of *MAT1-2-7* gene leads to changes in the pheromone response pathway of *Huntiella omanensis* **Brenda Wingfield** University of Pretoria

626W Reconstructing transcriptional networks governing fungal fruiting body development **Xiao-Bin Liu** Institute of Biochemistry, Biological Research Center, Szeged, Hungary

627T Investigating the regulatory networks governing morphology and virulence in *Histoplasma capsulatum* **Nebat Ali** University of California, San Francisco

628F Transcriptional profiling of the dbcAMP response of the human pathogen Histoplasma capsulatum identifies the WOPR-family transcription factor PAC2 as a regulator of cell morphology. **Dror Assa** University of California, San Francisco

629W The transcription factor Roc1 is a regulator of cellulose degradation in the wood-decaying mushroom *Schizophyllum commune* **Peter Jan Vonk** Utrecht University

630T Genome wide insights into signal integration by the G-protein pathway for regulation of carbon- and secondary metabolism **Miriam Schalamun** Austrian Institute of Technology

631F Genetic and epigenetic variants underpinning within-species transcriptional polymorphism in a major fungal pathogen **Leen Abraham** University of Neuchatel

632W GWAS for investigating laccase expression in *Ceratocystis albifundus* **Magriet van der Nest** University of Pretoria

633T Overexpression of *BnNAC19* in *Brassica* napus enhances resistance to *Leptosphaeria* maculans, the blackleg pathogen of canola **Zhongwei Zou** University of Manitoba

634F Relevance of copper homeostasis in *Fusarium oxysporum* pathogenicity **Rafael Palos Fernández** Universidad de Córdoba

635W Exclusively RNAi-based antimicrobial drug resistance is inherited after meiosis in the mucormycosis pathogen Mucor circinelloides Carlos Pérez-Arques Duke University School of Medicine

636T Identification and deep analysis of the target genes of an RNAi mechanism involved in virulence of Mucor lusitanicus. Ghizlane Tahiri Murcia University ESQ3018001B

637F The development of siRNA-mediated mRNA knockdown in *Batrachochytrium* dendrobatidis Rebecca Webb James Cook University

638W Arginine Methylation of RNA Binding Proteins in Cryptococcal Virulence and Antifungal Resistance Murat Can Kalem SUNY University at Buffalo

639T The multi-KH domain RNA binding protein Khd4 orchestrates membrane trafficking to promote polar growth of infectious hyphae Srimeenakshi Sankaranarayanan Institute of Microbiology, Heinrich Heine University of Duesseldorf

640F An RNA-binding protein that evolved a change in function to control fungal growth: the surprising history, structure, and function of Ssd1 Edward W. J. Wallace The University of Edinburgh

641W A-to-I mRNA editing is catalyzed by FgTad2 and FgTad3 ADAT in Fusarium graminearum Zhuyun **Bian** Purdue University

642T The role of R3B2 in the RNAi mechanisms of Mucor lusitanicus is driven by both doublestranded RNA binding domains José Tomás Cánovas-Márquez University of Murcia

643F MERLIN unlocks the secrets to chitin signaling: Using gene-network inference to predict mediators of fungal response to lipo-chitooligosaccharides Cristobal Carrera Carriel University of Wisconsin–Madison

644W Ccr4 and Gcn2 contribute differentially to stress-specific translational repression in C. neoformans Corey Knowles SUNY Buffalo

645T White-opaque switching in *Candida albicans* as a model system for the quantitative and molecular analysis of stochastic cell fate switching Naomi **Ziv** University of California, San Francisco

646F Identifying global regulators of effector gene expression in the rice blast fungus Magnaporthe oryzae Camilla Molinari The Sainsbury Laboratory

647V Elucidating the composition and functions of the Remodels the Structure of Chromatin (RSC) complex in Candida albicans Santanu Ghosh Indian Institute of Technology Bombay

648V Functional analysis of the conserved chromatin modifier ASF1 in the filamentous ascomycete Sordaria macrospora Jan Breuer Ruhr-Universität Bochum

649V A fungal ING protein regulates H3 acetylation and H4 deacetylation by interacting with two distinct histone modifying complexes **Cong Jiang** Northwest A&F University

650V Understanding the histone dynamics and regulatory role of lysine methyltransferases Set2, Ash1, and PRC2 in Magnaporthe oryzae David **Rowe** Kansas State University

651V The histone code of the fungal genus Aspergillus uncovered by evolutionary and proteomic analyses **Xin Zhang** Utrecht University

652V Sirtuins in the control of virulence in the plant pathogen fungus Ustilago maydis. Blanca Navarrete Pablo de Olavide University (UPO)

653V The epigenetic regulatory mechanisms of effector genes in the wheat pathogen Zymoseptoria tritici Marta Suárez Fernández Universidad Politecnica de Madrid

654V The Elp3 GNAT superfamily protein modulates development, cell cycle progression and virulence in the fungal insect pathogen, Beauveria bassiana Qing Cai University of Florida

655V Functional analyses of predicted G-proteincoupled receptors in nematode-trapping fungus, Arthrobotrys oligospora Chih-Yen **Kuo** Institute of Molecular Biology

656V Systematic Analysis of Host-derived Cues for the Regulation of Pathogenicity-associated Transcription factors in Cryptococcus neoformans Seong-Ryong Yu Yonsei university

657V Unveiling the Roles of the Casein Kinase 2 Complex in the Growth, Differentiation, Stress Responses, and Pathogenicity of Cryptococcus neoformans Yeseul Choi Yonsei University

658V Cpk1, Mpk1, and Hog1, MAPK Pathways Coordinately Regulate the Growth, Thermotolerance, and Cell Wall Integrity of Cryptococcus neoformans Yu-Byeong Jang Yonsei University

659V Identification of novel transcription factors involved in Aspergillus fumigatus adherence Francois Le Mauff McGill University

660V Transcriptional and strain-dependent impact of C. Albicans HGC1, the hyphal-specific G1 cyclin **Anupam Mahto** University of Georgia

661V Role of calcineurin signaling components in cryptococcal Titan cell formation Julia Reuwsaat Universidade Federal do Rio Grande do Sul

662V Natural variation in the control of Candida albicans iron acquisition **Liping Xiong** University of Georgia

663V Leveraging machine learning essentiality predictions and chemogenomic interactions to identify antifungal targets Ci Fu University of Toronto

664V Fungal A-to-I mRNA editing controls lethality of a fungal meiotic drive gene in homologous and heterologous expression systems Jessica **Lohmar** USDA-ARS

665V Blue Mold's Clues: Comparative transcriptomics of blue mold fungi clue into biochemical processes associated with fungal aggressiveness and conidial germination in *Penicillium* spp. **Holly Bartholomew USDA-ARS**

666V The role of RNA helicases during *Ustilago* maydis teliospore dormancy and germination Amanda Seto Trent University

667V Role of Nuclear mRNA Degradation Pathway in the Regulation of Telomere Length in Saccharomyces cerevisiae Mayukh Banerjea Jadavpur University

668V Characterization of N6-methyladenosine RNA methylation factors in *Fusarium* graminearum Wonyong Kim Sunchon National University

669V Identification of a stage-specific co-factor required for A-to-I mRNA editing during sexual reproduction in fungi Huiquan Liu Northwest A&F University

670V Exploring the role of natural antisense transcripts in the stress response of *Ustilago* maydis Monique Lariviere Trent University

671V Gad1 functions as a negative regulator of A-to-I mRNA editing during sexual reproduction **Zeyi** Wang Purdue University

672V The role of COP9 signalosome complex in secondary metabolism in Fusarium Massimo Ferrara National Research Council

673V Culturing *Aspergillus nidulans* in soil microcosm elucidates its ecological behavior and interaction with soil microbiota **Daisuke Hagiwara** University of Tsukuba

674V Identification of co-culture responsive biosynthetic gene cluster in Aspergillus niger and Penicillium species Daisuke Hagiwara University of Tsukuba

675V Characterization of conidia-specific transcription factor CsgA in Aspergillus spp. He jin Cho Kyungpook **National University**

676V Transcriptome-based functional analysis of spore-specific transcription factors in *Aspergillus* species Ye-Eun Son Kyungpook National University

7. Pathogenic and Mutalistic Interactions

677W Probing the role of N6-methyladenine DNA modification within the Rhizopus microsporus and Mycetohabitans symbiosis Margaret **Branine** Cornell University

678T Hijacking time: How *Ophiocordyceps* fungi could be using ant host clocks to manipulate behavior Charissa de Bekker University of Central Florida

679F Characterizing variation within the European Batrachochytrium salamandrivorans epidemic Moira Kelly Ghent University

680W Deciphering the potential niche of novel black yeast fungal isolates in a biological soil crust based on genomes, phenotyping, and melanin regulation Erin Carr University of Nebraska-Lincoln

681T Human p11-mediated re-direction of phagosomes to the recycling endosome-expulsion pathway induced by fungal pathogen Leijie Jia Leibniz Institute for Natural Product Research and Infection Biology - Hans Knöll Institute

682F Cryptococcus neoformans transcytosis of human brain endothelial cells likely begins with macropinocytosis. Dylan Lanser University of California

683W Unmasking chitin in *C. neoformans*: Panic or protection? Rajendra Upadhya Washington University, St. Louis

684T Connecting fungal genomes with the behavioral phenomes of ants, manipulated by Ophiocordyceps Charissa de Bekker University of Central Florida

685F Pyricularia HAG effector family interactions with rice candidate target proteins Nicholas Farmer Texas A&M University

686W Validation and characterization of *Pyrenophora* teres f. teres effectors VR1 and VR2 conferring virulence on Rika barley jinling li North Dakota State University

687T Unravelling the role of CRZ1 dependent F-BAR protein in mediating virulence of Ascochyta rabiei Ankita Shree National Institute of Plant Genome Research

688F Calcineurin regulates ß(1,3)-glucan exposure in Candida albicans Andrew Wagner University of Tennessee, Knoxville

689W Elucidating Fungal Immune Receptors and Testing the Potential Role of Nucleotide-binding Domain Leucine-rich Repeat-like Proteins (NLR-like) Against Bacterial Antagonists. Frances Stark University of California, Berkeley

690T Targeted delivery of antifungal liposomes to Rhizopus delemar Quanita Choudhury University of Georgia

691F Dectisomes Target Antifungal Drugs for Fungal Cells Zachary Lewis University of Georgia

692W Saccharomyces cerevisiae var. 'boulardii' host interactions and the virulence-related gene heme oxygenase-1 (HMX1) Alexandra Imre University of Debrecen

693T Pathogen carbon metabolism influences host immune response during infection by Cryptococcus neoformans Hannah Berguson Liberty University College of Osteopathic Medicine

694F Linkage analysis of clinical isolates in the Cryptococcus neoformans ST93 clade reveals two non-recombining populations with different in vivo disease manifestations Katrina Jackson University of Minnesota

695W Roles of candidalysin of *Candida albicans* in the gut permeability and brain pathology Courtney **Smith** The University of Texas at San Antonio

696T Elucidating key interactions between Coccidiodies and macrophages Jane Symington University of California, San Francisco

697F Roles of *Candida albicans* chromosome instability in the host **Huijuan Yan** University of California, San Francisco

698W Identification of the genetic basis of novel azole resistance mechanisms in Aspergillus fumigatus Asmaa Alghamdi University of Nottingham

699T A longitudinal study investigating patient acquisition of azole resistant Aspergillus fumigatus (ARAf) Amelie Brackin Imperial College London

700F Involvement of kinase genes in antifungal tolerance in the pathogenic yeast Candida glabrata Colin Clairet Institut Pasteur

701W Elucidation of Intrinsic Echinocandin Drug Resistance Mechanisms in Mucorales Fungi Alexis Garcia The University of Texas at San Antonio

702T Immunoprotection against cryptococcosis offered by Znf2 depends on capsule and the hyphal morphology Nhu Pham University of Georgia

703F Copper homeostasis and *Cryptococcus* neoformans cell surface architecture Corinna **Probst** Duke University

704W The Fungal Granuloma: Mechanisms of Fungal Containment and Persistence Calla L. Telzrow Duke University

705T Unfolded protein response is critical for the corneal pathogenesis of Aspergillus fumigatus Manali Kamath University of Oklahoma Health Sciences Center

706F Fungal hypoxia adaptation is critical for the establishment of keratitis Jorge Lightfoot University of Oklahoma Health Sciences Center

707W The *Aspergillus fumigatus* Spindle Assembly Checkpoint components, sldA and sldB, play roles in maintenance of triazole susceptibility Ashley Nywening The University of Tennessee Health Science Center

708T Extracellular vesicles and biofilms of the pine tree pathogen Fusarium circinatum Thabiso **Motaung** University of Pretoria

709F Identification of a gene cluster encoding at least two effector proteins involved in host-specificity of Sporisorium reilianum Jan Schirawski Friedrich-Schiller-Universität Jena

710W Chemical interactions between fungi and nematodes Reinhard Fischer Karlsruhe Institute of Technology (KIT)

711T Identification and functional characterization of a putative alternative oxidase (AOX) in the smut fungus Sporisorium reilianum f. sp. zeae. Emma **Lamb** University of Louisville

712F Metabolomic profiling of behaviorally manipulated insects infected by "zombie ant fungus" (Ophiocordyceps) Ian Will University of Central Florida

713W Genes for an extended phenotype: Biosynthesis of volatile sesquiterpenes in a pathogenic fungus is used to entice male flies into fatal mating's with infected female cadavers Henrik De Fine **Licht** University of Copenhagen

714T Genetic systems and pH stress in the laurel wilt-Ambrosia beetle symbiotic interaction Ross Joseph University of Florida

715F A shelter from the elements: understanding requirements for fungal chlamydospore formation and bacterial invasion Isabelle Ludwikoski University of Wisconsin-Madison

716W From iron to antibiotics: Bacterial-fungal interactions revealed by genome-wide mutational analyses Emily Pierce University of California, San Diego

717T Using random barcoded transposon-site sequencing (Rb-TnSeq) bacterial libraries to explore the effects of volatiles from Trichoderma atroviride Catharine Adams UC Berkeley

718F Heterothallic mutants of *Fusarium* graminearum and their use for Genetic Analysis of Fungal Pathogenicity and Toxigenicity Gabdiel Yulfo-**Soto** University of Kentucky

719W Deletion of the killer kinase *KIL1* abolishes penetration peg formation in the predator yeast Saccharomycopsis schoenii Mareike Rij Hochschule Geisenheim University

720T Conditional role of a signal peptidase component in the establishment of biotrophy by the maize anthracnose pathogen Colletotrichum graminicola Renata Belisario University of Kentucky

721F Cytoplasmic effector translocation during early biotrophic invasion by the rice blast fungus Ely Oliveira-Garcia Louisiana State University

722W Defining the septin interactome and its role in appressorium-mediated plant infection by the rice blast fungus Magnaporthe oryzae Iris Eisermann The Sainsbury Laboratory

723T Genotype and Fusarium head blight selection for microbiomes across barley spikes Brooke Benz North **Dakota State University**

724F Unraveling the role of effectors from Fusarium spp. in Fusarium wilt of banana Carolina Aguilera Galvez Wageningen University and Research

725W Transcriptome analysis and effector prediction in Fusarium spp. causing Fusarium wilt of banana Jelmer Dijkstra Wageningen University

726T Alternative sulfur scavenging and host colonization by the plant pathogen Raffaelea lauricola Joshua Konkol University of Florida

727F Fighting fungi with fungi: the biocontrol potential of Trichoderma against Armillaria root rot M Millen University of Bristol

728W Characterisation of novel effectors from the wheat pathogen, Zymoseptoria tritici Eli **Thynne** Christian-Albrechts University

729T Fungal Pathogens Utilize Extracellular Vesicles for Transport of Effector Proteins into Plant Host Cells Claire Whitaker UC Riverside

730F GWAS for identifying genes associated with virulence in F. circinatum Emma Steenkamp University of Pretoria

731W A new pathosystem to study the plant-fungal interactions underlying Cercospora leaf blight of soybean Kona Swift University of Arkansas

732T Convergent recognition of the *Magnaporthe* oryzae host specificity determinant PWL2 in divergent grass species Diana Gómez De La Cruz The Sainsbury Laboratory

733F Secreted in xylem (SIX) 6 mediates *Fusarium* oxysporum f. sp. fragariae race 1 avirulence to strawberry cultivars with FW1 resistance Christine Jade Dilla-Ermita University of California, Davis

734W Pathotypes of Fusarium oxysporum f. sp. fragariae express discrete repertoires of accessory genes and induce distinct host transcriptional responses during root infection. Peter Henry United States Department of Agriculture

735T Differences in fungal aggressiveness and host susceptibility revealed key drivers of Fusarium Head Blight infection in wheat Florian Rocher INRAE

736F Analysis of Superoxide Dismutase Activity in Fusarium oxysporum Manuel Sánchez López-Berges Universidad de Córdoba

737W Effector proteins of *Botrytis elliptica* as tools for resistance breeding in lily against fire blight disease Michele Malvestiti Wageningen University and Research

738T Extracellular vesicles of and biofilm formation in a maize fungal pathogen Fusarium verticillioides Thabiso Motaung University of Pretoria

739F A GPI-anchored protein gene from the chestnut blight fungus Cryphonectria parasitica is a hypovirusspecific virulence factor and a tolerance factor against hypovirus infection Dae-Hyuk Kim Chonbuk National University

740W Functional analysis of Heat Shock Protein 90 co-Chaperon p23, CpCo23, of chestnut blight fungus Cryphonectria parasitica in variety of stress Yo-Han Ko Jeonbuk National University

741T Unconventional suppression of plant defence responses by the signal peptide peptidase Spp1 in the Ustilago maydis - maize interaction Kai **Heimel** Georg-August-University

742F Identification and characterisation of an expanded family of effector from Asian soybean rust, Phakopsora pachyrhizi Kelly Robinson The Sainsbury Lab

743W Fungal alcohol oxidase (AOX): a broadly conserved protein facilitating ascomycete invasion of plants Nathaniel Westrick University of Wisconsin-Madison

744T Extracellular vesicle-mediated transfer of plant mRNA into fungal cells to suppress pathogenicity shumei wang University of California, Riverside

745F Functional analyses of genes involved in disease development in rice caused by both pathotypes of Fusarium fujikuroi Sang-Won Lee Soonchunhyang University

746W The monothiol glutaredoxin Grx4 is a key regulator of secondary metabolism, iron homeostasis, nitrogen sensing and virulence in *Ustilago* maydis Sean McCotter Michael Smith Laboratories, University of British Columbia

747T Co-transcriptomic time course analysis for mechanistic understanding of the Arabidopsis-Botrytis pathosystem Anna Muhich University of California, Davis

748F Botrytis cinerea secretes small RNA containing extracellular vesicles that enter plant cells through clathrin-dependent endocytosis Baoye He University of California, Riverside

749W Characterising an effector from the fungal pathogen of wheat, Zymoseptoria tritici Nikolaos Mastrodimos University College Dublin

750T Unexpected fitness advantage from hydrophobin loss in *Penicillium expansum* upon apple co-inoculation Dianiris Luciano-Rosario University of Wisconsin-Madison

751F The *Zymoseptoria tritici* effector *Zt-11* is involved in the switch to necrotrophy and contributes to virulence in wheat Paola Pilo University College Dublin

752W RNA interference affects fungus-fungus interactions in the biocontrol agent *Clonostachys* rosea Edoardo Piombo Swedish University of **Agricultural Sciences**

753T Mycangial colonization in the laurel wilt (Raffealea lauricola)-Ambrosia beetle symbiosis Ross Joseph University of Florida

754F The fungal root endophyte Serendipita vermifera displays inter-kingdom synergistic beneficial effects with the microbiota in Arabidopsis thaliana and barley Gregor Langen University of Cologne

755W The combined activity of two secreted fungal enzymes is implicated in fungal accommodation in the roots and triggers cell death in different host species Alga Zuccaro University of Cologne

756T Decoding the nuances of fungal symbiosis using ambrosia beetles-Raffaelea lauricola as a model system Kamaldeep Bansal University of Florida

757F Systems Biology of the Symbiosis of Arbuscular Mycorrhizal Fungi (AMF) in Sorghum Shufan **Zhang** University of Georgia

758W Testing the role of the transcription factor TvSom1 in adhesion of Trichoderma virens germlings Benjamin Horwitz Technion - IIT

759V The puzzle of mini-chromosomes and Fumonisins in Fusarium verticillioide Luigi Faino University of Rome "Sapienza"

760V Isolate specific effects of *Botrytis cinerea* on the expression of biosynthetic enzymes and stimulation of Jasmonic and Salicylic acid signaling in *Arabidopsis* thaliana. Jordan Dowell University of California, Davis

761V Transcriptomic approach to unveil the interaction between a biocontrol yeast and a postharvest fungal pathogen on the host fruit Giuseppe Ianiri University of Molise

762V Accessory chromosome loss contributes to increased symbiotic effectiveness of a tree root fungus Zhilin Yuan Research Institute of Subtropical Forestry, Chinese Academy of Forestry.

763V Comparative Genomics of Four Mollicutes-Related Endobacteria from the Mortierellaceae Reid **Longley** Michigan State University

764V Investigating microbial reservoirs for antivirulence compounds that attenuates dimorphism in the fungal pathogen Candida albicans. Jehoshua **Sharma** University of Guelph

765V Identification of novel effector proteins in Cercospora beticola Olivia Hamilton United States Department of Agriculture

766V Seasonal dynamics in the bacterial microbiome of field grown CLS-resistant and -susceptible sugar beet varieties Lorena Rangel United States Department of Agriculture

767V Impact of the

mycoparasite *Pythium oligandrum* on mutualistic interactions and disease resistance as well as growth induction in Medicago truncatula Maryam Hashemi Laboratoire de Recherche en Sciences Végétales, Université de Toulouse, CNRS, Université Toulouse II

768V Breakdown and maintenance of tree-fungal mutualism: why the nitrogen form matters? Long Peng State Key Laboratory of Tree Genetics and Breeding

769V Fusarium oxysporum induces the expression of the gene encoding the plant specific tissue protein 6 (ST6) involved in root and plant vasculature development Virginia Casado del Castillo University of Salamanca

770V Fusarium oxysporum FOSP1G 05432, the orthologous of B. cinerea Bcin04g03490, is involved in growth, sporulation and virulence Virginia Casado del Castillo University of Salamanca

771V Deep learning-based quantification of fungi in plant roots **Edouard Evangelisti** University of Cambridge

772V Genomic and associated soil microbioal community comparisons of two Armillaria species with different ecological behaviors Jane **Stewart** Colorado State University

773V Genetic mapping of new QTL conferring virulence in Pyrenophora tritici-repentis Jingwei **Guo** North Dakota State University

774V *Marchantia polymorpha* model reveals conserved mechanisms governing infection by the vascular wilt fungal pathogen Fusarium oxysporum Amey Redkar Universidad de Cordoba 775V Screening of small secreted proteins of Epichloë bromicola for Hypersensitive Response–Associated effectors in Nicotiana spp. Pranav Chettri AgResearch (Grasslands Research Centre)

776V Discovery and selection of fungal endophytes for disease resistance of barley Olga Lastovetsky University College Dublin

777V Characterization of urease in *Aspergillus* fumigatus: Biochemistry and implications for virulence Daniel Scharf School of Basic Medical Sciences, Zhejiang University

778V The pathogen-host interaction database in 2022: Providing FAIR data to explore human, animal and plant infecting filamentous pathogens Kim Hammond-Kosack Rothamsted Research

779V The diversity of mold warfare: a taxonomically wide investigation of Trichoderma - Pythium antagonism Sigiao **Chen** Nanjing Agriculture University

780V Heterologous expression of *Hanseniaspora* sp. transporters in Saccharomyces cerevisiae confirms their activity as pantothenate symporters, used by the yeast to obtain this vitamin from other organisms. Maria P. Rueda-Mejia Agroscope

781V Secreted proteins during interaction of mushroom-forming fungi against their competitors Marieke H. van Maanen Utrecht University

782V Ensembl Fungi: Melding data sets to explore species interactions Manuel Carbajo Martinez EMBL - EBI

783V Deciphering the mycovirome of *Botrytis* cinerea Ana Ruiz-Padilla Universidad Politécnica de Madrid. CBGP (UPM-INIA)

784V Exploring the Divergence of Interactions between Fungi and Bacteria Gayan Abeysinghe Graduate School of Science and Technology, University of Tsukuba

785V Mycovirus influences secondary metabolite production in Aspergillus flavus Misa **Kuroki** University of Tsukuba

786V Lactobacillus-secreted Yak1 inhibitor, 1-acetyl-beta-carboline, blocks *Candida* albicans morphogenesis and biofilm formation Jessie **MacAlpine** University of Toronto

787V The phospholipase VIPLA, from the plant pathogen Verticillium longisporum is a virulence factor targeting host nuclei and suppressing PTI-related hypersensitive response Georgios Tzelepis Swedish University of Agricultural Sciences

788V Dog9, a fungal protein involved in effectors secretion during plant infection María Dolores Pejenaute Ochoa Andalusian Centre for Developmental Biology, Pablo Olavide University, Seville, Spain.

789V Phosphoproteomic analysis of the Pmk1 MAP kinase pathway reveals novel phosphorylated virulence determinants in Magnaporthe oryzae Neftaly Cruz Mireles Norwich Research Park

790V Interactions Between the Diet and Mycobiome of Long-tailed Macagues (Macaca fascicularis) Vary Across Islands with Evidence of a Role for Antifungal Plants Benjamin Gombash University of Notre Dame

791V A major effect gene, *Bcin04g03490*, controls development and pathogenicity in Botrytis cinerea Ernesto Pérez Benito University or Salamanca

792V Impairment of the cellulose degradation machinery enhances Fusarium oxysporum virulence but limits its reproductive fitness Clara Sanchez-Rodriguez Department of Biology, ETH Zurich

793V Effector proteins of *Pseudocercospora fijiensis* as tools in resistance breeding of banana Maikel **Steentjes** Wageningen University

794V Identification of the Avr9B avirulence effector gene from the tomato leaf mould pathogen Cladosporium fulvum Silvia de la **Rosa** Massey University

795V Understanding the virulence molecular mechanisms of Neonectria ditissima, a necrotrophic fungal pathogen of apple. Liz Florez University of Auckland/Plant and Food Research

796V Functional characterisation of candidate Fusarium graminearum effectors Claire Kanja Rothamsted Research

797V Characterization of the role of the Parastagonospora nodorum effector SnTox267 in virulence on wheat using confocal microscopy **Ashley Nelson** North Dakota State University

798V Understanding the Molecular Bases of Adaptation of the Fungal Pathogen Zymoseptoria to Specific Host Species Andrea Sánchez-Vallet Universidad Politecnica de Madrid

799V Disruption of a *Dothistroma septosporum* cell death elicitor through CRISPR-Cas9 Mariana **Tarallo** Massey University

800V Functional characterization of *Fusarium* graminearum effectors inducing cell death Martin Darino Rothasmted Research

801V The conserved trichothecene biosynthetic cluster gene TRI14 is required for growth of Fusarium graminearum in wheat but not for trichothecene production Guixia Hao USDA, ARS

802V The Venturia inaequalis effectorome is expressed in waves, and is dominated by expanded families with predicted structural similarity to avirulence effector proteins Mercedes **Rocafort** Massey University

803V Spore-type specific chemotropic growth to maize roots determines root infection by the hemibiotrophic pathogen Colletotrichum graminicola Daniela Nordzieke Georg-August University Göttingen, Germany

804V Cross-kingdom RNA interference in early phases of the Botrytis cinerea - tomato interaction Si Qin Wageningen University

805V A novel RNA binding protein in table beet fungal pathogen, Cercospora beticola, regulates growth, secondary metabolism, and virulence. Sandeep Sharma Khatiwada Cornell University

806V Understanding the Molecular Bases of Adaptation of the Fungal Pathogen Zymoseptoria to Specific Host Species Coraline Praz Universidad Politecnica Madrid

807V Analysis of the microbial war between the Bioeffector Pythium oligandrum and the Pythium Soft-Rot of Ginger Pathogen Pythium myriotylum Taha Majid Mahmood Sheikh Jiangsu Academy of **Agricultural Sciences**

808V Functional analysis of putative protein glycosylation related genes in the plant pathogenic fungus Fusarium graminearum Heeji **Moon** Agriculture and Life Science

809V A spot type net blotch susceptibility locus in barley. Mariano Jordi Muria Gonzalez Curtin University

810V Spray-induced gene silencing (SIGS) against fungal and oomycete diseases in forest system Irene Teresa Bocos Asenjo Universidad de Valladolid

811V Differential physiological prerequisites and gene expression profiles of conidial anastomosis tube fusion and germ tube formation in Colletotrichum gloeosporioides Nikita Mehta Agharkar Research Institute

812V Spray-induced gene silencing (SIGS) using organic and inorganic based-nanoparticles ensures a steady RNAi effect against *Botrytis cinerea* infection on plant material Jonatan Niño Sanchez University of california, Riverside

813V Fungal Chemical Warfare: How Secondary Metabolites Influence Relationships in Maize Associated Fungi Tim Satterlee USDA/ARS

814V Establishment of functional symbioses between Epichloë endophytes and the modern cereals rye (Secale cereale) and hexaploid wheat (*Triticum aestivum*). **Richard Johnson** Agresearch Grasslands

815V Going Green: Evidence for acquisition and persistence of plant and algal plastomes in diverse fungi Julia Kelliher Los Alamos National Laboratory

816V Interactions between algal cells and

the dimorphic lichenized fungus Umbilicaria muhlenbergii Yuting Hu Purdue University

817V Genetic determinants of endophytism in the Arabidopsis root mycobiome Fantin Mesny Max Planck Institute for Plant Breeding Research

8. Population and Evolutionary Genetics

818W Long reads and Hi-C sequencing illuminate the two-compartment genome of the model arbuscular mycorrhizal symbiont Rhizophagus irregularis Gokalp **Yildirir** University of Ottawa

819T Emerging tree pathogen *Phellinus noxius* has a long evolutionary history in eastern Asia, Australia, and the Pacific Islands Olga Kozhar Colorado State University

820F Repeat-driven genome expansion and twospeed genome architecture of amphibian-infecting chytrids Theresa Wacker University of Exeter

821W Pangenomics of the 'death cap' mushroom, Amanita phalloides, and of Agaricales reveal dynamic evolution of toxinrelated gene family in an invasive range. Milton **Drott** University of Wisconsin–Madison

822T Births, deaths and survival of a retrotransposon family in the face of repeat induced point mutations (RIP) Ivar Westerberg Uppsala University

823F Evolution of a Large Effector Family in Pyricularia Daniel Ebbole Texas A&M University

824W Molecular evolution of virulence effectors of the rice blast fungus Magnaporthe oryzae Pierre **Gladieux** INRAE

825T An NLR-like system delimits individuals in the basidiomycete Coprinopsis cinerea Ben **Auxier** Wageningen University

826F Pararesistance: a non-genetic mechanism of antifungal drug resistance Jinglin Lucy Xie Stanford University School of Medicine

827W The molecular resistance mechanisms and population structure of azole-resistant Aspergillus fumigatus present on commercial agricultural products in the United States Caroline **Burks** University of Georgia

828T Identifying genes involved in the temperaturedependent morphological transition in Coccidioides posadasii Keith Walcott University of California, San Francisco

829F Population genetics and microevolution of clinical Candida glabrata reveals recombinant sequence types and hyper-variation within mitochondrial genomes, virulence genes and drugtargets Nicolas Helmstetter University of Exeter

830W A cystic fibrosis patient lung environment allowed for coexistence of multiple Exophiala dermatitidis clades over time Tania Kurbessoian University of California, Riverside

831T Global evolutionary patterns and drug resistance acquisition in the human pathogen Aspergillus fumigatus Johanna Rhodes Imperial College London

832F Parasexual recombination enables *Aspergillus* fumigatus to persist in cystic fibrosis Eveline **Snelders** Wageningen University

833W Transposon mobilization elevated by heat stress causes genome-wide mutations in the human fungal pathogen Cryptococcus deneoformans Asiya **Gusa** Duke University

834T Plants vs Botrytris: a model for quantitative interactions? Celine Caseys University of California Davis

835F Human mediated contact between amphibiankilling chytrid variants results in repeated recombination Thomas Jenkinson California State University, East Bay

836W Mushrooms without mating: the discovery haploid sporocarps in the invasive habitat of the heterothallic death cap, Amanita phalloides Yen-Wen Wang University of Wisconsin-Madison

837T Analysis of mitochondrial diversity in the smut fungus Sporisorium reilianum f. sp. zeae reveals

potential recombination events that alter predicted patterns of uniparental inheritance. **Hector** Mendoza University of Louisville

838F Extensive parasexual recombination promotes genetic diversity in Candida albicans progeny Matthew Anderson The Ohio State University

839W In-silico cross-contamination affects inference of genetic relationships in Saccharomyces cerevisiae Audrey Ward University of Georgia

840T Genomic and genetic analyses of antifungal drug resistance in Aspergillus fumigatus Jianping **Xu** McMaster University

841F Lineage structure of the *Fusarium* oxysporum Species Complex (FOSC) based on a dataset of 41 full-length genes from the core genomes of 545 isolates: its implications in taxonomy and diagnostics **David Geiser** Penn State University

842W Genetic diversity of the pea root pathogen Aphanomyces euteiches in Europe Carol Kälin Swedish University of Agricultural Sciences SLU

843T The *Parastagonospora nodorum* necrotrophic effector SnTox3 likely evolved from a duplication event of SnTox5 Gayan Kariyawasam North Dakota **State University**

844F Genome-wide association studies for the genetic basis of saprophytic fitness traits in samples of isolates of Fusarium graminearum from the Americas Christopher Toomajian Kansas State University

845W Using machine learning to gain insight on how environment and diet influence the evolution of galactose metabolism across the budding yeast subphylum Marie-Claire Harrison Pomona College

846T The role of DNA methylation in the evolution of two truffle-forming ectomycorrhizal sister species Emeline E. Pano California State University Fresno

847F Signaling Pathway Loss-of-Function Alleles and Evolutionary Hotspots in the Fungi Paul Magwene Duke University

848W Characterisation of the mating type loci in *Elsinoe*including the *Eucalyptus* pathogen *Elsinoe* necatrix Mike Wingfield University of Pretoria

849T Population genomics analysis of *Fusarium* graminearum isolates from the Americas Upasana **Dhakal** Kansas State University

850F Computational advances in the discovery of a new class of fungal natural products **Grant Nickles** University of Wisconsin-Madison

851W Genome-scale phylogeny of the fungal order Sordariales **Noah Lisa Hensen** Uppsala University

852T Analysis of 439 Cyp51 protein sequences shows 5 major Cyp51 gene family groups across Fungi Brandi Celia University of Georgia

853F Comparative genomics and population structure of South African Histoplasma isolates Rutendo Eugenia Mapengo National Institute for Communicable Diseases

854W Understanding the nature of the reproductive barriers within the wood decay species Trichaptum abietinum Dabao Sun Lu University of Oslo

855T Synonymous codon usage as a lens into the metabolic ecology of budding yeasts Abigail LaBella Vanderbilt University

856F The story behind the strains: using genomes to define wild yeast lineages from woodlands Jacqueline Peña University of Gerogia

857W Contrasting continental patterns of adaptive population divergence in a holarctic ectomycorrhizal fungus **Keaton Tremble** University of Utah

858T Molecular Characterisation of Candida auris Clinical Isolates at a Large Tertiary Academic Hospital in South Africa, 2016-2020 Dikeledi Kekana The National Institute for Communicable Diseases

859V Southwestern US-associated population of Cryptococcus isolates fills gaps in the family tree of molecular type VG-VI Juan Monroy-Nieto TGen North **860V** Global introduction patterns of the pine ectomycorrhizal fungus Suillus luteus Yi-Hong Ke Duke University

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863V Comparative genomics of Aspergillus oryzae genomes from different clades reveals signatures of artificial selection in primary and secondary metabolism in domesticate environments Katherine Chacon-Vargas University of Massachusetts

864V A global pangenome analysis of tan spot (Pyrenophora tritici-repentis) reveals an open genome and virulence factors nested in mobile elements Reem Aboukhaddour Agriculture and Agri-Food Canada

865V Analysis of pathogenicity genes in Batrachochytrium dendrobatidis Pangenome Mark Yacoub UC Riverside

866V The evolutionary analysis of *hac* BGC suggests the composite regulatory complex and the broad distribution of harzianic acid among metabolites of plant-associated ascomycetes Guan Pang Nanjing **Agricultural University**

867V Independent Expansion of the Hyr/Iff-like (Hil) Adhesin Family in C. auris and other Candida Yeast Pathogens Bin He University of Iowa

868V A Spot of Bother, transcontinental genetic diversity of Pyrenophora teres f. maculata. Kealan **Hassett** Curtin University

869V Ancient introgression between highly divergent fungal sister species Vilde Bruhn Kinneberg University of Oslo

870V Dynamics of *Verticillium dahliae* race 1 population under managed agricultural ecosystems Steven Klosterman USDA

871V Molecular determinants of host adaptation in a recombining population of Pyricularia oryzae infecting rice Marie Leys French National Research Institute for Agriculture, Food and Environment

872V An exploration into the differences in noncoding regions between Aspergillus fumigatus and close relatives and how these differences may influence virulence. Alec Brown Vanderbilt University

9. Synthetic Biology

873T The formation of a fuzzy negative arm protein complex is important for clock robustness in Neurospora crassa Meaghan Jankowski Rensselaer Polytechnic Institute

874F Program the Future with Ginkgo's Cell Development Kit Jesse Dill Ginkgo Bioworks

875W CRISPR/Cas9-based engineering of Aspergillus oryzae mycelium for meat-like flavor and appearance Vayu Maini Rekdal UC Berkeley

876T Use of CRISPR/Cas9 editing to generate mutations in erg27 gene of Botrytis cinerea associated with resistance to hydroxyanilides Anastasios Samaras UC Davis

877F Detection and engineering of rapidly evolving genomic regions in anaerobic microbes Amy Eisenberg UC Santa Barbara

878W Heterologous production of the fungal quinone polyketide bostrycoidin in Yarrowia lipolytica Mihaela **Bejenari** Aalborg University

879T Nature's Silent Pharmacy: Mining fungal genomes in the discovery of novel antibiotics. Sarah **Dodd** Univerity of Bristol

880F Structural characterization of secondary metabolites from filamentous fungi. Clay C. C. Wang University of Southern California

881W CRISPR-based transcriptional activation tool for silent genes in filamentous fungi Laszlo Mozsik University Leiden

882V Modular Synthetic Biology Toolkit for Filamentous Fungi Carsten Pohl Technische Universität Berlin

883V Development of CRISPR-Cas editing tools in Sphaerulina musiva towards controlling its establishment and pathogenicity in the model ecosystem, Populus Joanna Tannous Oak Ridge National Laboratory

884V Elucidation of pyranone pigment biosynthesis in fungi Yanfang Guo Westerdijk Fungal Biodiversity Institute

885V Secondary Metabolite Production in Aspergillus niger: methyltransferase specificity Susannah Selber-**Hnatiw** Concordia University

11. Other

886F Aspergillus nidulans Inhibitor of Apoptosis-like protein, AnBir1, is essential for survival and regulates fungal development Meareg Amare University of Wisconsin-Madison

887W Circadian Clock Control tRNA Synthetases in Neurospora crassa Griffin Best Texas A&M University

888T Spatio-temporal dynamics of the *Podospora* anserina fungus using a geomatic-based approach Cecilia Bobee Universite de Paris

889F Genetic and genomic analysis of Malassezia reveals pseudobipolar-tetrapolar mating-type locus transitions and early steps in sexual reproduction Marco A. Coelho Duke University Medical Center

890W Determining the carbohydrate profile of the Cryptococcus spore coat Eddie **Dominguez** University of Wisconsin–Madison

891T Developing genetic tools to unlock the biotechnological potential of anaerobic gut fungi Radwa Hanafy University of Delaware

892F Dynamic expanding fungal networks: characterization of the spatio-temporal hyphal growth in the filamentous fungus Podospora anserina Clara Ledoux Universite de Paris

893W Candida albicans and IL-17A stimulate cytokine production by oral epithelial cells via different mechanisms Jianfeng LIN The Lundquist Institute

894T Nanoparticles and pathogenic fungi: a nonuptake delivery Thomas Orasch Leibniz Institute for Natural Product Research and Infection Biology -Hans-Knöll-Institute

895F Mechanisms of circadian clock control of CPC-3 activity in Neurospora crassa Ebimobowei Preh Texas A&M University

896W Validating pantothenate kinase as a novel target for antifungal development Jessica **Regan** University of Tennessee Health Science Center

897T The role of ABC transporters in resistance to SDHI fungicides in the obligate fungal pathogen Erysiphe necator Anastasios Samaras UC Davis

898F Import and export of mannosylerythritol lipids by *Ustilago maydis* **Björn Sandrock** Philipps-University Marburg

899W The story of a sentinel tree, and the story of its fungal demise Jonathan Schilling University of Minnesota

900T Flotillin-dependent membrane microdomains are required for functional phagolysosomes against fungal infections Franziska Schmidt Leibniz Institute for Natural Product Research and Infection Biology Hans Knöll Institute

901F Signaling through the STRIPAK complex: Functional analysis of putative phosphorylation/ dephosphorylation targets Maria Shariatnasery Ruhr-**University Bochum**

902W Aspergillus fumigatus Septation Initiation Network (SIN) kinases contribute to fungal pathogenesis, cell wall construction, and rRNA metabolism. Xabier Guruceaga University of Tennessee Health Science Center

903V Structure-activity predictions from computational mining of protein databases to assist modular design of antimicrobial peptides Sascha Jung TU Berlin

904V Multiple tolerance mechanisms to the plant saponin α-tomatine in Botrytis cinerea Yaohua You Wageningen university and Research

905V Flower bulb waste material is a natural niche for the sexual cycle in Aspergillus fumigatus Jianhua **Zhang** Wageningen University

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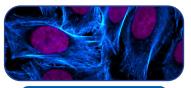
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