

Irish Plant Scientists Association Meeting 2016

27th & 28th April

Trinity College Dublin



Irish Plant Scientists' Association Meeting 2016

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IPSAM 2016 WELCOME

Dear Delegate,

Trinity College Dublin is delighted to welcome you to IPSAM 2016. This is a fantastic opportunity for plant scientists to showcase their research and network with their peers.

There is now greater than ever recognition by policy makers that plants provide the key to solving many of the principal challenges facing our planet – global climate regulation, feeding the growing population, replacements for fossil fuels, health and wellbeing.

IPSAM provides an important platform for our engagement with research into these issues; it also facilitates the broadcasting of the relevance of our research to a wider audience. We are thus particularly grateful to our sponsors LICOR Biosciences, and the International Association for Plant Biotechnology for their support.

I hope that you enjoy the meeting and that over the next two days you will be able to fully engage with the exciting range of talks, posters and social interactions that IPSAM offers.

Professor Fraser Mitchell

Head of the School of Natural Sciences, TCD

Irish Plant Scientists' Association Meeting 2016



Founded in 1963, the IAPB hosts a quadrennial congress - the next takes place in Dublin, Ireland in August 2018.

The association has as its objectives, to promote plant biotechnology, including cell and tissue culture applications.



DUBLIN 2018

International Association
for Plant Biotechnology
Congress

19th - 24th August 2018

Convention Centre,
Dublin, Ireland

For more information:

iapb2018.com



IAPB Executive Team (2015-2018)

(l-r) Eoin Lettice (Treasurer), Barbara Doyle Prestwich (President), Ewen Mullins (Editor-in-Chief)



Join the IAPB

The membership fee represents excellent value and the benefits include the following:

Access to a Newsletter published twice yearly which includes news of exciting developments in the industry and updates of the society. It also contains features and articles from individual members and groups.

Twice yearly publication of the Journal of the Society (In Vitro Cellular & Developmental Biology - Plant).

Access to a global network of Scientists working in the area.

Development of collaborative opportunities through competitively awarded travel scholarships.

Additional interaction with members through the use of social media on IAPB website, Twitter, Facebook and LinkedIn.

Reduced registration fee for the quadrennial congress in Dublin in 2018.

For more information on membership and the work of the IAPB:

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Trinity College Dublin
Coláiste na Tríonóide, Baile Átha Cliath
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Irish Plant Scientists' Association Meeting 2016

Irish Plant Scientists Association Meeting 2016

Wednesday 27th April

Speakers

Jane Stout – School of Natural Sciences, Trinity College Dublin.

09:40-10:00 – McNeill Lecture Theatre, Hamilton Building.

Title: Impacts of invasive plants on pollinators and pollination services.

Stout JC1 *

1 School of Natural Sciences, Trinity College Dublin, Dublin

*Presenting author



Introduced invasive plants have the potential to affect native pollinating insects both directly and indirectly. By affecting native plant community composition, they may have indirect impacts on pollinators, but those that are highly attractive to native flower-visiting insects have the potential to also exert direct impacts. Thus individual nutrition, health, behaviour and fitness may be affected, with knock-on implications for pollinator populations and communities. Furthermore, there may be implications for native plant-pollinator interactions and pollination services. Using the introduced, invasive

Rhododendron ponticum as a model system, I will synthesize data which test these potential impacts and consider whether they are as a result of *R. ponticum*'s non-native invasive status or could be applicable to any mass-flowering introduced species.

**Michelle McKeown-Bennett – School of Natural Sciences, Trinity College
Dublin.**

10:00-10:20 – McNeill Lecture Theatre, Hamilton Building.

Title: Characterisation of endophytic microbes within *Sphagnum magellanicum* from Clara Bog, County Offaly, Ireland: Implications for enclosed environment hydroponic systems in Space.

Michelle McKeon-Bennett*, Trevor R. Hodkinson

Botany, School of Natural Sciences, Trinity College Dublin, D2, Ireland

*Presenting author



This work investigates potential mutualistic relationships between endophytic microbes and species of native *Sphagnum* moss sampled from Clara Bog, County Offaly, Ireland. The application of the ion-exchange ability of *Sphagnum* moss to water remediation and resource recovery within an enclosed hydroponic system has been investigated by the author at NASA's Space Life Science Laboratory, Kennedy Space Centre, Florida. While this research indicated that *Sphagnum* could be utilized in this manner, it resulted in yet more questions, specifically in relation to microbial interactions and growth mechanisms within the *Sphagnum*:plant test bed. It is postulated that endophytic microbes growing mutualistically within *S. magellanicum* may be responsible for (a) anti-algae and anti-microbe effects within the hydroponic system and (b) increased nutraceutical content within the associated salad crop. Microbial DNA isolated from 100ug samples of *S. magellanicum*, was extracted and used to identify microbial endophytes using standard barcoding primers. Genetic fingerprinting is being utilised to type the endophytes. Isolation and culturing protocols from *sphagnum* plants have been developed and applied to characterisation of microbial species during hydroponic systems using *S. magellanicum* as a growth medium. Further investigation of mutualism between identified endophytes and a species of *Lactuca sativa* known as Lollo Rosso is ongoing.

Trevor Hodkinson – School of Natural Sciences, Trinity College Dublin.

10:20-10:40 – McNeill Lecture Theatre, Hamilton Building.

Title: Bleeding canker of horse chestnut (*Aesculus hippocastanum*) in Ireland: incidence, severity and molecular characterisation.

McEvoy Anna¹, O'Regan Frances¹, Fleming Colin C^{2,3}, Moreland Brendan², Pollock John², McGuinness Brian W⁴ and Hodkinson Trevor R^{5*}

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3 Molecular Bioscience-Parasitology, Institute for Global Food Security, School of Biological Sciences, Queen's University Belfast, Belfast, BT9 7BL, UK.

4 Teagasc, Ashtown Research Centre, Dublin 15, Ireland

5 Botany, School of Natural Sciences, Trinity College Dublin, the University of Dublin, Ireland

*Presenting author



A survey of bleeding canker disease, caused by *Pseudomonas syringae* pv. *aesculi*, was undertaken across Ireland. Incidence has become severe and can be considered epidemic, as 61% of the 1,587 trees surveyed showed symptoms of the disease. Bacteria were isolated from a sample of trees and characterised using *gyrB* DNA sequencing. DNA was also extracted directly from wound tissue. The Irish *P. syringae* pv. *aesculi* genotype was identical to genotypes previously sequenced with *gyrB* from the UK and some other locations in Europe. Real-time PCR using existing primers and a more pathovar specific primer set, designed here, was assessed for disease screening. It was more efficient to extract DNA directly from wound tissue, especially fresh bark, for disease detection than to undertake bacterial isolation with subsequent molecular analysis. A further set of sequencing primers was developed for the amplification of the *gyrB* gene from *P. syringae* pv. *aesculi* and their specificity shown using a diverse sample of bacterial isolate DNAs. The study also isolated and identified other bacterial species from diseased material. Some of these are known pathogens or have previously been identified as potentially beneficial endophytes of host trees.

**Ángel Cordero Vicente – UCD School of Biology and Environmental Science.
10:40-11:00 – McNeill Lecture Theatre, Hamilton Building.**

Title: Variation in leaf-level photosynthesis among Switchgrass genotypes exposed to low temperatures does not scale with final biomass yield.

Cordero Ángel 1,2*, Osborne, Bruce A1,2

1 UCD School of Biology and Environmental Science, University College Dublin, Belfield, Dublin, Ireland

2 UCD Earth Institute, University College Dublin, Belfield, Dublin, Ireland

*Presenting author



The effect of a 10 day low temperature treatment and subsequent recovery on 13 genotypes of Switchgrass resulted in significant variations in a number of leaf-level photosynthetic parameters. There was no clear separation of upland and lowland genotypes in terms of the resistance of leaf photosynthesis (A_{sat} , ϕ_{CO_2max} , V_p and V_{pmax}), respiration (R_d) or fluorescence (F_v/F_m) parameters to low temperatures, with lowland types achieving higher biomass yields than upland types. Examination of the reason for differences in the impact of low temperatures on leaf photosynthesis indicated that this could be due to both PEP carboxylase activity and/or PEP regeneration, but with some support for PEP regeneration being the more important. However, variations in leaf photosynthesis were not related to the final biomass yield in either control or low temperature exposed plants, and the best correlation was found with leaf area. Low temperatures were found to have a post treatment impact on leaf area development through a reduction in the formation of new leaves. Overall, these results suggest that more attention should be directed at variations in the effect of low temperature on leaf initiation and emergence in order to exploit the wider use of Switchgrass as a biomass-bioenergy crop.

Mike Williams – School of Natural Sciences, Trinity College Dublin.

11:30-11:50 – McNeill Lecture Theatre, Hamilton Building.

Title: N₂O emissions from legume crops in Europe.



Nitrous oxide (N₂O) makes up a large proportion of agriculture's contribution to greenhouse gas emissions. At a global level, there is a clear link between increases in fertiliser N use and the growth in N₂O emissions which show a long term growth rate of 0.5% (Tilman et al., 2002). However, agriculture receives nitrogen inputs from a variety of sources. Up until recently it had been assumed by the IPCC that a similar proportion of this N input was released as N₂O regardless of source. However, a number of reviews highlighted that where N was provided by biological nitrogen fixation (BNF) the associated N₂O emissions were significantly lower and in many circumstances no different to unfertilised control environments (Bouwman et al., 2002; Rochette and Janzen, 2005). This led to revisions of the National reporting guidelines prepared by the IPCC with the recommendation that no N₂O emissions would be associated with inputs of N by BNF (IPCC, 2006). The evidence for this revision remains somewhat circumstantial, and furthermore the extent to which decomposition of residues from legume plants contributes to emissions is highly uncertain (Baggs et al., 2000). In this talk I will be presenting field data from a European study where BNF has been calculated using plant biomass from a range of legume species and compared with direct measurements of N₂O. By this coupled approach and the use of field plots where no inorganic N had been applied, a more focussed assessment of the contribution of legume BNF to soil N₂O flux may be possible.

1Baggs, E. M., Rees, R.M., Smith, K.A., Vinten, A.J.A. (2000). Nitrous oxide emission from soils after incorporating crop residues. *Soil Use and Management*. 16 (2), 82-87. Bouman, A.F., Boumans, L.J.M., Batjes, 2N.H. (2002). Emissions of N₂O and NO from fertilized fields: summary of available measurement data. *Global Biogeochemical Cycles*. 16, 6-1. IPCC. (2006). 2006 IPCC guidelines for national greenhouse gas inventories, in: Rochette, P., Janzen, H.H. (2005). Towards a revised coefficient for estimating N₂O emissions from legumes. *Nutrient Cycling in Agroecosystems*. 73, 171-179. Tilman, D., Cassman, K.G., Matson, P.A., Naylor, R., Polasky, S. (2002). Agricultural sustainability and intensive production practices. *Nature*. 418(6898), 671-677.

Mohammad Ibrahim Khalil – UCD School of Biology & Environmental Science and Earth Institute.

11:50-12:10 – McNeill Lecture Theatre, Hamilton Building.

Title: Is sequestration of carbon in subsurface soils potentially sustainable for Irish agricultural land uses and the environment?

M.I. Khalil* and B. Osborne

UCD School of Biology & Environmental Science and Earth Institute, University College Dublin, Ireland.

*Presenting author



Agriculture and forestry are the dominant land use (>70% of the total) in Ireland. The recent intensification of agriculture has been increasing environmental pressure particularly on air, water, soil quality and biodiversity. The contribution of forest in terms of biomass and soil organic-C (SOC) to offset greenhouse gases (GHGs) is well documented but remains to be quantified at the national scale. Ireland has the lowest forest cover (11%) in European Union, indicating further potential for afforestation and thereby to partially offset GHGs emitting at an increasing rate particularly from livestock dominated agricultural systems (projected 45.6% of the national emissions in 2020). In addition to peaty soils, national soil information show relatively high SOC in surface mineral soils (3.2 to 6.3%), and that saturation concepts in most soils may apply. Unlike grasslands, potential loss of SOC can occur under continuous tillage. However, SOC density in grassland (except rough grazing) are lower at deeper layers compared to arable lands, and vice-versa. This clearly indicates huge potential of management and crop breeding approaches to increase carbon sequestration in major soils of Ireland. These co-benefit to offset and reduce GHGs, enhance nutrient use efficiency, attain environmental sustainability and the resilience of ecosystems functions.

Brian Murphy – University College Dublin.

12:10-12:30 – McNeill Lecture Theatre, Hamilton Building.

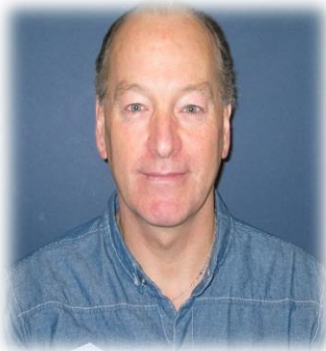
Title: Unlocking the Potential of Endophytes in Crops

BRIAN R. MURPHY^{1, 2*}, FIONA M. DOOHAN², TREVOR R. HODKINSON¹

¹ School of Natural Sciences & Trinity Centre for Biodiversity Research, Trinity College
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² UCD Earth Institute and UCD School of Biology & Environmental Science, University
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*Presenting author



Fungal and bacterial endophytes show great promise as biocontrol and biofertilisation organisms in agriculture. However, most of the research which has demonstrated endophyte benefits for crops has been conducted in controlled environments, and the few field experiments that have been carried out have produced inconsistent results. While we understand many of the mechanisms controlling beneficial interactions between endophytes and plants, there are still many aspects of the symbiosis that are proving difficult to elucidate in the complex environment of a field crop. Our research to date has found that benefits to barley cultivars arising from inoculation with fungal root endophytes are inconsistent and environmentally dependent. Here, we examine the environmental factors that influence the nature of the barley-endophyte relationship, and suggest profitable areas of research that may improve our ability to develop successful endophyte inoculants for cereal crops. These include: focused selection of host populations; building compatibility libraries for particular growing conditions; designing and testing endophyte consortia; understanding microbiome interactions in agricultural soils. We also stress the importance of understanding the needs of end users and of obtaining grower 'buy-in' in any venture to commercialise this promising biotechnology.

Matt Saunders – School of Natural Sciences, Trinity College Dublin.

12:30-12:50 – McNeill Lecture Theatre, Hamilton Building.

Title: Age does matter: Time-dependent implications for peatland restoration.

Saunders Matthew^{1,2*}, Hambley Graham³, Hill Timothy⁴, Levy Peter⁵, Cowie Neil⁶, Teh Yit Arn⁷, Robin Matthews²

1 School of Natural Sciences, Trinity College Dublin, Ireland

2 Environmental and Biochemical Sciences, The James Hutton Institute, Scotland

3 Department of Earth and Environmental Sciences, University of St. Andrews, Scotland

4 Geography Department, University of Exeter, England

5 Centre for Ecology and Hydrology, Scotland

6 Royal Society for Protection of Birds, UK

7 Institute of Biological and Environmental Sciences, University of Aberdeen, Scotland

*Presenting author



The peatlands of the Flow Country in Northern Scotland represent one of the largest areas of blanket bog in the UK and Europe, and are an important long-term carbon (C) sink. These peatlands underwent significant afforestation in the 1980s, when ~700 km² of bog were drained and planted with Sitka spruce (*Picea sitchensis*) and Lodgepole pine (*Pinus contorta*). This resulted in modifications to the hydrology, microtopography, vegetation and soil properties all of which are known to influence C sequestration and the production and emission of key greenhouse gases. Since the late 1990s restoration work has been undertaken to remove trees and raise the water table by drain blocking, to encourage the recolonisation of *Sphagnum* species and restore ecosystem function. Here, we report on the time-dependent impacts of peatland restoration by measuring and partitioning net ecosystem carbon exchange over a chronosequence of peatland sites. These included a near-natural peatland and two previously afforested sites that were restored in 1998 and 2005. The most recently restored site emitted ~80 g C m⁻² yr⁻¹, while the near-natural peatland and oldest restored site acted as a net C sink, sequestering ~114 and ~71 g C m⁻² yr⁻¹, respectively.

Plenary Talk 1: James Humphreys, Teagasc.

14:00-15:00 – McNeill Lecture Theatre, Hamilton Building.

Title: How sustainable are Irish dairy farms?

James Humphreys graduated with a master's degree in Agricultural Science from UCD before joining Teagasc in 1993. He completed his PhD in 1995. For most of his career he has been studying nutrient use efficiency in dairy production systems; conducting systems scale research at Solohead Research Farm and on-farm studies. He has been involved in a number of international projects examining resource use efficiency on European dairy farms including Green Dairy and Dairyman projects. He is married with four children and farms part-time on evenings and weekends.



James Humphreys, Donal O'Brien and John Upton

Livestock Systems Research Department, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland.

Ireland has a system of dairy production that is unique in Europe. In continental Europe milk production is focused on supplying short shelf-life products throughout the year in line with the demand of the enormous local market. Cows are increasingly confined indoors throughout the year and their diet is increasingly dependent on maize silage and concentrates imported from South America. A more traditional system has been maintained in Ireland where cows calve in spring and produce milk throughout the grass growing season and are dried off in the late autumn. Irish milk is processed into long-life products such as cheese, butter and milk powder, 85% of which is exported. Ninety per cent of the diet of Irish cows is low-cost grazed grass and grass-silage, and consequently Ireland has the lowest milk production costs in the EU. There are a number of additional benefits. Irish cows spend 10 months of the year at pasture which, along with a very effective quality assurance programme, underpins the positive image of Irish dairy products. Irish milk has the lowest carbon footprint in European Union (EU). Energy use on Irish dairy farms is also the lowest in the EU. Phosphorus losses from Irish agriculture have been brought under control by a 65% reduction in fertilizer use compared with the early 1970's and by substantial investment in slurry storage and management systems on farms. The Irish pasture-based system is relatively highly dependent on fertilizer N, which contributes to ammonia emissions (an important transboundary gas) to nitrous oxide (a potent greenhouse gas) and nitrate losses to water. Developing a more efficient nitrogen economy for Irish pasture based dairy production remains a challenge. Current research is examining the use of nitrification and urease inhibitors and the potential for making wider use of biological N fixation in grassland. Overall, Irish farms score well on any current scale or index used to measure sustainability compared with our international competitors. Nevertheless society is increasingly setting and demanding higher standards and challenges remain to meet these standards.

Yvonne Buckley – School of Natural Sciences, Trinity College Dublin.

15:00-15:20 – McNeill Lecture Theatre, Hamilton Building.

Title: Plant invasions now & in the future: challenges for science & society

Yvonne Buckley^{1*}

1 School of Natural Sciences, Zoology, Trinity College Dublin, Ireland

2 School of Animal & Plant Sciences, University of Sheffield, UK

*Presenting author



Humans have created novel ecosystems through environmental modification and mass movements of species around the planet. Many ecosystems are therefore composed of both native and non-native species. We face new challenges in understanding the functioning of these ecosystems and how we want to manage them. It is vital that we also understand the ecological role of humans in creating, shaping and determining future trajectories for these ecosystems. Differences between native and non-native species in novel ecosystems arise through multiple pathways including: biased sampling, different co-evolutionary histories with resident species, different species pools and pre-adaptation to human modified environments. I will present work from new global data sets that suggest that important differences in function between native and non-native dominated grassland ecosystems arise from biased species selection. I finish with a discussion of the challenges in the near to mid future which will shape how we think about and manage plant invasions.

Wuu Kuang Soh – School of Biology and Environmental Science, University College Dublin.

15:20-15:40 – McNeill Lecture Theatre, Hamilton Building.

Title: Increased global biome-level plant water-use efficiency in the past 25 years as atmospheric carbon dioxide concentrations rise.

Wuu Kuang Soh*, Michelle Murray, Conor Purcell, Jennifer McElwain

School of Biology and Environmental Science, University College Dublin

*Presenting author



Climate change will likely alter future ecosystems functioning however the magnitude and direction of such changes are unpredictable and difficult to quantify. One notable aspect of ecosystem functioning is the carbon and hydrologic cycles which are closely tied by gas exchange via plant stomata. Uncertainties in the magnitude and direction of the physiological responses of plants to elevated CO₂ at biome level hampers modelling of terrestrial water cycling and carbon storage. Furthermore, many existing studies focussed on long-term centennial effect of elevated CO₂ on a relatively few species in narrow ecosystem range while short-term effect on much broader ecosystem coverage is not known. Here we use stable carbon isotope, $\delta^{13}\text{C}$ leaf measurements, across seven major biomes to reconstruct the physiologically driven response of intercellular CO₂ caused by c. 40 ppm increase in atmospheric CO₂ over the last 25 years. We evaluate intrinsic water use efficiency (iWUE) trend for 264 woody angiosperm species for all seven biomes and show that the magnitude of iWUE change varied among biomes and plant functional types. Our finding is important because it shows that short-term increase in atmospheric CO₂ can potentially alter hydrologic cycle and its magnitude may differs among biome-plant functional type compositions.

Lynda Weekes – National Biodiversity Data Centre, Waterford; School of Biology and Environmental Science, University College Dublin.

15:40-16:00 – McNeill Lecture Theatre, Hamilton Building.

Title: National Vegetation Classification System: informing vegetation monitoring, planning and management - progress and development

***Weekes, Lynda^{1 2}, FitzPatrick, Úna¹**

1 National Biodiversity Data Centre, Waterford

2 School of Biology and Environmental Science, University College Dublin

*Presenting author



The National Vegetation Database (NVD) which is managed by the National Biodiversity Data Centre now holds over 30,000 Irish vegetation plots. It provides access to historical data to inform and direct both current habitat surveys and academic research and also contributes information to European vegetation initiatives. The NVD is the core building block from which an Irish vegetation classification system (INVC) can be developed which is a key objective in the 2011 National Biodiversity Plan (Action 3.2) allowing the description and quantification of our vegetation which provides sound scientific advice for nature conservation and management. The development of an INVC is a gradual process and is now underway, the aim is to provide user-friendly and freely accessible information on the web for surveyors, planners, policy makers and the like. A classification system for Irish semi-natural grasslands is now freely accessible at <http://www.biodiversityireland.ie/>, this facility provides information and the web application 'ERICA' that can statistically assign uploaded vegetation data to specific grassland plant communities. This is a valuable tool that aids vegetation surveying, mapping, and monitoring on a national scale. Current research, resulting in an Irish river vegetation classification system is also underway and will be available online in the near future.

Julio Isidro Sanchez – University College Dublin.

16:30-16:50 – McNeill Lecture Theatre, Hamilton Building.

Title: Improving genetic diversity in genomic selection by using the kinship matrix.

Isidro J^{1*}, Akdemir D²

1 Agriculture and Food Science, University College Dublin, Ireland.

2 Department of Plant Breeding and Genetics, Cornell University, USA.

*Presenting author



The enhancements in high throughput genotyping have transformed breeding pipelines in the last decade, letting to widespread use of genomic selection (GS) in plant and animal breeding. The concept of GS or genome wide selection [4] has brought new expectation and insight for the use of genomic information to make selection. Genomic Selection is a newly developed tool for animal and plant breeders in which dense markers covering the whole genome are used to estimate genomic breeding values. (GEBVs) for quantitative traits of selection candidates in breeding populations. Success of GS in breeding programs

lean on the improvement of prediction accuracies, which in turn depends on several factors. Selection of a good training population set (TRS) is very important for the success of GS. In this talk, I will present different statistical approaches to improve genetic diversity by using the relationship matrix in the process of optimization of the training population.

Rainer Melzer – School of Biology and Environmental Science, UCD.

16:50-17:10 – McNeill Lecture Theatre, Hamilton Building.

Title: Why do all orchids have six tepals? A developmental genetic hypothesis to explain asymmetries in species richness.

Melzer, Rainer

School of Biology and Environmental Science, University College Dublin, Ireland



One of the main conundrums in evolutionary biology is the asymmetry species richness between different taxa. Orchids, for example, constitute a huge family with more than 20 000 species, whereas many other flowering plant families only comprise a few dozen species. This differential success in terms of species numbers is at least partly ascribed to evolutionary innovations and ecological opportunities: taxa exposed to ecological opportunities and 'equipped' with a developmental genetic system capable of evolving innovations to seize those opportunities may become more species-rich than others. However, a currently underappreciated additional factor, developmental robustness, may play an important role in the origin of species-rich taxa. I will argue that evolutionary innovations need to be robustly integrated into the developmental genetic program to constitute a suitable substrate for natural selection and to 'explore' ecological opportunities. In this light, the six tepals of orchids may reflect a high degree of developmental robustness in perianth organ number determination. While this may not have been of direct adaptive value it may have facilitated the origin of evolutionary innovations superimposed on that robust bauplan and thus the species richness of the family.

Alwynne H. McGeever – Trinity Centre for Biodiversity Research, Trinity College Dublin.

17:10-17:30 – McNeill Lecture Theatre, Hamilton Building.

Title: Population dynamics of Pinus and Ulmus in Europe during the Holocene

McGeever, AH*1 and Mitchell, FJG2

1Trinity Centre for Biodiversity Research and Department of Botany, Trinity College Dublin, Dublin 2, Ireland

2Department of Botany, Trinity College Dublin, Dublin 2, Ireland

*Presenting Author



This work investigates and compares the population dynamics of Pinus and Ulmus in Europe, during the Holocene, at varying temporal and spatial scales, by using recently developed and novel modelling methods.

The first component characterises the European-wide post glacial rise and mid-Holocene decline experienced by both genera. Pollen data was extracted from 330 sites on the European Pollen Database (EPD). The depth of rise and decline events for each genus in each site core was defined by applying a spline curve, to remove stochastic noise from the pollen data, and identifying the range of depths along which the pollen values increased or decreased. The R package Bchron was used to calibrate radiocarbon dates and produce an age-depth model for each site, using stochastic linear interpolation and Monte Carlo methods. The age-depth model data was applied to the event depth range to produce a probability distribution of when the rise and decline events occurred.

The second component characterises Ulmus and Pinus when they were abundant on the European landscape. Depth and magnitude data of maximum pollen values for both genera were gathered from the EPD. The age-depth models were used to determine the age of the maximum pollen value depths.

These data were then plotted on maps and empirical Bayesian kriging was used to interpolate the spatial and temporal dynamics of these population events in the two tree genera.

This work, therefore, presents novel techniques to quantifying tree population dynamics, and also provides insight into the specific dynamics of two major tree genera in Europe.



Trinity College Dublin
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Irish Plant Scientists' Association Meeting 2016

Irish Plant Scientists Association Meeting 2016

Thursday 28th April

Speakers

Astrid Wingler – School of BEES, University College Cork

09:30-09:50 – Maxwell Lecture Theatre, Hamilton Building.

Title: Classification of intra-specific variation in plant functional strategies

Rose-Lucy May 1, Angela Connor 2, Astrid Wingler 2*

1 Research Department of Genetics, Evolution and Environment, University College London, United Kingdom

2 School of Biological, Earth and Environmental Sciences, University College Cork, Ireland

*Presenting author



Considerable intra-specific variation in key developmental processes, such as the timing of flowering or senescence, suggests that different functional strategies can be found within a plant species. A simple method for the classification of intra-specific variation of plant functional strategies would enable characterisation of evolutionary and ecological processes occurring in response to environmental change and during invasion or succession. Grime's C-S-R system was developed to assign functional strategies (competitor, stress tolerator and ruderal) to different plant species. Testing how this system can

be used to analyse intra-specific variation in *Arabidopsis thaliana*, we explore the potential and limitations of such an approach. In a genetically diverse set of accessions grown under controlled conditions, functional strategies varied along the stress-tolerant/ruderal spectrum. There was a positive correlation of temperature at the geographical origin with the S-dimension and a negative correlation with the R-dimension. The classification system also allowed prediction of important traits, such as fecundity, from vegetative characteristics. This approach could be extended to determine intra-specific variation in phenotypic plasticity. Further possible applications include investigations into the genetic basis of functional traits, e.g. in genome-wide association studies using wild species or crop plants.

Anna M. Csergő – School of Natural Sciences, Trinity College Dublin.

09:50-10:10 – Maxwell Lecture Theatre, Hamilton Building.

Title: Macroclimatic suitability predicts basic demographic processes but not population growth rates and extinction risk.

Anna M Csergő^{1,2*}, Roberto Salguero-Gómez^{2,3}, Olivier Broennimann⁴, Shaun R Coutts^{1,5}, Amy L Angert⁶, Erik Welk⁷, Brian McGill⁸, Jens-Christian Svenning⁹, Cyrille Violle¹⁰, Brian J. Enquist¹¹, Antoine Guisan^{4,12}, and Yvonne M Buckley^{1,2}

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Irish Plant Scientists' Association Meeting 2016



Climatic suitability is an important predictor of species distributions, which are ultimately driven by the population-level processes of birth, growth, reproduction, dispersal and death. However, the demographic mechanisms through which climate determine population extinction or persistence and species movement across large spatial extents are often unclear. Species distribution models (SDMs) typically model the probability of occurrence as a function of correlations between climate and other variables. However, there is often little empirical support for the implied relationship between

modeled habitat suitability and population performance that underlie species distribution patterns.

We used demographic data from the COMPADRE Plant Matrix Database and presence-based SDMs to test whether population performance and projected persistence can be predicted from macroclimatic suitability for 102 populations of 37 plant species worldwide.

While macroclimatic suitability was correlated with key demographic processes such as retrogression or progression, it did not directly predict population growth rate and extinction risk. To refine the use of SDMs as indicators of population performance, we need to improve the spatial and temporal replication of demographic data collection and to tailor SDMs to the complexity of environmental factors that modulate different types of demographic processes.

Conor Owens – Botany Department, Trinity College Dublin

10:10-10:30 – Maxwell Lecture Theatre, Hamilton Building.

Title: Biodiversity in willow evapotranspiration systems used for wastewater treatment

Owens Conor 1*, Mitchell Fraser 1, Stout Jane 1

1 Botany Department, Trinity College Dublin, Dublin 2, Ireland

*Presenting author



Constructed wetlands are increasingly seen in Ireland and abroad as a solution to the on-site treatment of wastewater from domestic and other sources in rural areas. They are likely permanent features in our landscape that will proliferate into the future. Willow evapotranspiration systems are a subtype suitable for application in areas with low permeability subsoils. These systems are often promoted as having a beneficial role with respect to biodiversity but this has not been rigorously evaluated. This project aims to assess the plant and invertebrate biodiversity of these systems and the contribution they make to the biodiversity of the wider landscape. The factors driving biodiversity in these systems are being investigated and thus this project will provide management recommendations to maximise this biodiversity. This project involves cross discipline collaboration, drawing on expertise from both the TCD School of Natural Sciences and the TCD School of Engineering.

Eduardo March – Plant Science, NUI Galway.

09:30-09:50 – Joly Lecture Theatre, Hamilton Building.

Title: Molecular characterisation of the CONFUSO protein of Arabidopsis.

March E^{1*}, Schubert D², Farrona S¹

1 Plant and Agricultural Biosciences Centre, NUI Galway, Ireland

2 Institute of Biology, Freie Universitaet Berlin, Germany



The study of how epigenetic processes affect developmental phase transitions in *Arabidopsis thaliana* (*Arabidopsis*) is important to reveal when and where expression pattern changes will occur allowing the phase transition, which ultimately enables reproduction and viability of the species. In these processes, Polycomb Group (PcG) proteins, which control the deposition of specific epigenetic marks, are essential for *Arabidopsis* development and cell lineage through the regulation of gene expression patterns. In particular, the POLYCOMB REPRESSIVE

COMPLEX 2 (PRC2) is responsible for the trimethylation of the histone 3 on lysine 27 (H3K27me3), an epigenetic mark for gene repression.

Previously in our lab novel interactors of CURLY LEAF (CLF), the catalytic subunit of PRC2, were discovered. One of these interactors is CONFUSO (COFU), a PHD domain protein with unknown function. Mutant plants affected in COFU present pleiotropic phenotypes that resemble mutants with a strongly impaired PRC2. We will present evidence revealing that 28% of the genes miss-regulated in COFU mutants are H3K27me3 target genes, including essential genes for SAM development like CLASS I KNOX, WUS and CLV3. If the role of COFU in deposition is direct or indirect, it still remains unveiled. All these results suggest a crosstalk between COFU and PRC2.

Peter Ryder – Plant and AgriBioSciences Research Centre (PABC), College of Science, National University of Ireland Galway.

09:50-10:10 – Joly Lecture Theatre, Hamilton Building.

Title: Deployment of genome editing in plants using the CRISPR/Cas9 system.

Peter Ryder^{1,*}, Marcus McHale¹, Antoine Fort¹ and Charles Spillane¹

¹Genetics and Biotechnology Laboratory, Plant and AgriBiosciences Research Centre (PABC), National University of Ireland Galway, University Road, Galway H91 REW4, Ireland.

*Presenting author



The targeted editing of DNA sequences in vivo (i.e. gene editing) has been desired for fundamental and biotechnological research since the advent of molecular biology. Early genome editing techniques including Zinc-Finger nucleases (ZFNs) and TAL effector nucleases (TALENs) have not been widely adopted due to difficulties in construction and laborious assembly of protein domains. The CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats)/Cas9 system has recently emerged as a powerful genome editing technology due to its ease of use, low cost and high reproducibility. Using the CRISPR/cas9 system, targeted gene cleavage of genomic DNA and subsequent DNA repair by either non-homologous end joining (NHEJ) or homology directed repair (HDR) can be achieved by simple alterations to a short RNA guide sequence. We have investigated the efficiency of the CRISPR/cas9 system as a system for genome editing in the model plant *Arabidopsis thaliana*. Through investigation of different CRISPR/cas9 vector constructs we have achieved high generation rates of T1 homozygous mutant plants. Using the CRISPR/cas9 system we have gene edited the trichome development gene *TRANSPARENT TESTA GLABRA 1* (TTG1) and also generated homozygous T1 generation triple mutants. CRISPR/cas9 is emerging as a powerful genome editing tool that will revolutionise biology, including plant biology.

**Brendan Hallahan – Plant and AgriBioSciences Research Centre (PABC),
College of Science, National University of Ireland Galway.**

10:10-10:30 – Joly Lecture Theatre, Hamilton Building.

Title: Investigating the relative contributions of hybridity and genome dosage to heterosis in sugar beet (*Beta vulgaris*)

Brendan Hallahan^{1,*}, Eva Fernandez-Tendero¹, Antoine Fort¹, Peter Ryder¹, Gilles Dupouy¹, Marc Deletre¹, Britta Schulz² and Charles Spillane¹

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²Molecular Breeding Sugarbeet, KWS Saat AG, Einbeck, Germany.

*Presenting author



Heterosis refers to an increase in size or other characteristics in F1 hybrid offspring that is not observed in the parents. Heterosis can occur when two genetically distinct inbred lines are crossed to generate a heterozygous F1 hybrid. Genome dosage effects can be observed when autopolyploid individuals of differing ploidy level display different characteristics, and is implicated in heterosis effects. Genome dosage (ploidy) effects have been utilised in commercial sugar beet (*Beta vulgaris*) breeding since the 1930s. However, a transition from polyploid (e.g. triploid) to diploid lines has occurred in sugar beet breeding. Sugar beet is a useful model for investigating contributions of genome dosage versus genetic hybridity on heterosis in a commercial crop. Using sugar beet lines with different ploidy levels we have investigated: (1) The effect of genome dosage increases on heterosis in F1 offspring, and (2) The effect of homozygous versus heterozygous tetraploid male parents on F1 triploid heterosis. Fruit and seed characteristics, germination rates and field yield performance were investigated. In sugar beet, we have determined that commercially important traits such yield, sugar content, germination and seed survival are more influenced by hybridity than genome dosage, which has implications for design of future hybrid breeding programs.

Antoine Fort – Plant and AgriBioSciences Research Centre (PABC), College of Science, National University of Ireland Galway.

10:30-10:50 – Joly Lecture Theatre, Hamilton Building.

Title: Disaggregating polyploidy, parental genome dosage and hybridity contributions to heterosis in *Arabidopsis thaliana*

Antoine Fort^{1,*}, Peter Ryder¹, Peter C. McKeown¹, Cris Wijnen³, Mark G.M Aarts³, Ronan Sulpice² and Charles Spillane¹

¹Genetics and Biotechnology Laboratory, Plant and AgriBiosciences Research Centre (PABC), National University of Ireland Galway, University Road, Galway H91 REW4, Ireland.

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*Presenting author



Heterosis is the phenomenon whereby hybrid offspring of genetically divergent parents display superior characteristics compared with their parents. While hybridity and polyploidy can influence heterosis in hybrid plants, the differential contributions of hybridity versus polyploidy to heterosis effects remain unknown. To address this question, we investigated heterosis effects on rosette size and growth rate of 88 distinct F1 lines of *Arabidopsis thaliana* consisting of diploids, reciprocal triploids and tetraploids in isogenic and hybrid genetic contexts.

“Heterosis without hybridity” effects on plant size can be generated in genetically isogenic F1 triploid plants. Paternal genome excess F1 triploids display positive heterosis while maternal genome excess F1s display negative heterosis effects. Paternal genome dosage increases plant size in F1 hybrid triploid plants by on average 57% (in contrast to 35% increase displayed by F1 diploid hybrids). Such effects likely derive from differential seed size, since growth rate of triploids was similar to diploids. Tetraploid plants display a lower growth rate compared with other ploidies, while hybrids display increased early stage growth rate. By disaggregating heterosis effects due to hybridity versus genome dosage, we advance understanding of heterosis in plants and facilitate novel paternal genome-dosage based strategies to enhance heterosis effects in crop plants.

**Plenary Talk 2: Deri Tomos - School of Biological Sciences, Bangor University.
11:30-12:30 – Joly Lecture Theatre, Hamilton Building.**

Title: Small volumes, large pressures. Adventures in *in situ* single cell analysis.

Prof Deri Tomos. (School of Biological Sciences, Bangor University)



PhD training in plant biochemistry (1977). Introduced to cell biophysics in Germany in 1980. Since then, at Bangor, developed an array of techniques to measure the mechanics, water relations, biochemistry and gene expression of individual cells *in situ* in fully physiological plants. This through the use of fine glass microcapillaries to sample cells. We describe the approach as SiCSA (single cell sampling and analysis). Analytical approaches include cell pressure-probe, pl-osmometry, X-ray microanalysis, enzyme-based fluorescence assays, pcr and capillary zone electrophoresis. Applications from the mechanics of solar tracking in beans, to the possible role of the apoplast in turgor regulation, to the foraging habits of roots for depleted uranium anti-tank shrapnel will be included in this presentation from across the Irish Sea.

Lynn Pillitteri – Western Washington University, Washington USA.

14:00-14:20 – Joly Lecture Theatre, Hamilton Building.

Title: A molecular look at stomata.

Lynn Pillitteri¹* and Aaron Mahoney¹

¹ Department of Biology, Western Washington University, USA

*Presenting author



Stomata are turgor-driven valves on the epidermal surface of all land plants that allow for efficient gas and water exchange between a plant and its environment. They play an important role in plant water-use efficiency and the global carbon cycle. The last decade has revealed many molecular components driving the production and density of stomata on the epidermal surface. Specifically, several basic helix-loop-helix (bHLH) proteins have been identified which directly regulate the differentiation of the cell types within the stomata lineage. The work presented here will describe some of the genes involved in the production of stomata and progress on identifying new regulators of these critical plant structures. The potential impacts of alteration of stomatal density/number in relation to climate change will be discussed.

Niall Brogan – School of Biology and Environmental Science (SBES), University College Dublin.

14:20-14:40 – Joly Lecture Theatre, Hamilton Building.

Title: Do mitochondria regulate plant programmed cell death?

Brogan Niall*, Reape Theresa, McCabe Paul.

School of Biology and Environmental Science (SBES), University College Dublin, Belfield, Dublin 4, Ireland

*Presenting author



Programmed cell death (PCD) is a fundamental biological process serving various cellular functions in plants. Some of its many functions include defence responses by restricting the spread of pathogens, and allowing for the development of the multi-cellular body plan. Understanding plant PCD may play a major role in future agricultural developments. The focus of this research is the role of mitochondria in the regulation of plant PCD, using the model organism *Arabidopsis thaliana*. Mitochondrial alterations such as the loss of transmembrane potential, production of reactive oxygen species (ROS) and in particular mitochondrial swelling, initiate PCD. Current studies suggest that the inhibition of mitochondrial swelling blocks plant PCD, the mechanism by which is still unclear. It is thought that the disruption of swelling prevents the release of specific mitochondrial molecules that once in the cytosol initiate the PCD process. The use of pharmaceutical agents such as lanthanum chloride (LaCl₃), cyclosporin A (CsA) and in particular 3-methyladenine (3-MA) inhibit mitochondrial swelling resulting in PCD suppression.

Saoirse Tracey – School of Agriculture and Food Science, UCD.

14:40-15:00 – Joly Lecture Theatre, Hamilton Building.

Title: Exploring the rhizosphere: Imaging root-soil interactions using X-ray Computed Tomography

Saoirse Tracy*¹, Malcolm Bennett², Tony Pridmore², Craig Sturrock², Sacha Mooney²

1.School of Agriculture, University College Dublin, Ireland 2. University of Nottingham, United Kingdom

*Presenting author



Although roots play a crucial role in plant growth and development through their acquisition and delivery of water and nutrients to the above-ground organs, our understanding of how they interact with their immediate soil environment largely remains a mystery as the opaque nature of soil has prevented undisturbed in situ root visualisation. The use of non-invasive techniques such as X-ray Computed Tomography (CT) means that it is now possible to visualise a growing root within an undisturbed soil core. X-ray CT is a technique that enables non-destructive 3-D investigations into root:soil interactions at the micro-scale. By imaging the actual 3D geometries of the soil structure and visualising the interfaces between roots, soil, water and air filled pores an accurate representation of water movement and root growth in soil is achieved. Previous commonly employed destructive methods for root studies, such as root washing could not provide detailed information on root architecture, including branching characteristics and extension rate, which are inherently linked to conditions within the soil matrix. Therefore this technique can enable root phenotyping of different crop species and varieties in soil. This information is crucial if laboratory research is to be translated to an understanding of responses under field conditions.

Catherine Gavin – Waterford Institute of Technology

CANCELLED 15:00-15:20 – Joly Lecture Theatre, Hamilton Building.

Title: Investigating the effects of pruning timings and regimes on the quality and yield of *Ozothamnus hookeri* 'Sussex Silver' for the cut foliage industry.

Catherine Gavin*, Dr. Nick McCarthy, Dr. Cara Daly

1 Waterford Institute of Technology, Ireland

2 Waterford Institute of Technology, Ireland

*Presenting author



Ozothamnus spp. are globally important plants in the cut foliage industry. Highly regarded for its grey foliage, *Ozothamnus hookeri* 'Sussex Silver' is grown commercially in Ireland for domestic and European markets. Research was required to fully understand the potential of this cut foliage crop when grown in Ireland's temperate climate. This study investigated the effects of pruning timings and regimes on the stem and spray yield of *Ozothamnus hookeri* 'Sussex Silver' on young and mature plantations grown in the South East of Ireland. The impact of rejuvenation pruning on a mature *O. hookeri* 'Sussex Silver' plantation was also examined. *Ozothamnus hookeri* 'Sussex Silver' plants were pruned in March or June using two pruning regimes: 'hard pruning' to 200 mm and 'light pruning' to 500 mm. Yields of saleable stems and sprays were collected for each plant and results indicated that higher yields of saleable single stems and sprays are obtained when *O. hookeri* 'Sussex Silver' was pruned in March rather than in June, regardless of whether it was pruned to 200 mm or 500 mm. Interestingly, rejuvenation pruning did not produce any harvestable stems in the subsequent year. These results suggest that *O. hookeri* 'Sussex Silver' is a commercially viable product.



Trinity College Dublin
Coláiste na Tríonóide, Baile Átha Cliath
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Irish Plant Scientists' Association Meeting 2016

Irish Plant Scientists Association Meeting 2016

Wednesday 27th & Thursday 28th April

Poster Sessions – SNIAM Building

**Alexandre Perochon - School of Biology and Environmental Science,
University College Dublin.**

**Title: NOVEL WHEAT GENES CONTRIBUTING IN PLANT RESISTANCE TO FUSARIUM
GRAMINEARUM AND THE MYCOTOXIN DEOXYNIVALENOL**

Alexandre Perochon^{1*}, Zsolt Váry¹, Jia Jianguang¹, Amal Kahla¹, Chanemougasoundharam
Arunachalam¹, Steven R. Scofield², Sarah Bowden³, Emma Wallington³ and Fiona M.
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*Presenting author



The disease Fusarium Head Blight (FHB) and deoxynivalenol (DON), its associated mycotoxin, are major factors limiting cereal production, in particular wheat, worldwide. DON acts as a virulence factor that facilitates *Fusarium graminearum* colonisation of wheat head during the disease development. Using wheat genomic resources, functional genomics techniques and virus-induced gene silencing (VIGS), we found that heads with less expression of some of new genes developed more DON damage. One example is an orphan gene identified to be taxonomically-restricted to the grass subfamily Pooidea. Expression analysis of the wheat gene show a rapid up-regulation in plant tissues in response to the infection with *F. graminearum* or DON. Using over-expressing transgenic wheat lines we present evidence that the wheat orphan gene is involved in plant resistance to *Fusarium*. We identify as interacting proteins a NAC-like transcription factor and a wheat SnRK1 (SNF1-Related Kinase 1). This evolutionarily conserved energy sensor protein is central integrators of stress and energy signalling in plants. Interestingly silencing of SnRK1 genes in wheat suggest a role in stress response induce by DON. This common role with the orphan protein in DON-induced bleaching tolerance and their physical interaction, propose that they act together in the same signaling pathway.

Alice Kennedy - UCD Earth Institute and School of Biology & Environment Science.

Title: Characterization of a wheat gene contributing to Fusarium Head Blight resistance.

Kennedy Alice^{1*}, Kahla Amal¹, Perochon Alexandre¹, Doohan Fiona¹

1 UCD Earth Institute and School of Biology & Environment Science, University College Dublin, Science Centre East, Belfield, Dublin 4, Ireland.

*Presenting author



The discovery of genes underlying resistance to globally significant diseases is of utmost importance to meet the demand of future food security in the face of increasing population and climate change. Fusarium Head Blight (FHB) caused by the fungal pathogen *Fusarium graminearum* is an economically important disease of wheat leading to direct yield loss due to shrivelled grains and indirectly due to contamination of grains by harmful mycotoxins. This project aims to characterize a novel wheat transcription factor and its role in resistance to *F. graminearum* and its mycotoxin deoxynivalenol (DON). Previous studies have shown this gene is induced by *F. graminearum* but not its tri5 mutant derivative leading to the conclusion that this gene is specifically DON-responsive. Preliminary studies show wheat lines overexpressing this novel transcription factor have greater resistance to Fusarium infection through spray inoculation trials of wheat heads and through detached leaf assays. Transgenic *Arabidopsis thaliana* lines expressing this gene have also shown increased resistance to DON in vitro. This project aims to characterize the mode of action of this novel gene in the defence against FHB.

Alysha Chua - School of Science, Waterford Institute of Technology.

Title: An investigation of the bio-fertilising and stress-mitigating effects of cyanobacteria strains on agricultural crop varieties.

Chua Alysha*, Connolly Damian, Daly Cara

School of Science, Waterford Institute of Technology

*Presenting author



Nostoc spp. are photosynthetic nitrogen-fixing cyanobacteria. Previous work has shown that the liquid media in which Nostoc spp. are grown - termed conditioned medium (CM) - suppresses stress-induced programmed cell death (PCD) in root hairs of the model plant organism *Arabidopsis thaliana*. PCD is a genetically controlled and conserved cell death mechanism in the plant life cycle; plant cells often undergo PCD to mitigate abiotic and biotic stress. Therefore, a novel Root Hair Assay will be used to screen for stress tolerance by enumeration of resultant cell viability and cell death (PCD and necrosis) levels after controlled abiotic and biotic stress treatment.

This project seeks to investigate the stress-suppressing and bio-fertilising properties of selected Nostoc spp. in important Irish crops (barley, wheat and maize) in response to applied abiotic (salinity, heat, and drought) and biotic stresses (salicylic acid, fumonisin B1). Cyanobacteria CM will also be tested for yield enhancement using a novel hydroponic system. The versatile hydroponic system streamlines handling of individual plants and treatments, enabling high-throughput testing of Nostoc spp. effects. The project findings have potential to develop a novel stress-mitigating and bio-fertilising product, as well as an early method of identification of crop varieties exhibiting enhanced stress tolerance.

Anindita Lahiri - Department of Botany, Trinity College Dublin.

Title: Fungal leaf endophytes of Irish ash (*Fraxinus excelsior*) threatened by ash dieback disease.

Supervisors: Trevor Hodkinson, Gerry Douglas, Brian Murphy and Colin Kelleher

PhD program title: Characterizing candidate disease resistance loci in ash (*Fraxinus*) and an assessment of ash fungal endophyte strain variation in Ireland

Presentation title: Fungal leaf endophytes of Irish ash (*Fraxinus excelsior*) threatened by ash dieback disease.



Ash is very useful and abundant tree found throughout Europe, which is now threatened considerably because of a disease called ash dieback. It is caused by a fungal pathogen known as *Hymenoscyphus fraxineus* Baral. It can damage plants irrespective of their age group but young plants are more susceptible to the disease. Ash dieback starts from the midrib of the leaves and travels through the midrib to the stem part of the plant where the fungal mycelia blocks the xylem and phloem vessels and the plant dies because of lack of water and nutrients.

This project is currently undertaking a comprehensive study of the leaf fungal endophytes of healthy plants to characterize their microbiome. We have cultured endophytes in a malt extract agar media and isolated them on the same media by sub-culturing. We are currently amplifying nuclear ribosomal bar coding DNA regions and sequencing them to identify the fungal isolates. We will then test the biocontrol potential of some of these against the disease pathogen.

Aude Perdereau - Teagasc Oak Park, Carlow.

Title: Using genome wide allele frequency fingerprints to identify allele frequency changes in seeded perennial ryegrass swards

Perdereau Aude^{1*}, Milbourne Dan¹, Byrne Stephen¹ and Barth Susanne¹

¹Teagasc, Crops, Environment & Land Use Programme, Oak Park, Carlow, Ireland

*Presenting author



Unlike varieties of many crops, in which all plants of a variety are identical, individual perennial ryegrass (PRG) cultivars are effectively genetically divergent populations of individuals that have been selected to have broadly similar characteristics. In addition, as opposed to annual crops, PRG cultivars are expected to remain in the field over a near decadal period before re-seeding. One consequence of these factors is that, once planted, the composition of perennial ryegrass swards can change over time in response to environmental variation and management practice.

In order to gain a better insight into this phenomenon, we will use cutting edge genetic fingerprinting approach called “Genome Wide Allele Frequency Fingerprints”, based on a genome-wide marker approach called genotyping by sequencing to monitor changes in the genetic composition of PRG swards over time. We will test whether these changes are random, or whether they can be related to management practices causing some plants to be preferentially selected over others. The ultimate goal of the research is to identify regions of the genome that are responsible for determining the lifetime performance characteristics of grazed swards and to use this information in the future to develop better performing PRG cultivars using genomic selection-based strategies.

Binbin Zhou - School of BES, University College Dublin.

Title: Identification of wheat proteins involved in the host response to *Zymoseptoria tritici*

Zhou, B. 1*, Christodoulou, T. 1, Brennan, C. 1, Feechan, A. 2 and Doohan, F. M. 1

1 UCD School of Biology and Environmental Science and UCD Earth Institute,

2 UCD School Of Agriculture and Food Science and UCD Earth Institute, University College Dublin, Belfield, Dublin 4, Ireland

*Presenting author



Septoria tritici blotch (STB) disease is the most significant threat to yield in most wheat growing regions. To identify the resistance gene in wheat, seven orphan genes have been selected from *Zymoseptoria tritici* (*Z. tritici*) and wheat interaction microarray database. We have selected orphan genes that play a role in the wheat response to STB disease. Orphans are taxonomically restricted genes and there is increasing evidence that they play a role in biological adaptation to environmental stress. The majority of orphan genes encode the orphan protein which have unknown function. In order to identify the interacting proteins of these orphan proteins, a yeast two hybrid library (Y2H) has been constructed. The third leaf of *Triticum aestivum* cvs. Stigg (resistant) and Longbow (susceptible) were inoculated with a mixed isolate inoculum of *Zymoseptoria tritici*. Leaves were collected at various time points post-inoculation, covering both the asymptomatic phase and the disease establishment phases. All the sample were bulked for RNA extraction. Y2H library construction and screening are being performing by Hybrigenics Services. The orphan proteins will be used as bait to screen the cDNA expression Y2H library. In addition, a *Z. tritici* candidate effector has been identified by our collaborating lab. This effector will also be used as a bait to screen the Y2H library. The host interacting proteins of both orphan proteins and the effector target proteins will be identified and characterized.

Ciaran Brennan - School of Environmental Science and Biology, UCD Earth Institute, University College Dublin.

Title: Mining for orphan genes of wheat during infection by the pathogenic fungus *Zymoseptoria tritici*

Brennan, Ciaran J.*, O'Driscoll, Aoife., Benbow Harriet., Mullins, Ewen and Doohan, Fiona M.

Molecular Plant-Microbe Interactions Laboratory, Earth institute, University College Dublin, Belfield, Dublin 4, Ireland.

*Presenting author

Zymoseptoria tritici is the fungal pathogen responsible for the disease commonly known as Septoria Leaf Blotch (STB) (Fig. 1). STB is currently the most prevalent foliar disease of Wheat in Ireland. Losses due to STB in Europe alone cost ~€300 million per annum. The exploration of uncategorized orphan genes is a relatively nascent and novel approach aiming to identify specially evolved genes involved in the amelioration of specific stresses. Using a custom pipeline, a collection of STB responsive microarray probes were screened to extract orphan genes potentially involved in the host/STB interaction.

Darren Heenan Daly – School of BEES, University College Cork.

Title: Isolation and Screening of Plant Growth-Promoting Rhizobacteria from Irish Potato Soils

Heenan Daly, Darren*1 Doyle Prestwich, Barbara1

*Presenting author



The Earth's population is set to burgeon to ~9 billion people by the year 2050. Food and energy security will be of paramount importance if we are to keep up with this projected figure. *Solanum tuberosum* is the fourth most widely-grown staple crop in the world and its popularity is set to expand outside its main world markets in the years to come. The potato industry in Ireland alone is worth more than €80 million at the farmgate. However, new E.U. regulations regarding the use of biocides and fertilisers in crop production will present a problem to farmers to keep up with demand in the coming years. This is exasperated even further by our warming climate in Ireland, creating ideal conditions for plant pathogens to thrive. Plant growth-promoting rhizobacteria represent a possible remedy to this problem. They can aid plant growth through direct and indirect mechanisms such as solubilising inorganic phosphates in the soil, reducing excessive plant stress responses and inhibiting the growth of plant pathogens respectively. An isolation campaign across Co. Cork on both organic and conventional potato crops yielded 120 isolates, 46 of which inhibit the growth of *Rhizoctonia solani* equal to or better than a commercial isolate.

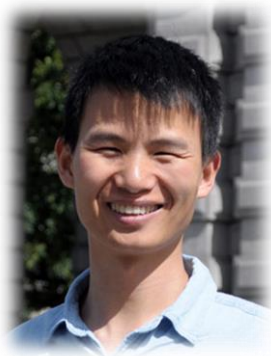
Dongwei Zhao – Botany Department, School of Natural Sciences, Trinity College Dublin.

Title: Phylogenetics and Biogeography of Camellia (Theaceae) in Indochinese Peninsula

Zhao Dongwei*, Parnell John, Hodkinson Trevor

Botany Department, School of Natural Sciences, Trinity College Dublin

*Presenting author



Tea, camellias and oil camellias from the genus *Camellia* L. are commercially highly important. About one third of all known *Camellia* species occur in the Indochinese Peninsula, of which half are endemic. Many new species of *Camellia*, including some golden camellias, are still being described from this area, suggesting that it was previously under-collected. Almost no work, however, has focused on the phylogenetics and biogeography of *Camellia* in this area. This project aims to address these issues using morphological and molecular approaches. Morphological studies, consisting of a comparison and description of various macro-characters of specimens, palynological analyses and leaf anatomical investigations, will be undertaken to clarify the boundaries of species in this notoriously variable genus. DNA markers derived from nuclear and chloroplast genomes will be selected to generate molecular sequence data, which will be used to reconstruct a robust phylogenetic tree. A new classification of this genus could then be proposed based on both morphological and molecular data. Species that have potential to supply new traits to facilitate the breeding of tea, camellias and oil camellias could also be identified.

Harriet Benbow – UCD School of Biology and Environmental Science and UCD Earth Institute, University College Dublin.

Title: Identifying genetic resistance to *Septoria tritici* blotch in wheat using next-generation RNA sequencing

Benbow Harriet^{1*}, Zhou Binbin¹, Christodoulou Thalia¹, Brennan Ciaran¹, Mullins Ewen², Doohan Fiona¹.

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Within this WHEATSECURITY project, we will employ next-generation sequencing to identify candidate genes involved in host resistance to septoria tritici blotch (STB); the most devastating foliar disease of wheat in Ireland. Using bulked-segregant analysis (BSA) of a doubled-haploid population of *Triticum aestivum*, which segregates for STB resistance, we will sequence RNA of inoculated and control plants in a time-series. The timepoints (0, 1, 4, 8 and 14 days post inoculations) were chosen to target differential gene expression between the resistant and susceptible hosts during early infection. In complement, we will perform BSA by RNAseq of a *Brachypodium distachyon* recombinant inbred population, which also segregates for STB resistance.

Following differential expression analysis, interesting candidates will be validated by RT-PCR, and a set will be chosen for characterisation. Using the most recent gene models available for wheat, we will identify varietal single nucleotide polymorphism (SNP) markers between the resistance and susceptible host plants. The putative SNPs will be validated using Kompetitive Allele Specific (KASP) PCR for their use in breeding programmes.

Joanna Kacprzyk – SBES, University College Dublin.

Title: The retraction of the protoplast during PCD is an active, and interruptible, calcium-flux driven process

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Programmed cell death (PCD) is a process of organized cellular destruction, playing an important role in developmental processes and responses to environmental stimuli. The protoplast retracts during apoptosis-like PCD (AL-PCD) and if this retraction is an active step of death programme, it should be used as a defining feature for this type of PCD. We used an array of pharmacological and genetic tools to test if the protoplast retraction occurring during AL-PCD can be modulated. Disturbing calcium signalling, ATP synthesis and mitochondrial permeability transition inhibited protoplast retraction and often the execution of the death programme. Protoplast retraction can precede loss of plasma membrane integrity and cell death can be interrupted after the protoplast retraction had already occurred. Blocking calcium influx inhibited the protoplast retraction, reduced DNA fragmentation and delayed death induced by moderate stresses. At higher levels of stress, where cell death occurs without protoplast retraction, blocking calcium flux had no effect on the death process. The results strongly suggest that retraction of the protoplast is an active biological process dependent on an early calcium trigger rather than cellular disintegration due to plasma membrane damage. Therefore, protoplast retraction is a quantifiable hallmark feature and consequently reporter of AL-PCD.

Emma Doyle – University College Dublin Earth Institute and School of Biology and Environmental Science.

Title: How does the wheat orphan gene TaFROG interact with plant defence pathways in providing resistance to FHB?

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Fusarium head blight (FHB) caused by the fungal pathogen *Fusarium graminearum* is one of the most economically important diseases of wheat and barley today, causing huge yield losses each year. Orphan genes of which the vast majority are of unknown function, are thought to have evolved in response to different environmental pressures. TaFROG is an orphan gene of the family Pooideae which has been shown to provide quantitative resistance to FHB in wheat. The expression of this orphan gene TaFROG is induced by the mycotoxin DON, a virulence factor produced by the fungus. While we know that this gene has the potential to be of benefit to disease resistance we know little about how it provides this resistance. This project aims to elucidate the pathways in which TaFROG is acting. A previous study has shown that Pathogenesis-Related (PR) Genes are upregulated by TaFROG in wheat without stimulation, while preliminary results also show that overexpression lines of TaFROG in *Arabidopsis* promote an enhancement of salicylic acid induced programmed cell death, both of which are characteristic responses to biotic stress. Gene expression analysis of TaFROG overexpression lines with *F. graminearum* will give a greater insight into how TaFROG provides resistance to FHB.

Enrique Alcalde – School of Biology & Environmental Science, University College Dublin.

Title: Elucidating the beneficial effects of two biostimulants in crop performance and stress resistance in cereals

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Increasing demand for sustainable alternative solutions against today's challenges, such as global warming, banning of pesticides and growing food demand, has led to an enormous rise in the use of products commercialized as bioestimulants. These products are used to enhance plant growth and increase yield, but little is known about their mode of action. They may either play a direct role by interacting with plant signalling cascades or by enhancing nutrient uptake. Using phenotypic and molecular biology approaches, we aim to quantify the beneficial effects of two biostimulants derived from microbial fermentation (Bio-1 and Bio-2), on cereals and also to determine the effects of the products on crops at the gene expression level, using next generation RNA-seq technology. A number of in vitro experiments were performed to determine the effect of the products in plant performance under non-stress conditions and salt, drought or heat stress situations. So far, Bio-1 and Bio-2 have had a positive effect on wheat seedling growth under saline conditions. These results will provide a better understanding of the mode of action of these products so that their efficacy can be improved. Furthermore, this study will contribute to unravelling the molecular mechanisms behind plant abiotic resistance.

John Conway – School of Biology & Environmental Science, University College Dublin.

Title: Changing Atmospheric Carbon Dioxide Concentrations Alters Plant Cell Sensitivity to Undergo Programmed Cell Death

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Programmed cell death (PCD) is an active, genetically controlled process in which cells are selectively eliminated in a highly co-ordinated step wise fashion. In plants PCD is involved from embryogenesis to death and plays a crucial role in a variety of processes - plant development, senescence, reproduction and defence against biotic and abiotic stresses. All cells can undergo PCD, and cells are constantly balancing pro and anti PCD signals. A cells sensitivity to respond to these signals depends on the health status of the cell and environmental factors. This study provides evidence that atmospheric CO₂ concentration is an environmental factor which can influence PCD sensitivity thresholds. A novel in-vivo PCD assay – which scores PCD based on morphology – is used to compare PCD initiation in root hairs of *Arabidopsis thaliana* seedlings grown in different CO₂ concentrations. Results show that growth in elevated CO₂ alters the sensitivity of *A. thaliana* root hair cells to undergo PCD. A change in PCD threshold sensitivity may have profound effects on many aspects of plant biology. Studies are continuing to quantify and evaluate the effect of CO₂ on PCD thresholds.

Keshav Bahadur Malla – Department of Biology and Environmental Sciences, UCD.

Title: Development of molecular marker for Fusarium Head Blight (FHB) resistance breeding in Wheat

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Fusarium head blight (FHB), caused by the fungal pathogens *Fusarium graminearum* and *Fusarium culmorum*, is an important disease of wheat. It causes loss in yield and contamination of grain with the mycotoxin deoxynivalenol (DON). Several resistance genes against FHB disease have been identified. However, very limited studies have been done in related to allelic diversity at the gene or gene promoter level associated with quantitative resistance. In our lab, several genes have been identified that (a) are up-regulated in response to FHB and DON and (b) that enhance DON and/or FHB resistance. These include TaCYP and TaLRR, the Pooideae-specific gene TaFROG, and the Ta-FROG-interacting proteins TaNAC5 and TaSnRK1a. In this study, we will determine the gene and promoter sequences of FHB DON-responsive homeologues of interest across a wide variety of wheat germplasm. Furthermore, we will identify SNPs within genes associated with DON/FHB resistance and develop molecular marker depending on the allelic variants within the resistance gene. These SNP markers will be used for Marker – assisted selection for Fusarium Head blight resistance breeding.

**Laura Gallego-Lorenzo – School of Biology and Environmental Science,
University College Dublin.**

**Title: Impact of Long Term Organic Fertilizer Amendments on Pasture on Greenhouse
Gases Fluxes**

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In order to assess the long term impact of pasture management practices on greenhouse gases emissions, nitrous oxide (N₂O), carbon dioxide (CO₂) and methane (CH₄) fluxes were measured in long-term managed grassland with different types and amounts of organic fertilizer amendments. The experiment was established in 1970 on a perennial ryegrass sward at Hillsborough, Northern Ireland. Eight treatments were established: unfertilized control, mineral fertilised control and pig and cow slurry at three different rates: 50, 100 and 200 m³ ha⁻¹ year⁻¹. The experimental design comprised of four replicates of each treatment in two randomized blocks giving a total of 32 plots. The plots were cut and fertilized three times a year. The discrete measurements of the gases were conducted using dynamic chambers connected onto PVC collars at two different depths to separate autotrophic and heterotrophic respiration (circa.5 cm and from 13 to 30 cm). The technique used to measure greenhouse gases are photoacoustic spectroscopy. Preliminary results showed that soil temperature is positively correlated with N₂O and CO₂ emissions and negatively correlated with CH₄ (P<0.01). The soil CO₂ and N₂O emissions increased with increasing fertiliser application rate, and pig slurry applications seemed to decrease the natural CH₄ sink capacity of soil.

Macdara O'Neill – Teagasc, Crops Environment and Land Use, Oakpark.

Title: Seasonal nitrous oxide emissions and emission factors for oilseed rape cultivations at different nitrogen levels under conventional and non-inversion tillage systems

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Oilseed rape (OSR) is the most important biofuel crop in Europe and shows high potential for future expansion in Irish agriculture. Conventional methods of cultivation involve mouldboard ploughing and relatively high levels of inorganic fertilizer to attain optimal yields, which promote emissions of greenhouse gases such as soil carbon dioxide (CO₂) and nitrous oxide (N₂O). Alternative management techniques, such as wider row spacing and non-inversion tillage practices, require further investigation with the prospect of potentially reducing overall greenhouse gas emissions and improving sustainability. This research examined the effect of different nitrogen rates (0, 160, 240 & 320kg N ha⁻¹) in ploughing and subsoiler based systems on nitrous oxide emissions and the emission factors over two growing seasons in 2014 and 2015. The results highlight that subsoiler systems enhance N₂O emissions compared to ploughing systems for all nitrogen rates, the sandy soil exhibited larger cumulative N₂O emissions than the loam soil and the majority of emission factors calculated were below those of the IPCC default value of 1%. Overall, subsoiler systems promote N₂O loss to the atmosphere at higher N rates and that both site-specific and climatic factors are necessary requisites for accurately modelling future emission factors for OSR cultivations.

Maurício Cruz Mantoani – Earth Institute, School of Biology and Environmental Sciences, University College Dublin.

Title: Early leaf development: a key-advantage of *Gunnera*'s invasion success?

Cruz Mantoani Maurício 1,2*, Gallego-Lorenzo Laura 1,2, Gilbert Maxime 3, Sweeney Lorna Marie 4, Osborne Bruce A. 1,2

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Early growth under sub-optimal conditions, may allow invasive species to out compete native species. One important invasive species that is causing problems in Ireland is *Gunnera tinctoria* Molina (Mirb.). To assess and quantify if *G. tinctoria* has an advantage over resident species, in terms of early development, six replicate (5x5 m) plots comprising invasive populations and nearby uninvaded grassland areas have been established on Achill Island, Co. Mayo, Ireland. In each plot, one individual of *Juncus effusus* L. and one individual of *G. tinctoria* (a total of six individuals of each species) were randomly assigned for measurements. Monitoring of leaf growth using linear dimensions and leaf number was started in February before any significant leaf emergence. Data on leaf length and breadth are being collected using a calliper ruler and a measuring tape. Conversion of the linear dimensions to leaf area values is being done using correlations with measured leaf areas based on photographic images and the software Easy Leaf Area. Leaf number is also being recorded. *G. tinctoria* is able to initiate growth significantly earlier than *J. effusus*, even in waterlogged environments characterised by anaerobic conditions where available nitrogen is low and mainly in the form of ammonium.

Myriam Deshaies – University College Dublin.

Title: Evaluation and development of a biostimulant for enhancing plant resistance against biotic and abiotic stresses

Myriam Deshaies

Earth Institute, University College Dublin, Ireland



The company Envirotech Innovative Products, Dublin, has developed a biostimulant product, Auranta Harvest, made of plant extracts and mainly composed of organic acids. The aims of the project are to evaluate the effects of the product on plant resistance against biotic and abiotic stresses and to understand its mode of action. Auranta Harvest is used as a seed coating or foliar treatment for wheat. Seeds and plants are being exposed to fungi to study their resistance against various diseases: Fusarium, Take-all, Eyespot and Sharp Eyespot. Drought and salt stress will also be experimented on wheat. Results will first be based on phenotypic observations. In a second part, genomics analyses will be effectuated to understand the mode of action of the biostimulant. Using this product could result in reducing the amount of fertilizers and fungicides applied in crop fields. It could become a tool for a more sustainable agriculture.

Patricia Coughlan – School of Natural Science, Botany Department, Trinity College Dublin.

Title: The phylogenetics of paclitaxel biosynthesis genes in *Taxus baccata*, *Taxus hybrids* and allies.

Coughlan, Patricia M.*¹, Carolan, James², Hook, Ingrid³, Hodkinson, Trevor R.¹

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Taxus baccata, the Irish yew is a natural producer of a diterpenoid alkaloid called Paclitaxel. Paclitaxel was first discovered in the Pacific yew *Taxus brevifolia*, and was developed by Bristol Myers Squibb into the anti cancer drug, Taxol used to treat ovarian, breast and lung cancer. Some knowledge has been generated about the phylogenetic relationships of *Taxus* species, however very little is known about molecular DNA variation in the genes leading to Paclitaxel production in the genus. This project is developing molecular primers to amplify and study the genes involved in the Taxol biosynthetic pathway, and take a phylogenetic approach to discover which genes are more important for paclitaxel production. More specifically, it aims to discover variation in these genes between *T. baccata* and *Taxus* hybrids such as *T. xmedia*. Progress has been made on isolating and sequencing Taxadiene synthase (TS) and DBAT (10-deacetylbaccatin III-10b-O-acetyltransferase) and considerable variation has been recorded among taxa. ITS and trnL gene regions of *Taxus* samples have also been sequenced to add to the existing phylogenetic knowledge and to help with correct identification of samples.

Samuel Belton – School of Biology and Environmental Science, University College Dublin.

Title: Characterisation of the de novo sphingolipid biosynthesis enzyme, serine palmitoyltransferase, in the multicellular cyanobacteria, *Nostoc punctiforme*.

Belton Samuel P1*, McCabe Paul F1,2,3, Ng Carl KY1,2,3

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Sphingolipids are a diverse group of amino alcohol-based lipids that function in signal transduction, lipid microdomain formation, protein sorting and cell death. Recent work in our lab has indicated that sphingolipids are produced by *Nostoc punctiforme*, a multicellular species of cyanobacteria which can enter symbioses with a wide range of different plant species. Unlike in eukaryotes, sphingolipid metabolism in prokaryotes, let alone cyanobacteria, has scarcely been studied. However, serine palmitoyltransferase (SPT) – an enzyme which catalyses the first step in the de novo sphingolipid biosynthesis pathway – has been characterised in a small number of gram-negative bacteria, including some species of the chemoheterotrophic genus, *Sphingomonas*.

Here, a putative SPT (Npun_R3567) was identified by BLAST comparison of the genome of *Nostoc punctiforme* ATCC 29133 using the SPT from *Sphingomonas multivorum*. In silico analyses of Npun_R3567 shows distinct phylogenetic clustering with other cyanobacterial and bacterial SPTs, and also contains a number of catalytically-important domains. We showed that Npun_R3567 is expressed in both the vegetative and nitrogen-fixing growth state of the cyanobacteria. Additionally, we have cloned Npun_R3567 in a bacterial expression vector and heterologously expressed Npun_R3567 in *E. coli* in preparation for enzymatic analysis and biochemical characterisation.

Saorla Kavanagh – School of Chemical Sciences, Dublin City University & Department of Botany, Trinity College Dublin.

Title: Does landscape structure impact the nutritional value of Irish honey?

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Honey contains bioactive compounds with potential antioxidative, antibacterial and anticarcinogenic effects. These compounds are beneficial not only to human health but also bee health. Honey can also contain many contaminants mainly due to anthropogenic effects.

Declines in bee populations have caused great concern due to the valuable ecosystem services they provide. Neonicotinoids have been implicated in these declines. Due to the wide application, persistence in soil and water and uptake by wild plants, neonicotinoids are widely bioavailable to bees. This can result in the presence of neonicotinoids in bee matrices (honey, pollen, wax). There has been a significant increase in the use of neonicotinoids in crop protection in recent years and their occurrence within bee matrices may become more frequent.

This research will combine analytical chemistry techniques with up-to-date geographical surveys to explore the relationship between landscape context and honey composition in terms of bioactive substances and contaminants. This will identify, for the first time, the extent to which land cover and land use impacts honey chemistry, and enable individual bioactive profiles of Irish honeys to be characterised.

Stephen Kehoe – The Earth Institute, UCD School of Biology and Environmental Science, University College Dublin.

Title: Investigating the potential of Auranta Harvest to increase the productivity of major crop plant species.

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Microbial plant pathogens attack plants, causing diseases that reduce yield. With European Union legislation limiting the number of products that can be utilized in the control of plant pathogens an ever increasing opportunity is opening for plant strengthening products. These products will boost plant health and natural defences from pathogens. A plant extract containing bioflavonoid and organic acids has a high potential to interact and increase a plants natural defences against pathogens. These compounds comprise some of the active ingredients in the product Auranta Harvest.

Auranta Harvest is a combination of a citrus extract, which contains a range of polyphenolic compounds, and natural organic acids. The product has demonstrated the ability to increase plant strength through increased production of phytoalexins in tomato plants in recent trials and has also shown some efficacy in controlling late blight in potatoes. This project will investigate the plant strengthening potential of the current Auranta Harvest formulation and the mechanisms involved using major crop plant species, including wheat and potatoes. The Auranta Harvest product will be tested against the take-all disease causing fungus *Gaeumannomyces graminis* Var. *tritici* on wheat and the blight causing fungus *Phytophthora infestans* on potatoes.

**Sukontip Sirimongkol – School of Natural Sciences, Department of Botany,
Trinity College Dublin.**

Title: The genus *Henckelia* Spreng (*Gesneriaceae*) in Thailand.

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The genus *Henckelia* is one of the most complicated genera in the family *Gesneriaceae*. Recent molecular phylogenetic studies on *Chirita* and *Henckelia* are presented. These have separated *Chirita* from other genera such as *Henckelia*, *Damrongia*, *Microchirita*, *Liebigia* and *Primulina*. Some members of *Henckelia* have been moved to other genera including *Codonoboea*, *Didissandra*, *Didymocarpus*, *Lindernia* and *Loxocarpus* resulting in a reduction in the number of *Henckelia* species to 57.

In Thailand, based on specimens received on loan, there are 5 species of *Henckelia*, i.e. *H. anachoreta* (Hance) D.J.Middleton & Mich.Möller, *H. grandifolia* A. Dietr., *H. pumila* (D. Don) A. Dietr., *H. rotundata* (Barnett) D.J.Middleton & Mich.Möller, *H. speciosa* (Kurz) D.J. Middleton & Mich. Möller. They are distributed over northern, central, eastern and southeastern Thailand.

Susan Foreman – UCD and Teagasc.

Title: Measuring the physiological and growth responses of potential short-rotation forestry species to variations in planting density

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Keywords: Short rotation forestry, gas analysis, biomass production, planting density.



The European Union has set targets for member countries to reach a minimum of 20% of energy supply from renewable-energy sources by 2020. The proportion of Ireland's gross consumption of energy from renewable sources in 2005 was 3.1%. The target is to produce 16% by 2020. One area in which Ireland might meet this target is through short-rotation forestry (SRF) biomass production. However, there is little information available on best practice for growing the main candidate SRF species, especially in relation to optimum planting density to maximise production. Therefore, the effects of planting density on the survival, growth and physiological response of three likely species are being examined in a controlled greenhouse experiment in Kinsealy and in a field trial at Johnstown Castle. The observations and measurements will include leaf-level gas exchange to assess photosynthetic activity, shoot growth phenology, height and diameter increments. The experiment with different tree densities in pots will inform a measurement strategy for use in field trials and involve scaling up from leaf- to canopy-level to enable differences in stand productivity to be modelled. Better understanding of the effects of competition stress on growth responses will allow optimal planting densities for such species to be optimised.

**Thalia Christodoulou – School of Environmental Science and Biology, UCD
Earth Institute, University College Dublin.**

Title: Screening a Wheat TILLING Population for Altered Susceptibility to Septoria Tritici Blotch Disease.

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Septoria tritici blotch disease is one of the major challenges faced by wheat-breeders. Reverse genetic approaches such as TILLING (Targeting Induced Local Lesions in Genomes) offers great potential for improving crop traits via a non-GM approach. We are screening the wheat cv. Cadenza population in order to identify mutants with altered susceptibility to Zymoseptoria tritici. To date we have screened 500 mutants. Plants were propagated in John Innes No.2 compost during the summer of 2015 in a polytunnel, with a temperature of aprox. 20-30 degrees celsius 80% RH during disease development on the flag leaf. The flag leaf of secondary or tertiary tillers was sprayed with pycnidia of a Dutch strain of Z. tritici (strain 94269) and disease (percentage of leaf area bearing pycnidia) was scored 21 days post-inoculation. This phenotypic evaluation highlighted seven lines heterozygous for enhanced resistance and five homozygous for an extremely susceptible phenotype, with wild type cv. Cadenza plants displaying a susceptible response. We are currently preparing to screen the remainder of the cv. Cadenza population for altered STB resistance, while at the same time we are cultivating and backcrossing (to cv. Cadenza) TILLING lines of interest arising from the initial screen. Anticipating the sequencing of these lines, we aim to use a combination of exome sequence data and phenotype analyses of progeny from a backcross with cv. Cadenza to identify the gene mutations responsible for the altered disease phenotypes. This work is funded by the Irish Department of Agriculture, Food and the Marine.

Anne Dubéarnès - Trinity College Dublin, Botany Department.

Title: Systematics of the genus *Embelia* Burm.f. (Primulaceae – Myrsinoideae)

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Within the Primulaceae (Primrose) family, the Myrsinoideae form a highly variable tropical group, ranging from climbers and shrubs to trees, and characterised by the presence of dark dots on the leaves and fruits. This subfamily contains over 1300 species, divided into approximately 40 genera. Many of these genera are in need of taxonomic revision, as their limits are poorly defined and sometimes rely on ambiguous characters. Among these genera is *Embelia*, a genus of climbing shrubs distributed mostly in South and South-East Asia, tropical Africa and Madagascar. *Embelia* displays extensive morphological variation - especially regarding the position, shape, size and merosity of the inflorescences and flowers. It is distinguished from other Myrsinoideae only by its climbing habit, and the relationship with morphologically similar genera has not been critically evaluated yet. The last monograph of *Embelia* by Mez (1902), recognised eight subgenera and 92 species, but the total number of species is currently estimated at 150-200, and the subgenera used by Mez must be assessed and refined. This project aims to combine morphological and molecular data in order to test the monophyly of *Embelia* and to provide a taxonomic framework of the subgenera.