New Phytologist

next generation scientists

22–25 July 2019
University College, Dublin, Ireland

Programme, abstracts and participants

New Phytologist

next generation scientists

O'Brien Centre for Science
University College Dublin

22–25 July 2019

Scientific Organising Committee, University College Dublin
Carl Ng (Organising Committee Lead)
Emma Doyle
David Hunt
Rainer Melzer
Sónia Negrão
Alexandre Perochon
Aisling Reilly

New Phytologist Trust Organisation
Jill Brooke *(Journal & Finance Administrator)*
Freja Kärrman-Bailey *(Events and Promotion Coordinator)*
Sarah Lennon *(Executive Editor)*
Mike Whitfield *(Development Coordinator)*

'New Phytologist next generation scientists' logo by Andy Crayston, Promotional Gods, Lancaster, UK

Contact email: *np-symposia@lancaster.ac.uk*.

Acknowledgements

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New Phytologist Trust

WILEY

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Information for delegates

Location
'New Phytologist next generation scientists' will take place at the University College Dublin O'Brien Centre for Science, Dublin from 22–25 July 2019. Oral presentations will take place in the George Moore Auditorium. Posters will be displayed in Zones 4 and 5.

Travel directions
Belfield, the main University College Dublin campus, is located 4km south of Dublin city centre.

Transport options
By bus: Dublin Bus provides a range of services to and from the Belfield campus (http://www.dublinbus.ie/PageFiles/10644/ucd_campus_map_2.pdf)

Bus Éireann provides a nationwide bus service with most major areas having a regular link to Dublin. The majority of Dublin services terminate in Busáras (Central Bus Station, Dublin) from where it is a short walk to O'Connell Street for connecting buses to UCD. Several Bus Éireann services from the Greater Dublin area directly serve the UCD Belfield Campus during morning peak times.

Aircoach operates a bus service (route 700) from Dublin Airport to Leopardstown / Sandyford / Stillorgan, which passes UCD.

By plane
Dublin is served by Dublin International Airport, which is located north of Dublin City Centre. There are frequent connecting buses from the airport to the city centre, including a special shuttle service, Airlink, which brings passengers directly to Busáras (Central Bus Station, Dublin).

Aircoach operates a service (route 700) that directly passes by UCD. The Aircoach bus stop is located just outside the main N11 (Stillorgan Road) entrance.

By ferry and train
Irish Ferries and Stena Line operate sailings between Dublin Port and Holyhead (UK) and Cherbourg (France). It is possible to book a combined Rail and Sail ticket that

includes rail travel within the UK and the ferry crossing from the UK to Ireland. Rail and Sail tickets can be booked via Loco2 (https://loco2.com/) or the ferry operators' websites. See The Man in Seat 61 (https://www.seat61.com/Ireland.htm) for more information and travel advice.

By train
Dublin is served by two main railway stations: Connolly Station and Heuston Station. It is a short walk from Connolly Station to O'Connell Street, where the Dublin Bus numbers 11 and 46A can be boarded for UCD. The route 145 provides a direct route from Heuston Station to Belfield via the city centre.

By taxi
There are usually taxis in operation in the city centre at any given time. It is possible to hail a taxi from the street, but convenient taxi ranks are located on O'Connell Street, Middle Abbey Street, Dame Street and St Stephens Green.

For further information, visit Iarnróad Eireann (Irish Rail, http://www.irishrail.ie/).

Catering and social events

Coffee breaks will take place in Zones 4 and 5 at set times as indicated in the programme.

Lunch on the 22nd of July will be available from 12:00 to 13:30 during registration. Food is not permitted in the auditorium so please arrive early if you intend to eat before the start of the meeting at 13:30. Lunch will be served 12:50–14:00 on the 23-24th July.

***Social event Monday evening*:**

Pizza will be served from 19:00.

Social event Tuesday:

A distillery trip has been arranged from 15:30, buses will take the group to The Powerscourt Distillery for a tour of the Distillery and Warehouse (https://powerscourtdistillery.com). The tour will be followed by drinks and canapés.

Social event Wednesday:

A BBQ will be set up at UCD Rosemount from 19:00.

Vegetarian, vegan, wheat- and gluten-free options will be available for all meals.

Accommodation
Accommodation for delegates is provided at the University College Dublin student residences.

Checking in to your accommodation

Please check in at the Central Reception Office located at UCD Merville (follow the purple signs). It is also adjacent the Centra Convenience Store.

The Central Reception is open 24 hours a day, and Reception staff will be there to welcome you and to direct you to your accommodation. Please note that there is no need to bring bed linen, or towels, as they are supplied.

If you have any difficulty locating the Merville Reception area, you can contact Reception on +353 1716 1008, or via email at summerreception@ucd.ie.

Check-in is from 15:00. You must check-out by 10:00 on the morning of Thursday 25th of July. A room for storing luggage will be available at the O'Brien Centre for Science on Monday 22nd July and on Thursday 25th July.

Please note that breakfast is not available at the residences, but coffee and breakfast pastries/fruit will be served in the O'Brien Centre for Science from 08:15 on Tuesday, Wednesday and Thursday. In addition, there are a variety of food and drink outlets on the Bellfield campus. For more details, see the interactive campus map here: http://map.ucdestates.ie/.

Posters
Posters should be prepared so that they are no larger than A0 size, portrait orientation (118 cm high x 84 cm wide). Posters should be put up during registration (12:00–13:30 on Monday 22nd July) and will be displayed for the duration of the meeting. There will be dedicated poster sessions throughout the meeting. We encourage you to return to the posters during the social events at the O'Brien Centre and during breaks.

***Prizes*:** Posters will be assessed by your peers (the other delegates) and the posters that gain the most votes will receive prizes. A scoring sheet is included in your delegate pack. Please fill out and return this sheet to the **registration desk by 10:00 on Thursday 25th July.**

***Abstracts*:** Abstracts are included in this abstract book which can also be found on the USB sticks in the delegate packs or online (https://www.newphytologist.org/nextgenevents/2019).

Internet Access

Free wireless internet will be available throughout the conference centre.
There are two wireless options: (1) UCDWireless - this is a non-secured link where no password is required; and (2) Eduroam - you must ensure that you are set up to access Eduroam via your home institution, this will allow you to connect to the UCD Eduroam network.

Social Media

We encourage all attendees to join in discussions on social media. Follow @NewPhyt on Twitter and Instagram, and fb.com/NewPhytologist on Facebook for updates during and after the meeting. The 'New Phytologist next generation scientists' Facebook group can be found at http://www.newphytologist.org/nextgensci/facebook.
The meeting hashtag is **#npnextgen**.

Filming and photography

Photography and/or filming will take place at the meeting. The resulting photographs and video footage will be used by the New Phytologist Trust for the purpose of promoting its activities, and may be published on the New Phytologist Trust's website and social media channels.
If you do not wish to appear in the photographs or video footage, please speak to one of the organisers or email np-symposia@lancaster.ac.uk.

Code of conduct

The New Phytologist Trust celebrates diversity and we expect participants in our meetings to be respectful, considerate and supportive of each other, to offer constructive critiques and embrace the variety of opinions on offer. New Phytologist next generation scientists 2019 is an opportunity to share, develop and broaden our viewpoints within a safe and inclusive setting, and we hope that you will enjoy the

meeting. If you have any concerns or suggestions, please speak to one of the organisers or email np-symposia@lancaster.ac.uk

Contact

For further information, and in case of any emergencies, please contact Sarah Lennon. Email: s.lennon@lancaster.ac.uk; np-symposia@lancaster.ac.uk; tel: +44 7811 37 10 19; or Carl Ng, Email: carl.ng@ucd.ie.

Meeting programme

Monday, 22 July 2019

Session 1. Chair: Grace Cott

12:00-13:30	Lunch and registration	
13:30-13:40	**Welcome**	
13:40-14:30	**Amy T. Austin** *Plenary Lecture, supported by the Environmental Protection Agency of Ireland*	**Diminishing the climate footprint with exotic pine afforestation in Patagonia, Argentina?**
14:30-14:50	Andrew Felton *Selected talk*	Spatiotemporal dynamics of net primary productivity sensitivity to precipitation
14:50-15:10	Francielli Bao *Selected talk*	Do neighbours matter? Density-dependent effects of intra and interspecific competition on seed germination in experimental microcosms
15:10-15:40	Tea/coffee break + Posters	

Session 2. Chair: Rainer Melzer

15:40-16:30	**Edwige Moyroud** *Plenary lecture*	**Bullseye! Understanding the mechanisms of petal patterning**

16:30-16:50	Chrysoula Pantazopoulou *Selected talk*	Every time we touch, I feel the static – molecular basis of touch induced leaf movement
16:50-17:10	Alvaro Montiel Jorda *Selected talk*	Characterisation of BML1, a novel protein linking brassinoteroid signalling with microtubules
17:10-17:30	Silvia Artuso *Selected talk*	Tempo and mode of flower shape evolution in a small-sized radiation of Madagascan Bulbophyllum orchids (clade 'C') using 3D geometric morphometrics
17:30-18:00	Break + Posters	
18:00-19:00	Flash Talks (12 speakers)	
19:00	Meet the Mentors (Pizza and posters)	

Tuesday, 23 July 2019

Session 3. Chair: Carl Ng

08:15-09:00	Coffee and pastries	
08:55-09:00	Announcements	
09:00-09:50	**Alistair Hetherington** *Plenary lecture*	**How stomata respond to environmental signals**
09:50-10:10	Sarah Carroll *Selected talk*	Guard cell wall structure and function
10:10-10:30	Cecilia Cheval *Selected talk*	A plasmodestmata-specific signalling cascade mediates chitin-triggered PD closure
10:30-11:00	Tea/coffee break + Posters	

Session 4. Chair: Angela Feechan

11:00-12:00	**Workshop: How to get published**	
12:00-12:50	**Stella Cesari** *Plenary lecture*	**Mode of action and engineering of a rice NLR immune receptor for broader recognition specificity of *Magnaporthe oryzae* effectors**
12:50-14:00	Lunch	

Session 5. Chair: Alexandre Perochon

14:00-14:50	**Catherine Feuillet** *Plenary lecture*	**A next generation wheat genome sequence for next generation breeding by next generation scientists**
14:50-15:10	Susanne Schilling *Selected talk*	MADS about wheat: genome-wide analysis of MIKC-type MADS-domain transcription factors in *Triticum aestivum*
15:10-15:30	Harriet Benbow *Selected talk*	The Serpin gene family contribute to disease resistance, yield, and grain quality in bread wheat
15:30	Visit to The Powerscourt Distillery and drinks reception	

Wednesday, 24 July 2019

Session 6. Chair: Sónia Negrão

08:15-09:00	Coffee and pastries	
08:55-09:00	Announcements	
09:00-09:50	**Jennifer McElwain** *Plenary lecture*	**Plant fossils, global change and evolution**

09:50-10:10	Jonathan Henn *Selected talk*	Winter climate, fire, and species characteristics affect prairie plant response to climate change
10:10-10:30	Juan Baca Cabrera *Selected talk*	Diurnal oscillation of leaf elongation rate is sensitive to atmospheric CO_2 and VPD
10:30-11:00	Tea/Coffee break + Posters	

Session 7. Chair: Paul McCabe

11:00-11:50	**Keith Lindsey** *Plenary lecture*	**Cellular pattern and growth in the Arabidopsis root**
11:50-12:50	**Workshop: Publishing Ethics**	
12:50-14:00	Lunch	

Session 8. Chair: Aisling Reilly

14:00-14:50	**Anna-Liisa Laine** *Plenary lecture*	**What keeps pathogens in check in the wild?**
14:50-15:10	*Xi Zhang, University* *Selected talk*	Evolution of plant defense resistance in natural enemies of an arthropod herbivore
15:10-15:30	Homero Garate Escamilla *Selected talk*	Range-wide variation in local adaptation and phenotypic plasticity of fitness-related traits in *Fagus sylvatica* and their implications under climate change
15:30-16:00	Tea/Coffee break + Posters	
16:00-16:20	Lisa Fürtauer *Selected talk*	Quantitation of subcellular plant metabolism

16:20-16:40	Alvaro Fernandez-Fernandez *Selected talk*	Getting to know plant metacapases: cues above, substrate identification and downstream signalling
16:40-17:10	Tea/Coffee break + Posters	
17:10-18:30	**Workshop: Careers**	
19:00	BBQ @ UCD Rosemount	

Thursday, 25 July 2019

Session 9. Chair: Joanna Kacprzyk

08:15-09:00	Coffee and pastries	
08:55-09:00	Announcements	
09:00-09:50	**Alexander J. Hetherington** *Plenary lecture*	**Getting to the root of roots: from fossils to transcription factors**
09:50-10:10	Marian Schubert *Selected talk*	Evolution of tolerance to temperate climates in the grass subfamily Pooideae
10:10-10:30	Victoria DeLeo *Selected talk*	200 years of *Arabidopsis thaliana* phenotypic variation
10:30-11:00	Tea/Coffee break + Posters	

Session 10. Chair: David Hunt

11:00-11:50	**Maarja Öpik** *Plenary lecture*	**Diversity of arbuscular mycorrhizal fungi: from local to global and back**
11:50-12:10	Tom Thirkell *Selected talk*	Changes in atmospheric CO_2 induce cultivar-specific carbon-for-nutrient exchange responses in wheat-arbuscular mycorrhizal symbioses

12:10-12:30	Aidee Guzman *Selected talk*	The relationship between aboveground diversity and arbuscular mycorrhizal fungi on agroecosystems
12:30-13:00	**Final comments**	

Speaker abstracts

22nd July

Diminishing the climate footprint with exotic pine afforestation in Patagonia, Argentina?

Plenary lecture

AMY T. AUSTIN **13:40-14:30**

austin@ifeva.edu.ar

IFEVA-CONICET, Facultad de Agronomía, Universidad de Buenos Aires, Buenos Aires, Argentina

Land-use change, including the conversion of natural ecosystems to produce tangible products such as food or wood, is one of the most prominent manifestations of global change in terrestrial ecosystems. In particular, the planting of tree species in previously non-forested ecosystems to achieve rapid growth and potential carbon sequestration has become an attractive option proposed for long-term carbon (C) storage and climate change mitigation. Nevertheless, there are many open questions regarding how ecosystem processes are modified as a function of this land-use change. We took advantage of an unplanned natural experiment involving a 40-year-old forestation project, where a single conifer species (*Pinus ponderosa*), was planted regionally in Patagonia, Argentina, replacing natural ecosystems ranging from semi-arid steppe to broadleaf forest along a broad range of precipitation (250-2200 mm mean annual precipitation [MAP]). We evaluated the effects of this change in dominant vegetation on ecosystem C and nitrogen cycling, net primary production (NPP) and decomposition, and modification of the soil fauna. Taken together, our results suggest that a change in the species composition of the dominant vegetation was sufficient to modify the major drivers of C and N cycling in these sites independently of climate constraints. Alterations of ecosystem processes due to afforestation were sufficient to significantly diminish, if not erase, the climate footprint along this broad precipitation gradient.

Spatiotemporal dynamics of net primary productivity sensitivity to precipitation

Selected talk

ANDREW FELTON
Utah State University, USA

14:30-14:50

Regional models of net primary productivity and precipitation predict declining sensitivity (S) of net primary productivity (NPP) to variation in PPT as mean annual precipitation (MAP) increases. However, previous assessments largely reflect differences in S that arise due to turnover of vegetation structure across ecosystems. It is uncertain whether previous S-MAP spatial patterns hold across a single vegetation type, and how 'with-region' S-MAP patterns may themselves vary across different vegetation structures. Utilizing the western United States grassland/rangeland region as a test bed and novel remote sensing data products, we analyzed within-region S-MAP patterns across a diversity of vegetation types; ranging from annual grasslands to shrub-dominated cold deserts. We find substantial variation in the S-MAP relationship when analyzing S-MAP patterns within vegetation types, which ranged from highly negative to near neutral, but became positive in the hot deserts ecoregion; opposite of what regional models predict. This suggests that previous S-MAP relationships developed across vegetation structures may not necessarily hold for predicting spatial patterns of NPP sensitivity within vegetation structures, especially in the driest ecoregions.

Do neighbors matter? Density-dependent effects of intra and interspecific competition on seed germination in experimental microcosms

Selected talk

14:50-15:10

F. BAO, D. R. ROSSATTO, A. POTT, T. ELSEY-QUIRK, M. A. ASSIS, R. ARRUDA, D. M. RAMOS

Instituto de Biociências, Universidade Estadual Paulista (UNESP), 13506-900, Rio Claro, SP, Brazil; Instituto de Biociências, Universidade Federal de Mato Grosso do Sul (UFMS), 79070-900, Campo Grande, MS, Brazil

The success of species colonization is unpredictable and varies by orders of magnitude from one place to another. Establishment of species in general related to density-dependent is still unclear when related to intra- or interspecific competition. What is the effect of the presence of neighbors on the germination of seeds? Experiments on the effects of seed density on the timing and magnitude during germination were conducted, with ten annual species, in the Pantanal, Brazil. We evaluated germination in three levels of intraspecific seed density: scarce seed, moderate and high density. And three levels in interspecific competition: low, medium and high density. The germination percentage was independent of type and intensity of competition. The density influenced both competition treatments. The shortest germination time occurred for *Borreria eryngioides*, *Diodia kuntzei* and *Richardia grandiflora* when intraspecific competition was high. Germination time was shorter with high density interspecific competition with *Euploca filiformis* and *Rotala ramosior*. In intraspecific competition, the germination is uniform independent of density. In interspecific competition they assume their characteristics of competition and exhibit different strategies of colonization. These findings illustrate that even species that have similar characteristics of colonization (rapid colonization) can change their time if they perceive danger from competition.

Bullseye! Understanding the mechanisms of petal patterning

Plenary lecture

EDWIGE MOYROUD **15:40-16:30**

edwige.moyroud@slcu.cam.ac.uk

The Sainsbury Laboratory, University of Cambridge, Bateman Street, Cambridge, CB2 1LR, UK; Department of Genetics, University of Cambridge, Downing Street, Cambridge, CB2 3EH, UK

Patterning mechanisms generate functional organs from undifferentiated cells in both plants and animals. Evolution acts on these mechanisms to generate morphological diversity. The patterns on the petals of flowering plants are striking examples of evolutionary diversification by natural selection and they play a crucial role in pollinator attraction. These patterns are often highly elaborated and combine differences in pigmentation, cell shape and ornamentation of the cuticle to generate neighbouring tissues with very distinct appearances. However, the mechanisms that permit the set-up of such patterns across flowering plants are not well understood. Our group investigates the mechanisms that regulate pattern formation and diversification in petals, using Venice mallow, a small hibiscus species with a striking bullseye pattern, as a model system. We combine genetic and phylogenomic approaches, with imaging and modelling to dissect those processes in Venice mallow and its close relatives.
Our results should help us understand how plants can set-up boundaries within their petal epidermis to produce cues for pollinators and how evolution tinkers with these processes to generate the diversity of patterns observed in nature.

"Every time we touch, I feel the static" – **molecular basis of touch-induced leaf** ***movement***

Selected talk

16:30-16:50

C. K. PANTAZOPOULOU[1], C. NGUYEN[2], E. E. FARMER[2], K. KAJALA[1] & R. PIERIK[1]

[1]Plant Ecophysiology, Department of Biology, Utrecht University, The Netherlands; [2]Department of Plant Molecular Biology, University of Lausanne, Switzerland

Plants growing at high densities compete for resources, including light. In dense stands, the light environment is already changing before true shading occurs, due to selective wavelength reflection by neighboring plants. Previous studies have shown that the earliest neighbour responses in dense stands of Arabidopsis are induced through touching of leaves and lead to upward leaf movement. This results in a vertical canopy structure that increases the horizontal reflection of FR light by the elevated leaves towards neighboring plants, subsequently inducing shade avoidance. It is currently unknown how touch is sensed and how the signal is transferred from the leaf tip to the base of the petiole where local cell expansion regulates hyponastic leaf moment. Our data show that touch-induced hyponasty is regulated differently from light-mediated hyponasty. Trichomes are the very first cells to interact between the two leaf tips and appear to have a key role in touch-induced hyponasty. Our transcriptome data suggest that detection of a mechanical stimulus regulates Ca^{2+}-dependent processes to regulate touch-induced hyponasty.

Characterization of BML1, a novel protein linking brassinosteroid signaling with microtubules

Selected talk

16:50-17:10

MONTIEL-JORDA ALVARO, VERT GRÉGORY
Laboratoire de Recherche en Sciences Végétales, UMR5546 CNRS/Université 3, 24 chemin de Borde Rouge, 31326 Castanet-Tolosan, France

Plant hormones regulate many developmental and adaptation processes. Among them, brassinosteroids are of special importance for plant growth, as evidenced by the extreme dwarfism of mutants lacking this pathway. To find new regulators of the brassinosteroid signaling pathway, we searched for new BRI1-interacting proteins. By performing a yeast-two-hybrid screen using BRI1 kinase as bait, we identified three novel proteins of unknown function named BMLs. Phylogenetic analyses revealed that orthologs of *BMLs* are present in lower plants such as liverworts and moss but absent in algae. We have cloned the three Arabidopsis BMLs (*AtBML1-3*) and chose to focus on BML1. We confirmed the interaction with BRI1 in yeast by Split Ubiquitin assays and *in planta* by BiFC and Co-IP. The BML1 protein was localized to microtubules, including cortical microtubules in close proximity to the plasma membrane. Interestingly, single *bml* knockouts display altered brassinosteroid responses, pointing to their functional importance. Overall, we have uncovered a new unexpected link between brassinosteroid signaling and cortical microtubules in the regulation of plant growth.

Tempo and mode of flower shape evolution in a small-sized radiation of Madagascan *Bulbophyllum* orchids (clade '*C*') using 3D geometric morphometrics

Selected talk

17:10-17:30

S. ARTUSO, A. GAMISCH, Y. STAEDLER, J. SCHOENENBERGER, H.P. COMES
Department of Biosciences, University of Salzburg, Hellbrunnerstrasse 34, 5020 Salzburg, Austria; Department of Botany and Biodiversity Research, University of Vienna, Rennweg 14, 1030 Vienna, Austria

How the tempo and mode of lineage diversification is linked to the evolution of phenotypic trait disparity remains poorly understood. Nonetheless, it is widely assumed that morphological change in reproductive traits predominantly occurs at speciation rather than during earlier periods of a radiation. To test this hypothesis, we generated 3D-flower-scans of 27 Madagascan *Bulbophyllum* orchid species (clade '*C*'), quantified flower shape variation using geometric morphometrics, and explored the shape evolution of this Late Miocene (*c.* 7.3 Ma) radiation using phylogenetic comparative methods. Regularized phylogenetic principal component analyses (rpPCA) reveal that the clade's main evolutionary shape trajectory relates to the degree of sepal opening and the position of the labellum. Moreover, this variation seems consistent with an evolutionary trait model assuming an optimal value (*Ornstein–Uhlenbeck*) rather than a purely stochastic model (*Brownian Motion*) or a model of decelerated evolution through time (*Early-Burst*). However, both rpPCA and ancestral shape reconstructions also indicate accelerated rates of shape evolution associated with two relatively recent (*c*. ≤ 1. Ma) speciation events. Overall, the present results suggest that flower shape evolution in these tropical orchids evolves under stabilizing selection, or even in an accelerating manner, as predicted for traits implicated in reproductive isolation and speciation.

23rd July

How stomata respond to environmental signals

Plenary lecture

ALISTAIR HETHERINGTON **09:00-09:50**

School of Life Sciences, University of Bristol, Life Sciences Building, 24 Tyndall Avenue, Bristol, BS8 1TQ, UK

Stomata are pores found on the surfaces of leaves. They open and close in response to alterations in environmental conditions. Changes in stomatal aperture regulate the uptake of CO_2 and the loss of water vapour which, in turn, impact on photosynthesis, the supply of mineral nutrients to the aerial parts of the plant, leaf cooling and the ability to withstand limited periods of reduced water availability. The aperture of the stomatal pore is controlled by the two guard cells surrounding the pore. When the guard cells are fully turgid the pore gapes open, whereas loss of turgor leads to stomatal closure. A complex signal transduction network is present in guard cells and is responsible for perceiving and responding to changes in environmental parameters such as light, CO_2, atmospheric relative humidity and internal signals such as the drought hormone ABA. The major topics to be discussed in this lecture will be how stomata integrate multiple signals and how they respond to UV-A radiation.

Guard Cell Wall Structure and Function

Selected talk

09:50-10:10

S. CARROLL[1], J.E. GRAY[2], A.J. FLEMING[1]
[1] The Department of Animal and Plant Sciences, University of Sheffield, Sheffield, S10 2TN, UK; [2] The Department of Molecular Biology and Biotechnology, University of Sheffield, Sheffield, S10 2TN, UK

Stomata are pores on the leaf surface which are surrounded by a pair of guard cells. The guard cells have specialised cell wall structures allowing them to expand and contract to control stomatal opening, thus regulating gas exchange for photosynthesis and transpiration. However, excessive transpiration results in detrimental water loss. We are interested in the structure of the wall that allows guard cells to repeatedly swell and deflate. This knowledge may also inform novel approaches to manipulating stomatal movement with the aim of conserving water loss in crops. We have performed our analyses in *Arabidopsis thaliana,* a eudicot, and in *Brachypodium distachyon,* a model monocot. Immunohistochemistry suggests that pectin is highly influential in guard cell walls in both these plants, yet the form and abundance differs. Enzymatic removal of the pectin side-chain arabinan impairs stomatal function in both *Arabidopsis* and *Brachypodium*, and genetically modified *Arabidopsis* arabinan synthesis mutants show altered stomatal movement. These transgenic lines are presently being assessed for whole-plant physiological traits including stomatal conductance and water-use efficiency. We are using a homology-based approach to identify and manipulate arabinan biosynthesis genes in *Brachypodium* to investigate the link of molecular wall structure to physiological function in these evolutionary distinct stomata.

A plasmodesmata-specific signalling cascade mediates chitin-triggered PD closure

Selected talk

10:10-10:30

C. CHEVAL, M. JOHNSON,S. SAMWALD, X. K. LIU,C. FAULKNER
John Innes Centre, Norwich Research Park, NR4 7UH, Norwich, UK.

Plants constantly face pathogen threads and have evolved different strategies to prevent fungal and bacterial infection. Among these strategies is the regulation of cell-to-cell communication via plasmodesmata closure, a newly identified immune response. Recent studies have demonstrated that the perception of the fungal elicitor chitin by a plasmodesmata-located LysM receptor protein LYM2 triggers plasmodesmata closure in *Arabidopsis* and contributes to resistance to *Botrytis cinerea* [1]. Using a combination of genetics, cell biology and biochemistry, we have dissected the hierarchy of molecular events that ultimately triggers the closure of plasmodesmata. Significantly, we found that LYM2 mediates plasmodesmata closure independently of other known plasma membrane-localised chitin-activated signalling pathways. We have identified two LysM receptor kinases LYK4 and LYK5 that are required for chitin-triggered plasmodesmata closure. LYM2, LYK4 and LYK5 can change their locations and interactions and form dynamic signalling hubs which is essential for their plasmodesmata-related signalling function. Downstream, LYM2 signalling involves site-specific phosphorylation of the NADPH oxidase RBOHD by calcium-dependent protein kinases and localised callose deposition that induces plasmodesmata closure. Our work demonstrates that an immune signal can trigger specific signalling cascades at plasmodesmata. The data generated from this project will enable us to understand how cells communicate during pathogen attack.

[1] Faulkner C, Petutschnig E, Benitez-Alfonso Y, Beck M, Robatzek S, Lipka V, Maule AJ (2013) LYM2-dependent chitin perception limits molecular flux via plasmodesmata. *Proceedings of the National Academy of Sciences of the United States of America* **110:** 9166-9170

Mode of action and engineering of a rice NLR immune receptor for broader recognition specificity of *Magnaporthe oryzae* effectors

Plenary lecture

STELLA CESARI
Tansley Medal winner

stella.cesari@inra.fr

INRA, UMR BGP, Campus International de Baillarguet, TA A-54/K, 34398, Montpellier, France

12:00-12:50

Plant nucleotide-binding domain and leucine-rich repeat containing proteins (NLRs) are intracellular immune receptors that specifically recognize pathogen effectors and induce immune responses. Based on our work on the detection of the *Magnaporthe oryzae* effectors AVR-Pia and AVR1-CO39 by the rice NLR RGA5, we developed the hypothesis that some NLRs recognize effectors through non-canonical integrated domains (IDs) that act as effector target decoys. We unravelled the molecular details of AVR-Pia and AVR1-CO39 binding to the integrated heavy metal-associated (HMA) domain of RGA5 through detailed structure-function analyses. Our results revealed that direct effector/HMA domain interactions are required for the specific recognition of both effectors by RGA5. However, the binding affinity between these effectors and the HMA domain is moderate but may be reinforced by additional associations of effectors on other sites in RGA5. This combination of effector-binding to IDs and to additional sites in the NLR seems to confer robust effector recognition. Here, I will also discuss how our knowledge of the molecular details of effector recognition by NLRs carrying IDs can be exploited to extend the recognition spectrum of plant immune receptors. Briefly, I have introduced point mutations in the HMA domain of RGA5 to investigate the possibility of modifying the recognition specificity of this receptor and enable the detection of AVR-PikD, another *M. oryzae* effector.

A next generation wheat genome sequence for next generation breeding by next generation scientists

Plenary lecture

CATHERINE FEUILLET **14:00-14:50**

Inari Agriculture, One Kendall Square, Building 600/700, Suite 7-501, Cambridge, MA 02139, USA

In 2005, a few wheat scientists supported by Kansas wheat growers launched the International Wheat Genome Sequencing Consortium with the vision of producing a high-quality reference genome sequence to provide breeders and scientist with a powerful new resource to accelerate wheat improvement. 14 years and more than 2000 IWGSC members later, the 16Gb hexaploid bread wheat genome sequence is available to all with a quality that is only matched by model crops such as rice. Since day one, the unwillingness to compromise on the completeness and quality of the sequence of bread wheat, the species which is grown on 95% of the wheat surfaces to generate a resource that can be used by breeders and scientists rather than just being published in a high impact factor journal, has driven technical and strategic choices of the consortium. It is paying off now, as gene discovery in wheat is at the same level of efficiency of model species thereby enabling the deployment of Next Generation Breeding, such as breeding by editing, in the very near future. Combined, with the advent of computational predictive modelling and elite germplasm plant transformation, the capacity to generate such high quality sequences even in large and complex genomes such as wheat will enable a complete paradigm shift in breeding with the opportunity to design varieties that perform optimally in their local environment with a minimum use of resources at a significantly reduced cost and time. It will enable the Next Generation Breeders who will bring together skills in agronomy, data science, and genomics to move breeding from an art into a science to cope with the challenges of agricultural production of the 21st century. Details of the strategy and achievements of the IWGSC as well as a perspective of Next Gen Breeding will be presented.

MADS about wheat: Genome-wide analysis of MIKC-type MADS-domain transcription factors in *Triticum aestivum*

Selected talk

14:50-15:10

S. SCHILLING, A. KENNEDY, S. PAN, L. S. JERMIIN, R. MELZER
School of Biology and Environmental Science, University College Dublin, Ireland

Wheat (*Triticum aestivum*) is one of the most important crops worldwide. Given a growing global population coupled with increasingly challenging cultivation conditions, facilitating wheat breeding by fine-tuning important traits is of great importance. Since they are involved in virtually all aspects of plant development and stress responses, MADS-box genes are prime candidates for improving wheat traits. Here, we present a detailed overview of number, phylogeny, and expression of 201 wheat MIKC-type MADS-box genes. Homoeolog retention is significantly above the average genome-wide retention rate for wheat genes, indicating that many MIKC-type homoeologs are functionally important and not redundant. Gene expression is generally in agreement with the expected subfamily-specific expression pattern, indicating broad conservation of function of MIKC-type genes during wheat evolution. We find the extensive expansion of some MIKC-type subfamilies to be correlated with their chromosomal location. A number of MIKC-type genes show novel expression patterns, pointing towards neofunctionalisation. Conserved, duplicated and neofunctionalised MIKC-type genes may have played an important role in the adaptation of wheat to a diversity of conditions, hence contributing to its importance as a global staple food. Therefore, we suggest that MIKC-type MADS-box genes are especially well suited for targeted breeding approaches and phenotypic fine-tuning.

The Serpin gene family contribute to disease resistance, yield, and grain quality in bread wheat.

Selected talk

15:10-15:30

HARRIET R. BENBOW[1], LARS S. JERMIIN[1,2] and FIONA M. DOOHAN[1]
[1]School of Biology and Environmental Science, University College Dublin, UCD Belfield, Dublin 4, Ireland; [2]Research School of Biology, Australian National University, Canberra, ACT 2600, Australia.

The serine protease inhibitor (serpin) gene family is the largest family of proteases inhibitors. We have identified and annotated the entire 'Serpinome' of wheat and constructed a high quality and robust phylogenetic analysis of the gene family. This has highlighted the Serpin-Z group of genes, known storage proteins that have been well characterised in barley but their expression in the developing grain of wheat has not been profiled. Using publicly available RNAseq data, expression profiles of the wheat serpins was explored across a variety of tissues from the developing grain, spikelet and spike. We show that certain clades of the serpin family are highly expressed during grain development, and that there appears to be some functional redundancy in this gene family. Serpins also play an important role in response to fungal pathogens. Using RNAseq data of wheat tissues infected with biotic stresses, we conducted differential expression analysis of 10 independent RNAseq datasets and identified Serpins with a significant disease response. The majority of these disease responsive serpins were upregulated by *Fusarium graminearum*, a devastating fungal pathogen that attacks the spike and developing grain of wheat.

24th July

Plant fossils, global change and evolution

Plenary lecture

JENNIFER McELWAIN

Botany Department, School of Natural Sciences, Trinity College Dublin, College Green, Dublin 2, Ireland

09:00-09:50

The fossil record of land plants extends over 450 million years of Earth history. This rich fossil archive documents plant evolution from the earliest simple and diminutive terrestrial ecosystems to complex and towering angiosperm dominated systems in more recent times. Fossil plant archives also provide a window on past atmospheric and climatic evolution and the nature of plant-atmosphere interactions on timescales of tens of thousands to millions of years. I will present on recent advances in our understanding on atmospheric evolution over the past 450 million years focusing in particular on trends in atmospheric CO_2 and O_2 as revealed from new and improved fossil plant-based proxies. The talk will explore current understanding on the deep-time history of plant ecophysiology, in particular photosynthesis and gas exchange based on new analyses of fossil plant chemistry, anatomy and inferred function, coupled with experimental data from simulated paleoatmosphere trials.

Winter climate, fire, and species characteristics affect prairie plant responses to climate change

Selected talk

09:50-10:10

JONATHAN J. HENN, LAURA M. LADWIG, ELLEN I. DAMSCHEN
Department of Integrative Biology, University of Wisconsin-Madison, 430 Lincoln Drive, 451 Birge Hall, Madison, WI 53706 USA

The winter season is warming faster than any other season in temperate regions, resulting in an overall loss of snow. In temperate grasslands, the loss of snow can substantially change the temperatures which organisms experience during winter as soils are exposed to colder conditions. Thus, plant tolerance of cold could be important in mediating responses to change. Fire is another important factor affecting ecosystem function in prairies. Here we combine long-term (60 year) observations of prairie and savanna plant community change across a gradient of winter climate change with a field experiment manipulating snow depth and fire and measurements of plant cold tolerance to better understand the consequences of winter climate change on prairie plant communities. Over the past 60 years, prescribed fire prevented local plant extinction and warming winter temperatures were related to increased extinction probabilities for spring-blooming species, but not summer-blooming species. Reductions in snow depth caused colder and more variable soil temperatures but did not significantly affect plant growth. Plant tolerance of cold varied by species and tissue type. Overall, these results suggest that winter climate has important effects on prairie plant health but that prairie plants are relatively resilient to changes in winter climate.

Diurnal oscillation of leaf elongation rate is sensitive to atmospheric CO_2 and VPD

Selected talk

10:10-10:30

J. BACA CABRERA, R. T. HIRL, J. ZHU, R. SCHÄUFELE, H. SCHNYDER
Grassland Group, Technical University of Munich, Alte Akademie 12, 85354 Freising, Germany

Leaf growth is considered an integrating plant behavior, given the vital role of leaves for light interception, photosynthesis, water status regulation and, ultimately, canopy development. Critically, leaf growth may show rapid or adaptive responses to changing environmental conditions. In a controlled chamber experiment we investigated the reaction of the leaf elongation rate (LER) of *Lolium perenne*, a temperate grassland species, to different atmospheric CO_2 (200, 400 or 800 ppm) and VPD (low or high) levels in the growth environment. Remarkably, we observed no effect of CO_2 or VPD on daily LER, leaf length, leaf width and epidermal cell length and number. However, diurnal oscillations of LER were influenced strongly by CO_2 and VPD, with oscillations decreasing with CO_2 and increasing with VPD. Based on measurements of stomatal conductance, transpiration and leaf water potential we conclude that the variation in the diurnal oscillation of LER was associated with leaf water status, the ability of the plants to regulate their growth under contrasting atmospheric conditions and the optimization of carbon gain versus water loss.

Cellular pattern and growth in the Arabidopsis root

Plenary lecture

KEITH LINDSEY

keith.lindsey@durham.ac.uk **11:00-11:50**

Department of Biosciences, Durham University, Durham DH1 3LE, UK

Plant development has in common with animals the establishment of patterning of cells, to provide organization to tissues and organs. Plant development contrasts with animal development by exhibiting a high degree of flexibility (plasticity), whereby final form is unpredictable. This plasticity represents a mechanism for responding to environmental change, such as variations in availability of water, nutrients, light, or attack by herbivores. While animals respond to such environmental challenges through behavioural change, plants use plasticity in development to adapt and survive, and this is mediated to a significant extent through the activity of meristems and control of cell elongation. In this talk I will present some of our work on the genetic and signalling mechanisms, and in particular the crosstalk between ethylene, auxin and cytokinin, that control meristem activity and cell elongation and regulate growth during root development in Arabidopsis. I will discuss new regulators of pattern and meristem activity in the Arabidopsis root, and the use of mathematical modelling to predict signalling-gene interactions leading to pattern.

What keeps pathogens in check in the wild?

Plenary lecture

ANNA-LIISA LAINE

anna-liisa.laine@ieu.uzh.ch **14:00-14:50**

Department of Evolutionary Biology and Environmental Studies, University of Zürich, Switzerland

Pathogens are prevalent across all ecosystems, yet we rarely witness devastating epidemics caused by pathogens in natural plant populations when they occur in sympatry. Understanding the mechanisms which keep pathogens in check in the wild may yield much needed insights and tools into the battle against disease in managed systems. In my talk, I will evaluate the relevance of classic evolutionary theory – namely life history trade-offs, multiple infection and coevolutionary theory – with respect to realized population dynamics of both hosts plants and their pathogens.

Evolution of plant defense resistance in natural enemies of an arthropod herbivore

Selected talk

14:05-15:10

X. ZHANG, D. VAN CONG, C.C.M. ARCE, L. HU, B. HIBBARD, M. HERVÉ, C.A.M. ROBERT, R.A.R. MACHADO, MATTHIAS ERB
Institute of Plant Sciences, University of Bern, Altenbergrain 21, 3013 Bern, Switzerland

Specialist herbivores can sequester plant defensive secondary metabolites for protection against natural enemies. Yet, whether sequestered chemicals can drive natural enemy adaptations is unclear. Here, we tested adaptations of 30 worldwide populations of entomopathogenic nematode (EPN) to benzoxazinoid (BX) sequestration by the western corn rootworms (WCR). We found a strong positive correlation between EPN co-occurrence history with WCR and their resistance to BXs. Rearing a susceptible EPN population in WCR larvae for five generations was sufficient to trigger significant physiological and behavioral adaptations to BXs. A model including the different adaptive traits of EPN demonstrates that EPN behavior is the main driver of BX resistance. Our study illustrates biochemical arm race among tri-trophic interactions and provides targets to increase the biocontrol efficiency of herbivore natural enemies.

Range-wide variation in local adaptation and phenotypic plasticity of fitness-related traits in *Fagus sylvatica* and their implications under climate change

Selected talk

15:10-15:30

H. GÁRATE-ESCAMILLA, A. HAMPE, N. VIZCAÍNO-PALOMAR, T. M. ROBSON & M. BENITO GARZÓN

BIOGECO, INRA-Université de Bordeaux, Bat-B2 Allée Geoffroy-St-Hilaire, 33615 Pessac, France

To more realistically predict future species distribution ranges, it is critical to account for local adaptation and phenotypic plasticity in populations' responses to climate. Phenotypic variation is trait-dependent with differential consequences for fitness. Our aim is to quantify local adaptation and phenotypic plasticity of vertical and radial growth, leaf flushing and survival across *Fagus sylvatica* (beech) range under current and future climate scenarios. We used fitness related traits of *beech* recorded in BeechCOSTe52 (>150,000 trees) to perform linear mixed-effect models that related trait variation and co-variation to local adaptation and phenotypic plasticity, and we made spatial predictions under current and RCP 8.5 climates. We found: the contribution of plasticity to intra-specific trait variation is higher than that of local adaptation; different traits constrain beech's distribution in different parts of its range; considering trait co-variation improved single-trait predictions. Our main conclusion is that population responses to climate across large geographical gradients are dependent on trait x environment interactions.

Quantitation of subcellular plant metabolism

Selected talk

16:00-16:20

L. FÜRTAUER[1], L. KÜSTNER[2], A.G. HEYER[2], W. WECKWERTH[3,4], T. NÄGELE[1]
[1] Ludwig-Maximilians-Universität München, Department Biology I, Plant Evolutionary Cell Biology, Planegg-Martinsried, German; [2]University of Stuttgart, Department of Plant Biotechnology, Institute of Biomaterials and Biomolecular Systems, Stuttgart, Germany; [3]University of Vienna, Department of Ecogenomics and Systems Biology, Vienna, Austria; [4]University of Vienna, Vienna Metabolomics Center, Vienna, Austria

Compartmentation is a key feature of eukaryotic cells though biological research is frequently limited by methods allowing for a subcellular resolution of the metabolome. We developed a new protocol based on the non-aqueous fractionation technique enabling the assignment of metabolites to their subcellular compartments. The method is applicable to resolve subcellular metabolite dynamics in a precise and statistically robust manner. Yet, only a very limited number of studies have addressed combined subcellular proteomics and metabolomics which strongly limits biochemical and physiological interpretation of large-scale *omics*-data. Methodologically, we combined non-aqueous fractionation, enzyme kinetics, proteomics and metabolomics approaches to reveal subcellular diurnal dynamics of plant metabolism in a 4-compartment model comprising chloroplasts, cytosol, vacuole and mitochondria. Wild type plants and hexokinase-1 (HXK1)-deficient *gin2-1* mutants revealed a strong impact of HXK1 activity on metabolome dynamics in multiple compartments. Subcellular levels of pyruvate, succinate and fumarate concentrations were significantly affected in *gin2-1*. Lowered mitochondrial glycine and serine concentrations together with reduced abundance of photorespiratory proteins indicated an effect of the *gin2-1* mutation on photorespiratory capacity. Our findings highlight the necessity to resolve plant metabolism to a subcellular level in order to provide a causal relationship between metabolites, proteins and metabolic pathway regulation.

Getting to know plant Metacaspases: cues above, substrates identification and downstream signalling

Selected talk

16:20-16:40

A. D. FERNÁNDEZ-FERNÁNDEZ, S. STAEL, K. GEVAERT, F. VAN BREUSEGEM
VIB-Ghent University, Ghent, Belgium

Plant metacaspases are cysteine proteases named after mammalian caspases due to their structural homology (Tsiatsianis, 2013). We have shown that METACASPASE4 remains as an inactive zymogen in normal conditions in the cell environment and its autolysis is dependent on calcium which can occur seconds after physical wounding (Hander, Fernandez Fernandez et al 2019). This autolysis leads to auto-activation and subsequent PROPEP1 processing minutes after damage. The C-terminal 23 amino acids is a known Damage-associated molecular pattern called PEP1 which after proteolysis is capable to remobilize from the vacuolar tonoplast to their specific receptors PEPR1 and PEPR2 on the membrane and alert surrounding cells of the wounded stress. Those downstream signals involve MAPK phosphorylation, transcription factor recruitment and expression of stress related genes which finalize with reduction in plant growth specially abolishing root elongation. We are using genetically tools and sensors to visualize cellular calcium and other signalling metabolites. We are interested to comprehend the cascades downstream of metacaspase activation in relation to wounding and transcriptional responses. Additionally we are expanding the current knowledge of additional unpublished METACASPASE4 substrates obtained combining N-terminal proteomics, validation of the substrates *in vitro* and specific protease sensors. Altogether, we expect to advance in the understanding of metacaspases and their interrelation with wounding.

Getting to the root of roots: from fossils to transcription factors

Plenary lecture

ALEXANDER J. HETHERINGTON
Department of Plant Sciences, University of Oxford, South Parks Road, Oxford, OX1 3RB, UK

09:00-09:50

The evolution of plant roots allowed plants to enormously increase their rooting function of anchorage combined with nutrient uptake and transport – charting the way for the diversification of vascular plants into new and previously unoccupied areas of the terrestrial surface. Despite the evolution of roots being central to the success of land plants their origin is still largely unknown. In the talk I will describe how recent advances made with both fossil plants and from comparative genomic and transcriptomic studies are shedding new light on the origin of roots. Fossil rooting systems are helping to unravel the gradual character evolution of roots. These fossils demonstrate that the origins of roots is far more complex than may be thought based solely on studies of living species. Alongside fossil studies, evidence from comparative genomics and transcriptomics is shedding light on the assembly of the root genetic toolkit. A toolkit that has its origin well before plants colonised the land. The study of rooting systems highlights the need to combine disparate lines of evidence to understand the evolution of complex plant traits.

Evolution of tolerance to temperate climates in the grass subfamily Pooideae

Selected talk

09:50-10:10

M. SCHUBERT[1,2], T. MARCUSSEN[3], A. S. MESEGUER[4], L. GRØNVOLD[5], S. R. SANDVE[5], T. R. HVIDSTEN[1], S. FJELLHEIM[5]

[1]Norwegian University of Life Sciences, Ås, Norway. [2]Stockholm University, Stockholm, Sweden. [3]University of Oslo, Oslo, Norway. [4]Université de Montpellier, Montepellier, France. [5]Norwegian University of Life Science, Ås, Norway

Frost is among the most dramatic stresses plants can experience and complex physiological adaptations are needed to endure long periods of sub-zero temperatures. Due to the need to evolve these complex adaptations, transitioning from tropical to temperate climates is regarded difficult. Using phylogenetic comparative methods and comparative transcriptomics, we studied the transition from tropical to temperate climates in the grass subfamily Pooideae, which dominates cool temperate, continental and Arctic regions. We found that Pooideae likely originated in a temperate niche and experienced cold temperatures and frost long before expansion of temperate biomes after the Eocene-Oligocene transition. Climate cooling was a probable driving force of Pooideae diversification. This suggests that the Pooideae ancestor had adaptations to temperate climate and that certain responses to low temperature stress are shared in extant Pooideae grasses. We found evidence for this hypothesis in our transcriptome analyses. Complex mechanisms such as cold acclimation and underlying genetic networks most likely evolved independently in daughter lineages. Our results reflect that selection pressure resulting from global cooling must have acted on already diverged lineages. Nevertheless, conservation of cold induced expression of certain genes indicates that the Pooideae ancestor may have possessed some molecular machinery to mitigate cold stress.

200 years of *A. thaliana* phenotypic variation

Selected talk

10:10-10:30

V. L. DELEO, D. N. L. MENGE, E. M. HANKS, T. E. JUENGER, J. R. LASKY
Department of Biology, The Pennsylvania State University, 405d Life Sciences Building, University Park, PA 16802 USA

Intraspecific trait variation, caused by genetic and plastic responses to environment, is captured in immense natural history collections across continents and through centuries. We measured phenotypes on a 216-year time series of *Arabidopsis thaliana* accessions across the native range. We applied spatially varying coefficient models to quantify region-specific trends in trait coordination and responses to climate gradients. All traits exhibited significant change across space and/or through time. $\delta^{15}N$ decreased over time across much of the range and leaf C:N increased, consistent with predictions based on changes in land use and atmosphere. Plants were collected later in the growing season in more recent years in many regions, possibly because populations shifted toward more spring germination. When climate variables were considered, collection dates were earlier in warmer years, while summer rainfall had opposing associations with collection date depending on region. There was modest correlation among traits, indicating that there is not a single life history/physiology axis. Regional heterogeneity in trends indicates complex responses to spatiotemporal gradients potentially due to geographic genetic variation and climate interactions with other aspects of environment. Our study demonstrates how natural history collections can be used to broadly characterize trait responses, revealing variation in response to environmental change.

Diversity of arbuscular mycorrhizal fungi: from local to global and back

Plenary lecture

MAARJA OPIK

11:00-11:50

Department of Botany, University of Tartu, 40 Lai Street, Tartu, 51005, Estonia

Soil biodiversity, its micro- and macrobiota, is increasingly recognized as provider of important functions of nature to the humans. These services of ecosystems range from maintaining clean air and water to supporting aboveground biodiversity and landscape diversity and to sustainable food and fodder production. Arbuscular mycorrhizal (AM) fungi can be considered as keystone members of soil microbiota because of their functions to plant nutrition, environmental and biotic stress mitigation and soil health maintenance. Therefore, there is increasing focus on the application of AM fungi in agriculture, restoration and conservation, including both direct inoculation with fungi as well as fostering growth and functioning of existing, indigenous species. I will summarise current knowledge on the biodiversity of AM fungi in natural and anthropogenic systems from local to global scales. Further, I will explore how anthropogenic activities including current agricultural practices influence AM fungal performance, and how this in turn relates to crop yield. Next, I present results on application of AM fungi to restore important nature value habitats, as well as revegetate abandoned mines. I will conclude by looking into how the knowledge of indigenous and natural AM fungal diversity and performance contributes to the wellbeing of both nature and humans

Changes in atmospheric CO_2 induce cultivar-specific carbon-for-nutrient exchange responses in wheat-arbuscular mycorrhizal fungal symbioses.

Selected talk

11:50-12:10

TOM THIRKELL, DARIA PASTOK, KATIE FIELD
Centre for Plant Sciences, School of Biology, Faculty of Biological Sciences, University of Leeds, Leeds, U.K. LS2 9JT, UK

Arbuscular mycorrhizal fungi (AMF) form symbioses with most crops, potentially improving their nutrient assimilation and growth. However, biotic (e.g. genotype) and abiotic (e.g. CO_2) factors sometimes cause AMF to act as parasites instead of mutualists. The effects of cultivar and atmospheric CO_2 concentrations (a[CO_2]) on wheat-AMF carbon-for-nutrient exchange remain critical knowledge gaps in the exploitation of AMF in agriculture. We used stable and radio-isotope tracers (^{15}N, ^{33}P, ^{14}C) to quantify AMF-mediated nutrient uptake and fungal acquisition of plant carbon in 3 wheat cultivars. We grew plants at current ambient (440ppm) and future projected atmospheric CO_2 concentrations (800ppm). We found significant ^{15}N transfer from fungus to plant in all cultivars, and cultivar-specific differences in total N content. There was a trend for reduced N uptake under elevated a[CO_2]. Similarly, ^{33}P uptake via AMF was affected by cultivar and a[CO_2]. Total P uptake varied significantly among wheat cultivars and was greater at future than current a[CO_2]. We found limited evidence of cultivar or a[CO_2] effects on plant-fixed carbon transfer to the fungus. Our results suggest that AMF will continue to provide a route of nutrient uptake to crops in the future, but consideration must be paid to cultivar-specific AMF receptivity and function.

The relationship between aboveground diversity and AMF on agroecosystems

Selected talk

12:10-12:30

A. GUZMAN, L. HUTCHINS, M. MONTES, A. KAKOURIDIS, M. FIRESTONE, T. BOWLES, C. KREMEN

Department of Environmental Science, Policy, and Management, University of California, Berkeley, 130 Mulford Hall, Berkeley, CA 94720 USA

Arbuscular mycorrhizal fungi (AMF) have the potential to benefit agroecosystems most notably through their role in nutrient cycling and soil structure. Yet, little is known about how AMF community composition varies within agricultural landscapes and, more so, through a range of farm management practices. AMF associate with more than 70% of vascular plants, including major crops. Still, while AMF not plant host-specific, mycorrhizal associations are also not random. In natural systems, greater plant diversity is often proposed to explain the patterns of increased soil microbial diversity. Thus, in agroecosystems, a relationship between managed aboveground diversity (e.g. crop diversity) and belowground AMF diversity is expected. In this study, we examine how AMF varies between high plant diversity (i.e. polycultures; >20 crop types) and low plant diversity (i.e. monocultures; 1 crop type) across 30 farms. We used microscopy and next generation sequencing on the fungal DNA barcode to characterize the AMF community. Our recent analyses demonstrate that AMF community composition correlates with greater crop diversity. Together, this research shows how diversifying farm management practices at the field-scale could foster potential beneficial soil ecosystem functions via crop plant symbiosis with AMF on agroecosystems and for farmers.

Workshops

Tuesday 23rd July

11:00–12:00 **How to get published**

The members of the panel will provide tips on how to get your work published and there will be time for questions – please come prepared!

Wednesday 24th July

11:50–12:50 **Publishing ethics**

In this 'Publishing Ethics' workshop, we will tackle some of the key questions that our community faces. The session promises to be interactive with opportunities to ask questions, to hear and draw lessons from stimulating stories, and to contribute to discussions.

17:10–18:30 **Careers**

In this workshop, we will explore careers outside academia. This will involve discussion and a Q&A with individuals with research backgrounds. The panel will discuss how their PhD or post-doctoral work has helped them develop their careers outside of academia.

Poster abstracts

P = poster abstract *** = flash talk**

P.1	Abid, Muhammad
P.2	Ahmed, Md Bulbul
P.3	Alabdallah, Osama M A
P.4	Alcantara, Andre Melao
P.5	Al Tamimi, Nadia
P.6	Andrade, Luis
P.7	Askani, Jana Christin
P.8	Bajhaiya, Amit
P.9	Bangash, Sajid Ali Khan
P.10*	Baz, Lina
P.11*	Brelsford, Craig
P.12*	Campos Dominguez, Lucia
P.13	Chakravarty, Dhiman
P.14	Chaudhary, Saurabh
P.15	Cosme, Marco
P.16	Cruz Mantoani, Mauricio
P.17	Doan, Van Cong
P.18	Doni, Febri
P.19	Dowling, Caroline
P.20	Dreyer, Bernd
P.21	Duminil, Pauline
P.22	Esperon, Manuel
P.23	Fattorini, Roisin
P.24	Forte, Flavia Pilar
P.25	Furtado, Bliss Ursula
P.26	Gamir Felip, Jordi
P.27	Giannakopoulos, George
P.28	Gómez Gallego, Tamara
P.29	Govi, Bianca
P.30*	Hahn, Florian
P.31	Hetherington, Katie
P.32	Ho Plágaro, Tania
P.33*	Hõrak, Hanna

P.34	Howard, Mia
P.35	Ikoyi, Israel
P.36	Ilesanmi, Ruth
P.37	James, Godwin
P.38	Kehoe, Stephen
P.39	Koppolu, Ravi
P.40*	Kouidri, Allan
P.41	Kozak, Katarzyna
P.42	Kroh, Gretchen
P.43	Kumarathunge, Dushan
P.44	Leyva Perez, Maria de la O
P.45	Liu, Bin
P.46	Looney, Caitlin
P.47	Lynn, Joshua
P.48	Malla, Keshav Bahadur
P.49	Margalha, Leonor
P.50	Martinez Berdeja, Alejandra
P.51	Meade, Fergus
P.52*	Mendez, Marcela Soledad
P.53	Middleton, Rox
P.54	Miricescu, Alexandra
P.55	Mooney, Brian
P.56	Moreno Garcia, Beatriz
P.57	Nemec Venza, Zoe
P.58	Nobrega, Rodolfo
P.59	Ozgur Uzilday, Rengin
P.60	Panter, Paige
P.61	Paolacci, Simona
P.62	Pidon, Hélène
P.63*	Pitaloka, Mutiara Kusumaningtyas
P.64	Pucker, Boas
P.65*	Quick, Susan
P.66	Rajewicz, Paulina
P.67	Rathore, Dheeraj
P.68	Rees, Helen
P.69	Ruiz Hernández, Victoria
P.70	Salazar, Bong
P.71	Sands, Betty
P.72	Sleczka, Katarzyna

P.73	Spencer, Victoria
P.74	Stricker, Eva
P.75	Tan, Huang
P.76	Thaowetsuwan, Pakkapol
P.77*	Thomas, Ben
P.78	Ticchiarelli, Fabrizio
P.79	Tumas, Hayley
P.80	Weiszmann, Jakob
P.81	Wilkinson, Samuel
P.82	Willing, Claire
P.83	Xie, Long
P.84*	Xu, Weimu
P.85	Zhang, Xi

Poster abstracts

Poster abstracts are ordered alphabetically by presenting author (underlined).

P.1 Screening of kiwifruit germplasm resources against salt stress and exploring tolerance mechanism

M. ABID, Y.J. ZHANG, M.Y. LIU, Y.P. ZHONG, J.B. FANG
Key Laboratory for Fruit Tree Growth, Development and Quality Control, Zhengzhou Fruit Research Institute, Chinese Academy of Agricultural Sciences, Zhengzhou 450009, P.R. China

Salt stress negatively affects many physiological processes in plants. Some of these effects may involve the oxidative damages within cell and cell organelles. In the past, NAC transcription factors have been reported in various salt stress related studies. We will investigate the protective role of NAC family genes in seven different *Actinidia* genotypes exposed to two salinization concentrations 0.3% and 0.6% by weight of pots. Plants will be grown into 18 X18 cm pots. Several quantitative and qualitative salt stress indices on plants will be measured. Leaf, shoot and root samples will be collected to analyze the changes of growth and morphology, antioxidant enzymes activities, osmotic regulator contents and ion contents after salt stress. PCA (Principal Component Analysis) will be used to comprehensively assess the salt tolerance. Moreover, high throughput transcriptomic sequencing will be used to mine the resistance-associated genes in tolerant genotype, such as NAC transcription factor and other functional genes (BADH and CMO). Gene functionality will be assessed in transgenic *Arabidopsis thaliana* plants. The overall results will help us to find out the tolerant *Actinidia* genotype against salt stress, to analyze the physiological mechanism of salt tolerance genotype and to obtain some resistance-associated genes. The overall experiment will help other researchers to further explore this study.

P.2 Unravelling mycorrhizal association can enhance cannabis production organically

MD BULBUL AHMED[1] AND MOHAMED HIJRI[1, 2]
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[2]*Department of Biological Sciences, Université de Montréal, QC, Canada*

Cannabis is among the oldest domesticated plants around 6000 years and it has been cultivated as a source of fibre, oil, and protein-rich food, psychoactive products and for medicinal purposes. Until now very few scientific investigations have been performed for microbiome analysis of *Cannabis* sp. The first report of *Cannabis* microbiome highlighted cultivar-specificity and soil determinants of microbiome but not much research has been carried out for microbiome interactions. For long time, the use of mycorrhizal fungi as natural fertilizers for crop productivity and ecosystem sustainability has been proven as a significant influence in organic farming. A limited number of studies using bioinoculant or PGPR have been done on hemp growing, which is only in the experimental level, not much in the field trial. Although hemp and cannabis are of same genus, but in terms of chemical properties and cropping practises there is a difference. As the demand of cannabis will increase and over the time cannabis growers will also face various problems for instance, nutrient availability, pathogens attack and so on. Currently, our research group at IRBV of University of Montreal located in the Montreal Botanical Garden is working on the understanding of microbial community structure of cannabis and trying to decode the molecular relationship between mycorrhizal fungi and cannabis plant, and we are also developing a minimal bioinoculant enriched with AMF for organic farming of cannabis. Until now, there is not molecular based studies has been done for the use of mycorrhizal fungi in cannabis production, however, the knowledge of molecular insights into mycorrhizal fungi-cannabis relationship will eventually boost up our knowledge of the application of mycorrhizal fungi in cannabis growth, as well as it will help our scientific community and growers for boosting up the knowledge of organic farming.

P.2

The Arabidopsis polyamine oxidase/dehydrogenase 5 interferes with cytokinin and auxin signaling pathways to control xylem differentiation

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In plants, the polyamines putrescine, spermidine, spermine (Spm), and thermospermine (Therm-Spm) participate in several physiological processes. In particular, Therm-Spm is involved in the control of xylem differentiation, having an auxin antagonizing effect. Polyamine oxidases (PAOs) are FAD-dependent enzymes involved in polyamine catabolism. In Arabidopsis, five PAOs are present, among which AtPAO5 catalyzes the back-conversion of Spm, Therm-Spm, and *N*1-acetyl-Spm to spermidine. In the present study, it is shown that two loss-of-function *atpao5* mutants and a *35S::AtPAO5* Arabidopsis transgenic line present phenotypical differences from the wild-type plants with regard to stem and root elongation, differences that are accompanied by changes in polyamine levels and the number of xylem vessels. It is additionally shown that cytokinin treatment, which up-regulates *AtPAO5* expression in roots, differentially affects protoxylem differentiation in *35S::AtPAO5*, *atpao5*, and wild-type roots. Together with these findings, Therm- Spm biosynthetic genes, as well as auxin-, xylem-, and cytokinin-related genes (such as *ACL5*, *SAMDC4*, *PIN1*, *PIN6*, *VND6*, *VND7*, *ATHB8*, *PHB*, *CNA*, *PXY*, *XTH3*, *XCP1*, and *AHP6*) are shown to be differentially expressed in the various genotypes. These data suggest that *AtPAO5*, being involved in the control of Therm-Spm homeostasis, participates in the tightly controlled interplay between auxin and cytokinins that is necessary for proper xylem differentiation.

P.4 A high-throughput screening assay for identifying proteins involved in unfolded protein response in plants

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The unfolded protein response (UPR) is a highly conserved process in eukaryotic organisms and plays a crucial role in adaptation and development. While the most ubiquitous components of this pathway have been characterized, a lot of effort is being focused in identifying and characterizing UPR components that play a role in specific conditions such as environmental changes, biotic stresses, or how pathogens can manipulate it to facilitate infection. We developed a high-throughput screen method to identify proteins that interfere with UPR signaling *in planta*. A set of 48 genes from a library of secreted proteins from the maize pathogen *Ustilago maydis* were transiently co-expressed with a reporter construct that upregulates YFP expression in *Nicotiana benthamiana*. After inducing UPR stress, leaf discs were placed in 96 well plates and YFP expression was measured. This allowed us to identify 2 previously undescribed proteins that inhibited UPR signaling, which were then re-tested using a more classical and laborious qPCR method. In summary, we established quick and reliable fluorescence-based method to identify heterologously expressed proteins involved in UPR stress in plants. This system can be used for initial screens of protein libraries that can then be validated and characterized in more detail.

P.5 One-step GWAS analysis identifies loci for rice photosynthetic traits

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Increasing the yield potential of rice is a vital requirement to feed the world's growing population. One way to achieve this is by improving rice photosynthetic efficiency. Yet, very little is known about the relationship between plant architecture and photosynthetic efficiency. Here, we used the *indica* diversity panel, which was established within the 'Phenomics of Rice Adaptation and Yield Potential' (PRAY) project. This panel was cultivated under irrigated field conditions in the Philippines, to investigate leaf anatomy and several photosynthetic parameters. Our study focuses on a new genome-wide association model using the 700k SNP high-density array with the aim to discover new genes associated with traits contributing to higher photosynthetic activity field conditions. This new association model is known as the one-step model which can simultaneously examine all raw data, such as all genotypes, all phenotype records (individual plants) and account for spatial variation and replication in a single step as opposed to conventional approaches that generally use the mean/median values of the phenotypic traits causing probable error inflation for the association analysis. Our results from the one step approach show an increase in statistical power as each individual plant is considered instead of using the means of each accession. This model allows the identification of previously undetected loci affecting photosynthetic parameters such as water use efficiency (WUE), Leaf intercellular CO_2 concentration (Ci) and Leaf chlorophyll content (SPAD). In recent years, this type one-step approach was efficiently implemented for many animal models but to our knowledge this is the first time this model has been applied to plant species and has yielded greater power and precise estimate values. To conclude, this approach has facilitated further exploration of the genetic diversity present in the PRAY *indica* panel, and helps towards the development of higher yielding rice varieties.

P.6 Low temperatures disrupt diurnal transcriptional dynamics in rice

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Rice is the staple food for more than 3.5 billion people and a model plant for genomic studies in cereals. Low temperatures are one of the major environmental stresses affecting rice productivity. Transcriptomic data can greatly improve our knowledge on how rice plants are affected by cold and several studies have identified genes whose expression under low temperatures can be correlated to rice's response to cold. However, these studies lack a comprehensive analyses on how the transcriptome of rice plants under cold behave throughout a period of 24 hours. This can limit our perception about the influence of cold in diurnal gene expression dynamics. Therefore, we performed a time course experiment to analyse the transcriptome of rice subjected to low temperatures over a day. Our results show that rice plants subjected to 10 ºC have a complete disruption of rhythmic transcripts when compared to plants at optimal 28 ºC. This phenomenon is characterized by an extensive dampening in the amplitude of rhythmically expressed genes, even those belonging to the circadian clock, which in most cases appear to become arrhythmic. We are now investigating whether and how the circadian clock related proteins mediate the response of the rice transcriptome to cold

P.7

Getting a grip on provacuoles

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Lytic vacuoles are essential for plant cells by fulfilling diverse functions, which require a massive amount of energy mainly provided by the V-ATPase (vacuolar H+-adenosinetriphosphatase), a proton pump localized at the vacuolar membrane. By examining how the V-ATPase arrives to the vacuole, a novel trafficking route was identified from the Endoplasmic Reticulum (ER) directly to the vacuole via so-called provacuoles. This transport pathway circumvents post-Golgi trafficking. For determining additional cargo proteins of provacuoles, we inducibly express the dominant-negative form of Sar1b, a COPII coat component to block ER-to-Golgi transport. First experiments identified several transmembrane proteins, which do not accumulate in the ER by blocking COPII-mediated export and therefore travel to the vacuole in a Golgi-independent manner. To learn more about the characteristics of provacuoles, we examined putative impacts of the membrane tethering complexes CORVET (class C core vacuole/endosome tethering) and HOPS (Homotypic Fusion and Protein Sorting) on fusion events with the vacuole. As *Arabidopsis* knock out mutants of CORVET and HOPS are embryo lethal, we created inducible artificial microRNAs. Thereby, we found that the HOPS complex facilitates homotypic vacuole fusion and that CORVET and HOPS are essential for proper endomembrane trafficking towards the vacuole by operating different transport routes.

P.8 Role of metacaspases in programmed cell death of the green algae *Chlamydomonas reinhardtii*

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Programmed cell death (PCD) is a planned cell suicide that removes damaged or unwanted cells. PCD occurs throughout the development from embryogenesis to death. Key effectors that control PCD are cysteine proteases called caspases, which are conserved from metazoans to humans. Structurally similar cysteine specific proteases called metacaspases (MCs) are reported in plants and algae. MCs are subdivided into type I and type II. The type I MCs have an N-terminal prodomain, which is absent in type II. Both type I and type II MCs contain a linker that connects the two catalytic caspase-like domains: the p20 and the p10. MCs are known to be implicated in cell-signalling and stress acclimation, however their molecular mechanism on PCD is not fully understood. Here in this study, we have performed the expression analysis of both type I and type II MCs under different abiotic stresses. Significant increase in expressions of CrMC1 was observed under salt and H_2O_2 stress, triggering the cell death. Knockdown line of both type I and Type II MCs were also investigated to confirm their role algal PCD.

P.9 (Sub)cellular glutathione homeostasis and secondary active transport of glutathione across the plasma membrane

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Glutathione (reduced form: GSH; oxidized form: GSSG) is a key player in maintaining cellular thiol-redox homeostasis. In plants, GSH synthesis is restricted to plastids and cytosol but there is requirement for glutathione also in other subcellular compartments. In several genetic screens, different *gsh1* mutants with defective GSH biosynthesis have been identified. However, the effect of these mutations at the subcellular level was still elusive. Monochlorobimane (MCB) labelling and HPLC measurements showed that the total amount of glutathione was affected in *gsh1* mutants. In addition, the relative glutathione redox potential (E_{GSH}) in different subcellular compartments measured with roGFP2, showed that these mutations differentially affect the subcellular glutathione pool. Furthermore, there is good indication pointing at long-distance transport of glutathione between different organs. However, transport of glutathione across the plasma membrane is poorly understood. To investigate the transport, we took advantage of the severely glutathione-deficient Arabidopsis mutant *rml1* expressing cytosolic roGFP2. Changes in the fluorescence ratio of roGFP2 in *rml1* with external supply of GSH in combination with inhibitor studies revealed a highly efficient secondary active uptake of GSH across the plasma membrane. The results have major implications for our understanding of the glutathione homeostasis in plants.

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P.10 3-Hydroxycarlactone, a Novel Product of the Strigolactone Biosynthesis Core Pathway

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Strigolactones (SLs), a novel class of carotenoids-derived plant hormones, mainly regulate plant architecture according to nutrient supplies in their environment. SLs are known as signaling molecules secreted by plant roots and released into the rhizosphere, initiating both parasitic and symbiotic interactions between plants and obligate heterotrophs in the soil. The study of SLs biosynthesis has demonstrated that three key enzymes, D27, CCD7 and CCD8, are involved in the sequential conversion of β-carotene to carlactone (CL), the main precursor of SLs. Like other SLs, CL can stimulate *Striga* seed germination, and can inhibit the shoot branching of rice SLs biosynthesis mutant*, d10*. In this study we identified a new signaling molecule (new carlactone), 3-OH-carlactone (H-CL) and investigated its biological activity. We showed that CCD8 can produce hydroxylated CL from the hydroxylated product of CCD7, 9-*cis*-3-OH-β-apo-10'-carotenal, *in vitro*. We also found H-CL present in *Nicotiana benthamiana* leaves infiltrated with carlactone biosynthesis enzymes. Results of biological activity assays revealed that H-CL not only induced seed germination of *Striga,* but also restored the wild type tillering phenotype of *d10.* Taken together, our study identifies 3-H-CL as a metabolite produced by the SL core pathway, which is likely the precursor of yet unidentified SLs.

P.11 Fear of the frost: predicting risk of late spring frost in *Fagus sylvatica* across Europe under climate change

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Late frosts in spring, once leaf out has occurred, cause ecological and economic damage. Climate change increases uncertainty in predicting risk of frost damage. Previous studies have used spring leaf out records, and freezing temperatures taken from large-scale climate data, to forecast frost risk. Our aims were: 1) to produce a model incorporating phenotypic plasticity of leaf out, to better predict frost risk under climate change, and 2) to assess the accuracy of using large-scale climate data to predict late spring frosts. We used spring leaf out data and frost damage records from the BeechCOSTe52 database, consisting of 166 provenances of *Fagus sylvatica,* across 6 trial sites in a common garden experiment. Large-scale climate data predicted which sites were affected, but not which trees within each site were damaged by frost; suggesting a need to increase our understanding of microclimates. Our model disagreed with studies suggesting that low elevation areas are most at risk, but agreed with others showing frost damage in *F. sylvatica* at high elevation areas in low latitude locations. Simulating future climate change scenarios suggests that the risk of spring frost to *F. sylvatica* will remain at high elevation areas in low latitude locations.

P.12 Studying the role of genome dynamics in the evolution of the fastest-growing genus Begonia

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Begonia is the fastest growing and one of the most species-rich angiosperm genera with c.1900 species currently identified. Recent studies on this genus provide robust phylogenetic background and confirm niche specificity cannot be the only factor driving speciation. Previous studies have also shown that *Begonia* species have very dynamic genomes, with highly variable chromosome and genome sizes. To better understand the role of genome dynamics in the evolution of this genus, Whole Genome Sequencing (WGS) strategies have been used to identify repeat content and variation among Begonia species. In addition, the genome of the only *Begonia* sister species *Hillebrandia sandwicensis* has been included in our study in order to compare these two genera at a genomic level and better understand the specific factors involved in the repeated radiation events described in *Begonia*. Our results suggest that *Begonia* species show more complex, repetitive and dynamic genomes overall than *Hillebrandia*. We have found a wide variation in both content and types of DNA repeats across most *Begonia* species radiations. We have been able to identify different Long-Terminal Repeat (LTR) copia expansions throughout the phylogeny. Future analyses and transposon-dating results will allow us associate these expansions to speciation patterns across the genus.

P.13 Adaptation to salinity stress in cyanobacteria: molecular insights into the physiological role of a salt-inducible Mn-catalase

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Due to their unique evolutionary association with plants, cyanobacteria are excellent model systems to understand the fundamental/applied aspects of stress biology. In the N_2-fixing cyanobacterium *Anabeana*, pre-treatment with NaCl resulted in unusual tolerance to H_2O_2. Genetic as well as biochemical analysis showed the increased accumulation of Mn-catalase, KatB, to be responsible for this protective effect. Furthermore, the *katB* mutant showed increased susceptibility to oxidative damage in response to salinity stress. The KatB protein was highly thermostable, robust Mn-catalase that was active even at alkaline pH. The crystal structure showed KatB to adopt a hexameric assembly and its active site was distinctly different from that of other Mn-catalases, resembling the ferritin protein. Interestingly, the N-terminal region of KatB was involved in oligomerization and in particular, the second residue (a non-active site residue) was essential for inter-subunit interactions and for the formation ofthe proper hydrophobic pocket that held the active site together. Overall, this study has demonstrated that (a) the oxidative stress response of an organism can be regulated by simple compound such as NaCl and (b) the 2nd N-terminal residue is crucial for the appropriate assembly, activity, and consequently the physiological response of KatB to H_2O_2 stress.

P.14

Epigenetics of alternative splicing in plants

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Alternative Splicing (AS) being largely co-transcriptional is strongly modulated by the epigenetic landscapes in higher eukaryotes. Recent evidence from animals and yeast suggest epigenetic marks such as DNA-methylation and nucleosome occupancy have significant impact on AS. However, the role of epigenetic landscapes on AS remains to be established in plants. Towards this goal and to elucidate the impact of DNA-methylation and nucleosome occupancy on AS, we generated RNA-Seq, bisulfite-Seq, and MNase-Seq data from Columbia (Col) and a selected Epigenetically Recombinant Inbred line of *Arabidopsis thaliana*, under normal (22°C) and cold (4°C) conditions. RNA-Seq analysis revealed high number of differentially expressed genes (DEGs) and differentially alternatively spliced (DAS) genes among both lines and treatments. Moreover, differential methylation and nucleosome occupancy levels were observed around splice-junctions predicted in RNA-Seq analysis. The differences in methylation, nucleosome occupancy and AS observed among Col-0 and epiRIL-368 lines were more pronounced under cold conditions. Our data supports the notion that genes expression and splicing is mediated by differences in epigenetic landscapes in plants. We envisage that using lines with identical DNA sequence and differential epigenetic landscapes (Col vs epiRIL) would help to understand how changes in the chromatin architecture alone could affect/modulate splicing outcomes in plants.

P.15 Interactions between arbuscular mycorrhizal fungi and non-host plants

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Arbuscular mycorrhizal (AM) fungi are unable to form symbiotic associations with approximately 29% of all vascular plants and often antagonize their growth. The underlying mechanism of this antagonism is still poorly understood. We deployed the AM fungus *Rhizophagus irregularis* against the nonhost plant Arabidopsis to analyze transcriptional changes and monitor fungal colonization and plant growth depression in Arabidopsis lines altered in phytohormone or microbe-associated molecular pathways. The early nonhost plant detection of AM fungi was not completely impaired. However, fungal nutrient transporters were inactive in colonized Arabidopsis roots. Although we observed defense-related GO term enrichment in colonized Arabidopsis, associated with mycorrhizal-induced resistance, neither the compromised defense nor growth phytohormone pathways affected the fungal antagonism against Arabidopsis. Moreover, Arabidopsis mutants susceptible to various pathogens were not susceptible to *R. irregularis*. Conversely, a coumarin exudation pathway stimulated asymbiotic colonization in Arabidopsis when *R. irregularis* was nursed by neighboring host plants. Altogether, *R. irregularis* did not acted like a typical pathogen nor Arabidopsis autoregulated growth-defense tradeoffs, which suggests that fungal antagonism against nonhosts may entangle a more specialized mechanism yet uncharted. Furthermore, we uncovered that plant coumarin exudation involved in responses to mineral nutrient depletion can excite AM fungi during the prepenetration dialogue.

P.16 Surviving the cold: impacts of an extreme weather event on the growth and phenology of *Gunnera tinctoria*

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Whilst it is often assumed that invasive plant species may benefit more from climate change than native species, there is little information on how they might respond to extreme weather events (EWE), the occurrence and magnitude of which are projected to increase with global warming. Here, we show that the benefits of an increase of two weeks in the length of the growing season were offset by an EWE (Storm Emma), characterised by low temperature extremes and snowfall. This resulted in a disproportionally greater impact on mature populations of the invasive species *Gunnera tinctoria* compared to native species. The EWE reduced the total leaf area of the invader by 11-fold, significantly delayed canopy development and reduced shoot biomass by > 85%, leading to a four-fold increase in the number of regenerating species in invaded areas. This also resulted in the loss of most of the inflorescences (83%) from mature plants, although it had a much smaller effect on seedlings of *G. tinctoria*. Thus, EWE may counteract early growth benefits, but the longer-term impacts will depend on the extent to which this compromises seedling growth and development as well as the ability of mature plants to recover vegetative and reproductive growth.

P.17

Belowground priming in maize

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Exposure to herbivore-induced plant volatiles (HIPVs) from neighbouring plants triggers increased resistance to future attack by herbivores, a process called priming. While this process is relatively well understood aboveground, it has rarely been investigated belowground. We exposed roots from maize (*Zea mays*) plants to root-volatiles from neighbouring plants that were attacked by larvae of the banded cucumber beetle (*Diabrotica balteata*) and investigated whether this resulted in defense priming. Exposure to an infested plant did not reduce the performance and survival of the root herbivore. We did not find any effects of volatile exposure on constitutive and herbivore-induced levels of soluble sugars, starch, total soluble protein, free amino acids, benzoxazinoid secondary metabolites, the root metabolome and defense-related gene transcripts. However, exposure to herbivory-induced volatiles altered the kinetics of root volatile production in response to root herbivory but not to root mechanical damage. Further experiments are currently in progress to evaluate if this phenomenon can be attributed to herbivore-specific priming or to differential larval feeding behaviour. We conclude that exposure to belowground HIPVs has a very different impact on plant-herbivore interactions below- and aboveground and discuss possible causes and ecological consequences.

P.18

New insights into symbiotic interaction between *Trichoderma asperellum* SL2 and rice plants: unraveling the ability of SL2 for modulating rice plants' growth, physiological processes and gene expression pattern

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The fungal species *Trichoderma* has exhibited evident potentials for useful applications in agriculture, in particular as a plant growth promotor. In this study, we aim to report our intensive study on the ability of a local *Trichoderma asperellum* SL2 isolate to enhance rice plants' growth, gene expression pattern, physiological processes, and yield. Results showed that the inoculation of SL2 into rice seedlings led to significant increases in rice growth (>40%), photosynthetic rate (>51.7%), stomatal conductance (>61%), stomatal density (>70%), tiller number (>29%) and filled grains (>44%). Numerous genes related to photosynthesis, RNA activity, stomatal activity, and root development were found to be up-regulated almost ten times in rice plants inoculated with SL2 than in inoculated plants. These up-regulation genes were significantly contributed to better energy metabolism, plant growth and other metabolic pathways in the rice plants. Furthermore, results on the application of SL2 in field condition showed that the grain yield of SL2-inoculated rice plants was found to be 30% more than that from the uninoculated rice plants. In conclusion, *Trichoderma* have the potential to enhance rice plant growth, physiological traits, gene expression, and yield. These abilities are of great agriculture importance for supporting more plentiful and sustainable rice production.

P.19 What does it take to make a plant? Genome analysis of a 30-year-old *Arabidopsis* cell culture

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Plant cell cultures are integral systems for basic research as well as for biotechnological metabolite production. However, long-term cell cultures cannot be regenerated back into their multicellular plant forms. The reasons for this loss of regenerative capacity remain elusive but are probably related to changes in the cell culture genome. Here, we investigate genomic changes in a 30-year-old *Arabidopsis thaliana* cell culture using next generation sequencing and computational methods. We find a high number of single nucleotide and short indel mutations (280,000) throughout the genome. 316 genes are severely impacted by mutations that cause massive alterations in length and sequence of the encoded proteins. We found no over-representation of severely impacted genes in developmental process gene ontologies. However, we identified an under-representation in cellular metabolism gene ontologies for highly impacted genes. This suggests that most mutation accumulation is random in the cell culture genome, while strong purifying selection is present for genes which are integral for basic cellular metabolism. The high number of mutations observed is probably a primary source for the loss of regenerative capacity of the cell culture.

P.20 The moonlighting function of superoxide dismutase depends on a novel class of transcriptional co-activators.

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Superoxide dismutase (SOD) has been regarded for more than 50 years as an important, pivotal antioxidant enzyme. However, recent work in yeast and humans indicate that copper-zinc SOD affects transcription inside the nucleus. Here we show that superoxide dismutase 1 (CSD1) from *Arabidopsis* and rice is a moonlighting protein. Next to its common scavenging function we reveal that CSD1 acts as a transcriptional regulator in the nucleus. Through fluorescent recovery after photobleaching (FRAP) experiments we found that CSD1 translocates to the nucleus upon stress. In addition, we revealed that CSD1 is a DNA-binding protein that recognizes a specific DNA motif. Moreover, we are using DNA affinity purification sequencing (DAP-seq) to uncover the genome-wide binding landscape of CSD1 in Arabidopsis. Interestingly, inside the nucleus CSD1 interacts with a member of the so far poorly characterized HEAVY-METAL-ASSOCIATED ISOPRENYLATED PLANT PROTEIN (HIPP) family. Our data demonstrate that HIPP proteins are a novel class of conserved transcriptional co-activators both to in Arabidopsis and rice. The rapid translocation and transcriptional complex formation with HIPP enables CSD1 to be an important early player in a so far unknown redox-sensing mechanism. Exploring and understanding the moonlighting features of CSD1 will have major impacts on fundamental biology and potentially results in novel breeding strategies for crops.

P.21 Phosphoregulation of the phosphoglycolate phosphatase (PGLP1), a photorespiratory enzyme, in *Arabidopsis thaliana*

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The most abundant enzyme in plant leaves is the ribulose-1,5-bisphosphate carboxylase/oxygenase (RuBisCO) that is a key enzyme of the Calvin cycle, via its carboxylase activity. However, RuBisCO has also an oxygenase activity that produces 2PG and 3PGA. The photorespiratory pathway allows recycling of the 2PG molecules to produce 3PGA, as well as the removal of other toxic metabolites (including 2PG). This pathway has a certain cost since it uses energy and reducing power and leads to the liberation of assimilated carbon and nitrogen as CO_2 and ammonia. Therefore, the photorespiratory cycle has been described as “wasteful” to plant productivity and has become a target to improve plant yield. Recent data indicate that phosphorylation may be a key regulatory component of the photorespiratory cycle. We investigate this on the first photorespiratory enzyme, the phosphoglycolate phosphatase (PGLP1) that dephosphorylates the 2-PG. Its mutation in *Arabidopsis thaliana* leads to a strong developmental phenotype. The measurement of PGLP1 activity *in planta*, and using recombinant proteins, mutated at four assumed phosphosites, allowed us to select two relevant amino-acids that could be phosphorylated. To go further, we complemented the homozygous mutant *pglp1*, to decipher the role of each phosphosite on the enzyme, *in vivo*.

P.22 Assessing the vulnerability of Australia's urban forests to climate extremes

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Urban forests (UFs) are recognised for the multiple benefits they provide to city-dwellers. However, global climate change will affect species' performance and survival in urban ecosystems. We assessed species composition and potential vulnerability of UFs in 22 Australian cities to heat and/or moisture stress. We evaluated species' realized climatic niches across their natural distributions in comparison to the climate in the cities where they are planted. We used three environmental variables (maximum temperature of the warmest month, precipitation of the warmest quarter, and potential evapotranspiration) to group species based on their potential climate vulnerability. Broadly, neither climate similarity nor geographical proximity were good predictors of species composition. Of 1342 tree species assessed, 53% were considered potentially vulnerable to heat and/or moisture stress in at least one city where they are currently planted. Our results highlight the climate vulnerability of current plantings across Australian cities and can be used to direct future species selection that considers climate change. UF planning can incorporate species from cities with similar climates and with low vulnerability to contemporary and future climate conditions. Species with high climate vulnerability, in contrast, may require more intensive management to avoid failure under future, hotter, drier climate conditions.

P.23 The evolution and development of petal spots in a South African daisy species

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The South African daisy species *Gorteria diffusa* is composed of several ecotypes which differ in floral morphology. Between ecotype variation in petal spot complexity and positioning is associated with differential pollinator behavioural responses. Petal spots are aggregations of pigmented cells in distinct petal regions, and this research aims to characterise the genes underlying *G. diffusa* petal spot pigmentation. Three homologous candidate *GdMYB8* genes encoding subgroup 6 MYB transcription factors have been identified. These genes are upregulated within spotted petal tissue and GdMYB8 overexpression in tobacco induces ectopic anthocyanin production. The expression patterns of anthocyanin pathway enzymes *DFR* and *ANS* indicate that they may be downstream targets of GdMYB8 proteins, and biochemical assays are being used to investigate this. Having determined the role of each *GdMYB8* homologue in spot development within the focal ecotype, gene function and expression patterns will be compared between several floral phenotypes associated with different pollinator behaviours. This study system provides a powerful comparative framework to investigate how *GdMYB8* homologues contribute to the intraspecific variation of a functionally relevant trait. Ultimately, this will enhance understanding of molecular evolution and diversification within *G. diffusa*.

P.24 Changes in endophyte and host associated with adaptation of the fungal endophyte *Epichloë festucae* to a new *Lolium perenne* host

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Epichloë festucae var. lolii is a fungal endophyte, which forms a mutualistic symbiosis with perennial ryegrass (*Lolium perenne*) conferring plant protection against biotic and abiotic stresses. The usefulness of new artificial plant-endophyte associations depends on reliable endophyte seed transmission from one plant generation to the next. To date, mechanisms leading to compatible and maintainable artificial associations are largely unknown. We studied a novel ryegrass-endophyte association that, by frequent selection for infection under the same breeding program, achieved a high proportion of infected seed (89-99%). We compared three generations (G2, G6 and G9) of endophyte-colonised and naturally endophyte-free plants, grown under controlled conditions, for plant and fungal characteristics by phenotyping and molecular analyses. Based on microscopy analysis and real-time PCR significant reduction in fungal biomass and higher vascular bundle colonisation occur in G9 compared to G2 and G6. Plant growth performances concerning tiller production did not change through generations. Conversely, plant population structure, from single-nucleotide polymorphisms (SNPs), revealed genetic divergence in naturally endophyte-free hosts. Symbiont-colonised plants, instead, shared similar genetic makeup. Expression of plant genes belonging to hormone pathways and membrane receptors resulted respectively downregulated and upregulated in endophyte-infected plants compared to endophyte-free ones, suggesting their involvement in this compatible interaction.

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P.25 Infect and reflect under salinity stress: role of Salicornia fungal endophytes in non-host perennial ryegrass

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Lolium perenne (perennial ryegrass) is a cool-season grass one of the major turf and forage species in the world. Increasing soil salinization has drastically affected its yield since this species is salt sensitive. However there are some microbes inhabiting inner parts of the plant called “endophytes” known to benefit many crops. But the question arises if they can confer these traits in non-host plant species. Hence, our study tests if the association between fungal endophytes from halophyte *Salicornia europaea* (Sfe) inoculated in non-host ryegrass is beneficial or detrimental under salt stress? Two selected grass varieties: one already Epichloë infected (E+) and other Epichloë free (E-) were chosen for Sfe inoculation. Our results from biochemical and transcriptome analysis support the two Sfe strains *Arthrinium gamsii* and *Stereum gausapatum* have beneficial effects on the growth and mitigate stress in grass. When compared to non-inoculated plants under salt treatments, a significant increase in grass biomass, chlorophyll content, proline, antioxidants and soluble oxidant was noted while lipid peroxidation levels decreased. Additionally, the E+ variety showed variations in the presence of Sfe suggesting this native grass endophyte could alter the action of Sfe. This study provides a promising basis for the use of Sfe endophytes in saline entrenched areas as a solution for future farming systems.

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P.26 Early recognition of the danger molecules oligogalacturonides is essential for mycorrhiza-induced resistance

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Arbuscular mycorrhizal fungi are beneficial microbe that establish mutualistic symbiosis with the roots of most vascular plants, improving plant nutrition and stimulating the plant immune system. The mycorrhiza-induced resistance (MIR) is associated to a faster and more efficient activation of plant defence mechanisms against a different variety of biotic stressors, for this reason. According to these observations, we hypothesized that MIR is based on a primed response to damage, through an optimized response to damage related signals, the so-called Damage Associated Molecular Patterns (DAMPs). Oligogalacturonides (OGs) are among the best characterized plant DAMPs. They are fragments of the plant cell wall that are released during herbivory or pathogen attack and they boost plant defence mechanisms when are sensed by adjacent cells. In the present work, we describe the tomato basal responses to OGs perception. In addition, we demonstrate that OGs triggers primed defence responses in mycorrhizal tomato plants at proteomic, metabolomic and transcriptomic. Finally, we provide evidences showing that MIR is not functional in tomato mutant lines lacking the OGs receptor, WAK1, supporting that OGs recognition is an essential event for a functional MIR.

P.27

Crop specificity of herbicide safeners

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Herbicide safeners, a diverse group of agrochemicals, have been developed to diversify the application of existing herbicides by selectively enhancing tolerance in large-grained cereal crops. While their exact site of action remains to be determined, safeners appear to exert their protective action through the induction of xenobiotic detoxifying enzymes and associated transport proteins collectively termed the xenome (Edwards, 2010). This study's aim was to investigate the molecular mechanism and selectivity of safeners in more detail in order to assist in predicting new applications for these compounds in crop protection. More specifically, a maize safener and its xenome-inducing and herbicide tolerance invoking activity was studied in different crops using a range of techniques (greenhouse trials, chromatography, gene expression studies), with the aim of dissecting the molecular basis of its differential activity in these species. Results suggested that a combination of the compound's behaviour upon uptake and its effect on key detoxifying enzymes correlated closely with its activity. The characterisation of the relationship between herbicide safeners and plant signalling mechanisms, despite appearing to be complex territory as demonstrated by this study and previous published articles (Riechers et al. 2010), can lead to the design of improved safeners, which will play an important role in the future of weed control.

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P.28 RiCRD, a *Rhizophagus irregularis* Cu efflux heavy metal ATPase with a dual key role on Cu detoxification and symbiotic Cu nutrition

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Arbuscular mycorrhizal fungi (AMF) are soil-borne microorganisms that establish mutualistic symbiosis with most plants. The fungus colonizes the root cortex while maintaining an extensive network of extraradical mycelium (ERM) that acquires low-mobility nutrients from the soil, which are then transferred to the plant. The symbiosis also increases plant tolerance to environmental stresses. AMF are able to increase fitness of their host plants under Cu deficient and toxic conditions. We have recently shown that Cu uptake by the ERM of the arbuscular mycorrhizal fungus *Rhizophagus irregularis* is mediated by a Cu transporter of the CTR family. However, it is currently unknown how Cu is transferred to the plant. Here, we report characterization of *RiCRD*, a *R. irregularis* gene encoding a Cu exporting ATPase. Expression of *RiCRD* transcripts in the intraradical fungal structures and, more specifically, in the arbuscules suggests a role for RiCRD in Cu release from the fungus to the symbiotic interface. In the ERM, *RiCRD* expression is highly up-regulated in response to Cu toxicity. Comparison of the expression patterns of different players of metal tolerance in *R. irregularis* under Cu toxic conditions suggests that this fungus mainly uses a metal efflux based-strategy to cope with metal toxicity.

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P.29 Investigating the diversity and role of culturable bacteria in the performance of duckweed ponds as wastewater bioremediation

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Duckweed ponds are a promising biotechnological solution for the treatment of dairy processing wastewater due to these plants' ability to uptake nutrients and store them in harvestable form. Duckweeds (family Lemnaceae) are not, however, the only biological agents in wastewater treatment ponds, with microbial processes also playing a major role in water chemistry regulation and nutrient cycling. The present study aims to investigate (1) the microbial diversity found in a commercial dairy processing wastewater treatment facility and (2) run a laboratory scale experiment to assess the impact of bacterial presence on growth, development and nutrient uptake by *Lemna minor*. Microbial diversity was assessed through culturing combined with 16S ribosomal RNA gene amplification, Restriction Fragment Length Polymorphism (RFLP) profiling and sequencing of unique representatives. For the second objective, once axenic duckweed cultures were established, *Lemna minor* was reinoculated with selected bacteria and growth experiments were run to assess the performance of axenic and re-inoculated plant cultures in terms of growth and water remediation. This research is designed to integrate knowledge about the different processes involved in the bioremediation of wastewaters and help develop next generation integrated systems employing cross-kingdom interactions for optimal remediation and recovery efficiency.

P.30 A Golden Gate based CRISPR toolkit will facilitate genome editing in wheat and other plants

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The CRISPR/Cas system has revolutionised the possibilities to modify the genome of plants. Using a single nuclease and a guide RNA, it is possible to target almost any sequence of interest in the genome of plants and other organisms and induce modifications. Here, we want to present our first results of successful genome editing in wheat, including the generation of mutations in all six homeologoues of a gene. Since the first application of the Cas9 nuclease from *Streptococcus pyogenes* for gene knockouts, the genome editing field has evolved rapidly. New applications have been described frequently, such as base editing, the discovery of new nucleases or multiplex gene editing using tRNA-gRNA modules.
A major bottleneck in the adoption of new CRISPR discoveries to the plant community is the time-consuming cloning of new nucleases and other essential components. We therefore adapted a large variety of nucleases, gRNA backbones, promoters, terminators and other components to the Golden Gate modular cloning system, which allows simultaneous assembly of multiple DNA fragments with high efficiencies. With this new community resource, we expect that plant genome editing will be facilitated greatly and that the latest developments in this field will be adopted rapidly amongst plant scientists.

P.31 Development of genomic prediction strategies for forage yield and reproductive traits in white clover breeding programmes.

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White clover (WC) is a perennial legume crop that has been shown to improve grazing sward productivity by incorporating additional nitrogen to the soil. This contributes to the economic and environmental sustainability of grassland production systems. In this study, two hundred and fifty-eight full-sib white clover families were evaluated over three harvest years after transplanting into a common perennial ryegrass background. Total forage yield of grass and clover was measured annually in a simulated grazing trial with up to eight cuts per year. Our objective is to develop a training population and models for genomic selection that would allow us to accelerate the rate of genetic gain in WC breeding programmes. Traits of interest included total forage yield (in grass-WC swards) and reproductive traits such as seed yield and inflorescence density (ID). Encouragingly, there is sufficient genotypic and phenotypic variation present within this population, and broad-sense heritability (H^2) for forage yield was calculated as 0.76. We have genotyped the F1-families and will use this data together with the phenotypic data to develop and evaluate prediction accuracy for genomic selection.

P.32 A novel MAP protein of *Solanum lycopersicum* involved in arbuscule formation during arbuscular mycorrhizal symbiosis

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Arbuscular mycorrhizal (AM) symbiosis formation requires plant root host cells to undergo major structural and functional modifications in order to house a new highly branched fungal structure for the reciprocal exchange of nutrients called arbuscule. These modifications are associated with changes in the cytoskeleton, and microtubule (MT) and actin filament remodelling has been observed in host cells colonized by AM fungi. In this sense, microtubule-associated proteins (MAPs) play a crucial role in the regulation of microtubule dynamics. In the present study, we found out that the tomato *tsb* gene, belonging to a *Solanaceae* group of genes encoding MAPs for pollen development, is also highly expressed in tomato roots colonized by AM fungi, particularly in cells containing arbuscules. In order to analyse the function of *tsb* in the mycorrhization process, hairy root tomato plants harbouring overexpression and RNAi constructs were generated. We observed alterations in the formation of arbuscules, as well as in the expression of marker genes for arbuscule functionality, and we also analysed possible microtubule rearrangements. Our results suggest that *tsb* encodes a MAP that induces modifications in the microtubule cortical array of arbuscule-containing cells, and has an essential role in AM functionality, and also probably in arbuscule development.

P.33 NPR1 protects young leaves from systemic salicylic acid-induced damage during bacterial infection

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Plant pathogens account for substantial yield losses in agriculture. Understanding the physiology and molecular mechanisms of plant-pathogen interactions will help in breeding for disease-resistant crops. *Arabidopsis thaliana* - *Pseudomonas syringae* pv *tomato* (*Pst*) model system has helped to identify many components of plant immune system, among them the protein NPR1 (NONEXPRESSER OF PR GENES 1), a central positive transcriptional regulator of salicylic acid (SA) responses that mediate plant immune response to *Pst* infection. We used chlorophyll fluorescence imaging of F_v/F_m in whole Arabidopsis rosettes to assess *Pst*-induced damage (manifested in reduction of F_v/F_m) in wild-type and *npr1-1* mutants, which express a dysfunctional version of NPR1. *Pst* infection in mature leaves triggered a systemic reduction of F_v/F_m in uninfected young leaves in the centre of the rosette in *npr1-1*, but not wild-type plants. Similar reduction of F_v/F_m in young leaves occurred, when SA was infiltrated to mature leaves of *npr1-1*. In the SA production deficient *npr1-1sid2-2* double mutant, there was no reduction of F_v/F_m in young leaves in response to *Pst* infection in mature leaves. We propose that NPR1 functions as a negative (auto)regulator of SA-mediated immune responses, thus protecting young leaves from autoimmune damage triggered by excess SA levels.

P.34 Soil microbes have the potential to mediate the escalation of plant herbivore defenses over succession

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Plant defenses typically escalate over the course of ecological succession, paralleling increasing pressure from herbivores. We observed increases in the herbivore resistance of tall goldenrod, *Solidago altissima* (Asteraceae), over the first 15 years of oldfield succession in a large-scale field experiment. While our previous work suggested that this increase in resistance is partially due to rapid microevolutionary shifts in the plant populations, plastic phenotypic shifts in response changing soil conditions also contribute. Our field surveys revealed significant shifts in the composition of bacterial and fungal communities in the *S. altissima* rhizosphere over succession. In order to assess the potential role of these soil microbial shifts in mediating changes in plant herbivore resistance, we performed a soil microbiome transplant experiment with *S. altissima* plants. We found that the specialist herbivore, *Trirhabda virgata* (Chrysomelidae), strongly preferred to eat leaves from *S. altissima* plants grown in soil media inoculated with early succession soil microbiomes (2 years post-agriculture community) over their later succession (15 years) counterparts in a feeding choice experiment, indicating that these successional microbial shifts can increase resistance to aboveground herbivores, likely contributing to the pattern of decreased herbivory on *S. altissima* plants we observed at later successional stages in the field.

P.35 Soil microbiota shifts in response to application of different rates and forms of phosphorus and sulfur fertilizer in grassland columns

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Phosphorus (P) and Sulfur (S) are essential macronutrients for living organisms, and used as fertilizers in agriculture. However, mineable P reserves are finite, excessive application leads to eutrophication and atmospheric deposition of S as pollution has reduced significantly. Reduced use of P and S fertilizers due to financial costs or increased use of manures requires efficient microbial mining of P and S from organic forms to ensure plant health and productivity. Soil column experiments were set up to provide a quantitative and qualitative understanding of how the soil microbiota and grassland plant *Lolium perenne* are affected by different rates and forms of P and S fertilization. The results showed that a positive effect of a single phosphate fertilization on grass growth in a soil can be largely cancelled out by its negative effect on the soil microbiota; grass growth benefits at 10-20 kg/ha sulfate S application outweighed the negative effects on the soil microbiota; and organic fertilizer P and sources favoured the soil microbiota involved in P and S cycling. Insights into cycling of P and S in a soil-microbe-plant environment will better our understanding of environmental risks including plant nutrient deficiency and groundwater pollution.

P.36 Investigating the maternal modifiers of the triploid block hybridisation barrier in *Arabidopsis thaliana*

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Triploid block is a reproductive isolation barrier that typically results in seed abortion in crosses between diploid seed parents and tetraploid pollen donors. This barrier is established in the endosperm and excess paternal genomic contribution results in over-proliferation of the endosperm, whereas, maternal excess results in smaller seeds that may also abort. In *Arabidopsis thaliana*, a triploid block is commonly observed in crosses between diploid accessions (as mothers) and pollen derived from Col-0 tetraploids (the Col-killer effect) however, the degree of F1 lethality has been found to be accession-dependent. Some accessions such as Col-0 and RLD are highly sensitive seed parents to Col-0 tetraploids resulting in a high frequency of inviable seeds. Other accessions, most especially Tsu-0 and Bla-1 are able to bypass this barrier to produce viable and bigger seeds. This study aims to unravel the maternal modifiers of the Col-killer effect, and we have identified two distinct major effect QTLs in Tsu-0 and Bla-1 accessions. A secondary F3 mapping population has narrowed the QTL locus in the Tsu-0 accession, enabling the identification of candidate genes. Work is in currently in progress to validate these candidates and define the genetic programme that underlies maternal rescue of Col-killing.

P.37 *AGAL2*, a possible marker of seed priming memory in Brassicaceae

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With the increasing world population and the threat of global warming hindering the crop production, new technologies must be developed to sustain food production. Efficient seed germination and early seedling establishment are important for commercial agriculture. However, seeds after dry storage often exhibit slow and non-synchronised germination due to poor vigour, especially when stored improperly. One of the methods established to improve seed vigour is seed osmopriming. However, the molecular memory instilled during seed priming is poorly understood. In our study, we have examined the expression pattern of genes between primed and non-primed seeds to understand short term memory establishment. *Brassica rapa* and *Arabidopsis thaliana* seeds were osmoprimed with Polyethylene Glycol (PEG) and sampled at different stages of seed germination to attempt to better understand the transcriptional changes occur during early stages of germination. We analysed the relative expression levels of germination related genes using qPCR. Our preliminary data shows that alpha-galactosidase 2 (*AGAL2*) gene expression levels was increased significantly during the priming process and increased further during post-priming germination stages compared to the non-primed seeds. Thus, *AGAL2* may have a possible role in establishing a molecular memory during seed priming of *B. rapa* and *Arabidopsis*.

P.38 The effect of different nitrogen rates on oat root phenotypes

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Few studies have currently investigated the root phenotypes of plants primarily due to the opacity of soil making it difficult to view roots. This lack of research is particularly evident in oats with fewer studies on it as a whole when compared to a close relative, wheat. Nitrogen can be considered the most important nutrient that roots uptake, yet detailed oat root phenotypes at different nitrogen rates are not known. This study started with field trials in 2018 using the shovelomics and WinRHIZO™ methods to identify root phenotypes. The aim of this investigation is to identify these phenotypes. This field trial has yielded interesting result with the root angle, as these preliminary results indicate that a higher nitrogen rate of application will result in roots being closer to the soil surface. This is being repeated in 2019 and will be followed by pot-based trials to confirm the root phenotypes found using X-ray computed tomography.

P.39 High-resolution spatial and temporal transcript atlas of barley spike meristems offers insights into the developmental dynamics of spike type inflorescences

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The gross morphology of an organism can be traced to its early developmental events, particularly to the changes in genes controlling development. In plants specification, of various organ primordia such as roots, leaves, and flowers is majorly driven by the local transcriptional regulation at the site of their specification. Hence understanding the precise control of organ specification, necessitates the need to dissect the transcriptional regulation at the site of organ initiation. Barley inflorescence called spike has a unique structure called triple spikelet (TS) [(one central (CS) and two lateral spikelets (LS)] along the inflorescence axis. The CSs are always fertile. The fertility of LSs at the TS distinguishes barley spike into, two- (sterile LSs) and six-rowed (LSs fertile). To understand the transcriptional regulation specifying LS development, we have precisely isolated immature LS and CS organs in a two-rowed barley cv. Bowman by laser capture microdissection across seven spike primordia developmental stages and subjected to RNA-seq analysis. We also analyzed inflorescence apical meristem, spike pro-vascular tissue, root apical meristem, and leaf meristems to understand the differences in transcriptional programs of various meristematic tissues. Our analysis of differential genes between CS and LS tissues revealed all known regulators of LS development along with several unknown genes. By mutational studies and phenotypic evaluation of four of the novel LS development genes identified, we validated the observed differential transcriptional regulation. In summary, we have developed a high-resolution tissue-specific transcriptome atlas of developing barley spike, illuminating the precise regulation of spike development.

P.40 Community resource for wheat and rice transformation

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The NIAB Crop Transformation facility has a proven track record in the transformation of a number of major crop species. The BBSRC BBR fund has recently awarded funding to NIAB for The Community Resource for Wheat and Rice Transformation. This project makes our wheat and rice transformation platform freely available to academic plant science researchers in the UK.
We are keen to engage with researchers working with genes from model species to test their hypotheses in wheat and rice. This will contribute to new genes being evaluated more efficiently in crop species essential to food security, and allow UK researchers to amass crucial data which can be used to seek follow-on funding.
Currently, there are an insufficient number of regulatory elements characterised for use in wheat or rice making challenging the transfer of multigene traits or complex pathways into these crops. Our aim is to characterise gene expression profiles using 50 different regulatory elements in stable wheat and rice transgenic lines. It will include both promoter and terminator sequences, fused to a reporter gene (e.g. GUS).

P.41 Unveiling molecular mechanisms of zinc accumulation in "Zn-storage cells" – the role of tobacco genes *NtNRAMP3*, *NtMTP2*, *NtZIP11* and *NtZIP1-like*

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One of the main factors determining plant's tolerance to zinc is the ability to store its high concentrations in leaves without revealing symptoms of toxicity. Recent studies performed on tobacco have proved the existence of "Zn-storage cells" (within leaf blade mesophyll) which accumulate large amount of Zn and thereby protect neighbouring "non-accumulating cells" from zinc excess. In the project, *NtNRAMP3, NtMTP2, NtZIP11* and *NtZIP1-like* were proposed as a candidate genes encoding proteins involved in zinc uptake. Their expression was up- or downregulated in the leaves of tobacco exposed to high Zn, which might indicate their role in a plant's response to Zn-toxicity stress. Accordingly, substrate specificity and subcellular localization of the proteins were determined, and the tissue-specific promoter activity (GUS staining) was compared with Zn accumulation pattern (Zinpyr1 staining). On this basis, the molecular mechanism of Zn transport in tobacco mesophyll cells was proposed. *NtZIP11* is probably involved in Zn uptake into "Zn-storage cells" while *NtNRAMP3* transports Zn only in Zn-excess conditions. *NtZIP1-like* protects "Zn-non accumulating cells" from Zn toxicity and *NtMTP2* is responsible for storing Zn in the vacuole (in Zn overabundance conditions). Funding: Polish Science Centre (NCN), HARMONIA-6 call (2014/14/M/NZ3/00527).

P.42 A regulated leaf Fe deficiency response sacrifices key photosynthetic and Fe-S cluster proteins

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Photosynthesis has an exceptionally high demand for iron (Fe). To avoid long term damage to plant health when Fe is limiting, plants can initiate an Fe deficiency response composed of efficient utilization of Fe, redistribution of Fe, remodeling of metabolism, and increased uptake of soil Fe. Here, we asked: does the leaf efficiently utilize Fe by prioritizing Fe for certain proteins or pathways during deficiency? We characterized molecular and physiological changes in the leaf over one week of Fe deficiency in 4-week-old *Arabidopsis*. Chlorophyll fluorescence indicated that Fe deficiency impacts photosynthetic electron transport downstream of photosystem-II. Changes at the molecular level showed ferredoxin (FD) and the cytochromeb_6f complex proteins to be sacrificed while photosystem-I (PSI) was relatively maintained. Additionally, SufB, a protein in the major scaffold of the Suf Fe-S cluster assembly, was strongly decreased in response to Fe deficiency. Gene expression changes preceded protein changes and showed FD2 and SufB to be downregulated after two days of Fe deficiency. These results suggest the leaf prioritizes chloroplast Fe for PSI during deficiency, and that changes to Fe utilization are transcriptionally regulated.

P.43 Acclimation and adaptation components of the temperature dependence of plant photosynthesis at the global scale

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The temperature response of photosynthesis is one of the key processes determining predicted responses to warming in terrestrial biosphere models (TBMs). The response may vary geographically, due to genetic adaptation to climate, and temporally, due to acclimation to changes in ambient temperature. Our goal was to develop a robust quantitative global model representing acclimation and adaptation of photosynthetic temperature responses. We quantified and modelled key mechanisms responsible for photosynthetic temperature acclimation and adaptation using a global dataset of photosynthetic CO_2 response curves including data from 141 C_3 species from tropical rainforest to Arctic tundra. We separated temperature acclimation and adaptation processes by considering seasonal and common-garden datasets, respectively. The observed global variation in the temperature optimum of photosynthesis was primarily explained by biochemical limitations to photosynthesis, rather than stomatal conductance or respiration. We found acclimation to growth temperature to be a stronger driver of this variation, than adaptation to temperature at climate of origin. We developed a summary model to represent photosynthetic temperature responses and showed that it predicted the observed global variation in optimal temperatures with high accuracy. This novel algorithm should enable improved prediction of the function of global ecosystems in a warming climate.

P.44 PotatoMASH - a low cost, genome-scanning marker system for use in potato breeding

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Potato breeding is a 10-year process that involves combining over 40 characteristics to produce varieties that have improved sustainability, utilisation and consumer characteristics. Genomic and marker assisted selection (GS and MAS) can make breeding faster/more efficient. Strategies for GS to date have tended to employ many thousands of markers; however, the economic burden of deploying such approaches on thousands of plants annually in a breeding programme may restrict the adoption of GS. The purpose of PotatoMASH (Potato Multi-Allele Scanning Haplotags) is to develop a novel, low cost, genome-scanning marker platform for use in simultaneous GS and MAS for multiple traits in potato breeding. Approximately 335 targets placed at 1Mb spacing throughout the euchromatic portion of the genome, and a further 15 SNPs linked to specific traits, will be targeted and assayed using an approach called GT-Seq, which uses combinatorial barcoding to allow multiplexing of thousands of samples in a single NGS run. The sequencing platform will be utilised in conjunction with 2 training populations to develop genomic prediction equations for yield and fry colour of potato. Subsequently, it will be deployed for combined GS and MAS on 1000 plants from the second field generation of a commercial potato breeding programme.

P.45 A HY5-COL3-COL13 regulatory chain for controlling hypocotyl elongation in *Arabidopsis thaliana*

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CONSTANS-LIKE3 (COL3) is a positive transcriptional regulator that mediates *Arabidopsis* hypocotyl elongation, flowering and lateral branch development under red-light conditions. However, the mechanism of COL3 action remains uncharacterized. In this study, we characterized the CONSTANS-LIKE13 (COL13) protein and showed that COL13 interacts with COL3 in yeast and *Arabidopsis* cells and inhibits hypocotyl elongation in red light. With various genetic and biochemical assays data, we proved that transcription factor LONG HYPOCOTYL 5 (HY5) directly bound to the promoter region of COL3, and COL3 directly targeted the promoter of *COL13* to regulate hypocotyl elongation. In addition, gene microarray analysis defined overlapping gene targets of COL3 and COL13 and showed these to be enriched for light-regulated genes and genes involved in cell-wall synthesis and photosynthesis/chloroplast function. The COL3-COL13 complex and the associated HY5-COL3-COL13 chain provide a new insight into the mechanism of regulating hypocotyl elongation in *Arabidopsis.*

P.46 Investigation of autumn defoliation date on shade avoidance response in perennial ryegrass

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Perennial ryegrass (*Lolium perenne* L) is the most commonly used species in pasture-based dairy production systems in temperate climates. Altered autumn management of pastures is one common way to overcome an acknowledged herbage deficit in spring. An investigation of shade avoidance response in swards as a result of altering autumn management using early(25th Sep-9th Nov), normal (10th Oct-24th Nov) and late (25th Oct-9th Dec) defoliation dates (DD) was carried out in spring 2018. Thirty mature vegetative tillers were randomly selected and harvested from within paddocks of different DD (n=18). The presence of stoloniferous growth was found in 37% of plants with lengths varying between 0.1 and 9.2 cm. A raised plant base between 0.1 and 4.9 cm (within the sheath) was found in 49% of plants and the presence of one or more aerial tiller was recorded in 5% of these. Both of these traits are unusual for perennial ryegrass within a well-managed system and are more than likely as a result of autumn defoliation impacting the shading to the base of the plant through increased senescent material and animal poaching as well as natural earthworm casting. The long term impact of both traits on sward persistency and quality must be further investigated.

P.47 Mammalian herbivores restrict the altitudinal range limits of alpine grasses in the Colorado Rockies

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As species ranges shift upward in elevation with climate change, the trailing edges of species ranges may become vulnerable to novel interactions with upwardly encroaching species. Dobzhansky and MacArthur hypothesized that species' low elevation (or latitude) range limits are constrained by antagonistic species interactions because these environments are less abiotically stressful than the high elevation limits of a species' range. We tested this theory for three alpine-restricted grass species by planting them below (novel), at (limit), or in the center (core) of their current elevational range and factorially excluding above- and belowground mammalian herbivores using fences. We monitored plant damage by herbivores as well as plant biomass, and reproduction for three years. The amount of herbivory was greatest below range limits and smallest within the plants' current ranges, suggesting herbivory could be a factor limiting the focal species range. Plants grew largest at novel sites below their current range limits, but only when above- and belowground herbivores were excluded. Reproduction declined at range limits, and the decline intensified with exposure to mammals. Our results suggest that increased herbivore pressure with climate change may cause population declines in alpine plants, potentially triggering local extinction for species that occupy mountain peaks.

P.48 Wheat mitochondrial phosphate transporter and methyltransferase genes contribute resistance to Fusarium Head blight disease and enhance grain yield

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Fusarium head blight (FHB), primarily caused by the fungus *Fusarium graminearum,* is an economically important disease of wheat that results in yield loss and grain contaminated with mycotoxins that are harmful to human and animal health. The mycotoxin deoxynivalenol (DON) is commonly found in *Fusarium*-diseased wheat; it is also a phytotoxic, facilitating fungal colonisation of the wheat spikelets. In this study, we cloned wheat mitochondrial phosphate transporter (*TaMPT*) gene located on chromosome 5A and methyltransferase (*TaSAM*) gene on 2D in two wheat cv. CM82036 and cv. Remus. Gene expression studies were conducted using *TaMPT* and *TaSAM* homoeolog-specific primers, which confirmed that the homoeologs were differentially expressed in response to FHB infection and the toxigenic *Fusarium* virulence factor DON in wheat cultivars CM82036 and Remus. Virus-induced gene silencing (VIGS) of either *TaMPT* or *TaSAM* enhanced the susceptibility of cv. CM82036 to FHB disease, confirming they both contribute to defence against FHB disease. VIGS of *TaMPT* and *TaSAM* also significantly reduced grain number and grain weight compared to control treatment. This indicates *TaSAM* and *TaMPT* genes also contribute to grain development in wheat. Hence, *Fusarium* responsive genes *TaSAM* and *TaMPT* warrant further study to determine their potential to enhance both disease resistance and yield of wheat.

P.49 Nuclear pore function regulates SnRK1 kinase distribution and plant stress tolerance

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The carbon sensing SnRK1 kinase functions as a metabolic regulator which promotes stress tolerance and influences a wide range of developmental processes. In response to declining energy levels, SnRK1 launches an energy saving program both through transcriptional reprograming and via direct regulation of key metabolic enzymes to restore homeostasis. Here, we show the *in vivo* interaction between SnRK1 and a component of the nuclear pore and demonstrate that the nuclear pore function affects SnRK1 kinase subcellular distribution. Accordingly, mutants of the nuclear pore display altered distribution of SnRK1 between the cytosol and the nucleus. Interestingly, nuclear pore mutants show compromised tolerance to dark-induced senescence similar to SnRK1 loss of function plants, but behave like SnRK1 overexpressor plants concerning ABA/salt stress hypersensitivity. These results correlate with the opposite changes on SnRK1 nuclear and cytosolic activities, respectively, observed in these mutants, and suggest that particular environmental stresses may require specific SnRK1 subcellular pools and/or activities for adequate responses. Furthermore, relevant crosses suggest genetic interaction between SnRK1 and nuclear pore components regarding the abovementioned phenotypes.

P.50 *DOG1* functional variation is associated with flowering and germination syndromes that determine life-history variation in *Arabidopsis thaliana*

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The seasonal timing of germination largely determines the environment that an annual plant will experience. Germination timing is controlled by physiological processes including dormancy and after-ripening, which are partially controlled by warm or cold temperatures. Our study characterizes natural variation in germination responses to cold across 500 fully-sequenced accessions of *Arabidopsis thaliana* from a wide climate range, and describes associations between germination and genetic variation, variation in flowering and senescence, and variation in climate of origin to understand the evolution of life-history variation in this species. We found a continuum of germination strategies varying in two axes: overall germination rate and responsiveness-to-cold, that result in different germination niches. Germination axes and their life-history syndromes are associated with *DOG1* gene functional variants. Individuals carrying a non-synonymous polymorphic allele in the self-binding domain of DOG1 flowered later and showed cold-induced dormancy, relative to individuals carrying the alternative allele. Environment influences correlated selection on multiple loci underlying these syndromes, to give rise to spring annuals, winter annuals, and rapid cyclers. *Arabidopsis thaliana*'s germination niche is defined by climate cycling during the Pleistocene that promoted *DOG1* haplotype diversification, and local adaptation to temperature gradients that structure *DOG1* allele turnover on the landscape.

P.51 Using genomic variants to predict fry colour in potato

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When potatoes for processing are stored below 8°C glucose can accumulate leading to dark fry colours. Sprouting occurs above 8°C and reduces quality. This demands the use of sprout suppressants such as chlorpropham, which is set to be phased out due to health concerns. Ideally we would be able to breed potatoes that do not suffer from low temperature sweetening (LTS). Using Teagasc breeding lines we have built up a training population for the development of models which would enable us to use genomic information to predict phenotypes. Data on fry colour for entries was collected at various time points after storage at 8°C and 4°C. Genotypes were collected using Genotyping-By-Sequencing. Together the data enables us to use genomic information to predict phenotypes. We demonstrate, through cross-validation, that high predictive accuracies can be achieved for traits such as resistance to LTS. Furthermore, these models have been validated in an independent collection of entries. Feature selection can be used to reduce the dimensionality of the data without significantly reducing predictive ability, opening up the possibility for the development of low cost, high-throughput assays based on hundreds of loci that are presumably in linkage disequilibrium with genes controlling the trait of interest.

P.52 Photodegradation in terrestrial ecosystems: processes and mechanisms that affect carbon cycling

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Decomposition is a critical step in the formation of soil organic matter in terrestrial ecosystems. The primary focus on the biotic controls of carbon turnover has masked the potential importance of other factors involved in determining the ecosystem carbon balance. Recently, photodegradation has been identified as an important factor in the degradation of senescent plant material (litter) in semi-arid ecosystems, but the interaction with biotic degradation is not well understood. We performed complementary experiments manipulating exposure of leaf litter to solar radiation, evaluating changes in: i) volatile emission of and chemistry of plant litter, ii) biotic decomposition and microbial enzymatic activity; and iii) degradation of plant litter in a time series of solar radiation exposure. We found a linear and positive relationship of litter carbohydrate availability for the microorganisms ($p < 0.05$, $r^2 = 0.80$) and a linear negative relationship for the concentration of lignin ($p < 0.05$, $r^2 = 0.70$) with the accumulation of radiation intercepted over time, both associated with a strong stimulation of biotically-mediated decomposition. The main conclusion is that solar radiation acts as a central control that affects carbon turnover, and highlighting the facilitative effects on biotic decomposition, which appear to be greater than direct effects, affecting a wide range of terrestrial ecosystems.

P.53 Structural colour in fruits for insight into cell wall growth

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Blue pigmentation in plant tissues is rare, due to the unusual biochemistry required for blue anthocyanins and the historic cultivation of truly blue fruits and flowers still inspires contemporary research. In nature, much blue reflectance has been explained by the interference of light with nanostructured surface tissue. The effect, called 'structural colour' because of its independence of chemical pigment, is famously responsible for the blues in peacocks and *Morpho* butterflies. Recently, blue-reflecting flowers, fruits, leaves and algae have been identified with structural colour, the strategies and materials of which inspire future biomimetic materials. However, the results bear on biological questions too: We demonstrate optical modelling to observe stability in the internal sub-wavelength length-scales of developing cell walls in living *Pollia japonica* fruits. This is possible by analysing the spectra which results directly from the nanostructure, thereby overcoming the optical diffraction limit. By comparing this nanostructured material with that of other newly described structurally blue fruits I'll explain how structural colour is a fantastic resource, not only for plants, but for plant scientists too.

P.54 Identification and generation of new barley germplasms with increased tolerance to waterlogging

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The ability to maintain high yields for barley production in Ireland is crucial for the indigenous brewing industry. However, high yields are threatened by global climate change, as Ireland is predicted to have increased flooding events. In consequence, the identification and development of barley varieties that are more tolerant to waterlogging has become an important research focus. The N-end rule protein degradation pathway has been shown to play an important role in the response of plants to flooding in *Arabidopsis thaliana*. Based on sequence similarities, N-end rule components were identified in barley and used as targets to develop new cultivars with increased waterlogging tolerance. Also, barley varieties that are part of AGOUEB population were tested for their waterlogging tolerance. Gene expression together with physiological parameters such as plant height, tiller number, chlorophyll content and root architecture were assessed in order to select varieties that are more tolerant to waterlogging.

P.55 The role of the PROTEOLYSIS1 E3 ligase in the regulation of plant-pathogen interactions

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Crop losses due to the impact of plant disease are a barrier to efforts to meet the food demands of a growing global population. The Ubiquitin Proteasome System (UPS) is involved in plant immunity and a greater understanding of its role could lead to the future development of disease-resistant crops. The UPS is primarily responsible for protein degradation in eukaryotes. E3 ubiquitin ligases confer specificity to the UPS by binding to degradation signals in substrate proteins and catalyzing ubiquitin attachment. The N-end rule pathway is a subset of the UPS that relates the stability of a protein to the identity of its N-terminal amino acid residue. The E3 ligase PROTEOLYSIS1 (PRT1) targets proteins for degradation via the N-end rule pathway and appears to play an important role in the regulation of plant-pathogen interactions. However, the molecular mechanisms underpinning PRT1's role in these processes are not well understood. My project addresses this using complementary approaches in *Arabidopsis thaliana*: (i) treatments with purified pathogen-associated molecular patterns to understand the role of PRT1 in pattern triggered immunity and (ii) inoculations with the model pathogen *Pseudomonas* D3000. Together, these experiments have yielded the first insights in the role of PRT1 during the immune response.

P.56 Combinational multigene engineering for the increase of photosynthetic efficiency

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With a predicted 100-110% increase in global crop demand by 2050, improving photosynthetic CO_2 assimilation is one of the most promising targets for increased yield. Targets for increasing photosynthetic efficiency include transgenic manipulation of the Calvin-Benson-Bassham cycle and the electron transport chain, and introduction of cyanobacterial CO_2/HCO_3^- transporters and photorespiratory bypasses. While these targets alone can lead to considerable increases in productivity, the benefits brought about by individual targets could be boosted by manipulating several target pathways simultaneously.
I have implemented a biolistic co-transformation experiment in the nuclear genome of tobacco, including twelve transgenes in individual expression cassettes involved in the abovementioned target pathways. This technique entails the co-integration of different combinations of genes into a single locus, leading to the generation of a library of combinatorial transformants. Screening this library can help identify the most promising transgene combinations, which would be challenging to achieve if all combinations were to be tested via transgene stacking. I have identified the best performing lines in terms of photosynthetic capacity, biomass accumulation, and physiological parameters. I am currently characterising the selected lines to identify the alterations underpinning the enhanced phenotypes. This will provide crucial information to lead coming efforts to increase crop productivity.

P.57 A CLAVATA pathway regulates cell identity in the filaments of the moss *Physcomitrella patens*

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The first stage of development in the moss *P. patens* involves the formation of photosynthetically active chloronema filaments, a subset of which then become foraging caulonema filaments. This transition involves an identity switch in the apical cell of each filament and is regulated by auxin. CLAVATA is mostly known for its role in flowering plant meristems, but it was recently shown to be a land plant specific regulator of stem cell function, being active in the bryophytes *M. polymorpha* and *P. patens* (Hirakawa et al. 2019, Whitewoods et al. 2018). To study the molecular function and evolution of CLAVATA, we are analysing mutant phenotypes and their interaction with auxin and cytokinin. Here we show that CLAVATA pathway gene expression is upregulated in foraging caulonema. The nature of filament types is altered in some mutants, and these react abnormally to hormonal treatments. We hypothesize that the CLAVATA pathway represses the identity switch between chloronema and caulonema in *P. patens* and current work aims to identify the downstream mechanisms involved.

P.58 Peeking through the stomata and seeing satellites: improving transpiration estimates using a bottom-up approach in a seasonally dry forest

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Plant transpiration and surface evaporation are often quantified together as a lumped sum, namely evapotranspiration (ET). Most of ET partitioning improvements in models have been overlooked in favour of satellite remote-sensing based ET estimates that allow high-spatial resolution and large-scale analyses. ET derived from most of these methods is quantified by extrapolation of an instantaneous measurement provided by non-stationary satellites, which relies on blanket assumptions with regards to atmospheric and plant physiological properties, e.g., stomata control, that are used equally for different ecosystems. Among these assumptions, one main concern is that the ratio of ET to available energy (A) is assumed to be constant. This can underestimate daily ET in dry climates where afternoon advection or increased afternoon wind speed may increase ET in proportion to A. Our study quantifies ET by using remote-sensing techniques and products in the Caatinga seasonally dry forest, in the Brazilian semiarid. We compare these results with outputs of a bespoke Caatinga terrestrial ecosystem model, which quantifies transpiration and evaporation independently, and uses ET measured by an eddy covariance system as an overall benchmark. We indicate how remote sensing methods and models should be adapted in conjunction with ecosystem models for these tropical dry conditions.

P.59 Interplay between proline and unfolded protein response in endoplasmic reticulum stress tolerance of *Arabidopsis thaliana*

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Accumulation of unfolded proteins in ER is called ER stress. In response to ER stress, the unfolded protein response (UPR) is triggered to increase the protein folding capacity. ER stress can also be induced with agents such as tunicamycin (Tm). Proline is a well-known amino acid that takes vital roles under environmental stresses. Previously, it has been observed that yeast strains deficient in proline biosynthesis were sensitive to ER stress. The aim of the study is to determine the effects of Tm induced ER stress at level of gene expression and enzyme activities of proteins related to proline biosynthesis and catabolism and to compare the ER stress tolerance of different *A. thaliana* genotypes that have low *(p5cs1-1)* and high (*prodh2-2, prodh1-4, R2M12-4*) endogenous proline levels to ER stress. For this aim, the effects of ER stress on these mutants were evaluated by phenotyping their root growth. Moreover, the responses to ER stress of these mutants were determined by measuring the transcript abundance of ER stress related genes by qRT-PCR. *p5cs1-1* mutant was more sensitive to ER stress and showed lower induction of UPR genes while the opposite was observed in genotypes with high proline levels.

P.60 Cell-wall fucose is essential for normal guard cell function in *Arabidopsis thaliana*

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The plant cell wall is a dynamic network of proteins and polysaccharides that is essential for plant growth, providing structural integrity, strength and protection against pathogens. Recent research has shown that the cell wall also plays a role in upholding normal stomatal dynamics dependent upon guard cell wall structure. In our lab we identified the *sensitive to freezing8* (*sfr8*) mutant, which is deficient in fucose biosynthesis. This leads to alterations in cell-wall structure due to the loss of fucose in wall polysaccharides. *sfr8* also exhibits a desiccation-sensitive phenotype; leaves lose water more quickly than wild type plants. This led to the discovery that guard cell dynamics are compromised in the *sfr8* mutant. Using a variety of techniques including infrared thermography, microscopy and stomatal conductance measurements, I have shown that *sfr8* stomata are more restricted in their movements than wild-type plants in response to ABA, CO_2 and changes in humidity. I have also used atomic force microscopy to probe the mechanical properties of the wall and show that this alteration in dynamics is likely due to decreased stiffness of the guard cell wall. Further study will identify the specific fucose-containing polysaccharides that are essential for normal stomatal function.

P.61 Aquaculture wastewater treatment using duckweed

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The present study aims to make freshwater aquaculture more sustainable by removing the excess of nutrients from the water using small free-floating freshwater plants called duckweed. The treated water can be re-used in a recirculating system or safely discharged in the environment. Valuable proteins are extracted from the biomass produced and used to integrate the fish diet. In order to develop and optimize the system, it is important to know the rate at which each square meter of duckweed can uptake nutrients. It is also important to identify the most efficient plant density so that we can learn how often we need to harvest the plants. An experiment was designed for this purpose. Four different plant densities were grown in synthetic aquaculture wastewater (SAW) and the concentration of N and P in the SAW was monitored daily until complete depletion. An uptake rate curve over time was determined for the four plant densities. A second experiment aimed to quantify the nutrients used by duckweed and the nutrients used by algae and bacteria also present in a real system. It was concluded that the plant density should be kept between 60 and 80% of the surface available.

P.62 Positional cloning of two resistance genes to barley viral diseases from a wild relative

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Virus diseases are causing high yield losses in crops worldwide. In Europe, *Barley yellow dwarf virus* (BYDV), transmitted by aphids, and the soil-borne *Barley yellow mosaic virus* (BaYMV) and *Barley mild mosaic virus* (BaMMV) complex, transmitted by *Polymyxa graminis*, are of prime importance in this respect in barley. To date, only two genes providing resistance to BaYMV/BaMMV have been cloned. To be able to achieve a durable protection of the crop, additional resistance genes are urgently needed. We are aiming at cloning *Ryd4^{Hb}* and *Rym14^{Hb}*, two dominant resistance genes from *Hordeum bulbosum*, a wild relative of barley, providing resistance to BYDV and to the BaMMV/BaYMV complex, respectively. In a previous study, *Ryd4^{Hb}* was allocated to chromosome 3H. Recombination in crosses between *H. vulgare* and *H. bulbosum* are scarce: by screening 16,000 F2 plants, we identified less than 120 recombinant plants in a 13.3 Mbp interval. However, by fine mapping we were able to reduce the interval to 67 kb on barley reference genome, in which a NB-LRR gene is annotated. Using GBS genotyping of 427 F5 plant, we reduced *Rym14^{Hb}* interval on chromosome 6H to 4 Mb. To further reduce it, 8,000 F2 plants are currently undergoing screening for recombination.

P.63 Clustered papillae on subsidiary cells of rice (*Oryza sativa*) promote plant responses to environmental cues

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Stomatal morphological feature is indeed holding a great value in supporting the efficiency of gas exchange between plant and environment. Stomata structure such as guard cells and subsidiary cells have been well studied and reported to be important in stomatal opening and closing. Given that the existence of those cells has strengthened leaf gas exchange, any other epidermal feature could also help on stomatal function. Our recent finding based on a stomatal trait screening in a rice germplasm revealed two rice cultivars exhibiting “mega-papillae” trait on stomatal subsidiary cells, which was fully formed on flag leaves. Based on a physiological measurement, the mega-papilla-containing lines had lower stomatal conductance and promoted water-use efficiency under changing environmental condition. Moreover, mega-papilla lines exhibited a slower stomatal response to dark light, but they responded faster when the light came back in. In addition, based on the leaf impression of a wide range of plant species, the “Mega papillae” trait on subsidiary cells likely occurred on only a few cultivars of *Oryza sativa*. Overall, our results demonstrated a new micro-morphological feature related to stomatal complex and its possible function towards a better understanding on stomatal function and in advance to improve climate-ready rice that can sustain the ability under environmental stresses.

P.64 Functional analysis of flavonoid biosynthesis genes in *Beta vulgaris*

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Beta vulgaris (sugar beet) belongs to the flowering plant order Caryophyllales, which is well known for a complex pigment evolution. Anthocyanins and betalains are considered mutually exclusive pigments thus different taxonomic lineages of the Caryophyllales are expected to produce either only anthocyanins or betalains. Although *B. vulgaris* produces betalains, the genes of the anthocyanin biosynthesis pathway are present in the genome. We set out to identify the genetic cause for the lack of anthocyanins in *B. vulgaris*.
Genes of the flavonoid biosynthesis, which provide anthocyanin precursors, were characterized through phylogenetic analysis, gene expression analysis, and complementation of *Arabidopsis thaliana* mutant lines. The binding and activation of candidate promoters by potential regulators of this pathway was studied through transient transfection of *A. thaliana* protoplasts.

Functionality of several enzyme-encoding genes was demonstrated. Although there are several gene copies for each step in the pathway, functionality was observed for only one or a few copies. Since committed enzymes of the anthocyanin biosynthesis appear functional, we speculate that the production of anthocyanins in sugar beet is possible, but hindered by reduced transcript abundances. Future research might identify betalain and anthocyanins production within the same species.

P.65 Linking soil water, xylem and transpiration in mature woodland responses to elevated atmospheric carbon dioxide

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Patches of deciduous woodland, dominated by 170-year-old *Quercus robur/* pedunculate oaks at the Birmingham Institute of Forest Research (BIFoR) Free-Air CO_2 Enrichment (FACE) facility, are being exposed to +150 ppm CO_2 above ambient, throughout growing season daylight hours. This environmental modulation simulates atmospheric CO_2 conditions predicted as the global annual average by about 2050. Earlier studies have enabled a greater understanding of water transport, water usage, and water efficiency by young trees under environmental modulation. There are sound theoretical reasons for hypothesising that mature trees, such as those at BIFoR FACE, will not respond in the same way as juvenile trees. We monitor inputs and outputs within the soil-plant-atmosphere continuum, studying plant responses focused on the dominant *Q. robur*, but with due consideration of the phytosociology with tree species such as *Acer pseudoplatanus* and ground cover plants e.g. *Rubus fruticosus*. Our early results are based on monitoring of xylem sapflow, soil moisture and transpiration in and around individual trees. Stomatal closure during high temperature and solar radiation periods appears to enable oaks to sustain plant water flow despite decreasing soil moisture availability. 2019 season will produce adequate xylem data enabling early responses to elevated CO_2 to be assessed.

P.66 Correlating leaf-level spectral and pulse-modulated chlorophyll fluorescence with photosynthesis-controlling factors during spring recovery of Finnish boreal forest

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Chlorophyll Fluorescence (ChlF) can serve as a tool for tracking variations in plants photosynthetic activity. At leaf-level, ChlF vary across species, canopy light gradients or in response to various stressors. The sum of leaves-level variations terms the observed remote sensing retrieval. Without defining factors that might control the ChlF variation at leaf-level, the precise interpretation of SIF remains difficult. We examined the ChlF variation at leaf-level for five months of spring recovery (2017), at Hyytiälä Forest Station, Finland. Both spectral and pulse-modulated fluorescence was measured. In addition, reflectance, absorption, photosynthetic assimilation and pigments concentrations were analyzed. We also estimated the light environment of canopy positions using Digital Hemispherical photography. Here we present the results of correlating the ChlF observations with accompanying leaf-level measurements. We show that the combination of environmental (light, temperature), structural (species-specific leaf morphology) biochemical (pigments composition) and physiological (NPQ, photosynthetic activity) factors can properly reflects the spatiotemporal dynamics in the intensity and shape of ChlF spectra.

P.67 Expanding the utility of *Ensifer*-Mediated Transformation (EMT) technology for crop genetic improvement

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Ensifer adhaerens OV14 underpins the successful plant transformation protocol termed as *Ensifer*-mediated transformation (EMT) technology. The efficacy of EMT to successfully transform dicots; *Arabidopsis*, tobacco, potato, cassava, oil-seed rape and monocot; rice, have been previously reported. This study aim to expand the utility of EMT and investigate the transcriptional response of plants to EMT and vice-versa. To this, a transient transformation method to facilitate comparable studies via EMT was developed as the *Ensifer*-mediated *Arabidopsis thaliana* Root Transformation (E-ART) protocol; first quantitative method of transient gene expression to facilitate the rapid evaluation of novel *E. adhaerens* strains in plant transformation and a platform for plant-bacterium interaction studies. Utilising E-ART, the plant transcriptome analysis revealed that EMT induced only 431 Differentially Expressed Genes (DEGs), while AMT induced 1906 DEGs. Whereas, the transcriptome profile of *OV14* identified a total of 2333 DEG's between bacterium treated with *Arabidopsis* roots and untreated. Combined, these results provide possibilities of future research focused to improve efficacy of EMT.

P.68 Getting to the root of the problem: controlling *Armillaria*

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Armillaria species are widespread fungal plant pathogens affecting a range of woody trees and shrubs. Due to a lack of practical and effective control options, there is a demand for a control which is pesticide-free with no negative cultural or environmental impact. In addition, little is known regarding the pathogenicity genes related to *Armillaria*. In attempt to find a biocontrol of *Armillaria* 40 *Trichoderma* endophytes were selected. *In vitro Trichoderma* rapidly overgrew and significantly reduced the growth of *Armillaria* cultures. *In planta* seven *Trichoderma* isolates offered plant protection. Further investigation into the potential of these seven isolates is being tested with strawberry and privet plants. To visualise interactions between *Trichoderma* and *Armillaria* isolates were transformed with GFP or dsRED. Finding seven *Trichoderma* isolates with the potential for biocontrol of *Armillaria* is an exciting start to preventing disease. Seven candidate pathogenicity genes in *Armillaria* with homologues to known pathogenicity genes in model plant pathogens (e.g. *M. oryzae* and *U. maydis*) were selected. These include homologues of MAPK cascades and Ras GTPases. Work is ongoing to construct plasmids with promoter regions of candidate genes, selective markers and fluorescent labels to locate gene activation in attempt to determine involvement in pathogenicity.

P.69 Visual traits override scent cues in *Bombus terrestris* floral selection

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Bombus terrestris is an important pollinator in both natural and agricultural ecosystems. We developed recombinant inbred lines (RILs) from *Antirrhinum majus* and *A. linkianum*. We analysed the scent emission of both species and studied some of the molecular reasons underlying their contrasting scent profiles. We developed a tool to automatically study scent profiles in depth. We phenotyped scent profiles and visual traits of different lines analysed. We studied the preferences of bumblebees for different floral scents and flowers of *Antirrhinum* spp. Bumblebees preferred, in general, flowers from wild species instead of RILs. Bumblebees showed contradictory behaviour when they had to choose between just scent and full flowers. Results indicate that visual cues are more important for bumblebees than floral scents when choosing the visitation of flowers.

P.70 Profiling and analysis of reproductive phenology of four coffee (*Coffea* spp.) species in the Philippines using the BBCH scale

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In the Philippines, asynchronous coffee flowering translates to laborious, expensive, and protracted harvesting. Sustainable management intervention to address this concern, however, is currently not available as basic information on coffee reproductive physiology are still wanting. Thus, this research aimed to elucidate the physio-morphological complexity of reproductive phenology of four coffee species (Robusta, Arabica, Excelsa, and Liberica) in the Philippines using the Biologische Bundesantalt, Bundessortenamt and CHemische Industrie (BBCH) scale. The experiment was conducted in Los Baños, Philippines from 2015-2017, wherein plagiotropic branches with emerging inflorescences (BBCH51) were tagged and monitored until the ripe-berry stage (BBCH88). Results showed that while the over-all developmental pattern was comparable across species, there were distinct species-specific variations in terms of phenophase timing, pacing, and duration. Two sigmoidal growth curves were noted: first, from inflorescence emergence until anthesis (BBCH69), and second, from pericarp development (BBCH71-77) to seed development (BBCH77-88). A spike in rainfall (≥ 320 mm) initiated bud break (BBCH 53), beyond which species variation became more significant. Large-fruited species (i.e., Excelsa/Liberica) had higher heat unit requirements (GDD) compared to small-fruited species (i.e., Robusta/Arabica). From inflorescence emergence to berry ripening, Arabica, Robusta, Excelsa, and Liberica required 6706 GDD, 7181 GDD, 7715 GDD, and 7519 GDD, respectively.

P.71 Sensing the rainbow: genetic and physiological light responses in the picophytoplankton *Ostreococcus*

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The photosynthetic activity of phytoplankton is vital, not only as primary production in the ocean and carbon sequestration, but also as a source of almost half the oxygen in our atmosphere. This is an investigation of the genetics and physiological consequences of light responses in *Ostreococcus*, a eukaryotic picophytoplankton. Understanding the responses of phytoplankton to their environment is particularly important due to climate change, it is not clear how these species will be affected. Two ecotypes, from the surface of Thau lagoon in South France, and from 100m deep in the euphotic ocean, were compared. It is known that some *Ostreococcus* ecotypes are adapted to high or low intensities of light, however the responses of ecotypes to light of different wavelengths, red, green, and blue, were unknown. Differential gene expression from RNASeq data under these light conditions was determined, and functional annotation used to describe the likely physiological effects of the transcriptional responses. Ecotype-specific light responses were detected and these changes were initially tested by measuring physiological photosynthetic parameters using Phyto-PAM technology. The transformation of cells using reporter constructs of promoter regions is now underway to investigate how the light responsive genes are controlled.

P.72 Identification and characterisation of novel wheat genes that confer resistance to Septoria Tritici Blotch disease during latent phase of the infection

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Septoria tritici blotch (STB) disease affecting wheat is caused by the fungal pathogen *Zymoseptoria tritici.* Early detection and initiation of defence responses during the latent phase of infection are crucial in allowing the host to prevent successful pathogen infection. RNAseq data from a doubled-haploid population derived from a cross between cvs. Stigg and Longbow representing the 96-hour response to the pathogen was conducted and a suite of early-response genes have been identified for further characterisation. A second bulk segregant analysis (BSA) RNAseq, composed of two bulks representing the 10-day response to the pathogen was conducted. The first bulk was comprised of six elite resistant cultivars and the second bulk comprised of six elite susceptible cultivars. Following the analysis of the BSA RNAseq data, a variety of candidate genes were identified to be involved in defence against STB. Induction of genes associated with catalytic activity and metal binding were prevalent in the resistant bulk compared to susceptible bulk. Expression of a set of homoeologous Reticulata-like genes were downregulated in the resistant bulk only suggesting, based on studies in other species, a potential burst of reactive oxygen species (ROS). Thirty-five common genes were identified across the two RNAseq datasets, including an adenosylhomocysteinase, a glutathione S-transferase and a serine-type endopeptidase inhibitor. This study shows that defence responses are conserved among wheat cultivars and highlights the importance of the early host response.

P.73

The innovation of branching in plants

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Vascular plants have elaborate branching shoot systems with leaves. In contrast, the earliest land plants had a single small stem, as in modern bryophytes. The evolutionary innovation of branching primed a tenfold increase in plant species numbers and changed the course of life on land. By comparing mechanisms for branching in groups whose shared ancestry dates back to the dawn of vascular plants, this project aims to identify the genes responsible for the origin of branching. The results will give exciting new insights into a major evolutionary change, and will ultimately enable modification of crop branching patterns to increase productivity.

P.74 Patterns of biocrust cyanobacteria ^{13}C values near plants not driven by composition

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Drylands are increasing in geographic extent and are key regulators of interannual variability in carbon (C) dynamics, and thus investigating how the producers (plants and cyanobacterial biocrusts on the soil surface) interact can improve understanding of C cycling. We observed ^{13}C values of biocrusts near multiple C_3 and C_4 species across regional sites to determine if biocrusts near plants have a C signature that is more similar to that of the adjacent C_3 or C_4 plant compared to the interspace microsite. We sampled biocrust composition and pure culture ^{13}C and chlorophyll content to determine if ^{13}C are related to biocrust characteristics, and we sampled leaf ^{13}C, root distribution, and organic matter as plant characteristics. We found that biocrusts near C_3 plants were depleted in ^{13}C compared to those in the interspace or near C_4 plants, but that this difference was not explained by cyanobacterial composition or chlorophyll content. Root abundance and organic matter were 83% and 11% higher near plants than interspace, respectively, suggesting biocrusts could fix root-respired carbon or integrate plant-derived compounds, but this does not explain difference in cyanobacteria ^{13}C by adjacent species. Understanding how carbon cycles through plants and microbes is critical for predicting global biogeochemical cycling.

P.75 Studying the role of pectin in pathogen associated molecular pattern (PAMP)-triggered immunity and inhibition of growth

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Plants utilize pathogen-associated molecular pattern (PAMP)-triggered immunity (PTI) to fend off pathogens. Activation of PTI responses leads to inhibition of plant growth; however, the molecular mechanisms underlying this trade-off are still largely unknown. Here, we used activation-tagging to identify mutants that show restoration of PAMP-triggered seedling growth inhibition (SGI) in the immunodeficient *bak1-5 bkk1-1* background, which lacks two major co-receptors in PAMP perception. We identified *GAE2*, which encodes a UDP-D-glucuronate 4-epimerase probably involved in pectin biosynthesis, as capable of partially restoring SGI in *bak1-5 bkk1-1* upon treatment with the active epitope of the bacterial PAMP EF-Tu, the peptide elf18, when overexpressed. Interestingly, *GAE2* specifically regulates the growth inhibition upon activation of PTI, since its overexpression cannot restore other PTI outputs, including the burst of reactive oxygen species (ROS), activation of MAPK, and elf18-induced anti-bacterial resistance. Arabidopsis double mutants in *GAE2* and its closest homologue *GAE3* show milder SGI when treated with elf18. Intriguingly, elf18 treatment caused a significant reduction of total content of uronic acid which is structural unit of pectin in WT plants, while triggering transcriptional changes in multiple pectin-related genes. Taken together, our results suggest that pectin content could be regulated by PAMP perception and affect the PAMP-induced growth inhibition.

P.76 The struggle for space: stamens packing strategies in male flowers of *Croton* and related genera

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Tribe Crotoneae (Euphorbiaceae) is a group of six genera with high diversity in male flowers, but remarkably stable female flower. To understand evolutionary processes underlying the male floral diversity, flower buds sampled from all genera were examined with light microscopy and scanning electron microscopy. Stamen shapes in bud are highly diverse ranging from erect (*Acidocroton*, *Brasiliocroton*, *Croton* section *Moacroton*), to sessile (*Sagotia*), twisted filaments (*Sandwithia*), and inflexed filaments (*Astraea* and *Croton*). Stamen arrangement in bud is also found to be variable in each genus. The diversity of stamen forms and arrangement within Crotoneae may be an independent innovative strategy of each genus to pack a maximum number of stamens in a limited space. Developmental studies revealed three main types of stamen development in *Croton*, i.e., the alternipetalous whorl develops first, followed by a centrifugally developing antepetalous whorl (most *Croton*), antepetalous whorl develops first (*Croton* with <10 stamens), and a chaotic development (*C. celtidifolius*). The first type is the most common pattern found in several sub-groups within *Croton* and also in *Astraea*, suggesting it may be an ancestral character. The study of androecial complexity in Crotoneae flowers will contribute to understanding floral diversity and evolution in other Euphorbiaceous taxa.

P.77 Drop it like it's hot: Snoopacin and nine other novel antimicrobials identified, synthesised and characterised from the *Cannabis sativa* genome by the AMPLY bioprospecting platform.

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Finding new antibiotics is a vital research area and can now be supported by a vast reservoir of readily available 'omic data on the back of the explosion of low-cost sequencing technologies. Antimicrobial Peptides (AMPs): endogenous peptides that provide a fast and effective means of defence against pathogens as part of the innate immune response. Large reservoirs of sequences exist to search for AMPs. A synthesis and screening program can screen 100s of prospects a day to test for activity and is an area of biomedical science that can scale to meet the data output from computational prediction toolkits. AMPLY, an in-house tool designed at Aberystwyth University, supported by Life Science Wales and working in collaboration with Tika Diagnostics at St. George's Hospital and Queen's University is part of a next wave of drug discovery platforms and is uncovering a treasure trove of novel AMPs in diverse environments: including 10 from *Cannabis sativa*. We highlight the significant benefits of forming a link between the understanding of plant-derived 'omic data, bioinformatics, peptide synthesis and confirmatory screening. We conclude with visualisations of these antimicrobials acting on pathogens as well as a variety of characterisation data to support the findings.

P.78 Strigolactone controls PIN protein accumulation patterns in the Arabidopsis stem via a region of the PIN hydrophilic loop

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Strigolactones (SLs) control a wide range of developmental programs. Upon SL perception the levels of PIN1, a key auxin efflux carrier, on plasmamembrane of xylem parenchyma cells (XPC) drop rapidly. It is therefore essential to understand how SL influences the establishment of auxin fluxes. Here we develop new image analysis tools to quantify the accumulation of PIN proteins in the stem, and use them to characterise PIN responses to SL perturbations. Our results show that SL induces removal of certain PIN proteins, but not others, from XPC plasmamembrane. This results in differential accumulation between responsive/non-responsive PINs. Furthermore, we show that response to SL can be conferred to non-responsive PINs via a PIN hydrophilic loop region. Our approach suggests that SL-dependent endocytosis of PINs controls their degree of polarity, thereby regulating the direction of auxin efflux. Finally, we present results suggesting that the response to SL is important to complement the *pin1* mutant phenotypes. In summary, we have provided a new perspective on the role of SL as a regulator development via the modulation of PIN levels and polarity.

P.79 Insect resistance in UK Sitka Spruce (*Picea sitchensis*)

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Herbivorous insects can cause large-scale damage to commercially grown conifer tree species, resulting in substantial value loss for the forestry industry. Resistance breeding is becoming an important mitigation tool due to the increasing restrictions on neonicotinoids. Insect resistance is well studied in the native range of Sitka spruce (*Picea sitchensis* (Bong.) Carr), the UK's main timber species, but was not assessed in the UK founder population. We performed a pilot study to assess presence and variation of resistance biomarkers in UK populations of *P. sitchensis* and examine the potential to breed for resistance based on heritability and tradeoffs with tree growth. Three terpenes ((+)-3-carene, terpinolene, and dehydroabietic acid) and two histology traits (sclerenchyma cells and resin canals) were measured across 50 full-sib families and 16 clonal genets. We used ASReml-R to estimate heritability of each biomarker and calculate genetic correlations among biomarkers and two growth traits. Histology across all samples resembled that of susceptible trees from previous studies. However, all three terpenes were present and variable across families and genets, and preliminary heritability estimates were high for (+)-3-carene and terpinolene. Results to date indicate high potential for use of resistance breeding to develop resilient *P. sitchensis* populations in the UK.

P.80 The role of vacuolar invertase in shaping photosynthetic stress response

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Survival under abiotic stress requires adjustments to primary carbohydrate and energy metabolism in plants. Stress responses regarding these metabolic pathways have been shown to not only comprise changes in metabolite levels but also contain intricate subcellular translocation and signalling mechanisms [1]. Furthermore, futile cycling of sucrose via sucrose cleavage and ATP-consuming hexose phosphorylation hampers the intuitive generation of hypotheses about stress responses. In the presented study, a cold susceptible and a cold tolerant natural accession of *Arabidopsis thaliana* were exposed to combined cold and high light stress, revealing significant differences in the dynamic stress response of sucrose and fumarate metabolism. Kinetic modelling of invertase-driven sucrose cleavage revealed differential subcellular invertase reprogramming, pointing to a substantial role of this enzyme in the initial stress response. The cold tolerant accession was shown to rely on sucrose cleavage in the vacuole during stress, while in the cold susceptible accession the cytosolic pathway of sucrose cleavage was more active. Finally, to verify the central role of this enzyme in stabilizing photochemical processes under freezing and high light conditions, the stress response of a mutant being dramatically impaired in vacuolar invertase activity was analysed[2].

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P.81 Long-lasting jasmonic acid induced resistance against a generalist herbivore comes at the cost of enhanced susceptibility to pathogens

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The phenomenon of induced resistance (IR), whereby exposure of plants to specific stimuli makes them more resistant to subsequent attack, could be more widely used in crop pest management if it was long-lasting. Previous studies have shown that long-lasting resistance can be induced by numerous stimuli including jasmonic acid (JA). We aimed to better understand the mechanisms underpinning long-lasting IR by treating two-week-old *Arabidopsis thaliana* seedlings with JA and then challenging these plants three weeks later. Interestingly, while the JA seedling treatment induced resistance against a generalist herbivore, it induced susceptibility against multiple pathogens. Transcriptome analysis demonstrated that JA seedling treatment primed herbivore defences for a faster and stronger upregulation upon subsequent attack. Whereas defences effective against pathogens were repressed long-term. JA induced resistance and susceptibility was compromised in DNA (de)methylation mutants. Thus, the altered defence responses and resulting changes in resistance are seemingly linked to JA induced epigenetic changes. To better understand the role of DNA methylation in long-lasting IR, we are currently analysing the JA-induced changes to the Arabidopsis methylome. This study highlights the importance of assessing how resistance inducing stimuli effect plants long-lasting defence responses against numerous biotic stresses, before using the stimuli in crop pest management.

P.82 Redwoods associate with multiple mycorrhizal types and harbor root organs that act as reservoirs of arbuscular mycorrhizal fungi

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Plant associations with fungi are ubiquitous and represent an important frontier in better understanding plant ecology. Leveraging improvements in DNA sequencing using the rRNA ITS2 region, we demonstrate strong biotic filtering in the rhizosphere of the iconic coast redwood (*Sequoia sempervirens*). Beyond the expected arbuscular mycorrhizal fungi (AMF) community, we find an abundance of ecto- and ericoid mycorrhizal fungi associated with redwood roots, potentially connecting redwoods to surrounding trees and shrubs in the understory. Further, we describe for the first time the previously unseen role of root structures (which we refer to as “rhizonodes”) as domiciles for AMF, demonstrating the capacity of plants to harbor fungal symbionts within a specialized root organ. These results challenge the common practice of AMF-specific sequencing that considers only a small portion of the diverse mycobiome. Additionally, we demonstrate that redwood-AMF association results in a cascade of consequences for shoot architecture, photosynthetic capacity, and drought response. Our study of a basal gymnosperm brings into question whether redwoods make or break rules about host specificity, the role of plant organs in mycobiome assembly, and the importance of mycorrhizal fungi not only in nutrient acquisition, but also for a diversity of architectural, hormonal, and physiological functions.

P.83

The effects of planting methods, plant species, beneficial microbes and their interactions on plant growth and microbial population on green roofs in southern Finland

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Green roofs are gaining increasingly popularity in urban areas. It becomes important to find effective methods to establish and maintain green roofs to provide ecosystem services at optimum. The present study investigated the effects of microbe-inoculation, plant species, planting methods, and their interactions on plant growth and microbial development under green roof conditions. The selected green roof plants were established with one of the three planting methods (mat, pot, and seed), and with or without co-inoculation with *Bacillus amyloliquefaciens* and *Rhizophagus irregularis*. Plant dry aboveground biomass and microbial population in soils and roots were measured as indicators of plant growth and microbial development respectively. This study confirmed that, on green roofs, co-inoculation of *B. amyloliquefaciens* and *R. irregularis* could significantly increase the growth of selected plant species. Seeded plants exhibited the highest *R. irregularis* colonization, followed by potted plants, and matted plants were the lowest. For plant species, *Thymus serpyllum* exhibited intermediate receptivity towards *R. irregularis*, which was significantly lower than *Fragaria vesca*, but higher than *Trifolium repens*. This study presents evidences that certain plant-growth-promoting microbes can successfully colonize green roof plants and effectively promote their growth. Moreover, by integrating suitable planting methods, the promoting effects would be further improved.

P.84 Exploration and optimization of a novel negative carbon emission technology using enhanced plant-mediated chemical weathering

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The recent Intergovernmental Panel on Climate Change (IPCC) 1.5°C Special Report suggests that CO_2 removal is required to achieve net negative emissions in the 21st century in order to limit the temperature rise below 1.5°C, in all future pathways. Enhanced chemical weathering offers one theoretical solution by increasing the rate at which plant mediated CO_2 helps to weather calcium silicate rocks which in turn increase the rate at which carbonates are deposited and stored in the ocean system. This study experimentally explores the carbon sequestration potential of the addition of volcanic ash to Irish grassland crops (model species *Lollium perenne*) under modern and future climate scenarios (IPCC). Experiments are carried out in controlled growth chambers using 8 treatments over 4 months. Preliminary results will be presented to show the impact of the volcanic ash addition to soil on the soil carbon storage and the alkalinity of the leachate. Ryegrass aboveground and belowground productivity as well as the uptake of the different elements will also be quantified for the different treatments. The results of the study will not only quantify the rate of carbon sequestration, it will also feed into optimizing a protocol for future field-based trials and large-scale agricultural practices.

P.85 Evolution of plant defense resistance in natural enemies of an arthropod herbivore

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Specialist herbivores can sequester plant defensive secondary metabolites for protection against natural enemies. Yet, whether sequestered chemicals can drive natural enemy adaptations is unclear. Here, we tested adaptations of 30 worldwide populations of entomopathogenic nematode (EPN) to benzoxazinoid (BX) sequestration by the western corn rootworms (WCR). We found a strong positive correlation between EPN co-occurrence history with WCR and their resistance to BXs. Rearing a susceptible EPN population in WCR larvae for five generations was sufficient to trigger significant physiological and behavioral adaptations to BXs. A model including the different adaptive traits of EPN demonstrates that EPN behavior is the main driver of BX resistance. Our study illustrates biochemical arm race among tri-trophic interactions and provides targets to increase the biocontrol efficiency of herbivore natural enemies.

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