New Phytologist
next generation scientists

Delta Centre
University of Tartu, Estonia

19–22 July 2022

Scientific Organizing Committee
Maarja Öpik (Organising Committee Lead)
Hanna Hõrak
Lauri Laanisto
Lena Neuenkamp
Ivika Ostonen
Kaido Soosaar
Leho Tedersoo
Tana Wuyun

New Phytologist Foundation organization
Christine Phillips (*Events & Promotion Manager)*
Mike Whitfield *(Development Coordinator)*
Sarah Lennon *(Executive Editor)*

‘New Phytologist next generation scientists’ logo by Promotional Gods, Lancaster, UK

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

Acknowledgements

New Phytologist next generation scientists is funded by the New Phytologist Foundation, with support from Wiley, and the University of Tartu.

Table of Contents

Information for online delegates

Hybrid Hub

New Phytologist next generation scientists is a hybrid event with delegates participating in-person and online. We are using Basecamp as our online Hub. All registered delegates have been sent details of how to register for Basecamp. If you have misplaced your email to access the Hybrid Hub, please contact np-symposia@lancaster.ac.uk. The Hybrid Hub will allow you to access the virtual poster exhibition, Flash Talks, and allow delegates to network with each other. The Hybrid Hub will also be home to the live feed from the symposium, and shortly after each session an unedited recording will be uploaded to view on demand.

Slido and Q&A sessions

During the symposium delegates will be able to ask questions via Slido. Join at Slido.com on any mobile device or laptop, and use the join code for the day. We will also have some short engagement activities on Slido, so we encourage you to sign in.

Online Poster exhibition (optional)

All in-person delegates are welcome to upload a PDF of their poster to the virtual poster exhibition in the Hybrid Hub on Basecamp. Please add it to the "in-person delegate posters" area. You are encouraged to view the online delegates' posters, and you will have the opportunity to vote for your favourite posters from online delegates after the close of the symposium.

Abstracts

Abstracts for in person posters are included in this abstract book which can also be found on the Hybrid Hub or online at https://www.newphytologist.org/nextgenevents/2022.

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**.

Code of conduct

The New Phytologist Foundation 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 2022 is an opportunity to share, develop and broaden our viewpoints within a safe and inclusive setting. The New Phytologist Foundation has established a set of core principles that outline the standards expected of individuals involved in the Foundation's activities, including symposia. We strive to treat all individuals with respect, and promote a safe environment free from discrimination, harassment, and victimization.

Expected behaviour

- We respect the rights of all individuals to dignity, privacy and confidentiality and delegates must treat everyone with respect.
- We ask delegates to respect their fellow participants and ensure they undertake good practices for intercultural collaborations.

- We ask that you remain mindful of your surroundings and respect the surroundings of your fellow participants.
- Do not share, copy or reuse any materials presented by speakers or in posters unless this is expressly permitted.
- All delegates must ensure they respect the staff, rules and protocols of the meeting venue, accommodation and online platform. This also includes protocols linked to Covid-19.

We will not tolerate behaviours that involve discrimination of individuals or groups on the basis of sex, race, ethnicity, gender identity, age, religion, disability, or any other characteristic protected by applicable laws. Sexual harassment, bullying, intimidation or harassment in any form will not be tolerated.

Any delegates that do not meet the expected respectful behaviour may be immediately removed from the online or physical meeting.

If you have any concerns or suggestions, please speak to the Events and Promotions Manager, Christine Phillips, the Executive Editor, Sarah Lennon, or one of the meeting organisers. Alternatively, you can email np-symposia@lancaster.ac.uk.

Meeting programme

All times are in EEST (UTC+3)
Registered Online delegates will receive links to join all the sessions
In-person delegates should refer to the in-person programme

Tuesday 19 July 2022

13:30–13:40	**Introduction and welcome, Alistair Hetherington and Maarja Öpik**

Session 1 (Chair: Maarja Öpik)

13:40–14:30 **Keynote talk**	**Hongzhi Kong,** Institute of Botany, Chinese Academy of Sciences **The making of the elaborate Nigella petals** *This talk will be given remotely*
14:30–14:50 Selected Talk	Marybel Soto Gomez, Royal Botanic Gardens, Kew Characterizing the impact of genome size on plant extinction risk
14:50–15:10 Selected Talk	Vicky Spencer, University of Bristol Redeployment of ancestral branching mechanisms in the evolution of lycophyte architecture
15:10–15:40	Break

Session 2 (Chair: Ülo Niinemets)

15:40–16:30 **Keynote talk**	**Andre Kessler,** Cornell University **Herbivore-induced volatile organic compounds: a chemical handshake mediating interaction contracts**
16:30–16:50 Selected Talk	Jamie Waterman, University of Bern The importance of continuous herbivory and HIPV emission for plant–plant information transfer
16:50–17:10 Selected Talk	Ivan De la Cruz Arguello, Swedish University of Agricultural Sciences Genomic basis of the evolution of resistance against its natural enemies in the poisonous and medicinal plant *Datura stramonium* (Solanaceae)
17:10–17:30 Selected Talk	Katherine Barragán-Fonseca, Wageningen University Amending soil with insect exuviae improves plant growth, pollinator attraction and fitness of flowering plants
17:30–18:00	Break

Session 3 (Chair: Ivika Ostonen)

18:00–18:50 **Keynote talk**	**Marina Semchenko,** University of Tartu **Plant functional traits and rhizosphere processes: from global patterns to local interactions**
18:50–19:10 Selected Talk	Katy Faulkner, University of Warwick High rainfall disturbs soil microbial structure and function in a mature temperate forest under elevated carbon dioxide
19:10–19:30 Selected talk	Xuan Zhou, University of Eastern Finland Microbial biodiversity contributes to soil carbon release: A case study on fire disturbed boreal forests

Wednesday 20 July 2022

08:55–09:00	Announcements

Session 4 (Chair: Tana Wuyun)

09:00–09:50 **Keynote talk**	**Shuhua Yang,** China Agricultural University **Molecular mechanisms of plant responses to cold stress** *This talk will be given remotely*
09:50–10:10 Selected Talk	Anna Sze Wai Tse, University of Cambridge Production of nanobodies in *Marchantia polymorpha*
10:10–10:30 Selected Talk	Katie Stevens, University of Birmingham The role of epigenetic in long-lasting post-harvest resistance in tomato
10:30–11:00	Break

Session 5 (Chair: Carl Ng)

11:00–12:00	**Panel discussion and Q&A – Taking the next step in your career** **Moderator: Holly Slater** • **Michał Bogdziewic,** Adam Mickiewicz University • **Charlotte Grossiord,** EPFL • **Anna Trugman,** University of California Santa Barbara • **Marjorie Lundgren,** Lancaster Environment Centre *(appearing remotely)*
12:00–12:50 **Keynote talk**	**Holger Puchta,** Botanical Institute, Karlsruhe Institute of Technology **Applying CRISPR/Cas to Plants: From Gene Editing to Chromosome and Tissue Engineering**
12:50–13:15	Break
13:15–14:00	**Virtual session – Meet Helen Pinfield-Wells,** Managing Editor *New Phytologist*

Session 6 (Chair: Carl Ng)

14:00–14:50 **Keynote Talk**	**Suayib Üstün,** University of Tübingen and Ruhr-University of Bochum **How proteostasis shapes the plant response to environmental stimuli**
14:50–15:10 Selected Talk	Febri Doni, Universitas Padjadjaran Isolation and molecular characterization of native Trichoderma isolates from West Java, Indonesia and the assessment of their roles for enhancing rice development and physiological traits
15:10–15:30 Selected Talk	Itumeleng Moroeyane, Donald Danforth Plant Science Center Engineering plant–microbe interactions to promote host health and resilience
15:30–16:00	**Break**
16:00–16:45	**Virtual session -** Meet Kai Zhu, Tansley Medal winner 2019
17:00–17:45	**Virtual session -** Meet Marjorie Lundgren, Tansley Medal finalist 2019

All times are in EEST (UTC+3)

Thursday 21 July 2022

08:55–09:00	Announcements

Session 7 (Chair: Martin McAinsh)

09:00–09:50 **Keynote talk**	**Teresa Fitzpatrick,** University of Geneva **B vitamins as cogs of plant metabolism**
Selected Talk	Jian You (Eric) Wang, King Abdullah University of Science and Technology Zaxinone: discovery, application, and mode of action
10:10–10:30 Selected Talk	Julien Agneessens, Durham University The Arabidopsis R-SNARE VAMP714 is essential for polarisation of PIN proteins and auxin responses

10:30–11:00	Break

Session 8 (Chair: Tiina Tosens)

11:00–11:50 **Keynote Talk**	**Carlos L. Ballaré,** Universidad de Buenos Aires and CONICET **Growth-defense tradeoffs in plants: myths, facts, and some mechanisms**
11:50–11:55	**Technical break**
11:55–12:55	**Publishing your work, a panel discussion with Q&A** **Moderator: Sarah Lennon** • **Susanne Brink** (*Trends in Plant Science*) (appearing remotely) • **Alistair Hetherington** (*New Phytologist*) • **Anne Knowlton** (*Current Biology)* (appearing remotely) • **Rosie Trice** (Wiley) (appearing remotely) • **Chris Surridge** (*Nature Plants*)
12:55–13:15	Break
13:15–14:00	**Virtual session – Meet Bennett Young,** Managing Editor *Plants, People, Planet*

Session 9 (Chair: Leho Tedersoo)

14:00–14:50 **Keynote talk**	**Bala Chaudhary,** Dartmouth College **Mycorrhizal fungal dispersal across spatial scales**
14:50–15:10 Selected Talk	Camille Delavaux, ETH Zurich Global evidence for a symbiotic bacteria filter on N-fixing plant establishment on islands.
15:10–15:30 Selected Talk	Mathu Malar, University of Ottawa The early branching arbuscular mycorrhizal fungus *Paraglomus occultum* carries a small and repeat poor genome compared to relatives in the Glomeromycotina

15:30–16:00	Break

Session 10 (Chair: Lauri Laanisto)

16:00–16:20 Selected Talk	Anis Mahmud Khokon, University of Hamburg Ectomycorrhizal diversity and community traits drive the N uptake of beech roots
16:20–16:40 Selected Talk	Besiana Sinanaj, University of Sheffield New ecological insights on Mucoromycotina ‘fine root endophytes’ (MFRE): their impact on plant growth under low nutrient conditions

16:40–18:15	Break
18:15–18:45	**Virtual session: Meet Rosie Trice, Wiley**
18:50–19:20	**Virtual session: Meet Susanne Brink, *Trends in Plant Science***
19:25–19:55	**Virtual session: Meet Anne Knowlton, *Current Biology***

All times are in EEST (UTC+3)

Friday 22 July 2022

08:55–09:00	Announcements

Session 11 (Chair: Hanna Hõrak)

09:00–09:50 **Keynote talk**	**Wei-Cai Yang,** Institute of Genetics and Developmental Biology, Chinese Academy of Sciences **The central role of the central cell in plant reproduction** *This talk will be given remotely*
09:50–10:10 Selected Talk	Jiaqi Shi, University College Dublin Morphological analysis of inflorescences and flower developmental stages in male and female hemp (*Cannabis sativa*)
10:10–10:30 Selected Talk	Rory Burke, University College Dublin Death by transcription: RNA-Seq identifies novel regulators of programmed cell death in Arabidopsis

10:30–11:00	Break

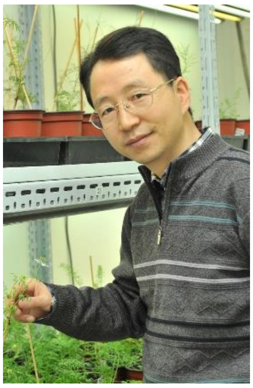
Session 12 (Chair: Kaido Soosaar)

11:00–11:20 Selected Talk	Renato Braghiere, NASA Jet Propulsion Laboratory, California Institute of Technology Global carbon cost of plant nitrogen and phosphorus acquisition
11.20–11.40 Selected talk	Sirgi Saar, University of Tartu Applying vegetation science concepts to crops: trait diversity across rice varieties increases complementarity effects and productivity
11:40–12:30	***New Phytologist* Editorial Meeting lecture – Andrea Polle,** University of Göttingen **Forest trees in the Anthropocene – feast, famine and failure** Q&A moderated by Alistair Hetherington
12:30–12:45	**Final comments, Alistair Hetherington, Maarja Öpik**

12:45	**Close of event**

Speaker abstracts
Tuesday 19 July 2022

Keynote lecture 13:40–14:30



The making of the elaborate *Nigella* petals

Hongzhi Kong

State Key Laboratory of Systematic & Evolutionary Botany, Institute of Botany, Chinese Academy of Sciences, Beijing, China

Biography:
Professor Hongzhi Kong graduated from Northwest University in 1995 and obtained his Ph.D. degree in Institute of Botany, the Chinese Academy of Sciences, in 2000. During 2002-2004, he worked for the Pennsylvania State University as a Visiting Postdoctoral Scholar. He became a full professor in Institute of Botany, Chinese Academy of Sciences, in 2006 and Director of the State Key Laboratory of Systematic and Evolutionary Botany in 2017. Professor Hongzhi Kong is broadly interested in the evolution of plants. He and his research group use morphological, phylogenetic, molecular, developmental, genomic and bioinformatic approaches to study how and why flowers have originated and diversified. The final goal of these "Evo-Devo" studies is to elucidate how changes in genomic sequences have led to evolutionary novelties in phenotype, and how diversity in floral characters has been generated and retained during plant evolution. Research projects in Kong's group cover a diverse set of topics, including: 1) evolution of the regulatory network for floral development; 2) molecular mechanisms underlying the origin and diversification of flowers and floral organs; and 3) generation and diversification of duplicate genes.
Read the *New Phytologist* profile of Hongzhi or Visit Hongzhi's website

Abstract:
Petals show tremendous diversity in shape, structure, color/coloration and function, and have increasingly been used as a model for the study of plant organ evolution. Petals of *Nigella* (Ranunculaceae) are of particular interest because they form highly elaborate, bilabiate structures with extensive modifications. To understand how elaborate *Nigella* petals were made through development and evolution, we conducted detailed morphological, micro-morphological, anatomical, developmental, transcriptomics, functional and evolutionary studies. We found that: 1) the complexity of elaborate *Nigella* petals can be measured at various levels; 2) the evolutionary elaboration of the *Nigella* petals is a gradual process, involving not only modifications of pre-existing structures but also *de novo* origination of new characters (e.g., pseudonectaries, short trichomes, and eyebrow-like stripes); 3) changes in the expression patterns of several transcription factor genes contribute to the formation of the upper lip (e.g., adaxial/abaxial polarity genes), the generation of pseudonectaries (e.g., *YAB5*), the bifurcation of the lower lip (e.g., *LMI1*), the development of long hairs (e.g., *GL3* and *GL2*) and short trichomes (e.g., *MYB5-2*, *GL3*, *TT8*, *GL2* and *LMI1*), and the production of eyebrow-like stripes (e.g., *MYB6*, *MYB20*, and *MYB113*); and 4) the evolutionary changes of some genes (e.g., *ARF3-1*, *ARF4*, *KAN1*, *TT8*, *GL3*, *MYB113* and *GASA14*) in the time and level of expression may have been the key to the elaboration of the *Nigella* species. These results not only uncover the mechanisms underlying the elaboration of *Nigella* petals but also pave the way for better understanding the genetic bases of plant lateral organ diversification.

Selected talk 14:30–14:50

Characterizing the impact of genome size on plant extinction risk

Marybel Soto Gomez
Royal Botanic Gardens, Kew

Abstract:

Genome size is a key biodiversity trait with increasingly recognized impacts on plant growth, adaptation, and survival. The emerging picture suggests that plants with bigger genomes are less able to compete and adapt in a range of environments, partly explained by having higher nutrient demands and lower photosynthetic efficiency compared to small-genomed plants. However, the influence of genome size on plant extinction risk has not been robustly tested to date, neither alone, nor in conjunction with potential covariates such as ploidy level, life form and distribution. Here we use phylogenetically-informed generalized linear mixed effect models to characterize the influence of genome size on plant extinction risk based on a global-scale sampling of angiosperms. Our preliminary results show that threatened species have slightly larger genomes than non-threatened ones. However, genome size differs substantially across plant life forms and sources of threats, with substantially larger genomes observed in threatened annual plants (compared to perennials and epiphytes) and species threatened by pollution. We are now characterizing this trend in diploid vs. polyploid and temperate vs. tropical species. Overall, our study suggests that genome size may be a useful trait to consider in the development of effective plant conservation strategies.

M. SOTO GOMEZ[1], M.J.M. BROWN[1], J. PELLICER[1, 2], S. PIRONON[1], P. BUREŠ[3], P. VESELY[3], T. ELLIOTT[3], F. ZEDEK[3], F. FOREST[1], E. NIC LUGHADHA[1], I.J. LEITCH[1]

[1] *Royal Botanic Gardens, Kew, Richmond, UK*
[2] *Institut Botanic de Barcelona (IBB, CSIC-Ajuntament de Barcelona), Spain*
[3] *Masaryk University, Faculty of Science, Department of Botany and Zoology, Brno, Czech Republic*

Selected talk **14:50–15:10**

Redeployment of ancestral branching mechanisms in the evolution of lycophyte architecture

Vicky Spencer

University of Bristol

Abstract:

Shoot branching is an evolutionary innovation that likely occurred once in the ancestor of vascular plants and was paramount to their subsequent success. Whilst lycophytes show ancestral apex bifurcation, flowering plants instead produce axillary branches at subtending leaves. Axillary branch initiation and outgrowth are regulated by transport of the hormone auxin via PIN protein efflux channels. However, it is unknown how widely auxin transport regulates branching in different lineages, and whether auxin transport was responsible for the innovation of branching in the vascular plant ancestor. To address this, we have studied bifurcation in the lycophyte, *Selaginella kraussiana*, along with a novel method of branching which is unique to the *Selaginella* genus. We performed surgical and pharmacological studies and found that both types are regulated by long range auxin transport from the shoot apex. We have identified four PIN orthologs in *S. kraussiana* and found gene-specific expression in the shoot apex (*SkPINR*), pre-vasculature (*SkPINR*, *SkPINS*), mature vasculature (*SkPINR, SkPINS, SkPINT*), and the developing angle meristem (*SkPINR, SkPINS*). Overall, our results suggest that long range polar auxin transport via PIN proteins controlled branching in the vascular plant ancestor. The redeployment of auxin transport to modulate a unique branching method in *Selaginella* highlights the flexibility of this molecular process. It is therefore likely that auxin transport patterns have been modified numerous times throughout evolution to create diverse and elaborate branching architectures.

V. SPENCER, C. J. HARRISON

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

Keynote lecture **15:40–16:30**

Herbivore-Induced Volatile Organic Compounds: A Chemical Handshake Mediating Interaction Contracts

André Kessler

Department of Ecology and Evolutionary Biology, Cornell University, United States

Biography:
André Kessler is Professor of Chemical Ecology at Cornell University, where he studies the chemical and molecular mechanisms, ecological consequences and evolutionary aspects of plant induced responses to herbivory. As a specific focus his group tries to understand how plant chemistry functions as a vehicle of information transfer between organisms and so affects ecological and evolutionary processes. His research includes a number of basic and applied study systems in North America, Kenya, Peru, Costa Rica and Colombia that use the concept of plant behavior to understand population, community, and ecosystem dynamics and develop sustainable technologies of pest control in agriculture. André Kessler did his undergraduate research and master thesis at the University of Würzburg, Germany and received a Ph.D. (Dr. rer. nat.) from the Max Plank Institute for Chemical Ecology and the University of Jena, Germany. Visit André's website

Abstract:
As sessile organisms, plants have to adjust their metabolism to ever-changing environmental conditions in order to stay in place and successfully reproduce. Thereby plants orchestrate interactions with other organisms (e.g. other plants, herbivores, pathogens, predators etc.) by providing cues or signals to whoever can read them. The seemingly universal language used to manipulate those interactions is chemical. This presentation reviews some of the Kessler Lab research on the ecological functionality and environmental context-dependency of chemical information transfer in the charismatic Northeastern goldenrod plants, *Solidago altissima*.

Selected talk **16:30–16:50**

The importance of continuous herbivory and HIPV emission for plant-plant information transfer

Jamie Waterman
Institute of Plant Sciences, University of Bern

Abstract:

Herbivore-induced plant volatiles (HIPVs) are emitted during herbivory and are critical for information transfer between plants. Upon perception of HIPVs released from herbivore-damaged plants, undamaged plants can activate their own defenses to proactively combat future herbivory. Additionally, there are many signals associated with herbivory that play an important role in inducing HIPV emission such as wounding created by feeding and chemical signals associated with herbivore oral secretions. Nevertheless, the importance of the temporal patterns of herbivory in HIPV-mediated information transfer between plants remains unknown. We tested the importance of continuous *Spodoptera exigua* (Lepidoptera) feeding in the induction of terpenoid defenses in *Zea mays* in real time using PTR-TOF-MS with a novel autosampler. Induction of mono- and sesquiterpene emission in undamaged neighboring plants was only observed during continuous herbivory and not simulated herbivory, despite higher maximum emissions in damaged plants under simulated herbivory. Further, we identify the importance of green leaf volatiles (GLVs) from damaged plants for terpene induction in neighboring plants, as the kinetics of GLV emission are dissimilar to other HIPVs and are released in bursts that coincide with active herbivore feeding. Collectively, we provide novel evidence that the timing of herbivory mediates information transfer between plants.

J.M. WATERMAN, M. ERB

University of Bern, Institute of Plant Sciences, Altenbergrain 21, 3013 Bern, Switzerland

Selected talk 16:50–17:10

Genomic basis of the evolution of resistance against its natural enemies in the poisonous and medicinal plant *Datura stramonium* (Solanaceae)

Ivan De la Cruz Arguello
*Department of Plant Protection Biology, Swedish University of Agricultural Sciences

Abstract:

Tropane alkaloids and terpenoids are widely used in the medicine and pharmaceutic industry and evolved as chemical defenses against herbivores and pathogens in the annual herb *Datura stramonium* (Solanaceae). Here, we present the first genomes of two plants from contrasting environments of *D. stramonium*. Using these de novo assemblies, along with other previously published genomes from 11 Solanaceae species, we carried out comparative genomic analyses to provide insights on the genome evolution of *D. stramonium* within the Solanaceae family, and to elucidate adaptive genomic signatures to biotic and abiotic stresses in this plant. Furthermore, we complemented this investigation with greenhouse and field experiments to elucidate the genetic basis of resistance to herbivores in this species. We also studied, in detail, the evolution of four genes of D. stramonium—Putrescine N-methyltransferase, Tropinone reductase I, Tropinone reductase II and Hyoscyamine-6S-dioxygenase—involved in the tropane alkaloid biosynthesis. Our analyses revealed that the genomes of *D. stramonium* show signatures of expansion, physicochemical divergence and/or positive selection on proteins related to the production of tropane alkaloids, terpenoids, and glycoalkaloids as well as on R defensive genes and other important proteins related with biotic and abiotic pressures such as defense against natural enemies and drought.

I. M. DE-LA-CRUZ AND J. NÚÑEZ-FARFÁN

Department of Evolutionary Ecology, Institute of Ecology, Universidad Nacional Autónoma de México,
Ciudad universitaria, Ciudad de México, México
**Current affiliation*

Selected talk 17:10–17:30

Amending soil with insect exuviae improves plant growth, pollinator attraction and fitness of flowering plants

Katherine Y. Barragán-Fonseca
Wageningen University

Abstract:

The production of insects as food and feed is increasing rapidly. Likewise, the resulting side-streams, such as insect exuviae (molted skins) do as well. To promote circularity in agriculture, these side-streams can be used as soil improver for crop production. We added different types of insect exuviae (*Acheta domesticus* L., *Hermetia illucens* L. and *Tenebrio molitor* L.) to the soil to investigate the effects on plant growth and resilience of *Brassica nigra* in a field experiment. We compared them with conventional organic soil amendments. The effects on plant traits, interactions with insects and seed set were investigated. Our findings show that insect exuviae had higher positive effects on the plant than the others soil amendments. Adding insect exuviae as soil amendment in the field benefits plant growth, plant-pollinator mutualism and fitness. Use of by-products from insect production as novel soil amendment can contribute to sustainable agricultural practices along with the conservation of ecosystem services.

K.Y. BARRAGÁN-FONSECA, D. MERTENS, J.J.A. VAN LOON, M. DICKE
Laboratory of Entomology, Wageningen University & Research, Droevendaalsesteeg 1, Wageningen 6708 PB, Netherlands

Keynote lecture **18:00–18:50**

Plant functional traits and rhizosphere processes: from global patterns to local interactions

Marina Semchenko
Institute of Ecology and Earth Sciences, University of Tartu, Estonia

Biography:

Marina Semchenko is an Associate Professor at the University of Tartu. The focus of her current research is on plant-soil interactions and the role of plant intraspecific variation and local adaptation in modifying soil functions and ecosystem stability. She started her studies at Tartu, did most of her PhD at the University of Sussex in the UK exploring plant root behaviour, and worked as an independent research fellow at the Soil and Ecosystem Ecology laboratory at the University of Manchester, UK, before recently moving back to Tartu, where she is doing a Marie Sklodowska-Curie Fellowship on plant-soil feedbacks and now starting an ERC consolidator grant on evolutionary responses of plant-microbial interactions to land use transitions.

Abstract:

Plant functional traits and their diversity across plant species are known to modify ecosystem functioning. However, mechanistic links between easily measured traits and rhizosphere interactions that determine species co-existence and drive carbon and nutrient cycling are still poorly understood. I will explore how plant functional traits modify feedbacks between plants and soil microbial communities. I will highlight root exudation as a poorly understood but crucial mediator of rhizosphere interactions across plant species as well as within species.

Selected talk **18:50–19:10**

High rainfall disturbs soil microbial structure and function in a mature temperate forest under elevated carbon dioxide

Katy Faulkner
University of Warwick

Abstract:

Climate change is expected to alter global precipitation patterns, with unknown impacts on biodiversity and ecosystem functioning. Temperate forests are one of the largest terrestrial carbon stocks, acting as sinks for greenhouse gases such as methane thus playing a major role in ameliorating global warming. Predicted changes to precipitation intensity and duration under future climates are likely to alter soil moisture dynamics in forest soils and the consequent impacts on the terrestrial carbon balance under future atmospheric carbon dioxide levels is not known. Here, we use a novel *in situ* approach to simulate high rainfall in soil plots within a mature temperate oak-dominated (*Quercus robur*) forest in Staffordshire, UK (Birmingham Institute of Forest Research Free-Air Carbon Dioxide Enrichment facility) where atmospheric CO2 levels are elevated 150 ppm above ambient levels. We show that an 8-week period of elevated rainfall and soil moisture had significant impacts on soil functioning. The forest soil methane sink was significantly reduced in the high rainfall treated soils by ~ 21-67%, resulting in greater methane accumulation in the atmosphere. Using molecular approaches, we show how the soil and fine root microbial communities are impacted by these climate stressors. The activities of soil extracellular enzymes were reduced during the high rainfall treatment. Our results demonstrate that important soil functional changes occur during high precipitation events and potential impacts of multiple climate stressors cannot necessarily be determined by the study of single stressors alone.

K. J. FAULKNER, **N.P. MCNAMARA, S. ULLAH, S. RAGUIDEAU, G. D. BENDING**

School of Life Sciences, University of Warwick, UK, CV4 7AL
UK Centre for Ecology & Hydrology, Lancaster, UK, LA1 4AP
School of Geography, Earth and Environmental Sciences, University of Birmingham, UK, B15 2TT

Selected talk **19:10- 19:30**

Microbial biodiversity contributes to soil carbon release: A case study on fire disturbed boreal forests

Xuan Zhou
University of Eastern Finland

Abstract:

Microbial communities often possess enormous diversity, raising questions about whether this diversity drives ecosystem functioning, especially the influence of diversity on soil decomposition and respiration. Although functional redundancy is widely observed in soil microorganisms, evidence that species occupy distinct metabolic niches has also emerged. In this paper, we found that apart from the environmental variables, increases in microbial diversity, notably bacterial diversity, lead to an increase in soil C emissions. This was demonstrated using structural equation modelling (SEM), linking soil respiration with naturally differing levels of soil physio-chemical properties, vegetation coverage, and microbial diversity after fire disturbance. Our SEMs also revealed that models including bacterial diversity explained more variation of soil CO2 emissions (about 45%) than fungal diversity (about 38%). A possible explanation of this discrepancy is that fungi are more multifunctional than bacteria and, therefore, an increase in fungal diversity does not necessarily change soil respiration. Further analysis on functional genes suggested that bacterial and fungal diversities mainly explain the potential decomposition of recalcitrant C than of labile C. Overall, by incorporating microbial diversity and the environmental variables, the predictive power of models on soil C emission was significantly improved, indicating microbial diversity is crucial for predicting ecosystem functions.

XUAN ZHOU, HUI SUN, JUSSI HEINONSALO, JUKKA PUMPANEN, FRANK BERNINGER

Department of Environmental and Biological Sciences, University of Eastern Finland, PL 111 80101 JOENSUU, Finland

Wednesday 20 July 2022

Keynote lecture 09:00-09:50

Molecular mechanisms of plant responses to cold stress

Shuhua Yang

State Key Laboratory of Plant Physiology and Biochemistry, College of Biological Sciences, China Agricultural University, China

Biography:

Shuhua Yang is a professor in the College of Biological Science, China Agricultural University. She received B.S. and M.S. degrees at Nankai University, China, and a Ph.D degree at National University of Singapore. After completing postdoctoral research at Cornell University, she joined the faculty at China Agricultural University. She is currently the Director for the State Key Laboratory of Plant Physiology and Biochemistry. Her laboratory mainly focuses on the study of molecular mechanism of plant responses to low temperatures. As one of important environmental factors, low temperatures restrict plant growth, development and distribution. How plants sense and respond to low temperatures is poorly understood. To understand the molecular mechanism underlying plants' response to low temperatures, her lab has been undertaking genetic, biochemical and molecular approaches to identify novel components essential for low temperature signaling pathway and investigate the functions of these components in cold responses using Arabidopsis thaliana and maize as research systems. She is also investigating the crosstalk of cold signaling and plant hormone signaling. Her research aims at deep understanding of how plants perceive and respond to the environmental temperature change. Visit Shuhua's website

Abstract:

Cold stress adversely affects plant growth and development, crop productivity and geographical distribution. Dissecting how plants respond to cold stress will provide molecular and genetic basis for breeding cold-tolerant crops. In this talk, I first report how this Ca2+ signal is produced, perceived and relayed to the downstream cold signalling pathway in Arabidopsis. Second, I report how cold signalling is attenuated by protein kinases, CRPK1, MPK3/6 and BIN2, in Arabidopsis. Third, the natural variations of two genes, ZmRR1 and ZmbZIP68, modulate cold tolerance in maize will be presented.

References

1. Ding et al. (2022) CPK28–NLP7 module integrates cold-induced Ca2+ signal and transcriptional reprogramming in Arabidopsis. Sci Adv accepted.
2. Li et al. (2022) The transcription factor bZIP68 negatively regulates cold tolerance in maize. Plant Cell doi: 10.1093/plcell/koac137.
3. Zeng et al. (2021) Natural variation in a type-A response regulator confers maize chilling tolerance. Nat Commun 12: 4713.
4. Liu et al. (2021) The calcium transporter ANNEXIN1 mediates cold-induced calcium signaling and freezing tolerance in plants. EMBO J 40: e104559.
5. Wang et al. (2019) PUB25 and PUB26 promote plant freezing tolerance by degrading the cold signaling negative regulator MYB15. Dev Cell 51: 222-235.
6. Ding et al. (2019) EGR2 phosphatase regulates OST1 kinase activity and freezing tolerance in Arabidopsis. EMBO J 38: e99819.
7. Ye et al. (2019) BRASSINOSTEROID-INSENSITIVE2 negatively regulates the stability of transcription factor ICE1 in response to cold stress in Arabidopsis. Plant Cell 31: 2682-2696.
8. Li et al. MPK3- and MPK6-mediated ICE1 phosphorylation negatively regulates ICE1 stability and freezing tolerance in Arabidopsis. Dev Cell 43: 630-642.
9. Liu et al. (2017) Plasma membrane CRPK1-mediated phosphorylation of 14-3-3 proteins induces their nuclear import to fine-tune CBF signaling during cold response. Mol Cell 66: 117-128.

Selected talk **09:50–10:10**

Production of nanobodies in *Marchantia polymorpha*

Anna Sze Wai Tse
University of Cambridge

Abstract:

Monoclonal antibodies (MAb) can serve as valuable therapeutic drugs and research reagents, but currently they remain inaccessible to most parts of the world due to low availability and high production costs. This problem can be addressed by producing an alternative with a simpler structure for easier production in more scalable and cheaper systems. We thus propose the production of nanobodies, smaller than but equally specific as MAb, in the model liverwort, *Marchantia polymorpha*, which is easier to manipulate and faster to grow than most other model plants. We designed and used *Escherichia coli* to trial the production of Green Fluorescent Protein (GFP)-binding nanobodies, tagged with mScarlet red fluorescent protein and 7 histidine residues for Ni-NTA purification, then developed a fast microscopy-based assay for verifying the binding of nanobody-mScarlet to GFP. We then demonstrated the expression of these nanobodies from the nuclear genome of Marchantia. This result shed light on plant-based production of more accessible nanobodies.

S. W. TSE, F. GUZMAN-CHAVEZ, F. ROMANI, J. HASELOFF

Department of Plant Sciences, University of Cambridge, Downing Street, Cambridge, UK, CB2 3EA

Selected talk **10:10–10:30**

The role of epigenetic in long-lasting post-harvest resistance in tomato

Katie Stevens
University of Birmingham

Abstract:

Tomato is a major crop world-wide however its production is heavily limited by *Botrytis cinerea*. Due to the toxicity of post-harvest pesticide application, alternative control methods such as priming are being investigated. Our work has shown that priming seedlings (2 weeks old) with the chemical β-aminobutyric (BABA) results in long-lasting resistance against *B.* cinerea in the fruit as well as transgenerational resistance. This work explores how changes in DNA methylation mark long lasting priming in fruit and explores the hypothesis that young plants display a greater epigenetic imprinting capacity. Using whole genome bisulphite sequencing analysis (WGBS), differentially methylated regions (DMRs) specific to the phenotype of long-lasting resistance have been identified. Our results illustrate that BABA treatment impacts CHH context methylation depending on timepoint of application, confirming our hypothesis. Interestingly however, changes in CHH methylation after BABA treatment are not maintained throughout the life of the plant. A transcriptomic analysis on *B. cinerea* infected fruit BABA treated plants identified differentially expressed genes (DEGs) associated with resistance against *B. cinerea*. By overlapping our DEGs of interest with our resistance associated DMRs we have identified markers of long-lasting priming in tomato fruit which could serve for targets of durable resistance in other crops.

KATIE STEVENS, VICTORIA PASTOR, MIKE ROBERTS, MARCO CATONI, ESTRELLA LUNA

School of Biosciences, University of Birmingham, Birmingham, UK

Keynote lecture **12:00–12:50**

Applying CRISPR/Cas to Plants: From Gene Editing to Chromosome and Tissue Engineering

Holger Puchta
Karlsruhe Institute of Technology, Germany

Biography:
Holger Puchta is director of the Botanical Institute and holds since 2002 the Chair of Plant Molecular Biology and Biochemistry at the Karlsruhe Institute of Technology (KIT) in Germany. After his study of biochemistry at the University of Tübingen and his PhD at the Max-Planck-Institute for Biochemistry in Munich he joined the laboratory of Barbara Hohn at the Friedrich Miescher Institute in Basel, Switzerland before he became in 1995 group leader at the Leibnitz Institute for Plant Genetics in Gatersleben (IPK). In 2000 he obtained his habitation in genetics from the University Halle. He was worldwide the first scientist to demonstrate that site-specific nucleases can be applied to induce different kinds of controlled change in plant genomes. His group elucidated major mechanisms of DNA double strand break repair and he was one of leading scientists adopting the CRISPR/Cas technology to plants. Recently his group was able to achieve another important breakthrough for breeding: CRISPR/Cas mediated plant chromosome engineering. For his work on plant genome engineering, he was named "Pioneer of Plant Biotechnology" by the Plant Biotechnology Journal and he was awarded twice with an advanced grant of the European Research Council. Visit Holger's website

Abstract:
The CRISPR/Cas technology has been applied in plants mainly on genes for the improvement of traits. However, breeding also requires the breaking or establishing genetic linkages. Using egg-cell specific expression of SaCas9 nuclease and optimizing screening protocols we were able to change genetic linkages by inducing non-homologous end joining (NHEJ)-mediated heritable translocations in the Mb range between heterologous chromosomes in Arabidopsis thaliana. By molecular and cytological analysis, we could confirm that the chromosome arm exchanges we obtained between chromosomes 1 and 2 as well as 1 and 5 are conservative and reciprocal3. Recent improvements in sequence analysis of crop plants reveal that multi Mb long inversions occur with high frequency between different genotypes, leading to crossover suppression. Therefore, we set out to revert the 1.1 Mb long heterochromatic knob (hk4S) inversion on chromosome 4 of the accession Arabidopsis Col-0. If a knob carrying accession like Col-0 is crossed with a knob-less accession like Ler-1 meiotic recombination is completely suppressed within the inverted region. Crossing Col-0 with the rearranged chromosome 4 with Ler-1, we were able to target meiotic crossovers into a region that was inaccessible for genetic exchange before. Moreover, we were able show that meiotic recombination can be suppressed in nearly an entire chromosome by inducing a heritable inversion of more than 17 Mb, covering most of chromosome 2 of Arabidopsis Col-0. This left only a 2 and 0.5 Mb telomeric end in their original orientation. By performing SNP marker analysis with the offspring of crosses with the accession Ler-1 we detected a massive reduction of crossovers (CO) within the inverted region, coupled with a shift of CO to the telomeric ends. Interestingly, the few genetic exchanges detected within the inversion all originated from double CO. Our results demonstrate that restructuring of plant genomes by chromosome engineering has the potential to revolutionize plant breeding. Using the SaCas9 nuclease to induce multiple DSBs in functional repetitive DNA, namely the 45S rDNA or the centromeric repeats, we became aware that cell death can be induced in a controlled way in Arabidopsis. This approach, named CRISPR-Kill, can be used as tool for tissue

engineering. By simply exchanging the constitutive promoter of SaCas9 with cell type-specific promoters, it was possible to block organogenesis. By AP1-specific expression of CRISPR-Kill, we were able to specifically eliminate petals. In addition, by expressing CRISPR-Kill in root-specific pericycle cells, we were able to dramatically reduce the number and the length of lateral roots.IN the future, the application of CRISPR-Kill may not only help to study and control development but could also be used to change the biochemical properties of plants by tissue engineering.

Keynote lecture **14:00–14:50**

How proteostasis shapes the plant response to environmental stimuli

Suayib Üstün

University of Tübingen/Ruhr-University of Bochum, Germany

Biography:

Suayib studied cell and molecular biology at the Friedrich-Alexander University in Nürnberg-Erlangen, Germany. In 2010 he started his PhD in the lab of Prof. Frederik Börnke, where he worked on the functional characterization of bacterial type-III effectors from Xanthomonas targeting the proteasome. Suayib completed his PhD in 2013 and continued to work in the same lab as a postdoctoral researcher. In 2016 he joined the lab of Prof. Daniel Hofius at the Swedish University of Agricultural Sciences in Uppsala/Sweden with his FEBS long-term Fellowship. Here, he initiated the project to study the crosstalk between proteasome and autophagy degradation pathways in Pseudomonas infection. Since September 2018, he is Emmy Noether Group Leader at the ZMBP trying to understand how proteolytic degradation pathways influence plant immunity. In 2020 he received the ERC Starting Grant to study the role of autophagy in plant-microbe interactions on a broader scale. Since 2022 he is a Professor for Plant Cell Biology at the Ruhr-University of Bochum in Germany.

Visit Suayb's website

Abstract:

Protein homeostasis is epitomized by a tight equilibrium of protein biosynthesis and degradation; the 'life and death' of proteins. Approximately one-third of newly synthesized proteins are degraded. As such, regulated protein turnover is required to maintain cellular integrity and survival. Autophagy and the ubiquitin-proteasome system (UPS) are the two principal intracellular degradation pathways in eukaryotes. Both degradation pathways orchestrate many cellular processes during plant development and upon environmental stimuli. As such, both pathways play a major role during plant-microbe interactions. We have recently identified that autophagy and the proteasome system are exploited by bacterial pathogens to reprogram host cellular pathways. By studying this intimate interplay, we can utilize plant pathogenic bacteria as tools to understand host cellular degradation machineries and to decipher novel components and functions. In my presentation, I will not only cover our recent work on the role of autophagy and the proteasome in plant-microbe interactions but will report on our attempts to identify new autophagy regulators and new functions of known UPS components. I will highlight different examples and discuss our recent advances.

PAUL GOUGUET[1], GAUTIER LANGIN[1], JIA XUAN LEONG[1], MANUEL GONZALEZ FUENTE[1], SHANSHUO ZHU[1], MARGOT RAFFEINER[1], SUAYB ÜSTÜN[1,2]

[1]*University of Tübingen, Center for Plant Molecular Biology (ZMBP), 72076 Tübingen, Germany*
[2]*Faculty of Biology & Biotechnology, Ruhr-University Bochum, 44780 Bochum, Germany*

Selected talk **14:50–15:10**

Isolation and molecular characterization of native Trichoderma isolates from West Java, Indonesia and the assessment of their roles for enhancing rice development and physiological traits

Febri Doni

Universitas Padjadjaran

Abstract:

Trichoderma spp. are soil fungi that are highly interactive in soil and plants root. Due to their capability to form symbiosis association with plants, *Trichoderma* spp. have become one of the most studied filamentous fungi for improving the production and growth of numerous plant species. The comprehensive study of the ability of *Trichoderma* in increasing rice productivity is still limited. In this study, we aim to report our intensive study on the characterization of native Indonesian *Trichoderm*a isolates and their capability in improving rice plant growth, development, and yield. Our result indicated that *Trichoderma* spp. have unique characteristics with regards to their capability in producing plant-growth promoting compounds. Further studies showed that *Trichoderma* spp. are able to increase rice germination, vigor, vegetative growth, physiological characteristics (photosynthesis and transpiration rates), and yield. The result of this study adds to the further understanding of the role of symbiotic fungi in enhancing rice productivity.

F. DONI, S.I. AKBARI, M. MIRANTI

Department of Biology, Faculty of Mathematics and Natural Sciences, Universitas Padjadjaran, Jatinangor 45363, West Java, Indonesia

Selected talk **15:10–15:30**

Engineering plant-microbe interactions to promote host health and resilience

Itumeleng Moroenyane
*Donald Danforth Plant Science Center

Abstract:

Ongoing global climate change has unpredictable consequences for agriculture, changing the prevalence of pathogens and the severity of the diseases they cause. Emerging research shows that the plant microbiome affects immunity, nutrient acquisition, and stress tolerance. Although the role of stress in influencing the plant microbiome is well documented, a comprehensive understanding of successional patterns and prevailing assembly processes of soybean-associated microbes is still lacking. Here, we investigate different soybean microbial communities' spatial and temporal colonisation patterns and their overall ecological assembly processes using amplicon sequencing. The results highlighted that there were interactions between spatial and temporal dynamics that influenced microbiome diversity patterns. Moreover, there was an existence of a strong temporal dependence of communities. Additionally, the plant compartment and developmental stage modulated the balance between niche-based and neutral processes. The seed microbiome colonised the shoot compartment during early developmental stages, whilst the soil microbiome colonised the rhizosphere. Different microbiome sources also influenced the abundance of N-cycling genes across all plant compartments. This work, therefore, aims to improve our understanding of plant stress tolerance from a holobiont point of view (plants and their associated microbes), focusing on plant innate microbiome, to enhance plant resistance to biotic and abiotic stress.

ITUMELENG MOROENYANE[1], JULIEN TREMBLAY[2], AND ÉTIENNE YERGEAU[1]

[1]Centre Armand-Frappier Santé Biotechnologie, Institut National de la Recherche Scientifique,531 Boulevard des Prairies, Laval, Québec, H7V1B7, Canada
[2]Energy, Mining, and Environment, Natural Research Council Canada, 6100 Avenue RoyalMount, Montreal, Quebec, H4P 2R2, Canada
**Current affiliation*

Thursday, 21 July 2022

Keynote lecture **09:00-09:50**

B vitamins as cogs of plant metabolism

Teresa Fitzpatrick
University of Geneva, Switzerland

Biography:

Teresa Fitzpatrick did her undergraduate and PhD studies at University College Dublin (Ireland) finishing in 1998, followed by a short fellowship at the Imperial Cancer Research Fund laboratories in Clare Hall, London (now part of Cancer Research UK). She then did a post-doc at the Swiss Federal Institute of Technology in Zurich (ETHZ, 1998–2002), after which she became a group leader there, pursuing projects on vitamin metabolism. In 2008, Teresa was awarded a Swiss National Science Foundation professorship to be pursued at the University of Zurich but she moved to the University of Geneva as a tenured Associate Professor in 2009 and was awarded a Full Professorship in 2015. Teresa was Director of the Plant Biology Department from 2012 to 2017. The research in the Fitzpatrick laboratory focuses on the biochemistry and physiology behind vitamin metabolism in plants and how these processes interact with other aspects of general primary plant metabolism. Teresa's research also addresses aspects of plant stress physiology, more specifically how alteration of vitamin metabolism affects environmental stress responses. Recently, Teresa has also become interested in the association of vitamin metabolism and the circadian clock. Her work also involves applied aspects particularly in relation to enhancing nutritional content of crop plants (biofortification) in a bid to alleviate some of the deficiencies encountered by populations that rely on a sustenance diet. A range of multi-disciplinary biological and chemical techniques form part of the research programme, that include molecular cellular biology, biochemistry, genetics, protein chemistry and selected biophysical techniques. Read the *New Phytologist* Profile of Teresa. Visit Teresa's website

Abstract:

Vitamins (as vital organic micronutrients for animals) were first discovered over a century ago. Plants biosynthesize these compounds de novo and are a predominant source of vitamins for humans. While gathering the wealth of information on the impact of vitamins in human health and disease alleviation, the biology of these compounds in plants themselves was sidelined. Surprisingly, the pathways for biosynthesis of vitamin compounds in plants were only elucidated recently. Within the vitamin classes, the B vitamins are renowned for their biochemical function as coenzymes – facilitating catalysis by enzymes dependent on them. As plants require a daily metabolic reprograming due to light/dark cycles, timely provision of coenzymes may be an important controller of the level of enzyme activity, which in turn influences daily metabolic homeostasis. Furthermore, each B vitamin is a family of compounds and little is known about the importance of maintaining individual family homeostasis. In this talk, I will present examples of aspects that we uncovered that relate to the integration of B vitamins into plant nutrient and health status. An application of this work leads to the possibility of overproduction of these compounds to enhance plant nutrient status and even stress responses. In this context, I will also discuss our work on enhancing the levels of particular B vitamins in consumed parts of crop plants for biofortification purposes.

Selected talk 09:50–10:10

Zaxinone: discovery, application, and mode of action

Jian You (Eric) Wang
King Abdullah University of Science and Technology

Abstract:

The breakdown of carotenoids, catalyzed by the family of carotenoid cleavage dioxygenases (CCDs), provides signaling molecules and precursors of plant hormones, which play important roles in plant growth, development and response to biotic and abiotic stress. Recently, we characterized the enzyme Zaxinone Synthase (ZAS), a rice representative of an overlooked CCD subfamily, and showed that it forms the novel metabolite zaxinone. Application of zaxinone to rice seedlings led to a striking increase in root growth and biomass. Multi-omics analysis revealed that zaxinone promotes rice growth most likely by increasing sugar uptake and metabolism, leading to an elevated root starch content, and induced glycosylation of cytokinins. In addition, the loss-of-function rice mutant *zas* contained less zaxinone and showed retarded growth accompanied by enhanced levels of strigolactones (SLs) in roots and root exudates. Exogenous application of zaxinone restored several *zas* phenotypes, by reducing SL levels and promoting root growth in wild-type seedlings, confirming that they are caused by zaxinone deficiency. Finally, we developed easy-to-synthesize and highly efficient mimics of zaxinone (MiZax) for elucidating zaxinone biology and investigating rice development, which could be also applied in agriculture to improve crop performance.

Wang, J. Y., Haider, I., Jamil, M., Fiorilli, V., Saito, Y., Mi, J., et al. (2019). The apocarotenoid metabolite zaxinone regulates growth and strigolactone biosynthesis in rice. Nature Communications 10, 810. doi: 10.1038/s41467-019-08461-1.
Wang, J. Y., Jamil, M., Lin, P.-Y., Ota, T., Fiorilli, V., Novero, M., et al. (2020). Efficient mimics for elucidating zaxinone biology and promoting agricultural applications. Molecular Plant 13, 1654–1661.
Wang, J. Y., Lin, P.-Y., and Al-Babili, S. (2021a). On the biosynthesis and evolution of apocarotenoid plant growth regulators. Seminars in Cell & Developmental Biology 109, 3–11. doi: 10.1016/j.semcdb.2020.07.007.
Wang, J. Y., Alseekh, S., Xiao, T., Ablazov, A., Perez de Souza, L., Fiorilli, V., et al. (2021b). Multi-omics approaches explain the growth-promoting effect of the apocarotenoid growth regulator zaxinone in rice. Communications Biology 4, 1–11.
Wang, J. Y., Chen, G.-T.E., Jamil, M.,Braguy, J., Sioud, S.,Liew, K.X., Balakrishna, A., et al. (2022a). Protocol for characterizing strigolactones released by plant roots. STAR Protocols 3, 101352 doi.org/10.1016/j.xpro.2022.101352
Wang, J. Y., Jamil, M., Hossain, Md. G., Chen, G.-T.E., Berqdar, L., Ota, T., et al. (2022b). Evaluation of the Biostimulant Activity of Zaxinone Mimics (MiZax) in Crop Plants. Frontiers in Plant Science 13:874858. doi: 10.3389/fpls.2022.874858.

JIAN YOU WANG[1], MUHAMMAD JAMIL[1], VALENTINA FIORILLI[2], YOSHIMOTO SAITO[3], TAKASHI GOJOBORI[3], IKRAM BLILOU[4], LUISA LANFRANCO[2], PAOLA BONFANTE[2], TADAO ASAMI[5], ALISDAIR R. FERNIE[6], SALIM AL-BABILI[1]

[1]*King Abdullah University of Science and Technology, Division of Biological and Environmental Science and Engineering, Center for Desert Agriculture, the BioActives Lab, Thuwal, 23955-6900, Saudi Arabia*
[2]*Department of Life Sciences and Systems Biology, University of Torino, Italy*
[3]*King Abdullah University of Science and Technology, Computational Bioscience Research Center, Thuwal, Saudi Arabia*
[4]*King Abdullah University of Science and Technology, Division of Biological and Environmental Science and Engineering, Center for Desert Agriculture, the Laboratory of Plant Cell and Developmental Biology, Thuwal, 23955-6900, Saudi Arabia*
[5]*Graduate School of Agricultural and Life Sciences, The University of Tokyo, Tokyo, Japan*
[6]*Max-Planck-Institute of Molecular Plant Physiology, Am Mühlenberg 1, 14476, Potsdam-Golm, Germany*

Selected talk 10:10–10:30

The Arabidopsis R-SNARE VAMP714 is essential for polarisation of PIN proteins and auxin responses

Julien Agneessens
Durham University

Abstract:

The asymmetrical distribution of proteins at the plasma membrane is referred to as cell polarity and is a common feature of both unicellular and multicellular organisms. In plants, polar distribution of auxin efflux carriers PIN-FORMED (PIN) in cells allows the directional transport of the phytohormone auxin through the tissues which regulates organ architecture and development. Numerous studies have underlined the importance of constitutive endocytic recycling of PIN proteins to establish their polar distribution at the plasma membrane. We identified a gain-of-function mutant of *VAMP714*. This gene is encoding for a N-ethylmaleimide-sensitive factor adaptor protein receptor (SNARE) that mediates vesicle fusion at a target membrane. In *Arabidopsis*, VAMP71 family proteins are involved in endosomal trafficking. Using genetics, transgenic and cell biological approaches we investigated the function of VAMP714 and generated a new model of endocytic recycling of PIN that includes this SNARE protein.

XIAOYAN GU, KUMARI FONSEKA, JULIEN AGNEESSENS, STUART A. CASSON, ANDREI SMERTENKO, GUANGQIN GUO, JENNIFER F. TOPPING, PATRICK J. HUSSEY, KEITH LINDSEY

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

Keynote lecture **11:00–11:50**

Growth-defense tradeoffs in plants: myths, facts, and some mechanisms

Carlos L. Ballaré

Universidad de Buenos Aires and CONICET, Argentina

Biography:

Carlos L. Ballaré is professor of plant biology at the University of Buenos Aires and San Martín National University (Buenos Aires, Argentina), and a senior scientist with the National Research Council of Argentina (CONICET). He completed his MSc and PhD degrees at the University of Buenos Aires and at Oregon State University (USA), respectively, and was a postdoctoral scholar at Utah State University (USA). His laboratory has conducted pioneering research on the role of photoreceptors in regulating plant responses to the proximity of neighbors, and on the effects of ultraviolet radiation on plants and terrestrial ecosystems. The Ballaré lab (http://epl.agro.uba.ar/) uses a combination of genetic, physiological, and genomic and biochemical tools to understand the mechanisms by which photoreceptors regulate plant immunity against pathogens and herbivores. Carlos has received several awards including the recognition as one of the 50 Latin American leaders for the New Millennium by CNN and Time (1990), a Guggenheim Fellowship (2001), the Konex Merit Prize in 2013, awarded by the Konex Foundation (Argentina), and the Georg Forster Research Award from the Alexander von Humboldt Foundation (Germany) in 2017 and was elected to the National Academy of Exact, Physical and Natural Sciences of Argentina in 2021. Carlos has served on the editorial boards of several leading journals in the fields of plant biology and ecology, including *Plant Physiology* (2000-2005), *New Phytologist* (2017--) and *Oecologia* (2015--), where he is currently one of the Editors-in-Chief. As part of his outreach activity, Carlos has been a member of the Environmental Effects Assessment Panel of the United Nations Environment Programme, between 2002 and 2019. Visit Carlos' website

Abstract:

The growth-defense tradeoff in plant biology has attracted considerable attention in recent years, mainly in connection with studies of the mechanisms that allow plants to deal with competitors and consumer organisms (herbivores and pathogens). In this presentation, I will begin by briefly discussing some of the assumptions implicit in studies that describe negative relationships between plant growth and accumulation of defensive metabolites, including the idea that these negative associations reflect a direct tradeoff that depends on the allocation of limited resources to alternative, antagonistic physiological functions. I will then focus on the configurational tradeoffs that plants face when adjusting their phenotype to face competitors and consumers suggesting that rather than a direct tradeoff based on resource limitation, there are intrinsic configurational costs associated with the decisions to grow or defend. I will discuss recent advances in our understanding of the sensory and signaling mechanisms that plants use to choose the right configuration in complex environments. In particular, I will focus on the mechanisms by which competition signals, perceived by the photoreceptor phytochrome B, regulate plant defense responses controlled through the jasmonic acid signaling pathway. Finally, I will speculate about the ecological implications of these mechanisms and the possibility of manipulating them for agronomic purposes.

Keynote lecture **14:00–14:50**

Mycorrhizal fungal dispersal across spatial scales

Bala Chaudhary
Dartmouth College, United States

Biography:
Dr. Bala Chaudhary is a soil ecologist and Associate Professor of Environmental Studies at Dartmouth College. She earned her undergraduate degree from the University of Chicago and her M.S. and Ph.D. from Northern Arizona University, previously holding faculty appointments at DePaul University and Loyola University Chicago. Research in Chaudhary's lab focuses on plant-soil-microbial interactions and mycorrhizal symbioses with an emphasis on using trait-based approaches to study microbial dispersal at macrosystem scales. In 2019, she was awarded a National Science Foundation CAREER award to study mycorrhizal dispersal. Dr. Chaudhary also conducts research on ways to broaden scientific participation and promote racial and ethnic diversity, equity, and inclusion and has won awards for her work on promoting anti-racism in STEM. Visit Bala's website

Abstract:
Dispersal is a key process driving local-scale community assembly and global-scale biogeography of ecological communities. Plants in most ecosystems on Earth form close associations with mycorrhizal fungi, obligate root symbionts that improve plant access to soil resources in exchange for photosynthetically derived carbon. Significant knowledge gaps remain regarding the mechanisms of dispersal for these cryptic, yet common plant symbionts. Combining macrosystems ecology, trait-based methods, eDNA metabarcoding, and data synthesis, we address fundamental questions in the emerging field of microbial movement ecology.

Selected talk **14:50–15:10**

Global evidence for a symbiotic bacteria filter on N-fixing plant establishment on islands.

Camille Delavaux
ETH Zurich

Abstract:

Island biogeography has classically focused on abiotic drivers of species distributions. However, recent work has begun to highlight the importance of mutualistic interactions in structuring island floras. The limited occurrence of specialist pollinators and mycorrhizal fungi have been found to restrict plant colonization on oceanic islands. Another important mutualistic association occurs between plants and N-fixing bacteria. For an estimated nearly 15,000 plant species, association with these symbiotic bacteria can be essential to meeting nitrogen and energetic demands. Therefore, the availability of these symbionts could determine colonization success for those species, which would result in ecosystem impacts on N-poor island systems. We find that plants that associate with N-fixing bacteria are disproportionately underrepresented on islands relative to other plant species, with a 22% decline in the proportion of N-fixing plant species on islands. Further, the probability of island N-fixing plants on islands decreases with island isolation and the proportion of N-fixing plants decreases with distance for all but the smallest islands. These findings suggest that N-fixing bacteria serve as a filter to plant establishment on islands, altering global plant biogeography, with implications for ecosystem development and introduction risks.

C. S. DELAVAUX, P. WEIGELT, S. M. MAGNOLI, H. KREFT, T. W. CROWTHER, J. D. BEVER

[1]*Department of Environmental Systems Science, ETH Zurich, Universitätstrasse 16, 8092 Zurich, Switzerland*
[2] *Department of Biodiversity, Macroecology & Biogeography, University of Gottingen, Büsgenweg 1, 37077 Göttingen, Germany*
[3]*Department of Ecology and Evolutionary Biology, The University of Kansas, 2041 Haworth Hall, 1200 Sunnyside Avenue, Lawrence, Kansas 66045, USA*
[4]*Kansas Biological Survey, The University of Kansas, 106 Higuchi Hall, 2101 Constant Ave, Lawrence, Kansas 66047, USA*

Selected talk **15:10–15:30**

The early branching arbuscular mycorrhizal fungus *Paraglomus occultum* carries a small and repeat poor genome compared to relatives in the Glomeromycotina

Mathu Malar C

University of Ottawa

Abstract:

The arbuscular mycorrhizal fungi (AMF) are obligate root symbionts in the subphylum Glomeromycotina that can benefit land plants by increasing their soil nutrient uptake in exchange for photosynthetically fixed carbon sources. To date, annotated genome data from representatives of the AMF orders Glomerales, Diversisporales, and Archaeosporales have shown that these organisms have large and highly repeated genomes, and no genes to produce sugars, fatty acids. This led to the hypothesis that the most recent common ancestor (MRCA) of Glomeromycotina was fully dependent on plants for nutrition. Here, we aimed to further test this hypothesis by obtaining annotated genome data from a member of the early diverging order Paraglomerales (*Paraglomus occultum*). Genome analyses showed this species carries a 39.6 Mb genome and considerably fewer genes and repeats compared to most AMF relatives with annotated genomes. Consistent with phylogenies based on ribosomal genes, our phylogenetic analyses suggest *P. occultum* as the earliest diverged branch within Glomeromycotina. Overall, our analyses support the view that the MRCA of Glomeromycotina carried hallmarks of obligate plant biotrophy. The small genome size and content of *P. occultum* could either reflect adaptive reductive processes affecting some early AMF lineages, or indicate that the high gene and repeat family diversity thought to drive AMF adaptability to host and environmental change was not an ancestral feature of these prominent plant symbionts.

MATHU MALAR C, NICOLAS CORRADI

Department of Biology, University of Ottawa, ON, Ottawa, K1N 6N5, Canada

Selected talk **16:00–16:20**

Ectomycorrhizal diversity and community traits drive the N uptake of beech roots

Anis Mahmud Khokon

Functional Forest Ecology, Department of Biology, University of Hamburg, Germany

Abstract:

Roots of forest trees are colonized by a diverse spectrum of ectomycorrhizal (EM) fungal species differing in their nitrogen (N) acquisition abilities. Here, we hypothesized that root N gain is the result of EM fungal diversity or related to taxon-specific traits for N uptake. To test our hypotheses, we traced ^{15}N enrichment in fine roots, coarse roots and taxon-specific ectomycorrhizas in temperate beech forests in two regions and three seasons, feeding 1 mM NH_4NO_3 labelled with either $^{15}NH_4^+$ or $^{15}NO_3^-$. We morphotyped more than 45000 vital root tips and identified 51 of 53 detected EM species by sequencing. EM root tips exhibited strong, fungal taxon-specific variation in ^{15}N enrichment with higher NH_4^+ than NO_3^- enrichment. The translocation of N into the upper parts of the root system increased with increasing EM fungal diversity. We conducted LASSO regression to identify influential EM species predicting root N gain. We did not find any significant EM fungal taxon. Our results support that community but not individual EM fungal traits drive root N acquisition. We propose that this behaviour constitutes an ecological mechanism for the stability of diverse EM fungal communities and highlights the importance of EM diversity for tree N nutrition.

A.M. KHOKON, DENNIS JANZ and ANDREA POLLE

Forest Botany and Tree Physiology, University of Göttingen, Göttingen, Germany

Selected talk **16:20–16:40**

New ecological insights on Mucoromycotina ‘fine root endophytes’ (MFRE): their impact on plant growth under low nutrient conditions

Besiana Sinanaj

University of Sheffield

Abstract:

Mucoromycotina ‘fine root endophytes’ (MFRE) are an understudied group of mycorrhizal fungi that are challenging our notions of the diversity and complexity of plant-fungal symbioses in nature. MFRE, which are molecularly and morphologically distinct to arbuscular mycorrhizal fungi (AMF), have been identified across land plants and form nutritional mutualisms with liverworts and Lycopodiella inundata. It is now imperative that we learn more about the ecology and function of these fungi in a wider range of vascular plants to widen our understanding of their true ecological significance. Here, soil sieving methods were applied to obtain an MFRE-enriched soil inoculum, which was used to grow Holcus lanatus grass in a pot-based experiment, in parallel with a commercial AMF inoculum. Organic and inorganic 15N-labelled nutrient sources were introduced to pots, and it was found that the presence of MFRE in the microbial community did not impair fungal transfer of 15N to plants. Although initially, plants in symbiosis with only AMF grew largest, after the N sources were added to pots, these plants suffered a greater growth depression than plants in the presence of MFRE. This suggests nutrient availability may drive symbiotic benefits derived by host plants from MFRE associations.

B. SINANAJ, S. PRESSEL, M. I. BIDARTONDO, K. J. FIELD

School of Biology, Faculty of Biological Sciences, University of Leeds, Leeds, LS2 9JT, UK.

Friday, 22 July 2022

Keynote lecture 09:00–09:50

The central role of the central cell in plant reproduction

Weicai Yang

Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing, China

Biography:
Dr. Wei-Cai Yang is currently the Director and Principal Investigator of the Institute of Genetics and Developmental Biology (IGDB), Chinese Academy of Sciences, and the Deputy Dean of the College of Advanced Agricultural Sciences, The University of Chinese Academy of Sciences. Dr. Yang is a graduate of Lanzhou University, China where he received a BSc and MSc in cell biology, and obtained his Ph.D. from Wageningen University, The Netherlands. After his Ph.D., Dr. Yang continued his scientific career in Wageningen University, Cold Spring Harbor Laboratory, New York and Institute of Molecular Agrobiology in Singapore as research fellows during 1994-2000. He became a principal investigator at Temasek Life Sciences Laboratory, Singapore in 2000, and joined IGDB in 2003. Visit Weicai's website

Abstract:
Unlike that in animals and lower plants, the meiotic products-the haploid spores-undergo additional mitosis to produce a multicellular gametophyte in flowering plants where double fertilization was evolved. The male gametophyte (pollen) contains two sperms enclosed within the vegetative cell, the female gametophyte (embryo sac) contains seven-cells, namely an egg, two synergids, a central cell, and three antipodals. The central cell receives the large central vacuole and two polar nuclei during cytokinesis and is therefore the only diploid cell of the embryo sac. In past 20 years, it became clear that the synergid plays a critical role in pollen tube guidance, reception and sperm release. Accumulating evidences support a central role of the central cell in plant reproduction. First, central cell serves as the second female gamete to fertilize with one of the sperm to initiate endosperm development; Second, central cell regulates antipodal life span and egg cell development; Third, central cell also plays a critical role for pollen tube guidance; Fourth, our recent data also support a role of central cell in fertilization recovery. Recent progresses on these aspects will be discussed.

Selected talk **09:50–10:10**

Morphological analysis of inflorescences and flower developmental stages in male and female hemp (*Cannabis Sativa*)

Jiaqi Shi
University College Dublin

Abstract:

Hemp (*Cannabis sativa*) is a high-value crop with virtually thousands of different applications. Hemp seeds are used for high-quality oil, as human food, and as nutritional supplements. Hemp flowers contain secondary compounds that have multiple medicinal uses. Therefore, hemp research, breeding and applications are on the rise after a century long prohibition, making it necessary to understand flower development in hemp in detail.

Here, we show the development phases of male and female hemp inflorescence, and flower development stages of male and female hemp employing macrophotography, light microscopy, scanning electron microscopy and computed tomography scanning. We define landmarks of each developmental phase and stage by examining the shape, size, and surface features of developing floral organs. Complementary, we provide expression of hemp homologs of the key flower developmental genes *LEAFY*, *SUPPRESSOR OF OVEREXPRESSION OF CONSTANS1* (*SOC1*) and *AGAMOUS* at different developmental stages of male and female flowers using quantitative PCR (qPCR). We find that the expression pattern of these genes is highly conserved, with early upregulation of CsLEAFY and *CsSOC1* and later upregulation of *CsAGAMOUS*.

Together, morphological and molecular analysis build a comprehensive framework of reference points for studies of flower development, sex determination and secondary compound production in hemp.

JIAQI SHI, SUSANNE SCHILLING, CAROLINE A. DOWLING, RAINER MELZER

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

Selected talk **10:10–10:30**

Death by transcription: RNA-Seq identifies novel regulators of programmed cell death in Arabidopsis

Rory Burke
University College Dublin

Abstract:

Programmed cell death (PCD) is a genetically controlled pathway for selective cellular suicide. In plants, PCD contributes to normal development, as well as responses to abiotic and biotic stress stimuli. Consequently, detailed understanding of plant PCD and its regulation is urgently required to aid the development of climate change- and disease- resilient crops. Previous attempts to examine the transcriptional signatures associated with this fundamental process in plants were hindered by difficulties in sampling small groups of cells undergoing PCD that are often buried within the bulk of the tissue. We addressed this challenge by using *Arabidopsis thaliana* cell suspension, that allows precise tracking of PCD rates induced, to generate unique RNA-seq datasets providing a snapshot of transcriptional changes occurring in the plant cells committed to PCD. Combining range of stress treatments and chemical PCD modulators allowed inference of core and stimuli-specific gene regulatory networks. Analysis of upstream transcriptional regulators allowed identification of novel candidate PCD regulatory genes, such as *DTX1*, a detoxifying efflux carrier. Phenotyping of Arabidopsis T-DNA insertion mutants functionally validated the role of selected genes in PCD regulation and stress responses, expanding our understanding of this integral biological process and highlighting novel targets for crop improvement.

R. BURKE, **P. MCCABE, J. KACPRZYK**

School of Biology and Environmental Science, University College Dublin, Belfield Dublin 4, Ireland.

Selected talk 11:00–11:20

Global carbon cost of plant nitrogen and phosphorus acquisition

Renato Braghiere
NASA Jet Propulsion Laboratory, California Institute of Technology

Abstract:

Most Earth system models (ESMs) do not explicitly represent the carbon (C) costs of plant nutrient acquisition, which leads to uncertainty in predictions of the current and future constraints to the land C sink. We integrate a plant productivity-optimizing nitrogen (N) and phosphorus (P) acquisition model (Fixation & Uptake of Nutrients, FUN) into the Energy Exascale Earth System (E3SM) Land Model (ELM). Global plant N and P uptake are dynamically simulated by ELM-FUN based on the C costs of nutrient acquisition from mycorrhizae, direct root uptake, retranslocation from senescing leaves, and biological N fixation. We benchmarked the model with measurements (in-situ, remotely sensed, and integrated using artificial intelligence), and other ESMs in CMIP6; we found significant improvements in C cycle variables. Overall, we found N and P co-limitation for 80% of the land area, with the remaining 20% being either predominantly N or P limited. Global NPP is reduced by 20% with N costs and 50% with NP costs. Modeled and observed nutrient limitation agreement increases when N and P are considered together.

R. K. BRAGHIERE, J.B. FISHER, K. ALLEN, E. BRZOSTEK, M. SHI, X. YANG, D. M. RICCIUTO, R. A. FISHER, Q. ZHU, R. P. PHILLIPS

Jet Propulsion Laboratory, California Institute of Technology, 4800 Oak Grove Drive, Pasadena, CA, 91109 USA

Selected talk **11.20–11.40**

Applying vegetation science concepts to crops: trait diversity across rice varieties increases complementarity effects and productivity

Sirgi Saar

University of Tartu / CIDE Valencia

Abstract:

Biodiversity consequences for ecosystem functioning are among the most fascinating effects in community ecology because of their potential impact on ecosystem services like primary productivity and food production. Niche complementarity, caused by functional trait differences between organisms, is expected to increase ecosystem productivity. In monospecific crop production it could be expected that fields composed of genetically diverse varieties could induce biodiversity effects on ecosystem level. We tested this hypothesis in a pot experiment using six common rice varieties, grown in monocultures and all possible two-varieties mixtures, where vegetative biomass and seed production were measured in each individual plant. To quantify the weed suppression, we added a typical weed of rice fields, *Echinocloa crus-galli*, whose presence significantly reduced rice growth. Rice productivity increased when using taller varieties and when the mixed varieties had larger difference in leaf traits. The net diversity effect was mostly related to niche complementarity, rather than one variety dominating. These results demonstrate the potential of applying ecological theories to crop production, particularly suggesting the importance of intraspecific crop mixtures.

S. SAAR, C. DOMINGO CARRASCO, J. LEPŠ, F. DE BELLO

Desertification Research Centre CIDE, Crta. Moncada-Náquera, Km4,5. 46113 Moncada. Valencia, Spain;
University of Tartu, Department of Botany, Liivi 2, Tartu, Estonia

New Phytologist Editorial Meeting lecture 11:40-12:30

Forest trees in the Anthropocene – feast, famine and failure

Andrea Polle
University of Göttingen, Germany

Biography:
Andrea Polle is Professor of Forest Botany and Tree Physiology at Göttingen University. She is the vice-president of the Academy of Sciences Göttingen. She is interested in the physiology and molecular biology of stress responses in forests trees. Her groups try to understand the physiological plasticity and adaptability of trees in a changing environment. A focus is abiotic stress and how organismal interactions modulate tree performance. Andrea Polle did her undergraduate studies in biology at the University of Cologne (Germany) and received a PhD (Dr. rer. nat) from the University of Osnabrück, Germany. Visit Andrea's website

Abstract:
The present era is recognized as the Anthropocene because Man has become the main driver of global environmental change. Indicators of the man-made global ecological crisis are climate change, loss of biological diversity and drastic alterations of biogeochemical cycles. Long-living tree species have to cope with in unprecedented variations in site conditions imposed by weather extremes, nitrogen deposition and other anthropogenic pollutants. How do these shifts in site conditions impact on tree health and growth? Here, our work on tree nutrition, interaction with symbiotic fungi and acclimation to environmental cues will be reviewed through the lens of eco- and molecular physiology.

Workshops and Panel Discussions

Career development

In this workshop, we will explore developing your research programme and taking the next step in your career. This will involve a panel discussion and a Q&A.

Featuring:

- **Michał Bogdziewic,** Adam Mickiewicz University
- **Charlotte Grossiord,** EPFL
- **Marjorie Lundgren,** Lancaster Environment Centre *(appearing remotely)*
- **Anna Trugman,** University of California Santa Barbara

Publishing Q&A

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!

Featuring:

- **Susanne Brink** (*Trends in Plant Science*) *(appearing remotely)*
- **Alistair Hetherington** (*New Phytologist*)
- **Anne Knowlton** (*Current Biology)* *(appearing remotely)*
- **Rosie Trice** (Wiley) *(appearing remotely)*
- **Chris Surridge** (*Nature Plants*)

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. This workshop will not be recorded and is for in person delegates only.

Poster abstracts

Poster abstracts are ordered alphabetically by presenting author.

1. Akinyemi, Olusegun Olaitan
2. Araguirang, Galileo Estopare
3. Atta-Boateng, Acheampong
4. Avila-Lovera, Eleinis
5. Beatrice, Peter
6. Bedford, James
7. Bertic, Marko
8. Bhattarai, Biplabi
9. Briggs, Eleanor
10. Brunn, Melanie
11. Cano Ramírez, Dora Luz
12. Choi, Bae Young
13. Cordeiro, Daniela
14. Dale, Maeve
15. Didion-gency, Margaux
16. Dimitrova, Anastazija
17. (cancelled)
18. Dueñas, Conrado Jr (Mico)
19. Durodola, Blessing
20. Eggers, Reinmar Stefan
21. Eldridge, Bethany
22. Enderle, Eileen
23. Färkkilä, Sanni
24. Fischer, Felícia
25. Franzisky, Bastian
26. Gardner, Bryony
27. Gonzalez Fuente, Manuel
28. Gumus, Berivan Ozlem
29. Gupta, Apoorva
30. Holden, Claire
31. Hoosein, Shabana
32. Jablonski, Andrew
33. Jakobson, Liina
34. Journé, Valentin
35. Kanasugi, Makoto
36. Kask, Kaia
37. (cancelled)
38. Korkmaz, Yasin
39. Kouhen, Mohamed
40. Krasnova, Alisa
41. Krishnan, Vithya
42. Kumar, Amit
43. Lee, Jinsu
44. Leong, Jia Xuan
45. Lim, Hyungwoo
46. Link, Roman Mathias
47. Liu, Daijun
48. Liu, Siqiao
49. Lynch, Deirdre
50. Magkourilou, Emily
51. Marín, César
52. Matthus, Elsa
53. Meng, Yiming
54. Morales Sánchez, José Ángel
55. Moreno Beltran, Juan Camilo
56. Mottiar, Yaseen
57. Muthreich, Florian
58. Ning, Youzheng
59. Noothong, Fonthip
60. Pagano, Andrea
61. Parik, Helen
62. Pavanetto, Nicola
63. Pierick, Kerstin
64. Přibylová, Adéla
65. Puglielli, Giacomo
66. Rasool, Shumaila
67. Ritchie, Erin
68. Robson, Jordan
69. Ruiz de Diego, Paloma
70. Sanka Loganatha Chetti, Dinesh
71. ~~Sanz Puente, Irene~~ (Cancelled)
72. Sardar Ali, Muhammad Kamil
73. Schwenk, Philipp
74. Sell, Marili
75. Sharma, Upasana
76. Shethi, Kishwar
77. Shtin, Margaryta
78. Singh, Minerva
79. Sinnott-Armstrong, Miranda
80. Stangl, Zsofia Reka
81. Stroud, Sebastian
82. Sulaiman, Hassan Yusuf
83. Sustek, Ferenz
84. Tafuri, Andrea
85. Tejera-Nieves, Mauricio
86. Top, Oguz
87. Tordoni, Enrico
88. Trindade, Diego
89. Wipulasena, Ayesh
90. Yirmibesoglu, Side Selin Su
91. Yochikawa, Aline
92. Zeng, Ziyue
93. Zhou, Yanmin
94. Zhu, Lingping
95. Zhu, Shanshuo
96. Zhu, Xudan
97. Wuyun, Tana

P.1 Diurnal and within-crown variation of chlorophyll fluorescence kinetics in silver birch

Olusegun Olaitan Akinyemi
University of Eastern Finland

Abstract:

O. O AKINYEMI[1,2], J. ČEPL[2], S. KESKI-SAARI[1], I. TOMÁŠKOVÁ[2], J. STEJSKAL[2], M. KEINÄNEN[1], S. KONTUNEN-SOPPELA[1]

[1] University of Eastern Finland, Department of Environmental and Biological Sciences, Yliopistokatu 7, P.O. Box 111, 80101 Joensuu, Finland.

[2]Czech University of Life Sciences Prague, Department of Genetics and Physiology of Forest Trees, Kamýcká 129 165 00, Praha 6.

The JIP test is based on fast fluorescence transients for describing underlying photosynthetic processes in plants. We used OJIP test parameters to detect differences between Finnish silver birch originating from northern and southern (67°N and 62°N) provenances, growing in a common garden at 62°N. Diurnal and within crown variation was considered using information from the OJIP and normalised variable fluorescence (Vt) transient pertaining to fluorescence intensity and duration of steps in the polyphasic fluorescence induction. Diurnal variation and provenance differences were strongest around P-step of the Vt-transient. Both provenances show diurnal variation in trapping probability (Fv/Fm), probability of photon trapped by the PSII RC entering the electron transport (Psi o), quantum yield of an electron reaching the acceptor (I-P phase), maximum trapped exciton flux per PSII RC (TR_0/RC), and electron-transport flux from Q_A to Q_B per PSII RC (ET_0/RC). Provenances differed diurnally in performance index (PIabs) and average absorbed photon flux per PSII RC (ABS/RC). Fv/Fm, Psi_o, and I-P phase showed a linear relationship with photosynthetic photon flux density. Within the tree crown, ETo/RC and TRo/RC were higher at the top than at the bottom. Intraspecific variation and tree crown heights should be dutifully considered when planning forest research experiments.

P.2

When Plants Paint Their Leaves Purple: Analyses of New Factors Involved in the Regulation of Anthocyanin Biosynthesis in Arabidopsis during High Light

Galileo Estopare Araguirang
University of Rostock

Abstract:

G.E. ARAGUIRANG, T. KLEINE, D. LEISTER, A.S. RICHTER

University of Rostock, Institute for Biosciences, Physiology of Plant Metabolism, Albert-Einstein-Strasse 3, 18059 Rostock
Humboldt-Universität zu Berlin, Institute of Biology, Physiology of Plant Cell Organelles, Philippstrasse 13, 10115 Berlin

During high light (HL) exposure, plants accumulate flavonoids such as anthocyanins to protect the chloroplasts from excessive amounts of (UV) light. Although anthocyanin biosynthesis is already well-established, the regulatory network tuning the expression of its genes remains elusive. Here we show that knockout of *INCREASED LEVEL OF POLYPLOIDY-1 (ILP1),* a component of the spliceosome, results in faster activation of flavonoid biosynthesis and significantly increased anthocyanin levels compared to wild-type (WT) after HL. Time-resolved RNA-sequencing analysis and metabolic profiling were performed to dissect the molecular mechanism behind this response. Our data revealed dynamic and temporal changes in both the transcriptome and metabolome of *ilp1-1*. Of the differentially expressed genes before HL shift, *MYBL2*, a repressor of anthocyanin biosynthesis, and *PAP2*, a key transcription factor of the pathway, were significantly downregulated and upregulated, respectively. This indicates that ILP1 most likely functions as a transcriptional regulator upstream of *MYBL2* and *PAP2*. We also found notable differences in the metabolome between WT and *ilp1-1* during HL, suggesting a crucial function of ILP1 for metabolic adjustments of primary and specialized metabolism during acclimation. Our data collectively provide new insights on a previously unrecognized ILP1 function and its role in regulating gene expression and metabolism during acclimation.

P.3

Pollination and physiological yield limitation in cacao: evidence from Western Ghana

Acheampong Atta-Boateng
University of Oxford

Abstract:

A ATTA-BOATENG, M. TOLEDO-HERNÁNDEZ, J. GHALAYINI, T. C WANGER, Y. MAHLI & T.A LANDER

Environmental Change Institute, University of Oxford, South Park Rd, United Kingdom
School of Geography and Environment, University of Oxford, South Park Rd, United Kingdom

Cocoa production in West Africa appears to suffer from a 'yield gap', where field production is lower than estimated based on physiological models. There is evidence that the yield gap is due, at least in part, to pollination limitation, as well as physiological limits. Understanding the mechanisms underlying yield limitation is critical for prioritizing interventions to optimize production outcomes. Here, we use empirical data from a hand-pollination experiment in Ghana to estimate natural levels of pollination during both the dry and wet seasons, pollination-yield curves, pollination limitation, and yield potential. The results show strong support for pollination limitation at the study sites, with natural pollination producing yields below 30% of yields produced with 100% hand pollination. In addition, mixed effects modelling of the data suggests that the biotic and abiotic drivers of pod and flower production are distinct. Based on these results, we suggest farm management interventions to increase cocoa yield.

Keywords: cacao, cocoa yield, agroecology, pollination, pollination yield gap.

P.4

Stem photosynthesis is common in Neotropical trees and lianas

Eleinis Ávila-Lovera
Smithsonian Tropical Research Institute

Abstract:

E. ÁVILA-LOVERA, K. WINTER

Smithsonian Tropical Research Institute, PO Box 0843-03092, Balboa, Ancon, Republic of Panama

Plants with photosynthetic stems are common in both temperate and tropical regions, particularly drylands. Stem photosynthesis improves plant carbon balance via net carbon fixation or reduced respiratory carbon loss. However, little work has been done to study the occurrence and advantages of photosynthetic stems in moist tropical forests. We set out to test whether stem photosynthesis is widespread in tropical woody species, and we measured leaf and stem CO_2 exchange, chlorophyll concentration, stomatal density, and area and biomass investment into leaves and stems in trees and lianas at two tropical forest sites in Panama. We studied 51 species and all of them showed either stem net photosynthesis or stem recycling photosynthesis, both of which positively contribute to the carbon economy of the plants. Interestingly, lianas had greater stem CO_2 re-assimilation capacity than trees, although there was no difference in chlorophyll concentration. Investment in photosynthetic stem area compared to leaf area is greater in lianas than in trees. Our results suggest that the contribution of stem photosynthesis to overall carbon gain is particularly important in lianas. Improved carbon balance in lianas may be one of the mechanisms by which lianas increase in abundance in drier forests

P.5

Plants responses to a new biophilic lighting system

Peter Beatrice
University of Insubria

Abstract:

PETER BEATRICE, DONATO CHIATANTE, GABRIELLA STEFANIA SCIPPA, ANTONIO MONTAGNOLI

Department of Biotechnology and Life Sciences, University of Insubria, Via Dunant 3, 21100 Varese (VA), Italy

The LED-sourced CoeLux® lighting system reproduces the effect of natural sunlight entering through an opening in the ceiling, with a realistic sun perceived at an infinite distance surrounded by a clear blue sky. It has already been demonstrated that this new lighting system generates long-term positive effects on human beings; however, there are no investigations so far concerning the plant responses to CoeLux® lighting. We used the model plant *Arabidopsis thaliana* WT to characterize both morpho-physiological responses and gene expression of the main plant photoreceptors at different light intensities and at different times after the exposure to the CoeLux® light type, using high-pressure sodium lamps as control light type. Furthermore, mutants for the main photoreceptors' genes were used to evaluate the role of these genes in the response to this peculiar light type. Under the CoeLux® light type, Arabidopsis WT plants showed a delayed life cycle and were significantly smaller than plants grown with control light, showing clear symptoms of light-induced stress. The phytochrome A gene showed to be more expressed in WT plants grown under the CoeLux® light type, while mutants of the phytochrome B and cryptochrome 1 genes showed a reduced lamina-to-petiole ratio under the CoeLux® light type.

P.6

Genomics of local adaptation in wild rice *Oryza rufipogon*

James Bedford
University of Southampton

Abstract:

J. A. BEDFORD, M. CARINE, L. WILLIAMS, M. A. CHAPMAN

Biological Sciences, Life Sciences Building 85, University of Southampton, Hampshire, SO17 1BJ, United Kingdom

Oryza rufipogon is the wild progenitor of cultivated rice *O. sativa* and exhibits high levels of genetic diversity across its population. Population genetic diversity is generally regarded as being beneficial for adaptation to changing environments, therefore, studying wild rice populations may help identify abiotic stress tolerant varieties and genes that could limit climate-changed induced yield losses of rice in the future.
To investigate local adaptation in wild rice, we analysed single nucleotide polymorphism (SNP) data from a panel of 286 samples located across a diverse range of climates. Environmental association analysis (EAA), a genome wide association study (GWAS)-based method, was used and revealed 19 regions of the genome significantly associated with various climate factors. Genes within these environmentally associated regions have putative functions in abiotic stress response, phytohormone signalling and the control of flowering time. This provides an insight into potential local adaptation in *O. rufipogon* and reveals possible locally adapted genes that are currently being explored, and which may provide opportunities for breeding novel rice varieties with climate change-resilient phenotypes.

P.7 Metabolomics deciphers the herbivory resistance of European oak

Marko Bertic

Helmholtz Zentrum Munich

Abstract:

MARKO BERTIĆ[1], HILKE SCHROEDER[2], BIRGIT KERSTEN[2], MATTHIAS FLADUNG[2], FRANZISKA ORGEL[2], JÖRG-PETER SCHNITZLER[1], ANDREA GHIRARDO[1]

[1]HelmholtzZentrum München, Research Unit Environmental Simulation, Ingolstädter Landstraße 1, Neuherberg, Germany; [2]Thünen-Institute of Forest Genetics, Sieker Landstrasse 2, 22927 Grosshansdorf, Germany

Climate change increases insect pressure forcing plants to invest resources in defense mechanisms. However, plant defense uses limited recourses and reduces growth. Finally, plant growth-defense tradeoffs pose a fundamental dilemma for plants in the face of climate change: is it better to allocate resources toward defense or growth. We have performed a metabolomics study on field data from leaf extract of 120 oak (*Quercus robur* L.) trees growing in four forest stands in Germany. Metabolomic differences (biomarkers) distinguish insect-resistant(T-) oak phenotype with higher levels of defensive metabolites such as flavonoids from insect-susceptible(S-) oaks enriched in primary metabolites from groups of carbohydrates in regard to the oak pest *Tortrix viridana.* We further assessed the ecological significance of oak phenotypes by studying the saliva and fecal metabolome of the insects and their performance. Despite the advantage of the T-phenotype in counteracting the herbivore by impacting their mortality and development, natural forests are composed of both phenotypes, and intermediate chemotypes supported probably by a large intraspecific genetic variation, helping tree communities cope with upcoming environmental changes and increase species survival.

P.8

Soil warming duration and magnitude affects dynamics of fine-roots and rhizomes and related C and N pools in belowground of subarctic grasslands

Biplabi Bhattarai
University of Tartu

Abstract:

BIPLABI BHATTARAI[1], BJARNI D. SIGURDSSON, PÁLL SIGURDSSON, NIKI LEBLANS, IVAN JANSSENS, WENDELIEN MEYNZER, ARUN KUMAR DEVARAJAN, JAAK TRUU, MARIKA TRUU AND IVIKA OSTONEN

Institute of Ecology and Earth Sciences, University of Tartu, Estonia

Climate predictions for the subarctic region show a higher rise in atmospheric temperature than the global mean, which will subsequently raise the soil temperature (Ts). We know very little about belowground plant biomass (BPB) response to warming soils in subarctic grasslands. We investigated the effects of medium- and long-term soil warming (11-yr and >60-yr, respectively) duration and magnitude (from +0.2°C to +6.2°C) on total belowground plant biomass (BPB), carbon (C) and nitrogen (N) pools in geothermally warmed subarctic grasslands. Both duration and magnitude of soil warming significantly influenced the BPB in the topsoil, whereas only magnitude significantly affected BPB in the subsoil. The effect of Ts increase on C and N pools in belowground biomass was driven by a decrease in FRB and a change of C:N ratio in rhizomes. We found a negative overreaction in BPB in the high warmed plots of medium-term warmed grassland. The significant decrease of BPB and C and N pools in BPB after 11-yrs of soil warming recovered in >60-yrs. Belowground adaptation to soil warming in subarctic grassland communities occurred with changed biomass distribution into fine-roots and rhizomes and a change in their chemistry. Furthermore, plants belowground traits changed together with a shift in functional composition of plant community – ferns dominated plots with high Ts. The abundance of forbs increased toward long-term warmed plots.

P.9

The function of 1,3-ß glucan in *Zymoseptoria tritici* and the control of septoria leaf blotch

Eleanor Briggs
The University of Sheffield

Abstract:

E. BRIGGS, G. DEPIETRA, O. EMMS, J. HOBBS, A. FLEMING, S. AMSBURY

Plants, Photosynthesis and Soil, Department of Biosciences, The University of Sheffield, Sheffield, S10 2TN.

Zymoseptoria tritici (*Z. tritici)* is regarded as the most important pathogen of wheat at a global scale. *Z. tritici* causes the disease septoria leaf blotch, which in high disease pressure years, can cause up to 50% of wheat yield losses, hence, control of *Z. tritici* is crucial. *Z. tritici* has become resistant to major fungicide classes which target chitin synthesis in the fungal cell wall, demanding novel targets for fungicide development. (1,3)-ß-glucans provide a structural backbone for the attachment of other polysaccharides in the fungal cell wall, providing structural integrity and protection to the cell, making it an attractive fungicide target. This project aims to develop an in vitro assay for identification of compounds that inhibit (1,3)-ß-glucan synthesis. To further understand functions of 1,3-ß glucans in the fungal cell wall, and in the pathogenicity of *Z. tritici to wheat,* we assess the pathogenicity of *Z. tritici* knockout mutants in the 1,3-ß glucan biosynthesis pathway. The use of Atomic Force Microscopy enables extremely high-resolution images of the fungal cell wall, and we compare the structural and compositional features of wild type *Z. tritici* to (1,3)-ß-glucan mutants to understand how fungal cell wall structure is linked to plant pathogenicity.

P.10 Carbon allocation to root exudates is maintained in mature temperate tree species under drought

Melanie Brunn
University of Koblenz-Landau

Abstract:

M. BRUNN[1], B. D. HAFNER[2], M. J. ZWETSLOOT[3], F. WEIKL[4,5], K. PRITSCH[4], K. HIKINO[5], N. K. RUEHR[6], E. J. SAYER[7], T. L. BAUERLE[2]

[1]Institute for Environmental Sciences, University of Koblenz-Landau, Fortstraße 7, 76829 Landau, Germany, [2]School of Integrative Plant Science, Cornell University, Ithaca, NY 14853, USA, [3]Soil Biology Group, Wageningen University, 6708 PB Wageningen, the Netherlands, [4]Institute of Biochemical Plant Pathology, Helmholtz Zentrum München GmbH - German Research Center for Environmental Health, 85764 Neuherberg, Germany, [5]Technical University of Munich, TUM School of Life Sciences, Land Surface-Atmosphere Interactions, Ecophysiology of Plants, 85354 Freising, Germany, [6]Institute of Meteorology and Climate Research - Atmospheric Environmental Research (IMK-IFU), Karlsruhe Institute of Technology (KIT), 82467 Garmisch-Partenkirchen, Germany, [7]Lancaster Environment Centre, Lancaster University, LA1 4YQ Lancaster, UK

Carbon (C) exuded via roots is proposed to increase under drought and facilitate important ecosystem functions. However, it is unknown how exudate quantities relate to the total C budget of a drought-stressed tree, i.e. how much of net-C assimilation is allocated to exudation at the tree level. We calculated the proportion of C assimilation allocated to root exudation during early summer by collecting root exudates from mature *Fagus sylvatica* and *Picea abies* exposed to experimental drought, and combining above- and belowground C fluxes with leaf, stem, and fine-root surface area. Exudation from individual roots increased exponentially with decreasing soil moisture, with the highest increase at the wilting point. Despite *c.* 50 % reduced C assimilation under drought, exudation from fine-root systems was maintained and trees exuded 1.0 % (*F. sylvatica*) to 2.5 % (*P. abies*) of net C into the rhizosphere, increasing the proportion of C allocation to exudates two- to threefold. Water-limited *P. abies* released two-thirds of its exudate-C into the surface soil, whereas it was only one-third in droughted *F. sylvatica*. Across the entire root system, droughted trees maintained exudation similar to controls, suggesting drought-imposed belowground C investment, which could be beneficial for ecosystem resilience.

P.11 Big regulates the circadian clock and development

Dora Luz Cano Ramírez
University of Cambridge

Abstract:

D.L. CANO-RAMIREZ, E. BIDASH, S. WARD, O. LEYSER, A.A.R. WEBB

Department of Plant Sciences, University of Cambridge, Downing Street, Cambridge CB2 3EA, UK
Sainsbury Laboratory, Cambridge University, Bateman Street, Cambridge CB2 1LR, UK

Due to Earth's rotation on its axis, life exists in day-night cycles of approximately 24 hours. Circadian clocks are timing mechanisms that help organisms to organize and coordinate their activities, and to predict and adapt to fluctuations in their environment. It has been discovered that BIG (AT3G02260), functions in the establishment of a correct phase relationship between the internal timing of a plant and the environment and regulates development through strigolactone and auxin signalling. Our aim is to identify how BIG exerts regulatory control over the synchronisation of the circadian clock and strigolactone signalling through RNAseq, genetic, physiological, and protein-protein interaction studies. Results show that strigolactone treatment has no effect on the circadian rhythm in wild type *Arabidopsis thaliana*, however, three different alleles of BIG mutants have different degrees of splicing defects possibly explained by interaction of BIG with proteins from the splicing machinery found by yeast two-hybrid essays. Our results suggest a new role of BIG in splicing in plants.

P.12

Studies on two transcription factors important for stress responses in *Chlamydomonas reinhardtii*

Bae Young Choi
Chungnam National University

Abstract:

BAE YOUNG CHOI, HANUL KIM, DONGHWAN SHIM, SUNGHOON JANG, SEUNGJUN SHIN, TAKASHI YAMANO, MASATAKA KAJIKAWA, EONSEON JIN, PASCALINE AUROY, FANTAO KONG, YUREE LEE, YONGHUA LI-BEISSON, YASUYO YAMAOKA, HIDEYA FUKUZAWA, YOUNGSOOK LEE

Department of Life Sciences, Pohang University of Science and Technology, 77, Cheongam-ro, Nam-gu, Pohang, 37673, Korea

Microalgae accumulate high levels of triacylglycerol under stress, but the underlying molecular mechanisms are largely unknown. Here, we report two transcription factors important for stress responses in *Chlamydomonas reinhardtii*. First, we found that a bZIP transcription factor BLZ8 mediates responses to oxidative stress. BLZ8 induces the carbon-concentrating mechanism (CCM) to provide an electron sink pathway in chloroplast, reducing ROS production upon oxidative stress. This mechanism is likely to be especially important to water-dwelling photosynthetic organisms, since slow gas diffusion in aqueous environments limits CO_2 availability for photosynthesis, which can trigger ROS formation. Second, we found that the MYB1 transcription factor is an important positive regulator of lipid accumulation upon nitrogen-depletion. Two *myb1* mutants accumulated reduced amounts of total fatty acids and triacylglycerol than their parental strain upon nitrogen depletion. Transcriptome analysis revealed that the expression of some genes involved in the transport of fatty acids from the chloroplast to the ER was altered in *myb1* mutants, suggesting that MYB1 promotes lipid accumulation by facilitating the transport. MYB1's role in lipid accumulation is at least comparable to those of the previously described lipid regulators in *Chlamydomonas*. This work provides molecular tools to enhance microalgal production of lipids, without increasing atmospheric CO_2.

P.13

Functional analysis of miR399 and miR827 involved in phosphate and sugar homeostasis during the loss of the embryogenic competence in *Solanum betaceum* Cav.

Daniela Cordeiro
University of Coimbra

Abstract:

D. CORDEIRO[1], J. CANHOTO[1], S. CORREIA[1]

[1] *University of Coimbra, Centre for Functional Ecology, Department of Life Sciences, Calçada Martim de Freitas, 3000-456 Coimbra, Portugal*

Somatic embryogenesis (SE) is a valuable tool for micropropagation and improvement of numerous economically relevant crops, and therefore there is a great interest in understanding the gene regulatory networks underlying cell reprogramming during this process. Being a maintainable system by embryogenic callus subculturing, SE in tamarillo (*Solanum betaceum* Cav.) represents a good model to study embryogenic competence acquisition, expression and maintenance. miR399 and miR827 showed to be up-regulated in calli that lost their embryogenic potential throughout subcultures comparatively to embryogenic ones. Concomitantly, their target genes, involved in phosphate-transport responses in the cell (*PHOSPHATE2* and *PHOSPHATE TRANSPORTER 5*), were down-regulated in long-term calli. Since sugar signalling mediates phosphate starvation responses, our hypothesis is that the long exposure to high sucrose concentrations during tamarillo subcultures might be responsible for the loss of the embryogenic competence. The functional validation of both miRNAs/targets is being conducted by several approaches including validation of miRNA target genes by miR-RACE, virus-based miRNAs silencing, miRNAs overexpressing, highly sensitive miRNAs FISH techniques, phosphate and sucrose quantification, changes in sucrose and/or phosphate availability in culture media. The results so far obtained corroborate the hypothesis and allow a better modulation of plant regeneration processes in very often recalcitrant plant species.

P.14 cGMP signalling in Arabidopsis

Maeve Dale
University of Bristol

Abstract:

M. C. DALE, G. JONES, D. H. MCLACHLAN and A. M. HETHERINGTON

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

cGMP is a cyclic nucleotide involved in responding to external stimuli. Although cGMP is well established as an intracellular second messenger in animals the role it plays in plant cell signalling is less well characterised. Recently we characterised the Arabidopsis *PDE1* gene that encodes a cyclic nucleotide phosphodiesterase. We have been using this to investigate the relationship between cGMP and glutamate signalling. Our preliminary results suggest that cGMP is involved in glutamate-induced stomatal closure. To investigate the relationship between cGMP and glutamate further, RNA sequencing was carried out to identify differentially expressed genes and highlight areas of interest. Findings suggest cGMP is involved in glutamate signalling as mutants in the cGMP pathway show alterations in both their stomatal response and differential gene expression. As glutamate is involved in many important survival and stress responses the link between cGMP and glutamate could be important in a variety of different responses. Recent results will be presented.

P.15 Impact of warmer and drier conditions on tree photosynthetic properties and the role of species interactions.

Margaux Didion-Gency
Swiss Federal Institute for Forest, Snow and Landscape Research WSL

Abstract:

M. DIDION-GENCY, A. GESLLER, N. BUCHMANN, J. GISLER, M. SCHAUB, C. GROSSIORD

Swiss Federal Institute for Forest, Snow and Landscape WSL, Zücherstrasse 111, CH-8903 Birmensdorf, Switzerland.

Increased temperature and prolonged drought have distinct impacts on tree photosynthetic properties. Yet, our knowledge of their combined effect is limited. Moreover, how species interactions alter photosynthetic responses to warming and drought remains unclear. Using a full factorial experiment in open-top chambers, we studied how photosynthetic properties of European beech and downy oak were impacted by three years warming of +5°C and soil drought alone or combined, and how species interactions (intra- vs. interspecific interactions) modulated these effects. Warming enhanced photosynthetic properties in oak but not beech, while drought decreased them in both species. Combined warming and drought reduced photosynthetic responses for both species, but no exacerbated effects were observed. Oak was less impacted by combined warming and drought when interacting with beech than in intraspecific stands. For beech, species interactions had no impact on the photosynthetic properties to warming and drought, alone or combined. Warming had either no or beneficial effects on the photosynthetic properties, while drought and their combined effects strongly reduced photosynthetic responses in both species. However, interspecific interactions can mitigate the negative impacts of the combined warming and drought in oak, thereby highlighting the need to deepen our understanding of interspecific interactions under climate change.

P.16

Knowledge From Within: The Seasonal Dynamics of Root and Shoot Cambial Cells of *Populus sibirica* and *Ulmus pumila* Trees Used for Afforesting the Semi-arid Steppe of Mongolia

Anastazija Dimitrova
Department of Bioscience and Territory, University of Molise

Abstract:

ANASTAZIJA DIMITROVA[1] , DONATO CHIATANTE[2], GABRIELLA S. SCIPPA[1], SER-ODDAMBA BYAMBADORJ[3-4], BATKHUU NYAM-OSOR[3], ANTONIO MONTAGNOLI[2]

[1] *Department of Bioscience and Territory, University of Molise, Contrada Fonte Lappone SNC – 86090 Pesche, Italy*
[2] *Laboratory of Environmental and Applied Botany, Department of Biotechnology and Life Science, University of Insubria, Via Monte Generoso, 71 – 21100 Varese, Italy*
[3] *Laboratory of Forest Genetics and Ecophysiology, School of Engineering and Applied Sciences, National University of Mongolia, Ulaanbaatar, Mongolia,*
[2] *Laboratory of Silviculture, College of Agriculture and Life Science, Chungnam National University, Deajeon, South Korea*

Successful environmental restoration depends on high survival rate and good long-term growth of the used plant material. The seasonal dynamics of cambial cells production may unravel the impact of growth conditions on trees, thus contributing to predictive models on trees growth and resiliencies under climatic challenges.

Previous analysis on the output of afforestation in the Mongolian steppe have emphasised the differences between *Populus sibirica* and *Ulmus pumula* trees grown under a combination of watering regimes and soil fertilization[1,2,3,4]. Comprehensive analysis on morphological traits and above-/below-ground biomass, indicate higher sensitivity of *P. sibirica* to lack of water but greater biomass production capacity, while *U. pumila* is more resistant to drought and more negatively impacted by fertilizers.

In the present work, we focus on understanding how the different treatments over the seasons impact the cambial cells, by processing, visualizing, and analysing microcore samples from stem and root of both tree species. We expect the results to elude on the combined impact of the factors and further correlation with the previous data in terms of the plant's development. The insight would contribute towards understanding the behaviour of the structural cell components and be a tool for species selection suited for varying environmental conditions.

P.18 Variation in germination behavior of Italian rice varieties in response to water stress, iron pulsing and PGA treatments

Conrado Jr (Mico) Dueñas
University of Pavia

Abstract:

C. DUENAS[1,2], D. SRIKANTHAN[1], C. CALVIO[1], I.H. SLAMET-LOEDIN[2], A. MACOVEI[1]

[1] *Department of Biology and Biotechnology 'L. Spallanzani', University of Pavia, via Ferrata 1, 27100 Pavia, Italy*
[2] *Trait and Genomic Engineering Cluster, Strategic Innovation Platform, International Rice Research Institute, DAPO Box 7777, Metro Manila 1277, Philippines*

To meet the ZERO HUNGER target, agricultural productivity must double by 2030. This ambitious goal should be met by implementing versatile agricultural practices that addresses both increase productivity and nutritional quality. Water stress brought about by climate change is among the major global concern threatening food security by negatively affecting crop production, especially for rice. Among the so-called Hidden Hunger phenomenon, Iron Deficiency Anemia (IDA) affects 2 billion people globally, especially children and pregnant women, widely belonging in low-income countries where rice is the staple food. To address both concerns, the current work proposes to develop techniques directed to enhance iron content in rice grains and promote resilience to water stress, by implementing specific seed priming treatments. Seed priming is a process of regulating the germination process by tackling the first biochemical processes within the initial stages of germination. In this study, five popular Italian rice varieties were subjected to priming treatments using poly- γ-glutamic acid (γ -PGA) and iron pulsing, while the treated seeds were grown under physiological and water stress conditions. Preliminary data based on selected germination parameters show that γ -PGA is effective in buffering water stress while iron pulsing resulted in enhanced Fe uptake during germination.

P.19 Genotype impact on the response of *Picea abies* to the artificial inoculation of *Heterobasidion parviporum*

Blessing Durodola
University of Goettingen

Abstract:

B. DURODOLA[1,2], K. BLUMENSTEIN[1,3], and E. TERHONEN[1,4]

[1]Forest Pathology Research Group, Büsgen-Institute, Department of Forest Botany and Tree Physiology, Faculty of Forest Sciences and Forest Ecology, University of Göttingen, Büsgenweg 2, 37077 Göttingen, Germany
[2]Forest Genetics and Forest Tree Breeding, Büsgen-Institute, Georg-August University Göttingen, Büsgenweg 2, 37077, Germany
[3]Chair of Pathology of Trees, Institute of Forestry, Faculty of Environment and Natural Resources, University of Freiburg, Bertoldstr. 17, 79098 Freiburg, Germany
[4]Natural Resources Institute Finland (Luke), Forest health and biodiversity, Latokartanonkaari 9, 7 FI-00790 Helsinki, Finland.

Spruce is one of the major tree species in Europe. However, it is highly susceptible to attacks from the *Heterobasidion annosum* species complex. Increasing temperatures and prolonged droughts caused by climate change pose a threat to forest health and the distribution of pests and pathogens, which, in turn, limits the ability of some plants to fight off infections. We aimed to determine the factors influencing resistance or susceptibility of Norway spruce to *Heterobasidion parviporum* infection. We investigated the possible differences in the necrosis measurements between different families and genotypes of three-year-old *Picea abies* saplings under normal water availability and drought stress. We artificially inoculated 458 trees with two strains of *H. parviporum*; 226 plants as mock control, while 135 remained non-treated. The visible necrotic lesion length and width in phloem and sapwood were measured. Our results show that the factors impacting the necrosis are the families and genotypes. This understanding could help strategically select genetically resistant trees for breeding purposes.

P.20

From Alcohol to Aldehyde: Characterization of Monolignol Oxidoreductases in *Arabidopsis thaliana* and Their Possible Involvement in the Extracellular Phenolics Pool

Reinmar Stefan Eggers
Graz University of Technology, Institute of Biochemistry

Abstract:

REINMAR S. EGGERS AND PETER MACHEROUX

Institute of Biochemistry, Graz University of Technology, Petersgasse 12/2, 8010 Graz, Austria

The Berberine bridge enzyme-like (BBE-like) protein family are flavoproteins that are present in bacteria, fungi and plants. In *Arabidopsis thaliana,* seven subgroups have been identified with a total of 27 genes encoding BBE-like enzymes (*At*BBE-like). *At*BBE-like proteins are involved in stress-induced plant responses as well as developmental processes. Our work focusses on *At*BBE-like subgroup six, from which two members have been found to oxidize monolignols. We therefore hypothesize an involvement of *At*BBE-like enzymes in the regulation of the extracellular monolignol pool *in planta*.

In order to unravel spatiotemporal expression patterns of the five genes from *At*BBE-like subgroup 6 on the tissue level, we generated transcriptional reporter lines and found expression in roots, where the individual genes show different expression patterns on the tissue level. Additionally, *AtBBE*-like *15, 24* and *26* reporter lines show expression during flower development. For all genes from subgroup 6, qRT-PCR revealed high levels of expression in roots. Phenotyping of T-DNA insertion lines do not exhibit an obvious phenotype.

Further phenotypic characterization of loss-of-function mutants generated with CRISPR/Cas9, detailed description of reporter lines and generation of fluorescent reporter lines will widen our understanding of subgroup six of the *At*BBE-like protein family.

P.21

Why are plants clingy? Characterising an ABC membrane transporter that affects root stickiness

Bethany Eldridge
University of Bristol

Abstract:

B. M. ELDRIDGE, E. R. LARSON, L. MAHONY, J. W. CLARK, & C. S. GRIERSON

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

The physical presence of roots and the compounds they release affect the cohesion between roots and their environments. However, we know very little about the genetic factors involved in these interactions, which limits the ability to tailor plants with root systems that enhance root-substrate cohesion. To efficiently identify genetic factors that affect root-substrate adhesion, we developed a novel centrifugation phenotyping assay that measures the centrifugal force required to detach young *Arabidopsis thaliana* seedlings from agar. Using this assay, we identified a mutant in the uncharacterised ABC transporter, *ABCG43*, with enhanced root-substrate adhesion. Interestingly, we found *ABCG43* gene dosage affects the root adhesive phenotype without affecting visible root morphology, suggesting that this transporter could be contributing to root adhesion by affecting biochemical properties at the root-environment interface. Our work is now focused on assessing how ABCG43 shapes root-substrate cohesion and if this transporter can be manipulated in other important crop species to affect the root cohesive phenotype.

P.22 Drought legacy effects on plant-soil interactions in grasslands

Eileen Enderle
University of Amsterdam

Abstract:

E. ENDERLE, F. HOU, L. HINOJOSA, M. GLIESCH, H. BOUWMEESTER, F. T. DE VRIES

Institute for Ecosystem and Landscape Dynamics, University of Amsterdam, Science Park 904, 1098XH Amsterdam, The Netherlands

Increasing summer droughts in grasslands have direct effects on plant growth, but also indirect effects that are mediated by the soil microbial community, thus potentially affecting plant-soil feedbacks (PSF). Drought effects on PSF may be caused by differences in plant inputs into the soil such as root exudates. Here, we investigated the role of drought-induced root exudates and root litter in driving PSF. In a controlled greenhouse experiment, we assessed drought-legacy effects in the soil on plant growth and PSF for three grassland species. Additional to classical plant-conditioned soil, we assessed plant growth in soil treated with root exudates or root litter from previously droughted or well-watered plants. We found that across all species, previous drought in plant-conditioned soils negatively affected biomass production of subsequently grown plants, which was related to a decrease in microbial biomass in soil. PSF in plant-conditioned soils was dependent on the species and was generally negative but not affected by drought. However, this pattern could not be replicated by addition of root exudates or litter from droughted plants. Our results thus suggest that the soil microbial community might play a more important role in determining plant-soil interactions under drought conditions than rhizodeposition and root litter.

P.23 Shedding light on common mycorrhizal networks (CMNs) with fluorescent nanoparticles (FNPs)

Sanni Färkkilä
University of Tartu

Abstract:

FÄRKKILÄ S.M.A.[1], KIISK V.[2], JAANISO R.[2], MÄEORG U.[3], TEDERSOO L.[4]

1 *Department of Botany, University of Tartu, Juhan Liivi 2, 50409, Tartu, Estonia*
2 *Institute of Physics, University of Tartu, W. Ostwaldi 1, 50411, Tartu, Estonia*
3 *Institute of Chemistry, University of Tartu, Ravila 14A, 50411, Tartu Estonia*
4 *Mycology and Microbiology Center, University of Tartu, Estonia*

The most commonly known benefit of mycorrhizal symbiosis is the trade of carbon to nutrients, but the study of these trade dynamics, especially in CMNs, is still relying on old isotopic techniques with several downfalls. With isotopic tracking, one has little knowledge about what happens between the donor and the receiver, or the pathways which are at play. Furthermore, the technique requires destructive sampling, rendering observations throughout time difficult. To combat these problems, we present a novel method in which carefully designed growth containers enable the non-destructive monitoring of nutrient movement in natural soil via the visual observation of FNP fluorescence. With fluorescent images taken of the soil column, it is possible to obtain quantitative results about nutrient movement by comparing fluorescent intensities in regions of interest (ROIs) throughout time. Additionally, the pathway(s) involved can be visually confirmed.

P.24 Designing communities for trait-based-biodiversity-experiments: new tools to explore functional trait effects on ecosystem stability

Felícia M. Fischer
Centro de Investigaciones sobre Desertificación

Abstract:

F. M. FISCHER, P. FIBICH, G. DOMENECH, M. BAZZICHETTO, M. G. SPERANDII, A. F. SALES
D. A. RODRIGUEZ, L. NEUENKAMP, F. DE BELLO

*Centro de Investigaciones sobre Desertificación (CSIC-UV-GV), Carretera CV-315 Km 10.7,
46113 Moncada (Valencia), Spain*

Trait-based biodiversity experiments (TBBE) are an important tool to understand the role of plant communities on ecosystem functions and stability. Although, specific care is needed in designing of such experiments. The design should not only aim for maximizing the range of communities´ functional metrics, but also consider natural and random assembly processes taking place and possibly shifting the intended sown communities (rates of dominance, germination/death, and intraspecific trait variations). So, we propose two r functions to aid on the matter: 1) maxtraits, suggests the best combinations of species to maximize the range of FD and CWMs while minimizing their collinearity; 2) rabast, explores scenarios of mortality rates, dominance, and intra-specific trait variation. We applied the functions to simulated data and then and compared the results to real data from a 1-year greenhouse experiment. rabast showed different levels of intraspecific trait variation, dominance, and mortality, produce different shifts in CWM and FD metrics, but generally do not invalidate proposed communities from maxtraits. In the real data, we observed a relevant shift in community characteristics between the intended and the resulting combinations, however maintaining suitable ranges of CWM and FD

P.25

Guard cells under salt stress: early and late responses

Bastian Franzisky

Geisenheim University

Abstract:

B. L. FRANZISKY[1], A. ERBAN[2], J. KOPKA[2], C. ZÖRB[3], C.-M. GEILFUS[1]

[1]*Institute of Soil Science and Plant Nutrition, Geisenheim University, Von-Lade-Str. 1, 65366 Geisenheim, Germany*
[2]*Max-Planck-Institute of Molecular Plant Physiology, Am Mühlenberg 1, 14476 Potsdam-Golm, Germany*
[3]*Insitute of Crop Science, University of Hohenheim, Schloss Westflügel, 70599 Stuttgart, Germany*

Salt stress is considered being a biphasic stress event with first osmotic and later also ionic stress phase. We described that already in the early osmotic stress phase, chloride ions induce the pH of the leaf apoplast (pH_{apo}) to alkalinize transiently. This pH event leads to rapid abscisic acid (ABA)-mediated stomatal closure. By combined *in vivo* imaging of the pH_{apo} and analysis of ABA production and contents, we show that the pH_{apo} transient promotes stomatal closure via triggering *de novo* ABA synthesis in the leaves leading to ABA accumulation in guard cells. Experiments with artificially induced pH_{apo} transients demonstrate that the pH event acts like a 'stand-alone'-signal, irrespective of any Cl^- stress-component.

In the later ionic stress phase of salt stress, Na^+ and Cl^- accumulate in leaves. High concentrations of Na^+ and Cl^- perturb mesophyll metabolism, as indicated by a metabolomics analysis. Guard cells also accumulated excessive Na^+. Stress-responsive metabolites, i.e. cellular marker, and compatible osmolytes accumulated in leaves but not in guard cells. This diverging regulation of guard cell metabolism under salinity might be a prerequisite for maintaining guard cell functioning, because stomata remained able to open and close, albeit at slower rates.

P.26 Exploring root exudate traits for soil-free growing systems

Bryony Gardner
University of Bristol

Abstract:

B.C. GARDNER, K. HEBDITCH, V.A. PALUMBO, B.M. ELDRIDGE, E.R. LARSON, C.S. GRIERSON

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

Plants allocate 10-40% of fixed carbon to root exudates, which function in soil to improve the plant's growth environment. Published research using *Arabidopsis thaliana* null mutants to evaluate root exudate composition has focussed on transporter genes, for whom substrates are difficult to identify. We conducted a meta-analysis of proteomics datasets and identified common root exudate proteins in wild-type *Arabidopsis* as novel candidate genes for altered exudate compositional analysis. Null mutant lines for these genes have been obtained and are being phenotypically screened for traits linked to altered exudate composition. These traits include root hair length, lateral root number and root-substrate adhesion. Future work aims to utilise soil-free growth systems (e.g. hydroponics and aeroponics) as a tool to chemically analyse root exudates from these lines using mass spectrometry. Additionally, exploring the roles that exudates might play in plant growth in these soil-free growth environments is a novel research area that addresses important questions relevant to future food production industries, including vertical farming.

P.27 Processing bodies as a novel hub in protein homeostasis during plant-pathogen interactions

Manuel Gonzalez Fuente
Center for Plant Molecular Biology (ZMBP) - University of Tübingen

Abstract:

M. GONZALEZ-FUENTE, M. FRANZ-WACHTEL, B. MACEK, S. ÜSTÜN

Center for Plant Molecular Biology (ZMBP), University of Tübingen, D-72076 Tübingen, Germany
Proteome Center Tübingen, Interfaculty Institute for Cell Biology, University of Tübingen, D-72076 Tübingen, Germany
Faculty of Biology and Biotechnology, Molecular and Cellular Botany, University of Bochum, D-44780 Bochum, Germany

Compartmentalization of transcripts in membraneless aggregates allows rapid and cost-efficient responses to environmental stimuli. Processing bodies (PBs) are dynamic ribonucleoprotein aggregates formed by phase separation in the cytosol. PBs are conserved among eukaryotes and are involved in translational arrest, mRNA decay and RNA quality control. PBs regulate several developmental processes and responses to stresses, including plant-pathogen interactions. Basal plant defence responses trigger a quick disassembly of PBs, possibly deregulating the expression of immunity genes. Here, we show that during bacterial infection, PB assembly is enhanced in an effector-dependent manner. Moreover, PB-defective mutants are more tolerant to infection. These results reinforce the notion that PBs are negative regulators of plant immunity and reveal PBs as a novel target of pathogen effectors. Interactomic studies combining two different PB markers in the context of infection allowed us to identify new components potentially associated with PBs. Among these candidates, we found an autophagy receptor and several proteasomal subunits and ubiquitin-binding proteins. With the increasing evidence of ubiquitin-mediated phase separation being involved in proteasomal functioning as well as in autophagosome formation, these results point towards a possible role of PBs as a novel hub in protein homeostasis, connecting RNA metabolism and translation with protein degradation.

P.28

Interplay between circadian clock and endoplasmic reticulum stress in *Arabidopsis thaliana*

Berivan Ozlem Gumus

Ege University

Abstract:

OZLEM GUMUS[A], BUSE PINAR[A], BARİS UZILDAY[A], ISMAİL TURKAN[A], RENGİN OZGUR[A]

[a] *Department of Biology, Faculty of Science, Ege University, Bornova, 35100, Izmir, Turkey*

The circadian clock is a time keeper system that regulates the physiology of an organism to adapt to enviromental changes. Plants as sessile organisms, use this mechanism to anticipate to day and night transitions and alterations of temperature. Environmental fluctations such as high temperature or salt stress can cause endoplasmic reticulum stress (ER) by increasing misfolded/unfolded proteins. The unfolded protein response (UPR) is stimulated by ER stress, which induce transcription of a number a series genes to increase protein folding capacity. Aim of this work is to investigate interaction among circadian clock and protein folding capacity and ER stress response. For this aim, *Arabidopsis thaliana* plants were trained to 12/12h (LD) and to 24h constant light (LL) to determine their response to tunicamycin induced ER stress. Expressions of genes related to UPR were measured at 4,8,12,16 and 24h time points after onset of ER stress. We also investigated if ER stress can change period or amplitude of *A. thaliana* molecular clock. As results, Tm enhanced the expressions of ER stress sensor/transducer genes (*bZIP17, bZIP28, bZIP60, IRE1A, IRE1B*), ER chaperones and folding helper genes (*BiP1, BiP3, ERO1, CNX*), ER-associated degradation (ERAD) genes (*DER1, SEL, HRD1*) and ER stress associated apoptosis genes (AGB1, NAC089) in shoots. LL and LD treatments have different effects on UPR of A. thaliana whereas LL grown plants showed decreased ER stress response as compared to LD grown plants.

P.29

Deciphering the role of a HSF:miR169:NF-YA feedback loop in Arabidopsis and tomato thermotolerance

Apoorva Gupta
National Institute of Plant Genome Research, New Delhi, India

Abstract:

A. GUPTA, S. RAO, S. JHA, C. BANSAL AND S. MATHUR*

National Institute of Plant Genome Research, Aruna Asaf Ali Marg, New Delhi, India

Heat stress adversely affects the productivity of agriculturally important crops worldwide. Regulatory feedbacks are at the basis of different stress and developmental networks in plants. Here, we report that tomato and Arabidopsis plants improve their thermotolerance through Heat stress transcription factor (HSF)-mediated transcriptional regulation of microRNA169 and post-transcriptional regulation of Nuclear Factor Y-Subunit A (NF-YA) transcription factors. We show that HSFs recognize tomato and Arabidopsis MIR169 promoters using yeast-one-hybrid/ChIP-qPCR. Silencing tomato HSFs using virus-induced-gene-silencing reduce Sly-MIR169 levels and enhance Sly-NF-YA9/A10 target expression. Further, tomato transgenic plants overexpressing Sly-MIR169 and Sly-NF-YA9/A10-VIGS knock-down tomato plants as well as Arabidopsis plants overexpressing At-MIR169d and At-nf-ya2 mutants showed a link with increased heat tolerance. In contrast, Arabidopsis plants overexpressing At-NF-YA2, or those expressing a non-cleavable At-NF-YA2 form (miR169-resistant At-NF-YA2) as well as plants inhibited for At-miRNA169d regulation (miR169d mimic plants) were more sensitive to heat stress, highlighting NF-YA as negative regulator of heat tolerance. Furthermore, post-transcriptional cleavage of NF-YA results in alleviating the repression of heat stress effectors HSFA7a/b revealing a retroactive control of HSFs by the miR169:NF-YA node. Hence, a regulatory feedback loop involving HSFs, miR169s and NF-YAs plays a critical role in the regulation of heat stress response in tomato and Arabidopsis.

P.30 Regional differences in clonal Japanese knotweed revealed by chemometrics-linked Attenuated Total Reflection Fourier-Transform Infrared Spectroscopy

Claire Holden
Lancaster University

Abstract:

CLAIRE A HOLDEN‡, CAMILO LM MORAIS†, JANE E TAYLOR‡, FRANCIS L MARTIN∇, PAUL BECKETT¶, MARTIN MCAINSH‡

‡ Lancaster Environment Centre, Lancaster University, † School of Pharmacy and Biomedical Sciences, University of Central Lancashire, ∇Biocel Ltd, Hull HU10 7TS, UK, ¶Phlorum Ltd

Japanese knotweed (R. japonica var japonica) is one of the world's 100 worst invasive species, causing crop losses, damage to infrastructure, and erosion of ecosystem services. In the UK, this species is an all-female clone, which spreads by vegetative reproduction. Despite this genetic continuity, Japanese knotweed can colonise a wide variety of environmental habitats. However, little is known about the phenotypic plasticity responsible for the ability of Japanese knotweed to invade and thrive in such diverse habitats.

We have used attenuated total reflection Fourier-transform infrared (ATR-FTIR) spectroscopy, in which the spectral fingerprint generated allows subtle differences in composition to be clearly visualized, to examine regional differences in clonal Japanese knotweed.

We have shown distinct differences in the spectral fingerprint region (1800–900 cm−1) of Japanese knotweed from three different regions in the UK that were sufficient to successfully identify plants from different geographical regions with high accuracy using support vector machine (SVM) chemometrics.

These differences were not correlated with environmental variations between regions, raising the possibility that epigenetic modifications may contribute to the phenotypic plasticity responsible for the ability of R. japonica to invade and thrive in such diverse habitats.

P.31

Exploring AM fungal and bacterial cooccurrence network interactions to elucidate patterns in plant-soil diversity feedbacks

Shabana Hoosein
Colorado State University

Abstract:

S. HOOSEIN, M.W. PASCHKE, P. TRIVEDI

Department of Forest and Rangeland Stewardship; Department of Agricultural Biology; Colorado State University, Fort Collins, CO (USA)

The integral role of soil biological relationships in ecological restoration is widely acknowledged as critical for vegetation establishment and rehabilitation of ecosystem functions. Arbuscular mycorrhizal (AM) fungi may play a major role in the rhizosphere microbiome, but its role in relation to microbial community dynamics remains largely unknown. We investigated how changes to plant community diversity influence dynamics between AM fungi and bacteria within the rhizosphere microbiome. Using conditioned soils from field-established plant diversity plots, we inoculated mesocosm pots and designed plant communities to understand how field microbial interactions shift with changes to plant diversity. Soil from mesocosm pots were processed using amplicon-based sequencing and evaluated for microbial diversity and cooccurrence network dynamics. AM fungi dominated in contributions to network formation in all field inoculum treatments. AM fungi was also the hub taxa across most treatments. Along with the high alpha diversity of AM fungal and bacterial communities, our data inferred that these networks are self-maintaining and stable. Overall, this research aimed to find evidence for the assumptions often made in plant-soil feedback studies and utilizes diverse methodologies to better understand linkages between plant-soil microbial community dynamics and feedbacks.

Key words: arbuscular, bacterial, networks, diversity, feedbacks

P.32

Examining the controls of the relationship between near-infrared reflectance and solar-induced chlorophyll fluorescence in temperate vegetation.

Andrew Jablonski
University of Virginia

Abstract:

A.D. JABLONSKI, M.T. LERDAU, X. YANG

Department of Environmental Sciences, University of Virginia, 291 McCormick Road, Charlottesville, VA,22904-4123, USA.

Photosynthesis by terrestrial vegetation is an important regulator of the global carbon cycle. Across spatiotemporal scales, remotely-sensed observations of solar-induced chlorophyll fluorescence (SIF) and near-infrared reflectance (NIR_v) track with each other and with eddy-covariance derived estimates of gross primary productivity (GPP). If these measurements are to be used to infer responses of vegetation and GPP to environmental change, the mechanisms that control the relationships between SIF, NIR_v, and GPP, must be understood.

We present results from the first dataset combining diurnal observations of SIF and NIR_v measured from an unmanned aerial system (UAS) with 3D measurements of canopy structure using terrestrial laser scanning (TLS), measurements of leaf gas exchange and variable chlorophyll fluorescence, and leaf functional traits, across individual plant canopies of deciduous, evergreen, and grass species from a mixed forest located in in the Piedmont region of Virginia. Our results show that canopy leaf angle distribution is a strong determinant on the relationship between SIF and NIR_v across the growing season.

P.33 Genetic engineering of barley (*Hordeum vulgare*) strigolactone pathway to improve weed suppression

Liina Jakobson
Estonian Crop Research Institute

Abstract:

L. JAKOBSON, L. TIMOFEJEVA, L. RAUDVA, K. LAANEMETS

Department of Plant Biotechnology, Estonian Crop Research Institute, M. Pilli haru 1, Jõgeva borough, Jõgeva county, Estonia

Weeds can cause up to 30% yield loss. An alternative approach to herbicides is to breed crops with increased weed suppression. Genetic modification of the strigolactone (SL) pathway has shown promising results as a breeding tool to increase yield and modify plant architecture such as height and leaf area. Among cereals, barley has the second largest growth area in Europe but thus far little is known about its SL pathway.

We are creating genetic variation in barley SL pathway genes using CRISPR-Cas9 and transgenesis by utlising the knowhow from Arabidopsis and rice. Changes in the expression of SL pathway genes in rice has resulted in numerous examples of rice lines with high tiller number and short plant height. Similarly, *HvD14* mutation in barley was also shown to result in increased tiller number and reduced plant height (1). We have located and sequenced three SL pathway genes (*HvD14, HvMAX3, HvMAX2*) in barley and targeted for site-directed mutagenesis. This has led to two viable T0 *hvd14* plants.

Further research involves assessment of the tiller number, weed suppression ability, gas exchange and other agronomic traits of the new barley lines in order to evaluate the breeding potential of the modified SL pathway genes.

(1) Marzec M, Gruszka D, Tylec P, Szarejko I. 2016. Identification and functional analysis of the *HvD14* gene involved in strigolactone signaling in Hordeum vulgare. *Physiologia Plantarum* 158: 341–355.

P.34 Globally, tree fecundity exceeds productivity gradients

Valentin Journé
INRAE LESSEM

Abstract:

V. JOURNÉ, M. BOGDZIEWICZ,B. COURBAUD, G. KUNSTLER, T. QIU, J.S. CLARK

Université Grenoble Alpes, Institut National de la Recherche pour l'Agriculture, l'Alimentation et l'Environnement (INRAE), Laboratoire EcoSystemes et Societes En Montagne (LESSEM), 38402 St. Martin-d'Heres, France.
Department of Systematic Zoology, Faculty of Biology, Adam Mickiewicz University, Umultowska 89, 61-614 Poznan, Poland.
Nicholas School of the Environment, Duke University, Durham, NC 27708 USA.

Lack of tree fecundity data across climatic gradients precludes the analysis of how seed supply contributes to global variation in forest regeneration and biotic interactions responsible for biodiversity. A global synthesis of raw seed production data shows a 250-fold increase in seed abundance from cold-dry to warm-wet climates, driven primarily by a 100-fold increase in seed production for a given tree size. The modest (threefold) increase in forest productivity across the same climate gradient cannot explain the magnitudes of these trends. The increase in seeds per tree can arise from adaptive evolution driven by intense species interactions or from the direct effects of a warm, moist climate on tree fecundity. Either way, the massive differences in seed supply ramify through food webs potentially explaining a disproportionate role for species interactions in the wet tropics.

P.35 Fungal microbiome of perennial crop intermediate wheatgrass *Thinopyrum intermedium* for sustainable agricultural production

Makoto Kanasugi
Nicolaus Copernicus University in Toruń

Abstract:

KANASUGI M, DEJA-SIKORA E, THIEM D., HRYNKIEWICZ K.

Department of Microbiology, Faculty of Biological Sciences and Veterinary, Nicolaus Copernicus University (Ncu), Lwowska 1, Pl-89-100 Torun, Poland

Modern agricultural production, such as an intensive annual grain cultivation creates negatives impact on terrestrial ecosystems, emerging as land-use issue. Perennial grain crop Intermediate wheatgrass (IWG: *Thinopyrum intermedium*) are promising alternative grain crop for sustainable agricultural production, which can be harvested for multiple years. IWG provides long-term green cover and harbor intense root system; expected to contribute to the conservation of ecosystem service and soil biodiversity. Moreover, it is presumed that IWG may take advantage of microorganisms recognized as plant microbiome to improve its productivity. Fungal microbiome is recognized as crucial factor on plant productivity and ecosystem functions. Arbuscular mycorrhizal fungi (AMF) is obligate mutualistic symbiont with majority of land plants which has critical roles in host plant productivity terrestrial ecosystem function. We hypothesize that fungal microbiome including AMF play significant role in IWG productivity and conserving ecosystem services; however, their role in IWG cropping system is still unclear. In this study, field scale experiments are undergoing across European counties: France, Belgium, and Sweden and we apply high through-put sequencing-based meta-DNA barcoding approach to analyze fungal community, comparing IWG and annual wheat to reveal their potential role in IWG cropping system for sustainable manner of food production

P.36

Combined Acute Ozone and Water Stress Alters the Quantitative Relationships between O3 Uptake, Photosynthetic Characteristics and Volatile Emissions in *Brassica nigra*

Kaia Kask
Estonian University of Life Sciences

Abstract:

K. KASK, E. KAURILIND, E. TALTS, A. KÄNNASTE, Ü. NIINEMETS

Chair of Crop Science and Plant Biology, Institute of Agricultural and Environmental Sciences, Estonian University of Life Sciences, Kreutzwaldi 1, 51006 Tartu, Estonia

O_3 entry into plant leaves depends on atmospheric O_3 concentration, exposure time and openness of stomata. O_3 negatively impacts photosynthesis rate (A) and might induce the release of reactive volatile organic compounds (VOCs). Water stress reduces stomatal conductance (g_s) and O_3 uptake and can affect VOC release and O_3 quenching by VOC, but the interactive effects of O_3 exposure and water stress, as possibly mediated by VOC, are poorly understood. Well-watered (WW) and water-stressed (WS) *B. nigra* plants were exposed to 250 and 550 ppb O_3 for 1 h, and O_3 uptake rates, photosynthetic characteristics and VOC emissions were measured through 22 h recovery. The highest O_3 uptake was observed in WW plants exposed to 550 ppb O_3 with the greatest reduction and poorest recovery of g_s and A, and elicitation of lipoxygenase (LOX) pathway volatiles 10 min–1.5 h after exposure indicating cellular damage. Ozone uptake was similar in 250 ppb WW and 550 ppb WS plants, and O_3-dependent reduction in photosynthetic characteristics was moderate and VOC emissions were little affected. Water stress alone did not affect the total amount and composition of VOC emissions. The results indicate that drought ameliorated O_3 stress by reducing O_3 uptake through stomatal closure.

P.38

Invasive Pathogens responsible for Horse Chestnut (*Aesculus* spp.) disease symptoms in addition to Leaf Blotch

Yasin Korkmaz

University of Freiburg

Abstract:

Y. KORKMAZ[1,2], J. RIECKMANN[2], E. TERHONEN[3], K. BLUMENSTEIN[1,2]

[1]*Chair of Pathology of Trees, Institute of Forestry, Faculty of Environment and Natural Resources, University of Freiburg, Bertoldstr. 17, 79098 Freiburg, Germany*; yasin.korkmaz@forpath.uni-freiburg.de, kathrin.blumenstein@forpath.uni-freiburg.de
[2]*Forest Pathology Research Group, Department of Forest Botany and Tree Physiology, Faculty of Forest Sciences and Forest Ecology, Büsgenweg 2, Georg-August-University Göttingen*, *37077 Göttingen*, johanna.rieckmann@stud.uni-goettingen.de
[3]*Natural Resources Institute Finland (Luke), Forest health and biodiversity, Latokartanonkaari 9, 7 FI-00790 Helsinki, Finland*; eeva.terhonen@luke.fi

Horse Chestnut (*Aesculus*) is an ornamental tree typically found in urban areas in Europe. It is an aesthetically valuable and essential genus of trees with significant biodiversity. Increasing temperatures and the invasion of non-native pathogens, leaf dieback, and increasing tree mortality are caused by the leaf miner (*Cameraria ohridella*) and leaf blotch (*Guignardia aesculi*). 30 Horse Chestnut leaves with disease symptoms (e.g., necrosis) were collected in Göttingen, Germany. A high fungal diversity of Ascomycetes could be identified with several molecular markers. Saprobionts and the potential pathogens *Biscogniauxia nummularia*, *Colletotrichum* spp., *Alternaria* spp., and *Fusarium* spp. were found. A putative synergy between the isolated pathogens and *G. aesculi* was investigated by antagonism assays and comparing the nutrient profiles with Phenotypic MicroArrays. The results suggest that the fungi do not antagonize each other; thus, a co-existence on the leaves is likely. Horse Chestnut trees may suffer from various fungal pathogens possibly responsible for decreasing their hosts health condition. The situation may worsen with increasing temperatures and a rising number of alien species. The results suggest that usually, warm-loving fungi spread to temperate climate zones. More research is required to investigate pathogens and their possible correlation to the leaf miner infestations within Europe.

P.39 Mechanical stress perceived by roots: *status quo* and perspectives

Mohamed Kouhen
University of Molise

Abstract:

MOHAMED KOUHEN, GABRIELLA STEFANIA SCIPPA, DONATO CHIATANTE, ANTONELLO MONTAGNOLLI, DALILA TRUPIANO
Department of Biosciences and Territory, University of Molise, Contrada Fonte Lappone, Pesche, IS 86090, Italy

Mechanical stress is an understudied abiotic stimulus that continuously impacts plant growth and development. It includes rain, wind, gravity, soil impedance, wounding, and bending. Previous research from our group focused on the relatively long-term stress response (6-12 months) of the woody roots of poplar trees to the bending stress. Proteomic analysis (Scippa et al., 2008; De Zio et al., 2016), transcriptomics (Rossi et al., 2015), anatomic and hormonal analysis (Trupiano et al., 2012; De Zio et al., 2020), in addition to network-based bioinformatic analysis (Dimitrova et al., under review) revealed that bent roots were characterized by an asymmetric response between the concave and convex side of the root. Formation of new lateral roots was observed on the convex side, and the deposition of reaction wood (RW) on the opposite concave side. Both sides also displayed hormonal differences in terms of auxins, abscisic acid (ABA), cytokinins (CKs) and their metabolites. To better understand these differential responses, we will zoom in to the early stress perception in both *Arabidopsis* and poplar roots. Special emphasis will be given to calcium and ROS signaling as major stress signaling elements. Expression levels of membrane-bound calcium sensors (eg., CNGCs) and downstream signal transductors will be studied, in addition to *in vivo* calcium imaging using *Arabidopsis* lines expressing the calcium indicator UBQ10pro::GCaMP3. Moreover, apoplastic liquid will be extracted to look for early indicators of stress perception and possible hints explaining the root response to mechanical bending.

P.40 The European 2018 heatwave impact on the CO2 fluxes of hemiboreal forest ecosystems

Alisa Krasnova
University of Tartu

Abstract:

KRASNOVA A., MANDER Ü., NOE S.M., URI V., KRASNOV D., SOOSAAR K.

University of Tartu, Ülikooli 18, Tartu, 50090, Estonia;
Estonian University of Life Sciences, Fr. R. Kreutzwaldi 1, Tartu, 51006, Estonia.

Forest ecosystems play an essential role in the global carbon cycle acting. Their sink strength might diminish with the increasing frequency of extreme weather events. In 2018, Europe experienced a heatwave, accompanied by rainfall reduction. We assessed the influence of elevated temperatures on the carbon exchange of three forest stands of different types (coniferous, deciduous (alder), and conifer-broadleaved) and a clear-cut area located in the geographical vicinity of a hemiboreal zone. The carbon fluxes were calculated using the eddy-covariance technique. Upland coniferous forest net carbon uptake (NEE) was slightly reduced due to the increase in ecosystem respiration. It was the most resistant to the heatwave, most probably because of its adaption to low soil water content. Alder riparian forest gained higher NEE due to the favourable period in spring. Contrary to our expectations, a mixed conifer-broadleaved forest (pine, spruce, birch, clear-cuts) was more affected by the heatwave with almost three times higher amount of carbon was released in 2018 as a result of GPP reduction. The clear-cut carbon exchange was the most vulnerable, the warm days in spring and autumn did not offset the temperature anomaly impact, as was observed for the forested ecosystems.

P.41 The effects of nitrogen form on the water use of Australian tropical tree seedlings

Vithya Krishnan
The University of Queensland

Abstract:

V. KRISHNAN, N. ROBINSON, J. FIRN, J. HERBOHN, S. SCHMIDT

School of Agriculture and Food Sciences, The University of Queensland, Brisbane, Queensland, Australia 4072

Reduced rainfall and prolonged drought impact tropical forest restoration by causing high seeding fatality and slowing global reforestation efforts. To boost seedling resilience and resulting forest restoration success, we tested the hypothesis that a suitable nitrogen (N) environment in the nursery improves water use efficiency and drought resilience. There is evidence that inorganic and organic N sources differ in their effects on ecophysiology. Specifically, we aimed to determine if organic N confers resilience to rainforest species *Acacia mangium* and *Alphitonia petriei*. After 12 weeks in well-watered conditions with inorganic N (Osmocote™, ammonium nitrate) or organic N (Argrow™, liquid arginine), seedlings were exposed to four weeks of water limitation. *Acacia mangium* was unresponsive to N sources and water limitation universally decreased growth relative to well-watered seedlings. In contrast, *Alphitonia petriei* produced similar total biomass with both water regimes indicating lower water needs. Confirming our hypothesis, organic N-supplied seedlings had a 30% higher water use efficiency and less depleted leaf $\delta^{13}C$ signatures with organic compared to inorganic N. This indicates that arginine as N source regulates stomatal conductance in *Alphitonia petriei*. The findings demonstrate that organic N can enhance drought resilience traits in certain tropical tree species.

P.42 Distinct functional trait responses of wild and domesticated barley roots to soil biota

Amit Kumar
Leuphana University of Lüneburg, Germany

Abstract:

AMIT KUMAR, OLGA KUZNETSOVA, VICKY M. TEMPERTON

Institute of Ecology, Leuphana University of Lüneburg, 21335 Lüneburg, Germany

Crop domestication has led to remarkable changes in aboveground plant traits to improve their desirability to human needs. However, we know essentially very little about the impact of domestication on functional root traits and their plasticity. Further, it is not clear whether domestication has also affected root-microbial interactions, as one would assume that growing domesticated crops under high-fertilization and homogenized soil environments would deter such interactions. Therefore, we investigated how domestication and soil microbial diversity have affected key functional root traits of wild and domesticated barley. We found that root physiological and biological traits were strongly responsive to soil microbial diversity and varied between both barley species. For instance, root mycorrhizal colonization was higher for wild barley whereas root exudation rates were higher for domesticated barley. We also found that the shoot dry matter content decreased for domesticated barley and decreased with decreasing soil microbial diversity. Overall, our results demonstrated distinct root trait syndromes as a function of soil microbial diversity for both wild and domesticated barley.

P.43

MSD2-mediated ROS metabolism fine-tunes the timing of floral organ abscission in Arabidopsis

Jinsu Lee
Seoul national university

Abstract:

JINSU LEE, HUIZE CHEN, GISUK LEE, AURÉLIA EMONET, SANG-GYU KIM, DONGHWAN SHIM, AND YUREE LEE

Research Center for Plant Plasticity, Seoul National University, Seoul 08826, Republic of Korea;

Fruit and flower abscission is directly linked to the crop quality and yield, which is affected not only by intrinsic developmental program but also by environmental conditions. Recently, a lot of advance has been made to understand molecular mechanisms of the abscission, and key components and signaling pathways have been identified. However, our knowledge is still very limited, and molecular mechanisms of how environmental stimuli are integrated into the developmental program of abscission process are less understood. To find molecular links between the external cues and the intrinsic program, we performed mutant screens and identified a *MnSOD2* (*msd2*) mutant that accelerated in floral organ abscission. Moreover, RNA-seq results showed the regulation of MSD2 on floral abscission at stage 15 was mainly by affecting NO and ABA response which was also confirmed by in vitro pharmacological experiments. I will present our recent progress on cellular and physiological characterization of *msd2* and genetic analysis to understand MSD2-mediated signaling pathways. Results and knowledge arising from our study will provide a better understanding of signaling networks regulating abscission.

P.44 Battle between bacterial effector and plant autophagy

Jia Xuan Leong

ZMBP University of Tübingen

Abstract:

J. X. LEONG[1], M. RAFFEINER[2], D. SPINTI[2], G. LANGIN[1], M. FRANZ-WACHTEL[3], A. R. GUZMAN[4], J.-G. KIM[4], P. PANDEY[5], A. E. MININA[6], B. MACEK[3], A. HAFRÉN[8], T. O. BOZKURT[5], M. B. MUDGETT[4], F. BÖRNKE[2,7], D. HOFIUS[8], S. ÜSTÜN[1,9]*

1. University of Tübingen, Center for Plant Molecular Biology (ZMBP), 72076 Tübingen, Germany
2. Leibniz-Institute of Vegetable and Ornamental Crops (IGZ), 14979 Großbeeren, Germany
3. Interfaculty Institute for Cell Biology, Department of Quantitative Proteomics, University of Tübingen, 72076 Tübingen, Germany.
4. Department of Biology, Stanford University, Stanford, CA 94305, USA
5. Department of Life Sciences, Imperial College London, SW7 2AZ London, United Kingdom.
6. Department of Molecular Sciences, Uppsala BioCenter, Swedish University of Agricultural Sciences and Linnean Center for Plant Biology, 75007 Uppsala, Sweden.
7. Institute of Biochemistry and Biology, University of Potsdam, 14476 Potsdam, Germany
8. Department of Plant Biology, Uppsala BioCenter, Swedish University of Agricultural Sciences and Linnean Center for Plant Biology, 75007 Uppsala, Sweden.
9. Faculty of Biology & Biotechnology, Ruhr-University Bochum, 44780 Bochum, Germany

Plant pathogenic effectors perturb the proteolytic pathways autophagy and ubiquitin-proteasome system (UPS), disrupting host cellular processes to enhance virulence. We study the bacterial pathogen *Xanthomonas campestris* pv. *vesicatoria (Xcv)* which is a significant agricultural pest. Results from our lab show that *Xcv* subverts host autophagy during infection. We identified XopL as an effector with a role in this subversion of host autophagy. We showed that XopL interacts with and ubiquitinates a component of the host autophagic machinery, SH3P2. This results in SH3P2 degradation via the proteasome, which leads to higher *Xcv* bacterial growth. In turn, the plant defends itself using defence-related selective autophagy receptor NBR1. We showed that NBR1 is upregulated and accumulates during coexpression with XopL, colocalizes with XopL in aggregates, is present in a complex with XopL, and causes the autophagic degradation of XopL. Knockdown of NBR1 also resulted in higher *Xcv* bacterial growth. To provide further mechanistic insight, NBR1 mutants lacking ubiquitin-binding domains were tested for interaction with XopL. We found that ubiquitin-dependent and -independent mechanisms drive this interaction. Our study is a novel example in plants of "effectorphagy", where selective autophagy targets bacterial effectors, and further gives mechanistic insight behind this process.

P.45 The impact of bark beetle outbreaks on forest carbon accumulation

Hyungwoo Lim
Swedish University of Agricultural Sciences

Abstract:

H LIM, N HENRIKSSON, R LUTTER, S BUCKLEY, H GRIP, S HASEGAWA, D LUSSETTI, R MAGH, Z STANGL, A STEINHOF, T LUNDMARK

Department of Forest Ecology and Management, Swedish University of Agricultural Sciences, Umeå, SE-901 83, Sweden

Forests are at increasing risk of dieback due to pathogen outbreaks. Despite fertilization being the most common practice in boreal productive forests, it is not known how the fertilization-induced gains in soil carbon accumulation would fare after such a dieback event.

We examine the impact of bark beetle outbreak on soil carbon pools. To simulate bark beetle damage to forests, we employed a large-scale tree-girding (1000 m^2). Among three pairs of unfertilized control and three pairs of fertilized plots, the girdling treatment was randomly assigned to one of each pair, comprising a combination of girdling and fertilization treatments (n=3). Girdling was commenced in June 2002, resulting in actual outbreak of bark beetles, having killed all trees under the treatment.

Two decades after the bark beetle damage, soil carbon pool in girded-unfertilized plots was 15.9±3.9 Mg C ha^{-1} lower than non-girdled plots, and the reduction occurred mostly from the mineral soil (0–40 cm). Fertilized plots, however, did not show reduction of soil carbon by girdling, due to a sustained carbon influx via understory vegetation turnover and reduced decomposition.

Our finding highlights the importance of soil fertility and vegetation dynamics in predicting ecosystem carbon dynamics in response to a disturbance.

P.46 Mutually inclusive mechanisms of drought-induced tree mortality

Roman Mathias Link
University of Würzburg

Abstract:

ROMAN M. LINK, PETER HAJEK, CHARLES A. NOCK, JÜRGEN BAUHUS, TOBIAS GEBAUER, ARTHUR GESSLER, KYLE KOVACH, CHRISTIAN MESSIER, ALAIN PAQUETTE, MATTHIAS SAURER, MICHAEL SCHERER-LORENZEN, LAURA ROSE, BERNHARD SCHULDT

Plant Ecology and Ecophysiology, Julius-von-Sachs-Institute of Biological Sciences, University of Würzburg, Julius-von-Sachs-Platz 3, 97082 Würzburg, Germany

The unprecedented tree dieback caused by the 2018 summer drought in Central Europe highlights the need for a better mechanistic understanding of drought-induced tree mortality. While previous research has singled out numerous risk factors, the principal mechanisms are still debated.

We studied 9,435 young trees of 12 temperate species to assess how hydraulic traits, carbon dynamics, pest infestation, tree height and neighborhood competition influence individual mortality risk in the 2018 drought, which resulted in the loss of a third of the trees.

Species with narrower hydraulic safety margins and an increasing sugar fraction in their non-structural carbohydrate pool were more likely to die. Individual risk was higher for trees affected by bark beetles, smaller trees, and trees that received less shelter from their neighbors, though neighborhood interactions were strongly species-specific.

Our data show that while severe tissue dehydration driven by hydraulic failure marks the final stage of drought-induced tree mortality, it interacts with other, mutually inclusive processes. These include starch depletion for osmotic adjustment and pest infestation, and are modulated by size effects and neighborhood interactions. A more holistic view that accounts for multiple causes of drought-induced tree mortality is required to improve predictions of trends in global forest dynamics.

P.47

Whether long-term drought manipulation shift post-fire recovery pathways of Mediterranean shrubland?

Daijun Liu
University of Vienna

Abstract:

DAIJUN LIU

Department of Botany and Biodiversity Research, University of Vienna, Austria

Increasing water deficits and severe droughts are expected to alter vegetation post-disturbance recovery in semi-arid Mediterranean ecosystems in future. However, which vegetation metrics will be shifted and how they respond over time are not clear, and the experimental evidence is lacking. Here we assessed the impacts of continuous (20-year) experimental drought (-30% rainfall) on the pathways for an early-successional Mediterranean shrubland. The results indicate that the pathways of vegetation metrics were differently affected by experimental drought. The abundance of Globularia alypum follows pathway 1 (altered mature state). Simpson diversity and abundance of Erica multiflora follow pathway 2 (delayed succession) while species richness, community abundance and shrub abundance follow pathway 3 (alternative stable state). There were no significances for the resilience to extremely dry years between control and drought treatment. Principal component analysis (PCA) shows that the first two principal components explained 72.3 % of the variance in vegetation metrics, PC1 was mainly related to the changes in community abundance, shrub abundance and species richness while PC2 was related to Simpson diversity and abundance of G. alypum and E. multiflora. Further research should focus on successional pathways in more water-deficit conditions in Mediterranean ecosystems and the consequences on ecosystem functions.

P.48

Herbicide addition and mechanical disturbance differ in their effects on arbuscular mycorrhizal fungal communities

Siqia Liu

Institute of Ecology and Earth Sciences, Department of Botany, University of Tartu

Abstract:

S. LIU, M. VASAR, M. ÖPIK, K. KOOREM

Department of Botany, Institute of Ecology and Earth Sciences, University of Tartu, Juhan Liivi 2, Tartu, Estonia

Disturbances related to increasing land-use are shaping above-and belowground communities but reported effects of disturbances are often controversial. Arbuscular mycorrhizal (AM) fungi, which live in soil and associate with the majority of terrestrial plant species, are the key component of soil communities. Here we tested if the response of AM fungi to disturbances depends on the type of disturbance and initial species richness of AM fungal communities. In a greenhouse experience we applied mechanical disturbance and chemical disturbance as herbicide to AM fungal communities from field and meadow origin in a fully-factorial design. Our results indicated that mechanical disturbance alone increased AM fungal taxon richness, while the effect of herbicide addition alone or in combination with mechanical disturbance had no significant influence. All disturbances increased the abundance of cultured AM fungi and decreased phylogenetic structure of AM fungal communities but this trend was strongest when herbicide was applied alone. The effect of the disturbances did not depend on the initial richness of AM fungal communities. Our results suggest that considering the type of the disturbance can help to improve our understanding about the effects of disturbances on AM fungal communities.

P.49

The effect of seed set temperature upon circadian clock-associated developmental and physiological phenotypes

Deirdre Lynch
John Innes Centre

Abstract:

DEIRDRE LYNCH[1], PAIGE E. PANTER[1], JACK FARMER[2], STEVEN PENFIELD[1,] ANTONY N. DODD[1]

[1] *John Innes Centre, Norwich Research Park, Norwich NR4 7UH*
[2] *LettUs Grow Unit 4, Avon Valley Business Park, Chapel Way, Brislington, Bristol BS4 4EU*

Seasonal and geographical variation in temperature conditions during seed production may influence the circadian phenotypes of the progeny, potentially affecting agriculturally important traits in crops. I am investigating this concept at a mechanistic level, using Arabidopsis as an experimental model. I produced seeds under a range of temperature conditions and investigated circadian clock function and other clock-associated phenotypes including seed dormancy and flowering time of the progeny. This involved a combination of circadian bioluminescence imaging and targeted physiological assays. My experiments are identifying that seed production temperature affects features of circadian regulation in the progeny and have exciting effects upon the transition to flowering that suggest a transfer of temperature information between generations. The insights from my work have important implications for the consistency of crop production within artificial growing systems as light and temperature conditions can be aligned with the circadian clock to optimise crop performance.

P.50 The role of a common mycorrhizal network in modulating the symbiosis of potato with cyst nematodes

Emily Magkourilou
The University of Sheffield

Abstract:

E. MAGKOURILOU, C. A. BELL, P. E. URWIN, T. J. DANIELL, K. J. FIELD

Plants, Photosynthesis and Soil, School of Bioscience, University of Sheffield, Sheffield S10 2TN, UK
Faculty of Biological Sciences, School of Biology, University of Leeds, Leeds, LS2 9JT, UK

In nature, plants interact simultaneously with multiple above- and below-ground symbionts. These relationships range from mutualisms, for example, with arbuscular mycorrhizal fungi (AMF), to parasitism, with organisms such as plant-parasitic nematodes. However, research efforts have often focused on the patterns of plant resource allocation to the AMF alone, ignoring the role of other, potentially competing plant symbionts. Recently, the tripartite interaction between potatoes, AMF and potato-cyst nematodes has received more attention with findings suggesting that infection by nematodes can cause a 20-fold reduction in the allocation of plant-carbon to AMF whilst the supply of fungal-acquired nutrients to the host plant is largely maintained. However, the role of common mycorrhizal networks and their potential to also impact the resource allocation dynamics in these complex interactions remains unknown. Here, using stable and radioactive isotope tracing and an experimental set-up of two potato plants linked by the same AMF network, we show how the presence of potato-cyst nematodes on either, neither, or both plants influences the carbon-for-nutrient exchange between the AMF network and the two host plants. Our work highlights the importance of employing experimental designs of increasing ecological relevance in order to more fully understand the carbon-for-nutrient dynamics in AMF-plant symbioses.

P.51 South American and Chilean research gaps in soil and mycorrhizal biodiversity and functioning

César Marín
Universidad Santo Tomás, Chile

Abstract:

C. MARÍN[1], J. RUBIO[2], R. GODOY[3]

[1]Centro de Investigación e Innovación para el Cambio Climático, Universidad Santo Tomás, Chile. [2]Escuela de Geografía, Universidad Austral de Chile, Chile. [3]Instituto de Ciencias Ambientales y Evolutivas, Universidad Austral de Chile, Chile.

It is crucial to elucidate the relationship between soil biodiversity and ecosystem functioning to support the governance around soil biota. However, soil macroecological analyses show that there are significant environmental, taxonomic, functional, and temporal data gaps and that in very few sites (0.3%) both soil biodiversity and ecosystem functions are jointly studied. Here we analyzed the data gaps for i.) South American mycorrhizal biodiversity (4 types) and functioning (9 functions), and for ii. Chilean soil biodiversity (10 taxa) and functions (4 functions). For South American mycorrhizas, we found 532 articles and 1528 sampling sites (80% in Brazil, Argentina, and Chile). In 24.21% of the sites, mycorrhizal biodiversity and ecosystem functions were jointly investigated. Biomes like the Atacama desert, Patagonian steppe, Cerrado, Chaco, and the Amazonian rainforest were highly understudied, as were most mycorrhizal functions (except plant growth and soil aggregation) and orchid and ericoid mycorrhizal associations. For Chilean soil biodiversity, 741 sampling sites were obtained from 239 articles. In 18.10% of the sites, both soil biodiversity and ecosystem functions were jointly investigated. By far, Bacteria/Fungi and nutrient cycles were the most investigated taxa and function, respectively, mostly in specific areas of the Atacama desert and the Valdivian temperate rainforests.

P.52 The economic trade-off between root hairs and mycorrhizal partners along a land use gradient

Elsa Matthus
Leibniz Institute for Agricultural Landscape Research (ZALF)

Abstract:

E. MATTHUS, T. HENNING, F. HANSCH, K. BARFUSS, J. BERGMANN

Leibniz Centre for Agricultural Landscape Research (ZALF), Am Gutshof 7, 14641 Paulinenaue, Germany

Nutrient uptake in plants relies on direct soil-to-root uptake as well as on symbiosis with arbuscular mycorrhizal fungi (AMF). Recent studies have shown that fine root traits predict AMF colonization rates - the thinner the root, the lower the colonization with AMF. As data on root hairs, dedicated structures to take up nutrients, is scarce, it is however not known how plants partition resources between building root hairs or engaging with AMF. In this study, we are testing the concept of a plant-fungal root hair surface trade-off along a land-use gradient in the field. We sampled 82 grassland species (forbs, grasses, legumes) across a range of different land-use intensity plots in the framework of the Biodiversity Exploratories in the South, Centre and North-East of Germany. Root trait analyses, with particular focus on root hairs, sequencing-based AMF-community analysis and determination of extraradical hyphal length and mycorrhization of plant roots are on-going. Preliminary results suggest that fine root variation follows the concept of the root economics space. Root hair length aligns with increase of specific root length, indicative of root hairs being an alternative to AMF symbiosis in plant nutrient uptake.

P.53

Phylogenetic conservatism and environmental conditions shape plant mycorrhizal traits across the world's flora

Yiming Meng
University of Tartu

Abstract:

Y. MENG, J. DAVISON, M. MOORA, M. ÖPIK, C.G. BUENO

Department of Botany, University of Tartu, Liivi 2, Tartu 50409, Estonia

Mycorrhizal symbioses are known to strongly influence plant performance, structure plant communities and shape ecosystem dynamics. Plant mycorrhizal traits, characterizing either mycorrhizal type (arbuscular (AM), ecto-, ericoid, or orchid mycorrhiza) or mycorrhizal status, with plants being obligately (OM), facultatively (FM), or non-mycorrhizal, are among the most promising traits in terms of capturing plant belowground functionality. Here, we compile available plant mycorrhizal trait information for 11,780 vascular plant species worldwide. Using plant phylogenetic mega trees and 54 climatic and edaphic data layers, we assess the variance explained share and correlated of phylogenetic vs. environmental predictors for plant mycorrhizal traits. We found that plant mycorrhizal type showed higher phylogenetic conservatism when compared to status. Variance partitioning also revealed that phylogeny explained more of the variation in mycorrhizal type, while environmental variables explained more in status. We also mapped the global distributions of plant mycorrhizal type and status at a 50 km-grid scale. AM and OM were the dominant type and status, respectively, but as latitude increased, the share of AM species decreased. Similarly, as OM species decreased at higher latitudes, FM species increased. Our results demonstrate distinctive responses of plants with different mycorrhizal types to phylogenetic and biogeographical drivers at the global scale.

P.54 Volatile organic compounds (VOCs) of bryophytes in a changing climate

José Ángel Morales Sánchez
Estonian University of Life Sciences

Abstract:

JOSÉ ÁNGEL MORALES SÁNCHEZ[1], KRISTIINA MARK[1], JOÃO PAULO SILVA SOUZA[1], EERO TALTS[1], BAKHTIER RASULOV[1], ÜLO NIINEMETS[1,2]

[1] *Institute of Agricultural and Environmental Sciences, Estonian University of Life Sciences, Fr. R. Kreutzwaldi 1, Tartu 51006, Estonia*
[2] *Estonian Academy of Sciences, Kohtu 6, Tallinn 10130, Estonia*

Volatile organic compounds (VOCs) produced by plants are important signaling molecules with key roles in defense and stress response. Furthermore, VOCs alter the chemical composition of the atmosphere and affect the climate at local, regional and global levels. The emission of VOCs upon environmental stresses has been studied in vascular plants, serving as an important source of information to monitor plant physiology under environmental changes, while bryophytes have received little attention. However, bryophytes are fundamental constituents of ecosystems, and can dominate ecosystem functioning, especially in higher latitudes, where future climatic disturbances are expected to be more notorious. We studied the physiological responses of bryophytes and their stress tolerance to desiccation with a custom-made system that allowed collection and real-time measurement of VOC emission kinetics with simultaneous analysis of gas-exchange and chlorophyll fluorescence. We have identified an array of compounds emitted constitutively and induced as the result of the stress in bryophytes, where the species from moist and shaded habitats showed the largest magnitude of emissions. The obtained results highlight a high responsiveness of bryophyte flora to predicted future climatic repercussions and indicate that monitoring VOC responses can be used to assess the magnitude of stress experienced by bryophytes.

P.55

Single gene bioengineering as starting point to produce a new generation of super crops

Juan Camilo Moreno Beltran
King Abdullah University of Science and Technology

Abstract:

JUAN C. MORENO, JIANING MI, ALICE STRA, SALIM AL-BABILI

Center for Desert Agriculture, Biological and Environmental Science and Engineering Division (BESE), King Abdullah University of Science and Technology (KAUST), Thuwal, Saudi Arabia

Improving yield, nutritional value and tolerance to abiotic stress are major targets of current breeding and biotechnological approaches that aim at increasing crop production and ensuring food security. Metabolic engineering of carotenoids, the precursor of vitamin-A and plant hormones that regulate plant growth and response to adverse growth conditions, has been mainly focusing on provitamin-A biofortification or the production of high-value carotenoids. Here, we show that the introduction of a single gene of the carotenoid biosynthetic pathway in tobacco and different tomato cultivars induced profound metabolic alterations in carotenoid (UPLC), apocarotenoid (LC-MS) and phytohormones (hormonomics via LC-MS) pathways. Alterations in isoprenoid- and non-isoprenoid-derived hormones together with enhanced xanthophyll content influenced biomass partitioning (enhanced fruit and shoot biomass) and abiotic stress tolerance in both crop models. This manipulation also promoted growth in tobacco and tomato shoots, fruits, and roots. In addition, metabolic and hormonal changes led to accumulation of key primary metabolites contributing, for instance, to enhanced biotic stress tolerance and fruit shelf life in tomato. Our findings pave the way for developing a new generation of crops that combine high productivity and increased nutritional value with the capability to cope with climate change-related environmental challenges.

P.56 Lignin *p*-coumaroylation in eudicots may have arisen by convergent evolution

Yaseen Mottiar
University of Helsinki

Abstract:

YASEEN MOTTIAR,[1,2] REBECCA A. SMITH,[2,3] STEVEN D. KARLEN,[2,3] JOHN RALPH,[2,3] AND SHAWN D. MANSFIELD[1,2]

[1] *Department of Wood Science, University of British Columbia, Vancouver, BC, Canada*
[2] *Department of Energy Great Lakes Bioenergy Research Center, University of Wisconsin, Madison, WI, U.S.A.*
[3] *Department of Biochemistry, University of Wisconsin, Madison, WI, U.S.A.*

It has long been known that ester-linked *p*-coumarate (*p*CA) moieties decorate the lignin of commelinid monocot plants. These groups arise during lignification via the incorporation of monolignol conjugates assembled by *p*-coumaroyl-CoA:monolignol transferase (PMT) enzymes, members of the BAHD superfamily of acyltransferases. In this study, we found that lignin *p*-coumaroylation occurs in the stems of kenaf (*Hibiscus cannabinus*), which is a eudicot species, not a monocot. Furthermore, we identified a novel acyltransferase, *Hc*PMT, that shares less than 30% amino acid identity with monocot PMT sequences. Phylogenetics analysis suggests that *Hc*PMT and related homologues in eudicots may have arisen following the divergence of their common ancestor (*i.e.*, long after the division with monocots). To test its activity, *Hc*PMT was expressed in transgenic hybrid poplar trees and resulted in the novel incorporation of *p*CA into poplar lignin, a discovery which could be industrially useful for engineering the cell walls of biomass feedstock plants. This works highlights the importance of mining diverse plant taxa for new lignin engineering tools. Moreover, the occurrence of *p*CA outside of monocot lineages may represent a new example of convergent evolution in plant cell walls.

P.57 Pinus pollen chemistry response to UV

Florian Muthreich
University of Bergen

Abstract:

F. MUTHREICH, A.W.R. SEDDON, T.M. ROBSON

Department of Biological Sciences, University of Bergen, Thormøhlensgate 53A, 5006 Bergen, Vestland, Norway

Ultraviolet radiation has effects on the biosphere at the level of genes, species and ecosystems. Despite the significance of UV-B for ecosystems functioning and individual plant fitness, the response of plants to UV radiation remains poorly understood. One of these responses is the production of para-coumeric acid to protect cell contents from the adverse effects of UV. Para-coumeric acid is an important compound in the pollen grain wall and is theorized to act as a “sunscreen” for pollen grains and the genetic material within. Nevertheless, the relationship between dose and response of para-coumeric acid to UV in pollen grains is not fully understood.

We present the first results from field experiments to help understand the response between para-coumeric acid and UV-radiation. In the field experiment three filters were attached to branches of Pinus uncinata trees to shield the pollen from i. only UV-A and ii. UV-A and UV-B and iii. permit all UV light. After maturation of the pollen, chemical methods are used to identify the composition of the pollen (IR spectroscopy and mass spectrometry). This field experiment aims to identify the effects of natural UV radiation on pollen chemical composition in general and coumeric acid in particular.

P.58

The Role of Arabidopsis thaliana Cyclic Nucleotide-Gated Channel (CNGC) 2 and 19 in Extracellular ATP Signalling

Youzheng Ning
Department of Plant Sciences, University of Cambridge

Abstract:

YOUZHENG NING, LIMIN WANG, JULIA M. DAVIES

Department of Plant Sciences, University of Cambridge, Cambridge CB2 3EA, United Kingdom

Extracellular adenosine 5’-triphosphate (eATP) is an important signalling molecule but poorly understood in plants. eATP is accumulated in response to external stresses such as wounding, salinity, and pathogen attack. When plant cells perceive eATP, an elevation of cytosolic free Ca^{2+} ($[Ca^{2+}]_{cyt}$) occurs, with the production of reactive oxygen species (ROS) and nitric oxide (NO). In the past decade, the identification of plant plasma membrane eATP receptors DORN1/P2K1 and P2K2 provided a clearer insight into eATP signalling pathways, but the downstream Ca^{2+} channels involved in eATP signalling remain unknown.

Cyclic nucleotide-gated channels (CNGCs) are Ca^{2+}-permeable channels which are opened via directly binding with the cyclic nucleotides cAMP and cGMP. Among the 20 members of *Arabidopsis* CNGCs, we firstly found CNGC2 could mediate eATP-activated root plasma membrane depolarization by electrophysiological tests. The involvement of CNGC2 in eATP-induced $[Ca^{2+}]_{cyt}$ elevation was then evident by aequorin Ca^{2+} indicator. Furthermore, we also identified CNGC19 plays a crucial role in eATP signalling for root apex and works in downstream of CNGC2. Both CNGC2 and CNGC19 were implicated in eATP-induced defense-related gene expression and plant wound response Pep1 signalling. Therefore, CNGC2 and 19 could be possible Ca^{2+} channels involved in eATP signalling.

P.59

Stomatal responses of the Arabidopsis cyclic nucleotide phosphodiesterase 1 mutant.

Fonthip Noothong
University of Bristol

Abstract:

F. NOOTHONG, D. H. MCLACHLAN, A. M. HETHERINGTON

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

We recently isolated a gene encoding a cyclic nucleotide phosphodiesterase (cnPDE1) from Arabidopsis. We have been using this to investigate the role of cGMP signalling in guard cells. We have concentrated on the ability of apoplastic calcium to induce stomatal closure. This process involves an increase in the concentration of cytosolic calcium ions and an increase in guard cell ROS. Our findings show that the pde1 mutant is hypersensitive to apoplastic calcium -induced closure but retains the apoplastic calcium-induced increase in ROS. From this we conclude that ROS is upstream of PDE1 in this response.

P.60

Proteomic profiling of *Medicago truncatula* seed priming: highlighting novel players in pre-germinative metabolism

Andrea Pagano
University of Pavia

Abstract:

A. PAGANO[1], L. KUNZ[2], A. DITTMANN[2], S. DE SOUSA ARAÚJO[3], A. MACOVEI[1], S. SHRIDHAR GAONKAR[1], H. WAZEER[1], A. BALESTRAZZI[1].

[1]Department of Biology and Biotechnology 'L. Spallanzani', University of Pavia, via Ferrata 9, 27100, Pavia, Italy; [2]Functional Genomics Center Zurich (FGCZ), University of Zurich/ETH Zurich, Winterthurerstr. 190, CH-8057, Zurich, Switzerland; [3]Association BLC3-Technology and Innovation Campus, Centre Bio R&D Unit, Rua Comendador Emílio Augusto Pires 14, Edifício SIDE UP, 5340-257 Macedo de Cavaleiros, Portugal.

Seed priming represents a resource-effective route for seed quality improvement. Specifically, the rehydration-dehydration cycle at the basis of seed priming protocols activates pre-germinative metabolism, thus preparing seeds for a faster germination and an improved stress resilience.

Our work showed that two hours of hydropriming followed by four hours of dry-back accelerates germination in the model legume *Medicago truncatula*. However, it remains unclear which are the molecular mechanisms and the metabolic pathways implicated in the observed response. The present work investigates the changes in the proteome of primed *M. truncatula* seeds, focusing on the response to antioxidant and genotoxic stress. A label-free proteomic approach (LC-MS/MS) allowed to identify and quantify 2000-2200 protein entries for each pairwise comparison within the experimental system, highlighting those that were differentially accumulated with priming progression and/or in comparison with unprimed control seeds during re-imbibition, particularly those implicated in the antioxidant and genotoxic stress response. These results were correlated with the biometrical assessment of priming effectiveness, ROS accumulation profiles and gene expression analyses. This integrative characterization of seed priming in *M. truncatula* can be used to support the future development of seed priming protocols adapted to legumes.

P.61

Characterization of novel stomatal mutants identified in a large-scale mutant screen

Helen Parik
University of Tartu

Abstract:

HELEN PARIK, DMITRY YARMOLINSKY, CEZARY WASZCZAK, OLENA ZAMORA, TRIIN VAHISALU, MAIJA SIERLA, JAAKKO KANGASJÄRVI, HANNES KOLLIST

Institute of Technology, University of Tartu, Tartu 50411, Estonia. Division of Plant Biology, Viikki Plant Science Centre, Department of Biosciences, University of Helsinki, FI-00014 Helsinki, Finland

Since plants have a waxy cuticle acting as a barrier to withstand desiccation, their functioning requires specialized airways to facilitate gas exchange. These small pores, stomata, are formed by pairs of guard cells which are able to shrink and swell, thus controlling stomatal apertures. By triggering stomatal closure, plants reduce water evaporation as well as prevent entry of air pollutants and pathogens. Ozone is a major air pollutant, one of the main causes behind crop production losses worldwide. Tropospheric O3 enters plants through stomata and degrades to reactive oxygen species (ROS) in the apoplast. ROS act as signaling messengers inside plants, making ozone a valuable tool for investigating apoplastic ROS signaling. A forward genetic screen for mutants lacking the stomatal response to O3 was started to gain more insight into stomatal regulation of signaling pathways. Currently, 19 novel mutations have been mapped and 60 are currently being mapped. Here, by using gas exchange measurements, we describe the stomatal phenotypes of two lines identified in the screen. Mapping in these lines will help clarify ROS-dependent signaling pathways in guard cells.

P.62

Trait trade-offs underlying abiotic stress tolerance strategies in woody plants

Nicola Pavanetto
Estonian University of Life Sciences (Tartu, Estonia)

Abstract:

NICOLA PAVANETTO, CARLOS P. CARMONA, ÜLO NIINEMETS, LAURI LAANISTO, GIACOMO PUGLIELLI

Institute of Agricultural and Environmental Sciences, Estonian University of Life Sciences, Tartu 51006, Estonia, *Institute of Ecology and Earth Sciences, University of Tartu, Lai 40, 51005 Tartu, Estonia*

Climate change is altering abiotic stress regimes, and thus woody plants performance, at every scale. Functional traits have become a staple for understanding species' resistance to abiotic stressors. However, we still miss consensus on the set of traits defining general woody plant adaptations to tolerate multiple abiotic stresses. Recently, a stress tolerance trade-off space (STS) was formalized, defining the major axes of differentiation of woody plants' tolerance strategies towards drought, shade, waterlogging, and cold for 799 species of the Northern Hemisphere. Using the traits defining the global spectrum of plant form and function (GSPFF), we aimed to uncover multivariate patterns of trait-tolerance relationships. To this aim, using GAMs, we mapped the axes defining the STS within the GSPFF. Patterns were analyzed at the plant functional type-level (PFT, deciduous/evergreen angiosperms, evergreen gymnosperms) since PFTs occupy different GSPFF regions. Independently of PFT, specialized tolerance strategies towards considered stressors were associated with different positioning in the GSPFF, and thus to contrasting trait combinations. This marks the existence of pervasive functional constraints over polytolerance. However, the trait combinations underlying different stress tolerance strategies mostly differed between angiosperms and gymnosperms, suggesting contrasting trait trade-offs only at a broad taxonomic level.

P.63

Trait integration along elevation in tropical montane forests

Kerstin Pierick
University of Göttingen

Abstract:

KERSTIN PIERICK, CHRISTOPH LEUSCHNER, JÜRGEN HOMEIER

University of Goettingen, Albrecht-von-Haller Institute for Plant Sciences, Department for Ecology and Ecosystem Sciences, Untere Karspüle 2, 37073 Göttingen, Germany

The covariation of plant functional traits helps to understand plant ecological strategies and the trade-offs and constraints driving them. Commonly, ordination methods are applied to identify leading dimensions of trait variation. While this reduction of dimensionality is a useful tool for describing trait spectra, it conceals the degree of trait integration, i.e., the degree of overall correlative interconnectedness between traits. Trait network analysis is a novel method for quantifying trait integration, and allows visualizing and describing the complex relationships between functional traits.

In this study, we use trait network analysis to test whether trait integration depends on the environment, which to our knowledge has not been investigated yet. We collected 13 leaf, wood and fine root functional traits on 52 tree species of three elevational levels in hyperdiverse tropical forests in the southern Ecuadorian Andes. The results of our analysis reveal a stark increase of trait integration towards higher elevations. Presumably, this is a consequence of increasingly severe environmental filters under colder and less fertile conditions at higher elevations, which only allow for limited trait combinations, whereas a broader range of combinations can be successful at lower elevations.

P.64 5’ single-nucleotide microhomology-mediated DNA repair after CRISPR/Cas9 cut

Adéla Přibylová

Charles University, Faculty of Science, Department of experimental plant biology

Abstract:

ADÉLA PŘIBYLOVÁ, ATTILA MOLNAR, ANDREW BASSETT, LUKÁŠ FISCHER

Department of experimental plant biology, Faculty of Science, Charles University, Prague, 128 44, Czech Republic

CRISPR/Cas9 is a widely used tool to mediate target-specific double-strand breaks (DSBs). Such DSBs are repaired with or without mutation by one of the inner-cell DNA repair mechanisms. Individual DNA repair pathways differ in individual proteins, their activity during the cell cycle and their representation in individual organisms. To predict the CRISPR/Cas9 mutation outputs, the mechanisms affecting cleavage and subsequent repair must be known. These predictions are important, among other things, for the more accurate and faster production of genetically modified plants. In our previous study, Přibylová et al. (2022), we detected an unidentified 5’ single-nucleotide microhomology-mediated DNA repair mechanism which formed a significant proportion of deletion events. Subsequently, we analysed our Next-generation sequencing data together with plant and animal NGS data available in online databases and searched for similar outputs. We observed different deletion patterns and representations of 5’ single-nucleotide microhomology-mediated DNA repair in animal and plant models. In plants, deletion dominantly occurs on DNA strands without PAM, and at some targets, 5’ single-nucleotide microhomology-mediated DNA repair plays a significant role. On the other hand, in animals, deletions mostly extend to both sides of the cleavage site and are mediated by larger microhomologies.

P.65

Tackling the multiple dimensions of woody plant adaptations to tolerate abiotic stresses

Giacomo Puglielli
Estonian University of Life Sciences

Abstract:

G. PUGLIELLI

Institute of Agricultural and Environmental Sciences, Estonian University of Life Sciences, Kreutzwaldi 5, Tartu, 51014, Estonia

Understanding general multi-dimensional patterns of woody plants' adaptations to abiotic stresses is a pressing task for plant eco(physio)logy. This is especially relevant considering ongoing climate change, which will alter the relative importance of the different stress regimes experienced by plants. However, the lack of evidence for general patterns of plant adaptations to multiple stresses hinders our ability to predict how plants will endure future scenarios of multiple stresses.

Recently, a stress tolerance trade-off space (STS) was put forth, defining the major axes of differentiation of abiotic stress tolerance strategies towards drought, shade, cold and waterlogging for woody plants worldwide. By presenting the STS, I propose it as a strategy scheme for mapping important biological features into a single multi-stress tolerance framework. Such features can be selected from a set of multiple ecological dimensions recently proposed as key niche dimensions across the tree of life: functional traits, habitat climate, trophic, and defence dimensions. Adopting this framework has the potential to shed light on the multidimensional patterns of woody plants' adaptations to tolerate multiple abiotic stresses.

P.66

Unravelling plant-fungus alliances against herbivores

Shumaila Rasool
Netherlands Institute of Ecology (NIOO-KNAW)

Abstract:

S. RASOOL[1,2], A. BIERE[1], N. V. MEYLING[2]

Netherlands Institute of Ecology, Wageningen Netherlands[1]
University of Copenhagen, Copenhagen, Denmark[2]

Insect pathogenic fungi are commonly used in Integrated Pest Management to reduce crop pest insect incidence. Recently, it has been discovered that these fungi can also colonize plants and promote plant health and resistance. However, the mechanisms involved in this fungus-induced defense against biotic stress are mainly unknown. Focusing on this fundamental gap, we investigated the effect of colonization of plants by different insect pathogenic fungi on plant physiological responses and arthropod herbivore population growth. The fungi showed isolate-dependent effects on herbivores. Some isolates increased whereas others decreased population growth compared to a control treatment. The fungi strongly modulated of the production of specialized plant metabolites in an isolate-dependent way and the accumulation of certain compounds correlated negatively with herbivore growth rate. Endophytic colonization patterns did not correlate with herbivore numbers, supporting the hypothesis of indirect effects on herbivores by modulating plant metabolite profiles. In addition, the fungi overall increased above- and below-ground plant biomass and significantly increased root biomass in the presence of herbivory. These findings provide initial understanding of plant-fungus-herbivore interactions which are further explored in an ongoing H2020 project “EXCALIBUR”, to better understand the mechanisms involved in the observed effects of different microbes in plant production and protection.

P.67

Translational regulation of *arginine decarboxylase* transcripts by an ancient cis-element and its role in plant disease development

Erin Ritchie
ZMBP, University of Tübingen

Abstract:

RITCHIE ES[1], GALLAS N[1], WU D[2], AND LAHAYE T[1]

[1]*ZMBP, Eberhard-Karls-University Tübingen, 72076 Tübingen, Germany*
[2]*College of Biology, Hunan University, 410082, Changsha, Hunan, China*

The broad-host bacterial phytopathogen *Ralstonia solanacearum* injects a Transcription Factor-Like (TAL) effector called Brg11 into host cells to increase host susceptibility. We found that Brg11 binds to and activates host *arginine decarboxylase* (*ADC*) genes, encoding a rate-limiting enzyme in polyamine (PA) biosynthesis, leading to increased ADC activity and elevated PA levels, measured via liquid chromatography-mass spectrometry. Interestingly, the Brg11-binding target sequence upstream of the *ADC* CDS, is part of a sequence motif, called the *ADC-box*, that is conserved across land plant species and explains how Brg11 can act across multiple hosts. CRISPR mutagenesis of the *ADC*-box in tomato, Arabidopsis, and *Marchantia* results in elevated ADC activity and PA levels, demonstrating the regulatory function of the *ADC box* in PA homeostasis. We uncovered that the transcribed *ADC-box* is located in the 5'UTR of *ADC* transcripts and forms a hairpin structure that inhibits movement of the ribosome and translation of ADC. Current studies aim to clarify the molecular basis of *ADC-box*-dependent PA homeostasis. Metabolome profiling uncovered that PAs are conjugated to hydroxycinnamic acids (HCAs). PA-HCA conjugates have antimicrobial activity but can be degraded by *R. solanacearum*, possibly indicating a working model where Brg11 manipulates the host to combat *R. solanacearum* niche competitors.

P.68

Illuminating the genetic basis of Photosynthetic Heat Tolerance in Rice, through Chlorophyll Fluorescence and Genome Wide Association Studies

Jordan Robson
University of Nottingham

Abstract:

J. K. ROBSON[1], J. FERGUSON[1], A. PRICE[2], Z. A. WILSON[1], E. MURCHIE[1]

[1]*Department of Plant Sciences, University of Nottingham, Sutton Bonington Campus LE12 5RD*
[2] *School of Biological Sciences, University of Aberdeen AB24 3FX*

With global temperatures rising and causing huge losses in yield, the impact of heat stress on our staple crops is becoming a serious threat to food security. Since over half of the world's population rely on rice as a vital source of energy, the development of heat-tolerant rice varieties is key to tackling this threat. During vegetative development, minor heat stress causes a physiological reduction in rates of photosynthesis whilst high temperatures can irreversibly damage photosynthetic machinery, inhibiting the plant growth.

In this project, the maximum quantum efficiency of photosystem II (PSII) under increasing temperatures was assessed by a high-throughput chlorophyll fluorescence screen in two diverse African (*Orzya glaberrima*) and Asian (*O. sativa*) rice populations. The critical temperature (Tcrit) at which PSII is damaged, and the temperature at which PSII activity is at half of its maximum (T50), were fed into Genome Wide Association Studies (GWAS) to identify new QTLs underlying vegetative heat-tolerance in rice. A total of 893K and 2M single nucleotide polymorphisms (SNPs) in *O. glaberrima* and *O. sativa* respectively were screened for association with T50 and Tcrit using a multi-model approach. Significant SNPs formed 9 distinct putative QTLs in *O. sativa*, and 10 QTLs in *O. glaberrima*, according to global linkage disequilibrium. Here we identify a number of genes which co-localise with these QTLs as potential new candidates for generation of climate-resilient rice varieties.

P.69

The Odd Man Out pattern: a model-clade approach to a classic biogeographic riddle

Paloma Ruiz de Diego
Real Jardin Botanico - CSIC

Abstract:

P. RUIZ DE DIEGO[2], P. BARBERÁ[1], I. SANMARTÍN[2] AND R. RIINA[2]

[1]*Africa and Madagascar Program, Missouri Botanical Garden, St. Louis, Missouri, USA*. [2]*Real Jardín Botánico, RJB, CSIC, Madrid, Spain*

The “Odd-Man-Out” pattern [1] describes the observed lower plant diversity in tropical Africa compared to other tropical regions. Historical biodiversity loss linked to climate change is one of several existing explanations. Here, we examine long-standing hypotheses behind this pattern by adopting a model-clade approach that combines the in-depth knowledge of small-scale clade studies with the power of family-wide metanalysis, trying to reconcile opposing concerns in the field [2, 3]. We focus on 31 genera of family Euphorbiaceae, which form 19 clades [4] and include approximately 551 species. We first review each genus' alpha-taxonomy and compile information about traits linked to climate-change vulnerability: habit, geographic range and sexual system. Additionally, we assess the conservation status of selected species for the IUCN. Using the *Euphorbia* kit for HybSeq target sequencing, we generate robust, genome-wide phylogenies of 431 low-copy nuclear genes per genus. The resulting life-history, biogeographic and phylogenomic information are then used to examine the specific mechanisms working on a clade-level and the general drivers acting clade-wide on Afrotropical lineages. Currently, we have sampled more than 70% of the selected species; generated new genomic data on the Afro-continental Croton species, and produced the first phylogenomic time-tree for the African lineages of Acalyphoideae.

[1] Richards PW. 1973. Africa, the ‘Odd man out’. In: Meggers BJ, Ayensu ES, Duckworth WD, eds. Washington DC: Smithsonian Institution Press, 21–26. [2] Beaulieu JM, O'Meara BC. *American Journal of Botany* **106**(5): 613-617. [3] Donoghue MJ, Edwards EJ. *American Journal of Botany* **106**(3):327-330. [4] Wurdack KJ, Hoffmann P, Chase MW. *American Journal of Botany* **92**(8):1397-1420.

P.70

Date palm (*Phoenix dactylifera*) root and bulk soil associated bacterial communities are distinct and structured by irrigation water salinity

Dinesh Sanka Loganatha Chetti
United Arab Emirates University

Abstract:

D.S.L. CHETTI, S. CHANDRAN AND S. MUNDRA

Department of Biology, College of Science, United Arab Emirates University, Al-Ain, Abu-Dhabi, UAE

Abstract: The knowledge on date palm (*Phoneix dactylifera*) associated belowground bacterial communities and their response to irrigation water salinity is scarce. We collected root and bulk soil from different date farms across UAE and investigated how bacterial communities of different date palm compartments are affected by irrigation water sources (non-saline water vs saline groundwater). We found that bulk soil and root-associated bacterial communities are distinct. The decreased selection of unique OTUs (12.18%) in roots compared to bulk (41.55%) and a decrease in root bacterial diversity indicated root mediated effect. Root samples were dominated by *Ammoniphilus* and *Nitrospira,* whereas *Nocardioides* and *Gaiella* were abundant in bulk soil. Root-associated bacterial communities structured according to the irrigation water sources, wherein soil electrical conductivity (EC) and water pH were significant predictors. This is evidenced by the decrease in unique OTUs (26%) under saline groundwater irrigation conditions compared to non-saline water irrigation (40.5%). At genus level, the abundance of *Bacillus, Micromonospora and Mycobacterium* were higher in roots under saline groundwater irrigation while pattern contrasted for *Rhizobium, Streptomyces* and *Acidibacter*. Taken together, this study strongly supports that roots select specific bacterial communities compared to bulk soil and water pH and soil EC were important factors affecting them.

P.71

Potential role of wheat bacteria endophytes as an agri-food bioestimulant

Irene Sanz Puente
Instituto de Biomedicina y Biotecnología de Cantabria

Abstract:

I. SANZ-PUENTE[1], S. REDONDO[1,2], F. DE LA CRUZ[1], and M. ROBLEDO[1,2]

[1]Instituto de Biomedicina y Biotecnología de Cantabria, Universidad de Cantabria–CSIC, Santander, Cantabria, Spain. [2]Biomar Microbial Technologies, Armunia, León, Spain.

The price increment of chemical fertilizers and the problems derived from their excessive use, demand for environmentally sustainable solutions to the development of the agri-food industry. The role of certain microorganisms in plant growth promotion (PGP) by providing nutrients or increasing the plant tolerance to stress is well known. The most studied example is the nitrogen-fixing association of *Rhizobium* with legumes. In this work, we evaluate the role of endophytic bacteria from *Triticum* seeds and their potential as biostimulants. Commercial and ancestral wheat samples grown in North Spain under different irrigation regimes were harvested. 16S metataxonomical analysis reveal a predominant presence of Enterobacteriales, dominated by *Pantoea* and *Erwinia* genus*.* Endophytic bacterial isolated from these samples were screened *in vitro* for PGP-abilities (i.e mobilization of P K, siderophores production, synthesis of indole acetic acid (IAA), or ACC deaminase activity evaluation). Selected strains were further tested on *Arabidopsis thaliana* and several species of agri-food importance. Whole genome sequencing (WGS) analysis of some of these promising PGP strains reveals the acquisition of PGP-traits by mobilizable plasmids. Our findings show the biotechnological potential of *Pantoea* isolates. Furthermore, the promising results highlight relevance of seed-borne bacteria as plant biostimulants.

P.72

Fluxes of CO2, CH4, and N2O from drained nutrient-rich organic soils

Muhammad Kamil Sardar Ali
University of Tartu

Abstract:

MUHAMMAD KAMIL SARDAR ALI[1*], THOMAS SCHINDLER[1,2], AIN KULL[1], HANNA VAHTER[1], ÜLO MANDER[1,2], KAIDO SOOSAAR[1,2]

[1]*Department of Geography, Institute of Ecology & Earth Sciences, University of Tartu, 46 Vanemuise, EST-51014 Tartu, Estonia*
[2]*Department of Ecosystem Trace Gas Exchange, Global Change Research Institute of the Czech Academy of Sciences, Belidla 4a, CZ-60300 Brno, Czech Republic*

Organic soils are large carbon (C) reservoirs of the global terrestrial C-stock, and drainage produces significant greenhouse gas emissions. Draining creates aerobic conditions that increase the decomposition of the organic material and promote CH_4 oxidation and N_2O emissions in nutrient-rich sites in these naturally water-saturated organic soils. Our two full-year study is focused on ten sites: (I) five forest sites with different tree species, (II) three grasslands with different water regimes, (III) cropland, and (IV) a natural fen as a reference site; to assess the impact of drainage and land-use on CO_2, N_2O and CH_4 fluxes in hemiboreal Estonia.
Measurements were made biweekly using the manual static (CH_4 and N_2O) and dynamic (heterotrophic respiration (CO_2)) closed chamber methods in addition to environmental parameters from January 2020 to December 2021.
Our preliminary results show that all drained forest soils were annual methane sinks (−59.4±2.5 μg m^{-2} h^{-1}, mean±SE). However, CH_4 uptake from the studied fen, crop, and grasslands soils were lower –13.2±4.4, -12.2±2.0, and -8.2±3.3 μg m^{-2} h^{-1}, respectively, while grassland with poor drainage emitted CH_4. Most of the sites were annual emitters of N_2O; forest sites were higher emitters (15.9±2.3 μg m^{-2} h^{-1}) than cropland (12.7±4.1 μg m^{-2} h^{-1}) and fen soils (6.3±1.1 μg m^{-2} h^{-1}).
CH4 and N2O fluxes had a statistically significant correlation with soil moisture and soil temperature, respectively, while soil CO_2 fluxes peaked during the summer. Moreover, sites with high seasonal variations in water levels had higher temporal variability.

P.73 Cytosolic phytochrome A mediates the disassembly of processing bodies in far-red light

Philipp Schwenk
University of Freiburg

Abstract:

PHILIPP SCHWENK and ANDREAS HILTBRUNNER

Institute of Biology II, Faculty of Biology, University of Freiburg, 79104 Freiburg, Germany
Signalling Research Centres BIOSS and CIBSS, University of Freiburg, 79104 Freiburg, Germany

Phytochromes are red- and far-red light receptors that control the development of plants. They regulate plant growth and development to adequately respond to changing light conditions. It has been shown that translationally halted mRNAs stored in phase-separated RNA granulae called processing bodies (p-bodies) are released upon light perception and contribute to the adaption to the light environment. We recently described NOT9B as a novel phytochrome A interacting protein. NOT9B is part of the CCR4-NOT complex, an evolutionary conserved multi-protein complex, and negatively impacts phyA mediated signalling in the nucleus. In addition, we also observed a cytosolic NOT9B fraction that localises to p-bodies.

The photophysiological background of the disassembly of p-bodies remains unknown. Here, we show that phytochromes control this process in red- and far-red light, and that in far-red light cytoplasmic phytochrome A is sufficient and necessary for the disassembly of NOT9B-containing processing bodies. We found that light of different wavelengths can trigger this effect in a dose- and time-dependent manner. This adds a novel, unexpected cytoplasmic function to the reactions controlled by phytochromes. Therefore, a role of phytochromes in the control of translationally halted mRNAs via storage of mRNAs in processing bodies can be assumed. We expect our findings to facilitate understanding of how light and environmental cues control the assembly and disassembly of processing bodies. This could also have implications for the regulation of the abundance and stability of non-membraneous organelles in general.

P.74 Using mobile phones and teaching AI to measure fine root growth dynamics

Marili Sell
University of Tartu

Abstract:

M. SELL, A. G. SMITH, I. BURDUN, G. ROHULA-OKUNEV, P. KUPPER and I. OSTONEN

Institute of Ecology and Earth Sciences, University of Tartu, Vanemuise 46, 51003, Tartu, Estonia

Measuring continuous fine root growth with less time- and resource-intensive methods is challenging for plant ecologists. We propose an approach where pictures of fine root growth were taken with smartphones and analyzed by the deep learning method-based program RootPainter. *Picea abies* saplings were grown in transparent boxes in growth chambers at either moderate (mRH) or elevated air humidity (eRH) and in nitrate or ammonium-dominated soil. We aimed to measure the ability of RootPainter to pick up on variation in fine root ageing caused by changes in air humidity and soil nitrogen source. Trees growing at mRH and in ammonium-dominated soil had the highest fine root projection area. The relative growth of young root tips was highest a week after potting, followed by the root browning peak. Interestingly, at eRH the peaks of both young and brown roots overlapped. We did not discover treatment-specific bias in error measures. We conclude that the combination of smartphone images and RootPainter gives reliable results and is easy to use in future plant growth manipulation experiments.

P.75 Photosynthetic acclimation of five macrolichens to canopy light gradients: resolving structural and physiological controls

Upasana Sharma
Estonian University of Life Sciences

Abstract:

UPASANA SHARMA[1*]; KRISTIINA MARK[1]; JOSÉ ÁNGEL MORALES SÁNCHEZ[1]; TIINA TOSENS[1]; ÜLO NIINEMETS[1,2]

[1] *Institute of Agricultural and Environmental Sciences, Estonian University of Life Sciences, Kreutzwaldi 1, Tartu 51006, Estonia;* [2] *Estonian Academy of Sciences, Kohtu 6, Tallinn 10130, Estonia; *Email: upasana.sharma@emu.ee*

Light availability is a critical factor regulating plant photosynthetic activity. Compared with non-symbiotic organisms, the effect of light availability on acclimation of morpho-anatomical and photosynthetic characteristics is more complex in lichens due to the symbiotic nature of these organisms. We aimed to assess the acclimation of lichen morpho-anatomical structure, ecophysiological responses and share of photobiont and mycobiont in thallus to natural vertical light gradients along semi-boreal forest habitats. Vertical variation in direct and diffuse irradiance was estimated by hemispheric photography for each specimen of five common boreal forest macrolichen species: *Parmelia sulcata*, *Ramalina farinacea*, *Evernia prunastri, Xanthoria parietina*, and *Hypogymnia physodes*. A total of 532 lichen specimens were collected in the summer of 2021 from six sampling sites, including open and dense forests to obtain the widest possible light gradient. We estimated the maximum photosynthetic activity of lichens *via* CO_2 gas-exchange and chlorophyll fluorescence, and estimated the relative share of algal layer volume and algal cell ultrastructural characteristics using light and transmission-electron microscopy methods. We observed a strong variation in the share of algal and fungal lichen components along the canopy vertical light gradient. In addition, variation in light availability was associated with modifications in the cell density of and structural arrangement in the algal layer. These changes explained the vertical variation in lichen photosynthetic capacity. Our study highlights a significant variation in lichen physiological activity across canopy light gradients and reveals the underlying structural and physiological controls of this variability.

P.76 How does elevated CO2 regulate the Stomatal aperture? Is it a balancing act?

Kishwar Shethi
University of Sheffield

Abstract:

K.J. SHETHI, J. E. GRAY, S. CASSON
Plants, Photosynthesis and Soil, School of Bioscience, University of Sheffield, Western Bank, S10 2TN, Sheffield, UK

Stomata are microscopic pores surrounded by a pair of guard cells and found on the surface of land plants to maintain plant gas exchange with the environment. In response to diverse stimuli, the stomatal aperture is modulated through systematic opening and closure to balance carbon-water status and adapt to its surroundings. An elevated concentration of atmospheric CO2 (eCO2) is considered to be one of the major drivers of global climate change. Therefore, understanding stomatal behaviour in response to eCO2 is important to maintain or increase crop yields in future climates. The phytohormone abscisic acid (ABA) plays a major role in regulating both stomatal closure and inhibition of opening responses. Whilst research shows that CO2 responses require the capacity for ABA biosynthesis, there is no evidence of ABA concentration changes in guard cells following changes in CO2. We propose that eCO2 alters responses to ABA by changing the homeostasis between ABA and other phytohormones. Stomatal bioassay and mass spectrometry analysis examined these interactions and we observed gibberellins (GAs) negating the effect of ABA on the stomatal closure response to eCO2 treatment. Therefore, experiments are going on to investigate how GAs are involved in eCO2-mediated closure response.

P.77 Unraveling the molecular circuit governing the Lateral Root Cap Programmed Cell Death events

Margaryta Shtin
University of Rome La Sapienza

Abstract:

SHTIN M. [1,2], SVOLACCHIA N.[1,2], ARGIRÒ L. [1,2], TERENZI A. [1,2], DELLO IOIO R. [2], DI MAMBRO R.[1].

1 Department of Biology, University of Pisa, via L. Ghini 13, 56126 Pisa, Italy
2 Department of Biology and Biotechnology, Laboratory of Functional Genomics and Proteomics of Model System, University of Rome «La Sapienza», via dei Sardi 70, 00185 Rome, Italy

The lateral root cap is the outermost tissue of the root apical meristem. It is involved in the perception of environmental stimuli and their translation into internal signals capable of governing root growth and architecture, the penetration into the soil and the physical protection of meristematic cells population. The uppermost lateral root cap cells (ULRC) are characterized by a recurrent Programmed Cell Death (PCD) event, as a result of which ULRC are sloughed off the root into the soil. This cellular turnover ensures the correct development of the lateral root cap and guarantees its functions. Several evidence provided a correlation between the activity of the phytohormone auxin and PCD events, including those occurring in the ULRC. However, the molecular mechanism that triggers ULRC PCD is still not clear. By means of a cell biology approach, exploiting a novel live imaging analysis combined with cell type specific gene editing, we show that the auxin polar transport, by adjusting auxin levels, affects the timing of ULRC PCD occurrence. In particular, the dynamics of the auxin carrier PIN-FORMED2 in the ULRC, by modulating auxin efflux, underpins PCD. We thus suggest a ULRC-specific molecular circuit that confers positional cues to coordinate cellular turnover.

P.78 Changes in Mangrove Carbon Stocks and Exposure to Sea Level Rise (SLR) under Future Climate Scenarios

Minerva Singh
Imperial College London

Abstract:

MINERVA SINGH

The Centre for Environmental Policy, Imperial College London, The Weeks Building, 16-18 Princes' Gardens, London SW7 1NE, UK

Mangrove ecosystems are threatened by a variety of anthropogenic changes, including climate change. The main aim of this research is to quantify the spatial variation in the different mangrove carbon stocks, aboveground carbon (AGC), belowground carbon (BGC), and soil carbon (SOC), under future climate scenarios and sea-level rise (SLR). Different representative concentration pathways (RCPs) ranging from the most optimistic (RCP 2.6) to medium emissions (RCP 4.5) and the most pessimistic (RCP 8.5) were considered for 2070. Marine Ecoregions of the World (MEOW), a biogeographical classification of coastal ecosystems was used to quantify the variation in future carbon stocks and identify regions of potential carbon stock losses and gains. Mangroves of Central and Western Indo-Pacific islands (Andamans, Papua New Guinea, and Vanuatu), and north-eastern South America are projected to lose all three carbon stocks under all future scenarios. Andaman ecoregion is projected to have an 11–25% decline in SOC accumulation, while the Western Indo-Pacific realm is projected to undergo the sharpest declines, ranging from 10% to 12% under all three scenarios. These ecoregions should be prioritised for conservation

P.79

Structural color, cell walls, and the evolution of *Viburnum* fruits

Miranda Sinnott-Armstrong
University of Cambridge & University of Colorado-Boulder

Abstract:

M. SINNOTT-ARMSTRONG, R. MIDDLETON, Y. OGAWA, G. JACUCCI, E. MOYROUD, B. J. GLOVER, P. RUDALL, S. VIGNOLINI, M. J. DONOGHUE

[1]*Department of Chemistry, University of Cambridge, Lensfield Road, Cambridge CB2 1EW, UK;* [2]*Department of Ecology & Evolutionary Biology, University of Colorado-Boulder, Boulder, CO 80303, USA;* [3]*Department of Ecology & Evolutionary Biology, Yale University, PO Box 208106, New Haven, CT 06520, USA*

Although structural color (color derived from nanostructures causing interference) is common in animals, it is rare in plants. In fruits, only six species have been described, including in one species in *Viburnum, V. tinus*, which reflects blue light due to multilayered lipid globules in the cell wall. Here, we investigate the evolution of structural color across *Viburnum*. We use transmission electron microscopy and optical simulations to identify the presence or absence of lipid droplets in each species, understand the mechanism producing structural color in newly identified species, and characterize the evolution of cell wall architecture across the clade. Both major origins of blue fruit color (in *V. tinus* and its relatives, and *V. dentatum* and its relatives) produce lipid globules in the cell wall, either arranged in a layered or a highly disordered structure. Other relatives of *V. dentatum* produce similar structures, but with lesser density or thickness of the globular region. We show that modifying the cell wall by embedding lipids is relatively common in *Viburnum,* and under particular conditions results in structural color. Examining species that may exhibit structural color in combination with pigments may yield further insights into the ecology, evolution, and diversity of fruit color.

P.80 Contrasting strategies of photosynthetic light induction in upper- and lower canopy leaves of Fagus sylvatica

Zsofia Reka Stangl

Swedish University of Agricultural Sciences, Dept. of Forest Ecology and Management

Abstract:

Z. R. STANGL, M. DURAND, T. M. ROBSON

Viikki Plant Science Centre, University of Helsinki, Viikinkaari 1, Helsinki, Finland; and Dept. of Forest Ecology and Management, Swedish University of Agricultural Sciences, Skogsmarksgränd 17, Umeå, Sweden

Within a forest canopy, leaf anatomy and photosynthetic capacity changes along the gradient of average light intensity. However, the light conditions of individual leaves are rarely constant and fluctuate with varying amplitude and frequency. Consequently, leaves rarely operate at full photosynthetic capacity. Whether leaf physiology is adapted to mean light intensity or the dynamic fluctuation in light intensity is debated and has not yet been explored in detail in forest canopies. We investigated the temporal dynamics of biochemical- and stomatal limitations during photosynthetic induction of upper- and lower canopy leaves of Fagus sylvatica. Upper canopy leaves exhibited faster relaxation of biochemical limitation, but slower relaxation of stomatal limitation in contrast to lower canopy leaves. This resulted in longer relative induction time but higher water-use efficiency, pointing to adaptation to longer high-light periods and less fluctuation in light intensity. Our results suggest that leaf physiology within a forest canopy is adapted to the dynamic light environment in addition to average light intensity, highlighting the relevance of these conditions to whole-canopy carbon assimilation.

P.81

Botanical University Challenge; connecting and creating the next botanical community

Sebastian Stroud
University of Leeds

Abstract:

SEBASTIAN STROUD*, JOHN WARREN, AND JONATHAN MITCHLEY

School of Biological Sciences, Room 1.15 Health & Life Sciences Building, University of Reading, Whiteknights, Reading, RG6 6AS, UK

Botanical University Challenge (BUC) started as a friendly competition between several UK universities to showcase the talents of their botany students. Now in its fifth year, BUC is flourishing and supported by the New Phytologist Foundation, boasting an impressive 18 institutions with audience members tuning in from as far afield as Malaysia and Nigeria. Students compete in rounds covering topics from cell biology, field botany, and everything plant-related in-between. Importantly, BUC fills a niche found nowhere else in the UK, a space where young and early career botanists can meet, socialise, and importantly, form a community that they cannot find elsewhere.

BUC is more than just a competition between institutions, through a series of surveys, workshops, and discussions the BUC planning team has identified and highlighted various challenges to students currently studying botany and other plant-related disciplines within the UK. BUC as an community seeks to address these key challenges facing the botanical community. With an ambitious five-year plan BUC seeks to halt the growing disconnect that many students from the botanical world face, connect those disparate students of botany and plant science, and reinforce the value of plants not only in our students but across our communities and disciplines.

P.82

Crown rust (*Puccinia coronata*) infection is more virulent in the primary host *Avena sativa* than in the alternate host *Rhamnus frangula*

Hassan Yusuf Sulaiman
Estonian University of Life Sciences

Abstract:

H. Y. SULAIMAN, E. RUNNO-PAURSON, E. KAURILIND, Ü. NIINEMETS

Chair of Crop Science and Plant Biology, Estonian University of Life Sciences, Kreutzwaldi 5, 51006 Tartu, Estonia

Rust infection results in decreases in leaf photosynthesis and stress volatile compound emissions, but how these changes vary among host species has not been studied. We investigated the impacts of the obligate biotrophic fungus, *Puccinia coronata* f. sp. *avenae*, on foliage physiological processes in the primary host, *Avena sativa,* and the alternate host, *Rhamnus frangula*. Photosynthesis decreased with the increasing percentage of damaged leaf area (D_A) in both species, but the reduction was greater in *A. sativa*. In *A. sativa*, photosynthetic reduction resulted from reductions in stomatal conductance and photosynthetic capacity. whereas in *R. frangula*, the reduction was primarily due to reduced capacity. Infection reduced photosynthetic biomass and key leaf nutrients in *A. sativa*, but not in *R. frangula*. In *A. sativa*, stress-elicited emissions (lipoxygenase pathways volatiles, mono- and sesquiterpenes, long-chain saturated aldehydes, carotenoid breakdown products, and benzenoids) increased with increasing D_A from 0 to 40%, but decreased with further increases in $D_{A.}$ In *R. frangula*, volatile emissions were slightly elicited. Our results indicate fungal-elicited-reductions in photosynthesis scale uniformly with stress severity. Our results indicated that the biphasic scaling of fungal-elicited volatiles indicates the heavy spread of chlorosis/necrosis leads to the overall cessation of physiological functioning in the sensitive host, *A. sativa*.

P.83

Gene editing in the important forage grass species *Lolium perenne* L.

Ferenz Sustek Sanchez

Tallinn University of Technology

Abstract:

F. SUSTEK SÁNCHEZ, M. SÕMERA, C. SARMIENTO

Department of Chemistry and Biotechnology, Tallinn University of Technology, Akadeemia tee 15, 12618 Tallinn, Estonia

"EditGrass–4–Food" is an EEA/Norway Grant project that started in May 2021 and is coordinated by the University of Latvia. The three Baltic countries and Norway are members of the consortium.

The project aims to improve the adaptability and resilience of perennial ryegrass (*Lolium perenne* L.) for safe and sustainable food systems through CRISPR-Cas9 technology. Genes involved in the mechanisms of freezing tolerance and biomass growth under water deficit will be investigated and targeted via gene editing.

The initial phase of this project has aimed to establish protocols to generate, in an asexual manner, plant material that can be used for gene editing. For this, the in-vitro culture of tillers in solid media, supplemented with growth promoters, has been set up. Procedures for both the isolation of protoplasts and the generation of calli have been tested. For calli, a plasmid encoding a novel growth factor chimera (GRF4-GIF1) will be used, aiming to improve regeneration efficiency. *Agrobacterium tumefaciens* mediated co-cultivation will be used for the transformations.

P.84 Genome wide association study of free asparagine content in durum wheat grain

Andrea Tafuri

Institute of Agricultural Biology and Biotechnology (IBBA), National Research Council (CNR), via A. Corti, 12, 20133, Milano (MI), Italy. Department of Agriculture and Forest Sciences, University of Tuscia, Via San Camillo de Lellis, 01100, Viterbo (VT),

Abstract:

A. TAFURI[1,2,3], R. PIRONA[1], A. CERIOTTI[1], M. ZUCCARO[1], S. RAVAGLIA[2], M. GIORDANO[2], L. R. CAGLIANI[4], R. CONSONNI[4], A. FRICANO[5], E. MAZZUCOTELLI[5], E. BALDONI[1].

[1] *Institute of Agricultural Biology and Biotechnology (IBBA), National Research Council (CNR), via A. Corti, 12, 20133, Milano (MI), Italy.*
[2] *SIS Società Italiana Sementi, Via Mirandola, 5, 40068, San Lazzaro di Savena (BO), Italy.*
[3] *Department of Agriculture and Forest Sciences, University of Tuscia, Via San Camillo de Lellis, 01100, Viterbo (VT), Italy.*
[4] *Institute of Chemical Sciences and Technologies "G. Natta" (SCITEC), National Research Council (CNR), via A. Corti, 12, 20133, Milano (MI), Italy.*
[5] *Council for Agricultural Research and Economics (CREA), Research centre for Genomics & Bioinformatics, Via S. Protaso, 302, 29017, Fiorenzuola d'Arda (PC), Italy.*

Acrylamide (AA), a molecule classified as probable human carcinogen, has been detected in a wide range of foods. AA is generated during Maillard cascade reactions and free asparagine (fAsn) content has been identified as a key factor in wheat derivatives. The aim of the project is to study the natural variation for fAsn levels in durum wheat (*Triticum turgidum* L. ssp. *durum* (Desf.)) grains to identify candidate genes controlling fAsn seed content. To this purpose, 215 durum wheat genotypes, were selected from the international Global Durum Panel (GDP), whose collection was previously genotyped with Illumina iSelect 90K SNP array technology. Linkage Disequilibrium Decay was calculated with a distance of 4.4 Mbp.

These 215 genotypes were sown in single location for three years. The quantification of fAsn levels in whole-grain samples from the first two years of field trials was obtained using an enzymatic/spectrophotometric method. The analysis showed the presence of a good variability for fAsn in this population. A preliminary multi-locus genome-wide association study was performed, and SNPs associated with grain fAsn content were found. In addition, 100 genotypes were selected from first year field trial to be investigated by High Resolution ^{1}H-NMR (Proton Nuclear Magnetic Resonance) spectroscopy, to monitor metabolite composition.

This work was partially funded by the European Regional Development Fund under the ROP of the Lombardy Region ERDF 2014–2020—Axis I "Strengthen technological research, development and innovation"—Action 1.b.1.3 "Support for co-operative R&D activities to develop new sustainable technologies, products and services"—Call Hub.

P.85

Leaf-level 13C-CO2 labeling revels increased fluxes through photorespiration and the TCA cycle in the C4 perennial grass under drought.

Mauricio Tejera-Nieves

Michigan State University

Abstract:

M. TEJERA-NIEVES[1,2], X. FU[2], B. J. WALKER[1,2]

[1] *MSU-DOE Plant Research Laboratory, Michigan State University, East Lansing, MI, USA*

[2] *Great Lakes Bioenergy Research Center, Michigan State University, East Lansing, MI, USA*

Switchgrass (*Panicum virgatum* L.) is a perennial C4 grass, widely considered as a bioenergy crop given its low-input requirements, cold tolerance, and high yields even in marginal lands. Recently, changes in plant chemical composition under drought stress have been shown to inhibit downstream fermentation and ethanol production. While some inhibitory compounds have been experimentally identified, the physiological base of these responses remains elusive. During the 2020 growing season we installed 20m^2 rainfall exclusion shelters to impose drought treatment and study how switchgrass carbon assimilation and metabolism change under drought stress. Switchgrass CO_2 assimilation was only ~15% lower ($p < 0.05$) under drought treatments, despite a 90% decrease in soil water content. Samples from a 30-minute leaf-level ^{13}C-CO_2 labeling event showed that plants in drought treatments maintained larger fluxes through photorespiration, the TCA cycle and lignin synthesis. To better resolve the metabolic fluxes through these pathways and how they change during the season, in 2021 we conducted a series of leaf-level ^{13}C-CO_2 labeling events during the growing season. Preliminary results, show larger drought and seasonal effects on CO_2 assimilation, the upcoming analysis of the ^{13}C-CO_2 labeling data would provide valuable insight on the metabolic changes that led to switchgrass photosynthetic resilience.

P.86

Regulation of embryogenesis and sporophyte development by specific AGO1-dependent small RNA pathways in *Physcomitrium patens*

Oguz Top
Ludwig-Maximilians-University Munich

Abstract:

O. TOP, Y. AN, W. FRANK

Plant Molecular Cell Biology Lab, Faculty of Biology, Ludwig-Maximilians-University Munich, Planegg-Martinsried, 82152, GERMANY

Small non-coding RNAs modulate the expression of many important genes involved in cell growth, development, differentiation and stress responses through genetic and epigenetic silencing pathways. Key regulators in this process are members of the Argonaute (AGO) protein family that bind sRNAs that guide AGO complexes to RNA or DNA targets to mediate posttranscriptional or transcriptional gene silencing. The number of AGO proteins among organisms varies greatly and increased organismic complexity is often accompanied by a diversified AGO family. *Physcomitrium patens* harbors eight AGO proteins and based on their close relationship to the *Arabidopsis* AtAGO1 protein that binds microRNAs (miRNA), PpAGO1a, PpAGO1b and PpAGO1c are supposed to be acting in miRNA binding and conferring cleavage or translational repression of their cognate targets. Within the scope of this project, I particularly focus on *PpAGO1a, PpAGO1b* and *PpAGO1c* genes and generated single, double and triple knockout mutants by targeted gene disruption. The resulting Δ*PpAGO1* lines were compared to wild-type for overall growth and development and displayed abnormalities in gametophore development and/or sporophyte formation. Applying combined mRNA- and miRNA-sequencing, I am investigating redundant and non-redundant specialization of PpAGO1s, miRNA-mediated regulation through particular PpAGO1s and key regulatory genes in embryogenesis and the alternation of generations.

P.87

A synthetic evaluation of global plant diversity facets highlights the relative roles of historical, environmental and anthropogenic factors

Enrico Tordoni
University of Tartu

Abstract:

E. TORDONI, C. P. CARMONA, A. TOUSSAINT, R. TAMME, M. PÄRTEL

Department of Botany, University of Tartu, J. Liivi 2, 50409 Tartu, Estonia.

Although humans have transformed the terrestrial biosphere since the early Holocene, most research efforts have focused on recent human impacts, and considered solely species richness. We collated a database encompassing the most comprehensive and up-to-date information on traits and evolutionary history for more than 300,000 species of vascular plants and estimated a new metric (m-Diversity) synthetizing taxonomic, functional and phylogenetic information. We used random forest to disentangle the main drivers of the global geography of plant µ-Diversity, including the relative roles of climate variability since the Last Glacial Maximum (LGM), environmental features (e.g., actual evapotranspiration - AET), geological activity and anthropogenic factors (past and current). We found that higher m-Diversity is mainly observed in South East Asia, Central and South America and Australia, whereas the lowest values are located in Africa and the Northern Hemisphere. AET and climate variability since LGM are the most important determinants of µ-Diversity. Among human factors, the date of onset of pastoralism is more important than current human impacts, suggesting a role of old civilizations that date back at least to mid-Holocene which may have shaped plant diversity in the long run.

P.88 Observed and dark diversity dynamics over millennial time-scales: fast-life history traits linked to expansion lags of plants in Northern Europe

Diego Trindade
University of Tartu

Abstract:

DIEGO P.F. TRINDADE, CARLOS P. CARMONA, TRIIN REITALU, & MEELIS PÄRTEL

Institute of Ecology and Earth Sciences, University of Tartu, Juhan Liivi 2, 50409, Tartu, Estonia

Global changes (e.g. climate and land-use) affect the species and functional traits observed in a local site but also its dark diversity - set of species and traits locally suitable but absent. By depicting the biodiversity that is present in the region but locally absent, dark diversity links regional and local scales and, over time, it reveals how long this potential biodiversity remained suitable but absent - an indication of expansion lag. Although global change effects on biodiversity are both spatial and temporal scale dependent, the assessment of temporal observed and dark diversity dynamics is still lacking. Here we used sedimentary pollen data to test how both taxonomic and functional observed and dark diversity changed over the past 14500 years in Northern Europe. We found that climate warming, after the Late Glacial, and human activities, during the Late Holocene, were crucial drivers of increasing biodiversity, but dark diversity reveals that several taxa presented expansion lags due to their functional characteristics (high functional redundancy, as well as dispersal limitation and stress intolerance). Assessing temporal observed and dark diversity dynamics is a novel and promising tool to assess biodiversity change, revealing the extent and pace that species pools have changed.

P.89 A high throughput analysis method for soil phospholipid and neutral lipid-derived fatty acids

Ayesh Wipulasena
University of Tartu

Abstract:

A. Y. A. P. WIPULASENA[1], T. VAHTER[1], K. HERODES[2]
1. Department of Botany, Institute of Ecology and Earth Sciences, University of Tartu, Juhan Liivi 2, 50409 Tartu, Estonia
2. Chair of Analytical Chemistry, Institute of Chemistry, University of Tartu, Ravila 14a, 50411 Tartu, Estonia

Phospholipid fatty acids (PLFAs) and neutral lipid fatty acids (NLFAs) have been widely used in soil ecological studies as biomarkers indicative of main microbial groups. The Bligh and Dyer method of extraction and separation of PLFAs and NLFAs is considered the gold standard and is extensively used in the fatty acid analysis for soil microbial community studies. A high throughput method of soil fatty acid analysis was developed based on the classical Bligh and Dyer method, which involves the extraction of fatty acids, separation of the fatty acids to PLFAs and NLFAs using solid-phase extraction technique, and subjecting the fatty acids to mild alkaline methanolysis prior to analysis using a GC-FID. Where possible, stages were modified to be carried on a 96 well plate multi-tier unit, increasing the sample throughput and decreasing the overall consumption of solvents, cost of analysis, and time. The method performance was compared against the standard method on 47 soil samples. The novel high throughput method showed comparable biomass and community characteristics to that of the standard method and thus, could be proposed as a novel method of fatty acid analysis specifically applicable in large-scale ecological studies.

P.90

Involvement of Reactive Carbonyl Species (RCS) in Unfolded Protein Response (UPR) of *Arabidopsis thaliana*

Side Selin Su Yirmibesoglu
Ege University

Abstract:

S.S.S YİRMİBESOGLU[a], R. OZGUR[a], C. SAKURAI[b], B. UZILDAY[a], J. MANO[b], I.TURKAN[a]

[a] *Department of Biology, Faculty of Science, Ege University, Bornova, 35100, Izmir, Turkey,* [b] *Science Research Center, Organization of Research Initiatives, Yamaguchi University, Yamaguchi 753-8515, Japan*

Environmental stress conditions induce the accumulation of unfolded protein accumulation in the ER and trigger UPR which is responsible for maintaining ER homeostasis. RCS may take a signalling role just like H_2O_2 during ER stress and to enlighten this, UPR induction via RCS and involvement of RCS in ER stress tolerance in *A. thaliana* are investigated. For this aim, Schiff's staining, HPLC analysis and RCS scavenging pathway related gene expression analysis were conducted. The results showed that ER stress induces the accumulation of RCS and regulates the transcriptional pathways of RCS scavenging related genes. To understand RCS involvement in ER stress tolerance, growth parameters and expressions of UPR related genes were also measured after carnosine treatment which is a RCS scavenging dipeptide. Results showed that RCS is required for efficient induction of UPR. To elucidate temporal response to RCS, time dependent analysis on the expressions of UPR related genes were performed. Moreover, scavenging of RCS resulted in alterations on

P.91

UV-B negatively regulates *PHYTOCHROME INTERACTING FACTOR (PIF)* transcription in Arabidopsis

Aline Yochikawa
University of Bristol

Abstract:

ALINE YOCHIKAWA, KEARA A. FRANKLIN
School of Biological Sciences - University of Bristol, Tyndall Avenue, Bristol, City of Bristol, BS8 1TQ, United Kingdom.

UV RESISTANCE LOCUS 8 (UVR8) is a plant photoreceptor that perceives UV-B radiation (280-315 nm) and regulates defence responses to UV-B stress. In addition, UVR8 can control plant development in response to non-stressful levels of UV-B by regulating the abundance and activity of *PHYTOCHROME INTERACTING FACTOR (PIF)* transcription factors to promote photomorphogenesis, shade-avoidance or to repress thermomorphogenesis. Perception of UV-B leads to rapid degradation of PIF4 and PIF5 proteins, but the transcriptional regulation of PIFs by UV-B remains poorly studied. By performing gene expression assays in UV-B treated *Arabidopsis thaliana* seedlings, we have found that UV-B suppresses *PIF3*, *PIF4* and *PIF5* expression in an UVR8 dependent manner. Mutants of genes involved in the modulation of *PIF* expression were subjected to RT-qPCR post UV-B treatment, and CONSTITUTIVE PHOTOMORPHOGENIC 1 (COP1) has been identified as a possible component in this response. We further showed that *PIF4* transcript levels in UV-B are repressed in the presence and absence of proteosome inhibitor MG132, suggesting a proteosome-independent mechanism. Our results thus provide a global view of how UV-B regulates *PIF* transcript abundance.

P.92

Diversity, pathogenicity and stability of *Pseudomonas* population over distance, time and environment

Ziyue Zeng
NIAB

Abstract:

Z. ZENG, J. WEBLIN, A. VADILLO, M. T. HULIN, M. RABIEY, J. W. MANSFIELD, R. W. JACKSON, R. J. HARRISON

NIAB, Cambridge CB3 0LE, UK

Pseudomonas syringae is a widespread bacterial pathogen of a variety of plant species, cherry included. Despite the advances in disease control, *P. syringae* remains of great concern to the security of cherry production. Some *P. syringae* strains, such as *P. syringae* pathovars *syringae* (*Pss*) and *morsprunorum* (*Psm*), are known pathogens which infect and cause canker symptoms on cherry trees whilst some *P. syringae* bacteria proliferate silently as epiphytes without causing symptoms. However, the epiphytic *P. syringae* populations also play a potential role in the emergence of outbreaks of canker in cherry. In the previous sampling across cherry orchards around the UK, aside from the known *P. syringae* pathogens, a diversity of non-pathogenic *P. syringae* strains were also isolated from the leaf and shoot surface of undiseased trees. Intriguingly, these non-pathogenic epiphytes were extremely widespread and display the hallmarks of a pathogenic strain, although they had not been described as a pathogen in prior studies. Moreover, interesting regional variations in *P. syringae* populations were observed. Extending the previous work, the current study further investigates the diversity, heterogeneity and pathogenicity of environmental *P. syringae* in cherry trees via multi-year, multi-site samplings from orchards in four regions in the UK. In addition, as varied levels of resistance to *P. syringae* has been found in wild cherry, the sampling also includes the wild cherry in the woodlands nearby. In the May and September samplings in 2021, a total of 6000 bacterial strains have been isolated from leaves and shoots samples. A multiplex PCR method has been devised to identify the potentially pathogenic *Pseudomonas* bacteria. By using repeated sampling and genome sequencing of these environmental isolates, we aim to enrich the insights on the temporal and spatial variation in the epiphytic populations of pathogenic and potentially pathogenic *P. syringae* in cultivated and wild cherries.

P.93

Stomatal responses to a fluctuating environment: depend on photosynthetic pathways and guard cell size?

Yanmin Zhou
University of Sheffield

Abstract:

Y. ZHOU, C. P. OSBORNE

School of Biosciences, University of Sheffield, Western Bank, Sheffield, S10 2TN, UK

Stomatal behaviour mainly determines the balance between carbon gain and water loss. Rapid stomatal responses to environmental changes can improve intrinsic water use efficiency and reduce the risk of transient water deficits. *Alloteropsis semialata* has unequalled intrinsic variation in photosynthesis and genome size, and a diversity of habitats, this species represents an ideal system in which to investigate how natural variation in guard cell length and photosynthetic pathway impact stomatal responses to a fluctuating environment. By testing the relationships among guard cell length, photosynthetic pathway, and the speeds of stomatal opening and closure, we have found smaller guard cell length is associated with faster stomatal response to increasing light. For a given guard cell length, C_4 grasses have slower speed of stomatal opening than non-C_4 grasses. However, for stomatal responses to decreasing light, stomata in C_4 grasses close as fast as non-C_4 grasses. In addition, stomata take a shorter time for closure than opening. This finding may indicate that faster stomatal closing has potential improvements in water use efficiency.

P.94

Polyketide reductases in gerbera parasorboside biosynthesis: Recruitment from ancient sporopollenin biosynthesis

Lingping Zhu
Department of Agricultural Sciences, University of Helsinki, Finland

Abstract:

L. ZHU, M. PIETIÄINEN, J. KONTTURI, A. TURKKELIN, P. ELOMAA, T. T. TEERI

Viikki Plant Science Centre, Department of Agricultural Sciences, University of Helsinki, Finland

Polyketides are a diverse group of secondary metabolites in plants. They are synthesized by type III polyketide synthases (PKSs) and their final functional diversity is determined by post-PKS tailoring enzymes. *Gerbera hybrida* is rich in two defensive polyketides, gerberin and parasorboside. Their biosynthesis is initiated by the gerbera 2-pyrone synthase 1(G2PS1), while the accessory polyketide reductases (PKRs) have been missing. By conducting coexpression analysis, we identified two *PKR* candidates, *gerbera reductase 1* (*GRED1*) and its close paralogue *GRED2*. Both *GRED1* and *GRED2* are similar to *tetraketide α-pyrone reductase 2 (TKPR2)*, a gene encoding a reductase in anther-specific sporopollenin biosynthesis. We showed by expression and metabolite analysis of different gerbera tissues, cultivars, and overexpression and RNAi downregulation transgenic gerbera lines that both GRED1 and GRED2 are involved in parasorboside biosynthesis. Further *in vitro* enzymatic assays showed that the two PKRs act on linear intermediate prior to its lactonization, suggesting an update of the pathway. We also showed that GRED1 and GRED2 have maintained a minor function in gerbera sporopollenin biosynthesis. Our work elucidates a crucial tailoring step in an important gerbera PKS pathway and shows an example of how plants achieve secondary metabolic innovation through gene duplication and functional diversification.

P.95 Studying the role of autophagy at cell-type specific resolution

Shanshuo Zhu
ZMBP University of Tübingen

Abstract:

S. ZHU[1], P. SOLANSKY[1], T. DENYER[1], M. TIMMERMANS[1], S. UESTUEN[1,2]

1, Center for Plant Molecular Biology (ZMBP), University of Tübingen, 72076 Tübingen, Germany
2, FACULTY of Biology & Biotechnology, Ruhr-University Bochum, 44780 Bochum, Germany

Maintaining cellular proteome homeostasis is essential for plants to respond to new environmental signals. During plant immune reactions, the initiation and maintenance of defense responses not only involves a de novo synthesis of regulatory proteins and enzymes, but also their regulated degradation. Recent evidence indicates that autophagy is required for proteome adjustments to remodel cellular environment for stress tolerance and it is also responsible for cellular quality control by removing protein aggregates, organelles and specific proteins. Autophagy can be activated by various stress condition, but the autophagic degradome can be very specific to the stimulus, as well as in different cell types and even in subcellular compartmentalization. To identify tissue and cell-type specific autophagy modulation, we utilize single-cell RNA sequencing analysis by combining both autophagy-induced conditions (by microbes or TOR inactivation) and autophagy-defective mutants. In addition, we also generate cell-type specific autophagic mutants to access the autophagic response in pathogen infection assays and obtain autophagic degradome in certain cell types. With this approach we will be able to decipher cell-type specific autophagy mechanisms in leaves and shoots in response to different environmental stimuli.

P.96

The role of terrestrial productivity and hydrology in regulating aquatic dissolved organic carbon concentrations in boreal catchments

Xudan Zhu
University of Eastern Finland

Abstract:

XUDAN ZHU, LIANG CHEN, JUKKA PUMPANEN, ANNE OJALA, JOHN ZOBITZ, XUAN ZHOU, HJALMAR LAUDON, MARJO PALVIAINEN, KIMMO NEITOLA, FRANK BERNINGER

Department of Environmental and Biological Sciences, Joensuu Campus, University of Eastern Finland, FI-80101 Joensuu, Finland

The past decades have witnessed an increase in dissolved organic carbon (DOC) concentrations in the catchments of the Northern Hemisphere. Increasing terrestrial productivity and changing hydrology may be reasons for the increases in DOC concentration. The aim of this study is to investigate the impacts of increased terrestrial productivity and changed hydrology following climate change on DOC concentrations. We tested and quantified the effects of gross primary production (GPP), ecosystem respiration (RE) and discharge on DOC concentrations in boreal catchments over 3 years. Wavelet coherence analysis and the distributed-lag linear model were applied. Our results showed that the combined impacts of terrestrial productivity and discharge explained 62% of aquatic DOC variations on average across all sites. The impact of GPP and discharge on DOC changes was directly related to catchment size: GPP dominated DOC fluctuations in small catchments (<1 km^2), whereas discharge controlled DOC variations in big catchments (>1 km^2). The direction of the relation between GPP and discharge on DOC varied. This study reveals that climate change-induced terrestrial greening and shifting hydrology change the DOC export from terrestrial to aquatic ecosystems and confirms the importance of DOC fluxes in regulating ecosystem C budgets.

Citation:

Zhu, X., Chen, L., Pumpanen, J., Ojala, A., Zobitz, J., Zhou, X., Laudon, H., Palviainen, M., Neitola, K., & Berninger, F. (2022). The role of terrestrial productivity and hydrology in regulating aquatic dissolved organic carbon concentrations in boreal catchments. Global Change Biology, 00, 1–15. https://doi.org/10.1111/gcb.16094

P.97

Ubiquitous and unique methyl jasmonate-induced volatile defense responses in the lycophyte *Selaginella martensii*: timing, sensitivity, and gene expression

Tana Wuyun
University of Tartu

Abstract:

Tana Wuyun, Hanna Hõrak, Bin Liu, Eero Talts, Kalle Kilk, Eve Kaurilind, Caihong Li, Lu Zhang, Ülo Niinemets

Institute of Agricultural and Environmental Sciences, Estonian University of Life Sciences, Kreutzwaldi 1, 51014 Tartu, Estonia

Methyl jasmonate (MeJA) induces various defense responses in seed plants, but there is limited information of MeJA responses in early plant lineages such as lycophytes. Responses of photosynthesis, volatile organic compound (VOC) emissions, phytohormone concentrations, and gene expression were studied in the spikemoss *Selaginella martensii*. in response to a range of MeJA concentrations (0, 10, 25, and 50 mM). Reductions in foliage net assimilation rate and stomatal conductance, and elicitation of emissions of methanol, lipoxygenase (LOX) pathway volatile and linalool were MeJA dose dependent. 12-oxo-phytodienoic acid (OPDA) had largest share of phytohormone and increased fast after stress. Jasmonic acid (JA) was found before and increased continuously after MeJA treatment. Genes involved in the synthesis of lignin, production of LOX volatile emissions via the arachidonic acid pathway, linalool biosynthesis, and OPDA -specific response, were upregulated at 0.5 h after MeJA treatment. Unlike a previous report, we show that *S. martensii* can accumulate JA, but probably utilized OPDA as a signaling molecule upon MeJA at the early hours. The results suggest MeJA suppressed the primary metabolism and boosted the secondary metabolism where the fast-emitting linalool may play a role as a stress marker in lycophytes.