41st New Phytologist Symposium

# Plant sciences for the future

11 – 13 April 2018
Nancy, France

New Phytologist

arbre

## Programme, abstracts and participants

# $41^{st}$ New Phytologist Symposium

# Plant sciences for the future

**Présidence de l'Université de Lorraine,**
**Nancy, France**
**11 – 13 April 2018**

## Scientific Organizing Committee

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# Acknowledgements

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www.newphytologist.org

The New Phytologist Trust is a non-profit-making organization dedicated to the promotion of plant science. It owns and produces the international journal *New Phytologist*. The Trust receives income through subscriptions to *New Phytologist* and any excess revenue from the publication of the journal is put straight back into supporting plant science. This is achieved by funding a wide range of activities: the organisation and sponsorship of symposia, workshops and meetings; numerous grant schemes; sponsorship of various awards for early-stage career scientists including the Tansley Medal; and ensuring that research published in the journal is as widely and openly available as possible, as such, all of our Tansley series reviews and Forum articles are immediately available to access free of charge upon publication. All of these actions have a common goal to promote emerging areas of plant science and to encourage continued progress and innovation in the field.

Labex ARBRE - Advanced Research on the Biology of Tree and Forest Ecosystems
http://mycor.nancy.inra.fr/ARBRE

The overarching goal of the Laboratory of Excellence for Advanced Research on the Biology of TRee and Forest Ecosystems (ARBRE) is to guarantee forests sustained ability to produce quality goods and services in a changing environment. Recognizing that forest resilience, and its productivity both stem from a wide range of biological and biophysical processes, ARBRE centers its research agenda on the interactions between processes at micro-, meso-, and macro-scales.

Programme, abstracts and participant list compiled by Ashley Pridgeon
‘Plant sciences for the future’ logo by A.P.P.S., Lancaster, UK, concept by Ella Crouch
Contact email: *np-symposia@lancaster.ac.uk*

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# Information for Delegates

## Symposium location

The 41st New Phytologist Symposium will be held at the Headquarters of the Université de Lorraine, 34 Cours Léopold, Nancy, France. All presentations will be given in the Grand Amphithéâtre (1st floor) and posters will be displayed in the lobby of the Grand Amphithéâtre and adjoining rooms.

## Catering

All coffee breaks will be served in the lobby of the Conference Theatre. Lunches on Wednesday, Thursday and Friday will also be in the lobby of the Conference Theatre and adjoining rooms.

## Welcome Dinner

The Welcome dinner is included for all delegates and speakers. It will be held at the Grands Salons de l'Hôtel de Ville de Nancy on the famous Stanislas Square. See map on page 90.

If you have special dietary requirements please do make yourself known to the catering staff or ask Helen or Mike from *New Phytologist*. All our requirements have been provided to the catering team and they will have meals prepared accordingly.

## Restaurants

If you are staying in Nancy downtown there are a number of restaurants and pubs close to the Stanislas Square. Discover the restaurants located on the 'Rue des maréchaux', a 5 min walk from the Stanislas Square, and in the Old City. For a nice selection, see also: https://www.thefork.com/restaurant+nancy

## Excursions in Nancy

On Friday afternoon there will be three different excursions. If you have not replied to the email asking you to state your preference you will have been allocated to an excursion. For excursion 3, buses will leave from the Headquarters of the Université de Lorraine, 34 Cours Léopold. Buses will return to Headquarters of the Université de Lorraine.

- Group 1: Visit to the historic centre of Nancy and Fine Arts Museum. No public transportation is required for this. Visit will be approx. 3hrs.

- Group 2: Arts Nouveau Mansions/Architecture + visit of the Art Nouveau Museum. Public transportation needed (with a guide), about a 15 min tramway ride. Visit will be approx. 4hrs.
- Group 3: Visit of the Toul Vineyards (1hr west of Nancy by bus). Visit will be approx. 4hrs.

**Posters**

Posters should be prepared so that they are no larger than A0 size, portrait orientation (118 cm high x 84 cm wide). Posters should be put up during registration (12:00–13:30 on Wednesday 11 April) and will be displayed for the duration of the meeting. Delegates are welcome to view posters during coffee and lunch breaks; there will also be a dedicated poster session from 18:00 to 19:30 on Thursday 12 April. Please stand by your poster for part of these sessions (we appreciate as poster presenters you will also want to view and discuss the other posters). Posters will be assessed by your peers (the other delegates) and the posters that gain the most votes will receive prizes. A scoring sheet is included in your delegate pack. Please fill out and return this sheet to the registration desk by 9:00 on Friday 13 April.

**Internet access**

Please use the below details

Log in : col_inra
Password (Mot de passe) : wndm2LVJ

**Social media**

We encourage all attendees to join in discussions on social media sites. Follow @NewPhyt on Twitter and fb.com/NewPhytologist on Facebook for updates before, during and after the meeting. Please use the hashtag #41NPS in all of your tweets.

**Taxis**

At the railway station: 2 Place de la République, 54000 Nancy.
Tel : +33 383 37 65 37

Banks : BNP Paribas, 58 rue Saint Jean, 54000 Nancy; Société Générale, 42 Rue Saint-Dizier, 54000 Nancy.

**Video recording and photography**

Video recording and photography will take place at the 41st NPS.

The resulting videos and photographs will be used by the New Phytologist Trust for the purpose of promoting its activities and may be published on the New Phytologist Trust's website and social media channels.
If you do not wish to appear in the videos or photographs, please speak to one of the organisers.

## Code of conduct

The New Phytologist Trust celebrates diversity and we expect participants in our meetings to be respectful, considerate and supportive of each other, to offer constructive critiques and embrace the variety of opinions on offer. The 41st NPS is an opportunity to share, develop and broaden our viewpoints within a safe and inclusive setting, and we hope that you will enjoy the meeting. If you have any concerns or suggestions, please speak to one of the organisers.

## Contact

For further information, and in case of any emergencies, please contact Helen Pinfield-Wells.
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tel: +44 7966 450 389.

# Meeting Programme

**Wednesday 11th April**

| | |
|---|---|
| 12:00–13:30 | Registration and lunch |
| 13:30–13:45 | Welcome: **Alistair Hetherington & Francis Martin** |
| 13:45–14:30 | **Keynote: Liam Dolan**<br>Evolution and development of the earliest land plant rooting systems |

**Session 1: Physiology and Development**
**Chair: Alistair Hetherington**
**14:30–18:00**

| | |
|---|---|
| 14:30–15:00 | **S1.1 Andrew Groover**<br>Evolution and development of wood formation in forest trees |
| 15:00–15:30 | **S1.2 Colin Brownlee**<br>Animal, vegetable and mineral: Understanding the unique physiology of biomineralizing phytoplankton in a changing ocean |
| **15:30–16:00** | **Coffee/Tea break** |
| 16:00–16:15 | **Selected talk 1: Cecilia Brunetti (P7)**<br>A possible role for abscisic acid in restoring water transport in embolized vessels |
| 16:15–16:30 | **Selected talk 2: Tracy Stevenson (P40)**<br>Understanding the mechanism of decoding of calcium signatures regulating transcript and protein expression in *Arabidopsis thaliana* |

| | |
|---|---|
| 16:30–17:00 | **S1.3 Alison Smith**<br>What plants do in the dark |
| 17:00–17:30 | **S1.4 Keith Lindsey**<br>Control of root growth in Arabidopsis |
| 17:30–18:00 | **S1.5 Shuhua Yang**<br>Phosphorylation-regulated plant freezing tolerance |
| **19:30** | **Welcome Dinner - Grands salons de l'Hotel de Ville de Nancy** |

## Thursday 12th April

**Session 2: Interaction**
**Chair: Maarja Öpik**
**09:00-12:30**

| | |
|---|---|
| 09:00–9:30 | **S2.1 André Kessler**<br>Plant-to-plant communication and its role in driving herbivore population dynamics |
| 09:30–10:00 | **S2.2 Anne Osbourn**<br>Finding drugs in the garden: Mining plant chemical diversity |
| 10:00–10:15 | **Selected talk 3: Diana Ramirez-Garces (P34)**<br>Roles of Malectin-like kinases FERONIA and HERK1 in plant immunity |
| 10:15–10:30 | **Selected talk 4: Veronica Basso (P2)**<br>Fungal manipulation of plant jasmonate signaling in *Populus- Laccaria* bicolor ectomycorrhizal symbiosis |
| **10:30–11:00** | **Break** |
| 11:00–11:30 | **S2.3 Björn Lindahl** |

| | |
|---|---|
| | Sequencing the mycobiome of boreal forest soils |
| 11.30–12:00 | **S2.4 Ralph Panstruga**<br>Durable disease resistance by loss of plant ‘susceptibility factors’ |
| 12:00–12:30 | **Tansley Medal winner talk: Stella Cesari**<br>Multiple strategies for pathogen perception by plant immune receptors |
| **12:30–14.00** | **Lunch** |
| **Session 3: Environment**<br>**Chair: Richard Norby**<br>**14:00–18:00** | |
| 14.00–14.30 | **S3.1 Andrea Polle**<br>Molecular ecophysiology of wood formation under drought |
| 14:30–15:00 | **S3.2 Belinda Medlyn**<br>Recent advances in stomatal conductance |
| 15:00–15:15 | **Selected talk 5: Charlotte Grossiord (P14)**<br>Reductions in tree performance during hotter droughts are minimized by shifts in nitrogen cycling |
| 15:15–15:30 | **Selected talk 6: Nadia Maaroufi (P21)**<br>Shifts in ectomycorrhizal and saprophytic fungal communities mediate litter and humus decay in response to chronic nitrogen enrichment |
| **15:30–16:00** | **Break** |
| 16:00–16:30 | **S3.3 Amy Austin**<br>Plants in the sun: new insights on the role of solar radiation in terrestrial ecosystems |
| 16:30–17:00 | **S3.4 Owen Atkin** |

| | |
|---|---|
| | Thermal biology of plant metabolism: Insights into global patterns |
| 17:00–18:00 | **Discussion** ‘How plant sciences can be harnessed to help solve societal issues’<br>Discussion leaders: **Marc-André Selosse & Richard Norby** |
| **18:00–19:30** | **Poster session** |
| **Friday 13th April** | |
| **Session 4: Evolution**<br>**Chair: Simon Hiscock**<br>**09:00-11:45** | |
| 09:00–9:45 | **Keynote: Lynda Delph**<br>It's the phenotype... |
| 09:45–10:15 | **S4.1 Elena Kramer**<br>Exploring the genetic basis of floral novelty in *Aquilegia* |
| 10:15–10:30 | **Selected talk 7: Shihao Su (P42)**<br>The origin of corolla neck in *Torenia fournieri* |
| 10:30–10:45 | **Selected talk 8: Babu Ram Paudel (P30)**<br>Interspecies variation in reproductive strategy of co-existing alpine gingers (*Roscoea purpurea* and *R. tumjensis*): implication for reproductive isolation and species integrity |
| **10:45–11:15** | **Break** |
| 11:15–11:45 | **S4.2 Hongzhi Kong**<br>The making of elaborate petals in *Nigella* (Ranunculaceae) |
| 11.45–12:30 | **ARBRE lecture: David Beerling**<br>Can we achieve multiple gigatonne $CO_2$ capture by farming with crops and rocks? |

| | |
|---|---|
| 12:30–12:45 | Closing comments: **Alistair Hetherington** |
| **12:45–13:30** | **Lunch** |
| 13:30–18:00 | *Excursions in Nancy* |
| 18:15–19:30 | **Public lecture (*in French*): Marc-André Selosse**<br>Plants, from head to toe in symbiotic love with microbes<br>Grand Salon de l’Hôtel de Ville, Stanislas Square |

# Speaker Abstracts

*S=speaker abstract; P=poster abstract; Bold indicates presenting author*

| | |
|---|---|
| Atkin, Owen | **S3.4** |
| Austin, Amy | **S3.3** |
| Beerling, David | **ARBRE lecture** |
| Brownlee, Colin | **S1.2** |
| Cesari, Stella | **Tansley Medal winner** |
| Delph, Lynda | **Keynote** |
| Dolan, Liam | **Keynote** |
| Groover, Andrew | **S1.1** |
| Kessler, André | **S2.1** |
| Kong, Hongzhi | **S4.2** |
| Kramer, Elena | **S4.1** |
| Lindahl, Björn | **S2.3** |
| Lindsey, Keith | **S1.4** |
| Medlyn, Belinda | **S3.2** |
| Osbourn, Anne | **S2.2** |
| Panstruga, Ralph | **S2.4** |
| Polle, Andrea | **S3.1** |
| Selosse, Marc André | **Public lecture** |
| Smith, Alison | **S1.3** |
| Yang, Shuhua | **S1.5** |

# Speaker abstracts

## Evolution and development of the earliest land plant rooting systems

## Keynote

**LIAM DOLAN**

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*Department of Plant Sciences, University of Oxford, Oxford, OX1 3RB, UK*

**13:45–14:30**

The evolution of the first rooting systems some time before 400 million years was a key innovation that occurred when the first complex multicellular eukaryotic photosynthetic organisms – plants – colonized the land. The evolution of land plants resulted in dramatic changes to the Earth System. For example, changes in the Carbon Cycle contributed to dramatic global cooling between 470 and 300 million years ago.

Rooting systems are important for land plants because they facilitate the uptake of most chemical elements that are required for growth, water update and anchorage. The rooting systems of the earliest diverging group of extant land plants comprised unicellular tip-growing filaments called rhizoids and are morphologically similar to cells that develop at the interface between the plant and the soil in vascular plants – root hairs. Subsequently specialized axes – multicellular structures that develop from self-renewing populations of cells called meristems – with evolved that carry out rooting function.

A major aim of our research is to use fossils and genes to understand key events in the evolution of land plant rooting systems. Fossils demonstrate the variety of forms that existed and how these forms developed. We have identified the oldest rooting structures with meristems. Genetics has allowed us to define the regulatory mechanisms that controlled the development of the first land plant root system and demonstrate how these mechanisms changed during the course of evolution. This positive regulatory mechanism is preserved in most land extant plant lineages. By contrast, negative regulatory components of the mechanism evolved independently in different lineages and some are more than 300 million years old.

By combining evidence from paleontology, genetics and development we can construct a picture for the evolution of rooting systems in the 100 million years after plants colonized the land and radiated across the continental surfaces.

## Session 1: Physiology and Development

***Chair: Alistair Hetherington***

### Evolution and development of wood formation in forest trees

## S1.1

**ANDREW GROOVER**

agroover@fs.fed.us

*US Forest Service, Pacific Southwest Research Station, Davis CA; Department of Plant Biology, UC Davis, United States*

**14:30–15:00**

Forest trees are wonderfully diverse organisms that share the common features of perennial growth and the production of wood. Tree stems contain a lateral meristem, the vascular cambium, which divides to produce cells that differentiate into cell types within wood or secondary phloem (the inner bark of the tree). In this talk, I will present an overview of how vascular cambia and wood evolved in different plant lineages, as well as insights into the molecular genetic evolution of wood formation and forest trees that are coming from advances in genome sequencing and computational analyses of gene expression data.

# Animal, vegetable and mineral: Understanding the unique physiology of biomineralizing phytoplankton in a changing ocean

## S1.2

**COLIN BROWNLEE**

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*Plymouth Marine Laboratory, Marine Biological Association,*
*Plymouth PL1 2PB, UK*

**15:00–15:30**

The marine phytoplankton account for approximately half of global productivity, play a major role the regulation of atmospheric carbon dioxide levels and underpin global fisheries. Two broad groups, the diatoms and coccolithophores are distinguished by their ability to produce biomineralized structures (silica frustules and calcite coccoliths respectively). Together they account for much of biogenic silica and calcium carbonate formation on Earth. At a cellular level these processes require exceptional fluxes of substrate and products into and out of the cell. How these processes of biomineralization occur in harmony with other essential cellular processes, such as cell signalling is a major theme of our research. Unlike plants, marine phytoplankton possess animal-like cation channels in their plasma membrane that underlie rapid electrical and calcium signalling. We are also studying the roles of a novel class of bacterial-like eukaryotic cation channels recently discovered in both diatoms and coccolithophores. We have also demonstrated a mechanism for pH regulation in coccolithophores, intimately associated with the calcification process, and based on voltage-dependent proton channels. In diatoms, new roles for cation channels in calcium signalling will be described. Characterising these complex physiological interactions will allow better understanding of how phytoplankton populations in the oceans will respond in a warming and acidifying ocean.

## What plants do in the dark

**S1.3**

**ALISON SMITH**

**16:30–17:00**

alison.smith@jic.ac.uk

*John Innes Centre, Norwich Research Park, Norwich NR4 7UH, UK*

When they can’t photosynthesise, how do plants survive? The starting point for plant growth is the synthesis of sucrose from atmospheric carbon dioxide, driven by energy from light. But what happens at night, and when seeds, tubers and so on start to grow in darkness under the soil? In most plants this problem is solved by synthesis of starch as well as sucrose as a product of photosynthesis in the light. Starch accumulates in plastids, then during darkness it can be converted to sucrose to fuel growth.

This apparently simple story hides a wealth of complexity and diversity, and several important aspects are not understood. I will describe our present understanding of how starch is converted to sucrose in leaves at night, and our efforts to discover how this process is controlled so that there is a steady supply of sucrose that lasts until dawn. I will discuss to what extent, and indeed whether, the picture emerging from our studies of Arabidopsis leaves is generally applicable to leaves of other species and to starch in other organs of the plant.

## Control of root growth in *Arabidopsis*

**S1.4**

**KEITH LINDSEY**

**17:00–17:30**

keith.lindsey@durham.ac.uk

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

Plant development contrasts with animal development by exhibiting a high degree of flexibility (plasticity), in which final form is unpredictable. This plasticity represents a mechanism for responding to environmental change, such as variations in availability of water, nutrients, light, or attack by herbivores. While animals respond to such environmental challenges through behavioural change, plants use plasticity in development to adapt and survive, and this is mediated to a significant extent through the activity of meristems and control of cell elongation. In this talk I will present some of our work on the genetic and signalling mechanisms, and in particular the crosstalk between auxin, ethylene and cytokinin, that control meristem activity and cell elongation, that regulate growth during root development in *Arabidopsis*.

# Phosphorylation-regulated plant freezing tolerance

## S1.5

**YANGLIN DING, ZIYAN LIU, HUI LI, SHUHUA YANG**

17:30–18:00

yangshuhua@cau.edu.cn

*State Key Laboratory of Plant Physiology and Biochemistry,*
*College of Biological Sciences, China Agricultural University,*
*Beijing 100193, China*

Cold stress is an environmental factor that adversely affects plant growth, development, productivity, and ecological distribution. The CBF-dependent cold signaling pathway has been extensively characterized in *Arabidopsis*; however, the underlying protein kinases remain unknown. Here, we identified three protein kinases regulating this signaling pathway. First, we found that SnRK2.6/OST1 (OPEN STOMATA1) is activated by cold stress. Activated OST1 phosphorylates ICE1 and suppresses HOS1-mediated ICE1 degradation under cold stress, thereby enhancing CBF expression and plant freezing tolerance. Moreover, OST1 phosphorylates BTF3 and BTF3L, subunits of the nascent polypeptide-associated complex, leading to stabilization of CBF proteins and increased plant freezing tolerance. Second, we found that MPK3/MPK6 phosphorylate and destabilize ICE1, which negatively regulate CBF expression and plant freezing tolerance plant freezing. Third, we identified a plasma membrane-localized kinase CRPK1 (Cold-responsive protein kinase 1) which is activated by cold stress, and phosphorylates its interacting proteins 14-3-3s. The 14-3-3 proteins shuttle from the cytosol to the nucleus to promote CBF protein degradation under cold stress, thus fine-tuning CBF cold signaling. Our data thus uncover the distinct molecular mechanisms by which different kinases regulate CBF-dependent cold signaling in *Arabidopsis*.

Key words: cold stress response, protein kinases, ICE1, CBFs, *Arabidopsis*

## Session 2: Interaction

***Chair: Maarja Öpik***

### Plant-to-plant communication and its role in driving herbivore population dynamics

**S2.1**

**ANDRÉ KESSLER**

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*Ecology & Evolutionary Biology, Cornell University, Ithaca NY 14853, United States*

**09:00–09:30**

Plant secondary metabolites mediate a large diversity of interactions from the cell over the tissue and whole plant to the community levels. Thus, their most basic and common function is information transfer and chemical signaling and communication should underlie the same principles as other types of information, such as acoustic and optical. Plant volatile organic compound emissions include secondary metabolites with the seemingly most obvious functions as information vehicles and thus provide a nice example of how to apply information theory to chemical information transfer.

The application of information theory to plant secondary metabolite production allows deriving new questions and hypotheses about the ecological roles and functions of noise in chemical signaling and, in consequence, the evolution of plant chemical signaling in different information landscapes.

Here I use tall goldenrod, *Solidago altissima*, as a model to illustrate various aspects of information theory for plant secondary metabolite production. More specifically, I review induction characteristics and ecological functions of volatile-mediated plant-plant information transfer in this community ecology model species. The special environmental circumstances in *S. solidago* habitats as well as the importance of herbivore dominance patterns provide strong agents of natural selection on plant chemical traits as vehicles of information.

# Finding drugs in the garden: Mining plant chemical diversity

## S2.2

**ANNE OSBOURN**

anne.osbourn@jic.ac.uk

*John Innes Centre, Norwich Research Park, Norwich NR4 7UH, UK*

**09:30–10:00**

Plants produce a wealth of natural products that are valuable as industrial or pharmaceutical products. The growing reliance on chemicals from plants is driving demand for green, environmentally friendly and sustainable feedstocks across industrial sectors in order to enable us to reduce our dependence on products derived from chemical refineries. Importantly, many of the natural products that are produced by plants are structurally complex and beyond the reach of chemical synthesis. These compounds are commonly extracted from plant material either growing in the wild or in cultivation. Availability is limited by difficulties in accessing and cultivating source species, low yield and problems of purification. The scale of the economic opportunity for improving the supply of high value products from plants is therefore enormous.

The vast majority of the natural product diversity encoded by plant genomes remains as yet untapped. The explosion in plant genome sequence data, coupled with affordable DNA synthesis and new DNA assembly technologies, now offer unprecedented opportunities to harness the full breadth of plant natural product diversity and generate novel molecules in foreign hosts using synthetic biology approaches. The recent discovery that genes for the synthesis of different kinds of natural products are organised in biosynthetic gene clusters in plant genomes opens up opportunities for mining for new pathways and chemistries. This advance, in combination with powerful new transient plant expression technology, is enabling the development of rational strategies to produce known and new-to-nature chemicals tailored for particular applications. This presentation will focus on our work on developing a translational synthetic biology pipeline for rapid preparative access to plant natural products and novel analogs using synthetic biology approaches.

# Sequencing the mycobiome of boreal forest soils

## S2.3

**BJÖRN LINDAHL**

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*Department of Soil and Environment, Swedish University of Agricultural Sciences, Uppsala 750 07, Sweden*

**11:00–11:30**

Boreal forest soils store significant amounts of organic carbon and nutrients, but drivers of decomposition and soil fertility are poorly understood, contributing uncertainty in global models of climatic feedbacks. We systematically sampled soil DNA from the entire latitudinal range of Swedish boreal forests and assessed fungal communities by sequencing ITS markers. Predictors of organic matter accumulation in the topsoil were evaluated by statistical modelling, combining fungal community data with climatic, edaphic and productivity parameters. Fungal community composition was identified as the principal determinant of organic matter accumulation, with a positive impact of ectomycorrhizal *Piloderma* species but a negative impact of other ectomycorrhizal species within the genus *Cortinarius*. Stress tolerant ascomycetes were associated with larger organic stocks. Organic matter accumulation increased with declining pH and tree biomass, but these effects seemed to be indirect and mediated by their interplay with fungal communities. Our findings highlight the regulatory importance of soil fungi in boreal ecosystems. The results contribute correlative support for the idea that certain ectomycorrhizal fungi and stress tolerant ascomycetes that are poor decomposers drive organic matter accumulation, but that other ectomycorrhizal species (e.g. in the genus *Cortinarius*) are efficient decomposers that counteract organic matter accumulation. Intense forestry has large effects on fungal communities and indirect impacts on organic matter turn-over is to expect. Potentially, forestry may have a positive effect on below-ground carbon storage, but there is a major risk that long-term soil fertility is under threat.

# Durable disease resistance by loss of plant 'susceptibility factors'

## S2.4

**RALPH PANSTRUGA**

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*Institute for Biology I, RWTH Aachen University, Aachen 52056, Germany*

**11:30–12:00**

Plant diseases are a serious threat to agriculture and worldwide cause enormous yield losses every year. The two-layered plant immune system is able to prevent or restrict the attempted attacks of many potential microbial intruders. The two tiers of plant immunity rely on cell surface receptors that perceive highly conserved microbial patterns and cytoplasmic receptor proteins that recognize – either directly or indirectly - very specialized microbial virulence molecules (e.g. so-called effector proteins). However, some pathogens evolved molecular tools to either overcome or evade plant immunity and cause disease. Since even these 'successful' microbial invaders typically depend on particular host factors during pathogenesis, absence or non-functionality of such host components – which are also termed 'susceptibility factors' – can result in highly effective disease resistance. In my presentation, I will introduce and discuss this concept with examples from different patho-systems, focussing in particular on the well-known *mlo* mutants that confer durable broad-spectrum powdery mildew resistance. Apart from the beneficial aspects of disease resistance conferred by loss of plant 'susceptibility factors' also limitations and potential problems of this approach will be considered.

# Multiple strategies for pathogen perception by plant immune receptors

**Tansley Medal winner**

**12:00–12:30**

**STELLA CESARI**

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*Institut National de la Recherche Agronomique, UMR de Biologie et Génétique des Interactions Plante-Pathogènes, TA A-54/K Campus International de Baillarguet, 34398 Montpellier Cedex 5, France*

Plants have evolved a complex immune system to protect themselves against phytopathogens. A major class of plant immune receptors called nucleotide-binding domain and leucine-rich repeat-containing proteins (NLRs) is ubiquitous in plants and is widely used for crop disease protection, making these proteins critical contributors to global food security. Until recently, NLRs were thought to be conserved in their modular architecture and functional features. Investigation of their biochemical, functional and structural properties has revealed fascinating mechanisms that enable these proteins to perceive a wide range of pathogens. Here, I review recent insights demonstrating that NLRs are more mechanistically and structurally diverse than previously thought. I also discuss how these findings provide exciting future prospects to improve plant disease resistance.

## Session 3: Environment

## *Chair: Richard Norby*

### Molecular ecophysiology of wood formation under drought

### S3.1

**ANDREA POLLE[1] AND THE WATBIO CONSORTIUM[2]**

apolle@gwdg.de

[1]*Forest Botany and Tree Physiology, University of Göttingen, Göttingen 37077, Germany;* [2]*http://www.watbio.eu/*

**14:00–14:30**

Woody biomass can substitute many oil-based products because of its multiple usages, for example, as construction material, as raw material for added-value wood products, as feedstock for the chemical industry and as a resource for energy generation. The demand for sustainable production of renewable resources is increasing but climate change with increasing periods of drought limits productivity and enhances the risk of mortality for trees species with high water demand. Drought acclimation of trees involves structural changes in wood anatomy with thicker cell walls and smaller vessel lumina to avoid cavitation. Consequently, wood of drought-stressed trees exhibits higher densities than that of well-watered trees. While the ecophysiological responses to drought have been well characterized, the time course of the molecular responses to gradually increasing stress across different tissues that eventually lead to changes in wood anatomy have barely been studied. Here, we show results of poplar ecophysiological, anatomical and molecular acclimation to moderate, gradually increasing drought stress. We uncovered divergent, tissue-specific networks that were correlated with hormonal changes in roots, stem and leaves. To unravel a potential role of abscisic acid, we analyzed a range of transgenic poplar plants with modification in ABA signal perception and response. Our results provide insights into the genomics and ecophysiology of wood formation, which are an essential basis securing sustainable wood production in a future climate.

Funding: WATBIO (Development of improved perennial non-food biomass and bioproduct crops for water stressed environments) is funded by the European Union’s Seventh Programme for research, technological development and demonstration under the grant agreement FP7-311929.

## Recent advances in stomatal conductance

**S3.2**

**BELINDA MEDLYN**

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*Hawkesbury Institute for the Environment, University of Western Sydney, Penrith 2750 New South Wales, Australia*

**14:30–15:00**

The finding that empirical models of stomatal conductance can be interpreted in terms of optimal stomatal theory has opened up a wide range of new avenues for research into stomatal behaviour. In this talk I will review recent advances in optimal stomatal theory, describing new model developments and how they help us predict stomatal responses to light, drought and heat. I will also survey how stomatal behaviour varies within and across species and highlight outstanding questions and promising areas for future research.

# Plants in the sun: new insights on the role of solar radiation in terrestrial ecosystems

## S3.3

**AMY AUSTIN**

16:00–16:30

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*Principal Investigator, CONICET, Associate Professor, University of Buenos Aires, Buenos Aires C1417 DSE, Argentina*

Human activities are altering biogeochemical cycles globally, and our understanding of the controls on carbon and nutrient turnover in terrestrial ecosystems is essential for our ability to mitigate and minimize human impact in natural ecosystems. Plant litter decomposition is an essential process in the first stages of carbon turnover in terrestrial ecosystems, and provides some of the principal inputs of carbon for the formation of soil organic matter. Our research focuses on the role of photodegradation, the photochemical transformation of organic matter due to exposure to solar radiation, as a mechanism for previously unexplained high rates of carbon loss to the atmosphere in terrestrial ecosystems. In addition, we have demonstrated indirect effects of photodegradation on biotic stimulation of carbon turnover in a wide range of species. Field studies in Patagonian woodland ecosystems confirm the importance of biotic facilitation on litter decomposition, which appears to have larger stimulatory effects than those observed in controlled conditions. The generalized positive effect of solar radiation exposure on subsequent microbial activity appears to be mediated by increased accessibility to cell wall polysaccharides, which is consistent in both field and controlled condition experiments. These results suggest that photodegradation is quantitatively important in affecting the global carbon cycle, which has implications for the potential alterations in carbon turnover in terrestrial ecosystems to predicted climate or land use change.

# Thermal biology of plant metabolism: Insights into global patterns

## S3.4

**OWEN ATKIN**

16:30–17:00

owen.atkin@anu.edu.au

*Building 134, ARC Centre of Excellence in Plant Energy Biology, Research School of Biology, Australian National University, Canberra ACT 0200, Australia*

Being sessile organisms, plants often experience large variations in temperature through time. Temperatures also vary markedly across landscapes. Changes in temperature can affect metabolic processes that underpin plant growth and survival, with the impacts of temperature on leaf photosynthesis and respiration being particularly important. Short-term changes in temperature alter metabolic rates via changes in the maximum catalytic activity of key enzymes, and influence the fluidity of biological membranes with consequences for metabolism. While rising temperatures generally increase metabolic rates, exposure to heat waves can cause irreversible damage to photosynthesis and respiration, suggesting that global warming could have a detrimental effect on the processes of carbon gain and release in plants, depending on the extent to which carbon metabolism acclimates to sustained increases in growth temperature. In this talk, I will discuss recent global surveys of plant metabolic responses to short- and long-term changes in temperature, focussing on: (1) the impacts of temperature on leaf respiration and the role respiratory acclimation may play in mitigating the negative effects of sustained climate warming on respiratory $CO_2$ release; and (2) global patterns in high temperature tolerance of respiration and photosynthesis. The implications of plant metabolic temperature responses for survival of plants in hot climates and future atmospheric $CO_2$ concentrations will be discussed.

## Session 4: Evolution

### *Chair: Simon Hiscock*

### It’s the phenotype …

**Keynote**

**09:00–09:45**

**LYNDA DELPH**

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*Department of Biology, Indiana University, Bloomington IN 47405, United States*

Science often progresses when ideas merge with new technologies that allow scientists to answer questions in ways that were previously not possible. That said, inordinate focus on results garnered from new methodologies can direct research down paths that are not necessarily those that will produce breakthroughs in our understanding of nature. I will draw from recent commentaries, talks, and my own work on sexually dimorphic dioecious plants to highlight the importance of retaining a focus on plant phenotypes as we attempt to understand how selection operates to produce the diversity of plant form and function. Knowledge of plant traits, when coupled with advances in genomics, will propel us into the future.

# Exploring the genetic basis of floral novelty in *Aquilegia*

## S4.1

**09:45–10:15**

**<u>ELENA KRAMER</u>[1], YA MIN[1], MOLLY EDWARDS[1], CLARE MEADERS[1], EVANGELINE BALLERINI[2], SCOTT A. HODGES[2]**

ekramer@oeb.harvard.edu

*[1]Dept. of Organismic and Evolutionary Biology, Harvard University, Cambridge MA 02138, United States; [2]Dept. of Ecology, Evolution and Marine Biology, Univ. of CA, Santa Barbara, United States*

The lower eudicot model system *Aquilegia* possesses several novel morphological features that have the potential to shed light on the evolution of novelty, particularly in the context of complex organ form. We have been studying two key features of the *Aquilegia* flower: the three-dimensional petal nectar spur and a fifth floral organ type, the staminodium. In the case of the petal spur, we have found that *Aquilegia* petal spurs initiate due to a localized region of cell division in which cell wall formation is radially organized around the presumptive nectary. This lays the ground pattern of the spur, which is then realized through rapid, anisotropic cell elongation that is the major determinant of spur length and curvature. Diversification of spur morphology has involved multiple factors, including heterochronic shifts that generate much longer, narrower cells; differences in cell numbers around the radial axis of the spur; and independent control of cell elongation on different surfaces of the spur, which generates curvature. We are now combining transcriptomics, candidate gene approaches, and QTL mapping to explore the genetic architecture of spur development and understand its evolution. In the case of the staminodium, we have previously discovered that this novel organ identity is determined via the combinatorial activity of paralogs of the genes that normally confer stamen identity, such that the stamens and staminodia now have distinct genetic codes via sub- and neofunctionalization. We are further exploring the developmental and morphological oddities of the staminodia, what their ecological function may be, and how their developmental program diverges from that of stamens.

# The making of elaborate petals in *Nigella* (Ranunculaceae)

# S4.2

**XU YAO, RUI ZHANG, HONG LIAO, XUEHAO FU, YI YUAN, HONGZHE WANG, HONGYAN SHAN, GUIXIA XU, HONGZHI KONG**

hzkong@ibcas.ac.cn

*State Key Laboratory of Systematic and Evolutionary Botany, Institute of Botany, Chinese Academy of Sciences, Beijing 100093, China*

**11:15–11:45**

As a special type of floral organs, 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 *Nigella* petals have become elaborate and diverse, we first investigated the morphology, micro-morphology and development of *Nigella* petals. We found that the degree of petal complexity increases gradually during the evolution of the genus, likely through modification of pre-existing characters (e.g., the elongation of stalk and the alteration of the upper and lower lips in shape) as well as de novo origination of new features (e.g., pseudonectaries, short trichomes, and conical cells). By conducting extensive digital gene expression (DGE) analyses, we further identified the genes that play key roles in the elaboration and diversification of *Nigella* petals. We found that: 1) changes in the expression domains of adaxial/abaxial polarity genes may have led to the formation of the upper lip; 2) ectopic expression of *LMI1*, a class I HD-Zip family transcription factor gene, may be responsible for the bifurcation of the lower lip; and 3) *YAB5-1*, a *YABBY* family transcription factor gene, is involved in the formation of pseudonectaries and short trichomes. There results confirmed that *Nigella* is an excellent model for the study of petal elaboration and pave the way for better understanding the basics and underlying mechanisms of plant organ diversification.

## Can we achieve multiple gigatonne $CO_2$ capture by farming with crops and rocks?

**ARBRE lecture**

**11:45–12:30**

**DAVID BEERLING**

d.j.beerling@sheffield.ac.uk

*Department of Animal & Plant Sciences, University of Sheffield, Sheffield S10 2TN, UK*

Global warming is a problem that affects everyone on the planet. Scientists have generally done a poor job of getting across the point that the world must reduce emissions of greenhouse gases from fossil fuels and combine this with strategies for extracting carbon dioxide from the atmosphere to avoid a climate catastrophe. Enhanced rock weathering is carbon dioxide ($CO_2$) removal strategy that can work together with existing managed croplands. It may offer a pragmatic carbon cycle intervention strategy for the safe removal of some of our anthropogenic $CO_2$ emissions while addressing sustainable development goals linked to safeguarding food and soil security, and the oceans. Unlike other carbon removal strategies being considered, it doesn't compete for land used to grow food or increase the demand for freshwater, but what would deployment look like and what would it cost? This lecture will address these issues.

# Plants, from head to toe in symbiotic love with microbes//Jamais seule: pourquoi il n'y aurait pas de plante sans microbes

**Public lecture**

**MARC ANDRÉ SELOSSE**

ma.selosse@wanadoo.fr

*Département Systématique et Evolution, Muséum national d'Histoire naturelle, Paris 75005, France & University of Gdansk, Poland*

**18:15–19:30**

Recent research has demonstrated the amazing extent to which microbes (mainly bacteria and fungi) facilitate the generation of a plants structure and function. Plants are born microbial, since their photosynthesis and respiration are carried out by intracellular bacteria, inherited over generations. Plants also receive nutrients from microbes that allow their nutrition in soil: roots are fed by soil fungi, without which most plants could not grow. Leaves and roots are protected by microbes living between cells in the tissues, from which they get nutrients to develop. Last, plants can be seen as microbial sculptures, since microbes shape development: microbes contribute to establish mature plant immunity, but also morphology, and even reproduction. This new, holobiontic vision of plants offers promising tools for future management of plants and ecosystems.

Les recherches récentes ont montré à quel point les microbes (bactéries et champignons) fabriquent les plantes, de leurs structures à leurs fonctions. Les plantes sont nées microbiennes, car leur photosynthèse et leur respiration sont réalisées par des bactéries contenues dans leurs cellules, héritées de génération en génération. Les plantes vivent de microbes car ceux-ci façonnent leur nutrition dans le sol: des champignons nourrissent leurs racines, sans lesquels la plupart des plantes ne pousseraient pas. Feuilles et racines sont protégées par des microbes qui s’insinuent dans leurs tissus, où ils se nourrissent en retour. Enfin les plantes sont sculptées par les microbes car ces dernières années, il est apparu que ceux-ci façonnent le système immunitaire végétal, mais aussi le développement de la forme, et jusqu’à la reproduction de la plante. Demain, il nous faudra gérer la plante comme un écosystème microbien!

# Poster abstracts

*P=poster abstract. S=speaker abstract.* Bold=presenting author

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# Poster abstracts

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

## P1

## Are nodule specific genes NCRs under the regulatory control of ancient protein family?

**MINGKEE ACHOM[1], ROXANNA BONYADI POUR[1], CHARLOTTE RICH[1], SASCHA OTT[2], MIRIAM GIFFORD[1]**

*[1]School of Life Sciences, [2]Department of Computer Science, University of Warwick, Coventry, CV4 7AL, UK*

Legumes house nitrogen-fixing endosymbiotic rhizobia in specialised polyploid cells within root nodules. The model legume *Medicago truncatula*, one of the members of the inverted repeat lacking clade (IRLC) of legumes are known to have a class of multi-gene family encoding for NCRs (Nodule Cysteine Rich peptides). Until now, studies have suggested that this large family acts as anti-microbial defensins keeping the rhizobial population in balance. However, these functional insights come from only a few of more than 500 NCRs that have diversified spatio-temporal expression. Due to their occurrence in large numbers from genome amplification, it is possible that these NCR genes have evolved gain of novel functions beyond just bacterial regulation.

Using transcriptomic analysis from microarray data and promoter study we have revealed the presence of six conserved promoter motifs that are over-represented in subsets of NCRs that are regulated in different ways by combinations of rhizobia and nitrogen. Our hypothesis is that the NCR promoter motifs may be acting as transcription factor (TF) binding sites for the regulation of nodulation and we have identified protein family of AHL, ATHB, CCA1 and RVE1 as putative TF regulators. Our results support an expanded role of NCRs in signaling and development during symbiosis.

## P2

# Fungal manipulation of plant jasmonate signaling in *Populus- Laccaria* bicolor ectomycorrhizal symbiosis

**V. BASSO[1], Y. DAGUERRE[1,2], R. SCHELLENBERGER[1], S. WITTULSKY[1], A. KOHLER[1], F. MARTIN[1], C. VENEAULT-FOURREY[1]**

*[1]INRA, UMR INRA-Universite´de Lorraine 'Interactions Arbres/Microorganismes', Laboratoire d'Excellence ARBRE, INRA Grand Est-Nancy, Champenoux, France; [2]Forest Genetics and Plant Physiology, Umeå Plant Science Centre, Swedish University of Agricultural Sciences, 90183 Umeå, Sweden*

Jasmonates (JAs) are a class of phytohormones involved in plant defense against insects and necrotrophic pathogens, primary root length regulation, anthocyanin production and other physiological and developmental processes. Evidence is emerging that exogenous-JA perception by a host plant is deleterious for the establishment of the ectomycorrhizal (ECM) symbiosis, in accordance with the pivotal role of this hormone in defense against fungi. However, we showed that the ectomycorrhizal basidiomycete *Laccaria bicolor* secretes the Mycorrhiza-induced Small Secreted Protein 7 (MiSSP7), which penetrates cortical cells nuclei of the host plant *Populus trichocarpa* and interacts with its jasmonate-zim-domain protein 6 (JAZ6), blocking JA signaling and promoting fungal colonization. We aim at elucidating the structure of the JA perception complex targeted by MiSSP7, as well as the transcriptomic consequences of this interaction. Using Yeast Two Hybrid (Y2H), Yeast Three Hybrid (Y3H) and co-immunoprecipitation (Co-IP) in tobacco, we dissect the composition of the poplar JA perception complex. Next step will be the identification of genes targeted by JAZ6-interacting bHLH transcription factors, using ChIP-Seq assay and transcriptome analysis of overexpressing and silencing mutants.

# P3

# Transcriptomic effect of phytohormone treatment on *Populus-Laccaria* ectomycorrhiza

**VERONICA BASSO[1], ANNEGRET KOHLER[1], KERRIE W BARRY[2], VASANTH SINGAN[2], IGOR GRIGORIEV[2] ONDREJ NOVACK[3], FRÉDERIC GUINET[1], FRANCIS MARTIN[1], CLAIRE VENEAULT-FOURREY[1]**

*[1]INRA, UMR 1136 INRA-University of Lorraine, Interactions Arbres-Microorganismes, Laboratory of Excellence ARBRE, INRA-Nancy, 54280 Champenoux, France; [2]US Department of Energy Joint Genome Institute (JGI), Walnut Creek, California, USA; [3]Laboratory of Growth, Palacký University & Institute of Experimental Botany AS CR, Šlechtitelů 27, 783 71 Olomouc, The Czech Republic*

Ectomycorrhiza (ECM) are symbiotic interactions occurring between the roots of about 400 tree species and several fungi of the *Basidiomycota* and *Ascomycota* phyla; they are pivotal for nutrient cycling in forest ecosystems. However, not much is known about the molecular and physiological mechanisms underpinning the establishment of such interactions. Therefore, using the tree *Populus tremula x alba* INRA 717-1B4 and the basidiomycete *Laccaria bicolor* as model organisms, we assessed the role of phytohormones in the plant and fungal transcriptomic reprogramming at the onset of ECM formation. We focused on jasmonic acid (JA), ethylene (ET), gibberellic acid (GA) and salicylic acid (SA). The perception of JA and ET by the plant was previously demonstrated to inhibit ECM formation. Here we show the transcriptomic profiling of poplar roots, *Laccaria* free mycelia and *Populus-Laccaria* ECM treated with one or two phytohormones. We will (i) identify relevant *Populus* marker genes for JA, SA, GA, ET-signalling pathways in roots, (ii) investigate the antagonism/ synergy between phytohormone signalling pathways and finally (iii) study responses of *Laccaria* hyphae to exogenous plant hormones. These results, coupled with morphological phenotyping, will suggest hints as to the molecular mechanisms needed for the onset of the ECM symbiosis.

# P4

# Immunocytochemical and gene expression analyses of the bast fibres in the developing hemp hypocotyl

M. BEHR[1,3*], C. FALERI[2*], S. LUTTS[1], JF. HAUSMAN[3], G. GUERRIERO[3], G. CAI[2]

**Equal contribution as first authors. [1]Earth and Life Institute, Université catholique de Louvain, 5 (Bte 7.07.13) Place Croix du Sud, 1348 Louvain-la-Neuve, Belgium; [2]Dipartimento Scienze della Vita, Università degli Studi di Siena, Via Mattioli, 4-53100 Siena, Italy ; [3]Dpt Environmental Research and Innovation, Luxembourg Institute of Science and Technology, 41 rue du Brill, 4422 Belvaux, Luxembourg*

Hemp (*Cannabis sativa* L.) cultivars grown for biomass production present in the stem hypolignified extraxylary fibres (aka bast fibres) rich in crystalline cellulose. The specification and functional characteristics of this cell type is of major interest for future technical applications. The cellulose network of these cells is embedded in a pectic matrix whose composition has an important role for its mechanical properties. In flax for instance, the molecular composition of rhamnogalacturonan I has a crucial importance in this respect. However, the composition of bast fibre cell wall is not yet precisely known in hemp. We have therefore investigated this point through immunocytochemistry using confocal and electronic microscopy in hypocotyls aged between 9 and 20 days. Specific monoclonal antibodies recognising cell wall polysaccharides (crystalline cellulose, hemicelluloses and pectins) and cell wall proteins were used. The expression of some genes involved in the biosynthesis of these polysaccharides was investigated by targeted RT-qPCR and RNA-Sequencing. By combining these two techniques, we show that the gelatinous layer of the bast fibres has its own signature.

# P5

# A novel role of the soybean circadian clock gene in reproductive development

**LC. LIEW, MB. SINGH, PL. BHALLA**

*Plant Molecular Biology and Biotechnology Laboratory, Faculty of Veterinary and Agricultural Sciences, The University of Melbourne, Parkville, Victoria 3010, Australia*

Soybean is a major oilseed legume crop used for human and animal feed, and its genome palaeopolyploid has been duplicated several times. Moreover, legume crops such as soybean have unique vegetative and floral complexities. Expanding the cultivation areas of crops such as soybean requires optimization of environmental and development responses suitable for changing climate regimes.

The internal circadian clock has emerged as a key regulator of different biological functions. Studies have shown that the circadian clock enhances the adaptation, fitness, and survival of plants. However, it is not known whether clock genes regulate plant development directly. The evening complex, a tripartite protein complex of ELF4-ELF3-LUX, is an integral component of a plant circadian clock for maintaining circadian rhythms. *LUX ARRHYTHMO* (*LUX*) has been shown to play a key role in circadian rhythms and flowering. However, it is not clear how the evening complex connects with other pathways to regulate plant development and physiology. Our study on soybean *LUX* revealing the novel function of a clock gene in controlling fertility and seed yield by affecting stamen development and function.

# P6

# Regulatory mechanisms of tomato glandular trichomes against the aphid *Macrosiphum euphorbiae*

**L. BLANCO**[1*], **JA. DÍAZ-PENDÓN**[1], **E. de la PEÑA**[1,2]

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Alternative pest management to pesticide use, requires a solid knowledge on the plant-pest-natural enemy relationship. In tomato (*Solanum lycopersicum*), one of the most important crops worldwide, the presence of type IV glandular trichomes and acylsucrose production is associated with high levels of resistance to diverse arthropod species. Some species of aphids as *Macrosiphum euphorbiae* are of particular importance as they not only produce severe plant damage but also act as vectors of viruses. Nonetheless, it remains undescribed whether this resistance trait protects tomato plants from aphids.

The aim of this study is to unravel the mechanisms driving this resistance trait from a molecular and an ecological perspective. Firstly, we analyzed the performance of *M. euphorbiae* on two near-isogenic lines (ABL 10-4 and 'Moneymaker') that vary in the presence of type-IV trichome density and acylsugar production. Because of the significant reduction on aphid's growth found on ABL 10-4 line, we studied the role played by the acylsucroses. Since phytohormones can modulate the density of defense-related glandular trichomes, transcriptomic analyses were also conducted to monitor changes in JA and SA signaling pathways. We noticed that previous herbivory, both by sap-sucking and leaf-chewing insects, had an antagonist effect on aphids´ performance attributed to the display of type-IV trichomes. In addition, a series of experiments were also performed to assess aphids' performance on tomato lines impaired in the JA/SA signaling pathway.

# P7 A possible role for abscisic acid in restoring water transport in embolized vessels

**C. BRUNETTI[1], T. SAVI[2], A. NARDINI[2], A. GORI[3], F. LORETO[4], M. CENTRITTO[1]**

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Under drought conditions plant are more vulnerable to the formation of embolism within the xylem conduits. The possibility of plants to refill embolized xylem conduits may rely on up-regulation of carbohydrate metabolism to create an osmoticum. On this basis, we explored: 1) xylem hydraulic during drought and subsequent re-watering to investigate the vulnerability to embolism and eventual refilling processes in *Populus nigra*; 2) the role of abscisic acid in mobilization of non-structural carbohydrates for embolism repair processes. We conducted physiological (leaf conductance to water vapour (gL), leaf water potential($\Psi W_{leaf}$), leaf osmotic potential ($\Psi\pi$), stem water potential ($\Psi W_{stem}$), loss of stem hydraulic conductance (PLC)) and biochemical measurements (ABA and its metabolites, starch and carbohydrates). Our results confirm a relatively high vulnerability to embolism in P. nigra. Under drought the decline in ΨWstem and ΨWleaf led to a significant reduction in gL and a marked increase of PLC (>60 %). Embolism, alongside $\Psi W_{stem}$ and $\Psi W_{leaf}$, recovered fully after re-watering. However, gL values remained low, suggesting efficient recovery mechanisms. Interestingly, during rewatering we observed an increase both in ABA and hexoses concentration, both in the wood and in the bark. These results suggest a possible role for ABA in the restoration of xylem transport capacity via regulation of stem carbohydrate metabolism during drought relief.

# P8

# Future flowers may not smell the same, but will that matter to their pollinators?

**<u>JOYSHREE CHANAM</u>[1], DHARMENDRA LAMSAL[1], YUVARAJ RANGANATHAN[2], SHANNON OLSSON[1], MAHESH SANKARAN[1,3]**

*[1]National Centre for Biological Sciences, TIFR, Bangalore, India; [2]GNOBIOSYS, Thiruvananthapuram, India; [3]School of Biology, University of Leeds, Leeds LS2 9JT, UK*

Climate warming is reported to affect biosynthesis and volatility of plant Volatile Organic Compounds (VOCs), which mediate plant–insect interactions. However, little is known about climate warming effects on plant–insect interactions in tropical alpine ecosystems, such as the Himalayas, where average temperature increase is higher than global average, and hence more vulnerable. With Eastern Himalayas as study site, we investigated the effect of *in situ* warming on floral VOCs, compared floral VOCs of four species across elevation gradient, and also noted pollinator visitation on three flower species across elevation gradient. We found intraspecific variation in floral VOCs between 'warmed' and control plants, as well as across elevations. Further, cluster analysis with all species from all elevations showed that VOC samples of each species grouped together, independent of elevation, and were separated from groups of other species. This indicates that despite intraspecific variation in VOCs due to environmental factors, pollinators might still recognize a flower species as long as the community structure is stable and pollinators can differentiate specific flowers from other flower species in the community. This hypothesis is supported by our finding that there is no trend in pollinator visitation rate to the same flower species across elevations.

# P9

# Functional analysis of gibberellic acid-related early signaling in soybean (*Glycine max*) nodulation

**XITONG CHU, SATOMI HAYASHI, HUANAN SU, MENGBAI ZHANG, APRIL HASTWELL, PETER GRESSHOFF, BRETT FERGUSON**

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Legume nodulation is critical to food security, improved soil fertility and sustainability. Like most legume species, soybean (*Glycine max*) is characterised by its ability to form root nodules in response to compatible nitrogen-fixing rhizobia bacteria (*Bradyrhizobium diazoefficiens*). Nodule formation and development both require complex molecular mechanisms involving an array of plant hormones, including gibberellic acid (gibberellin; GA). GAs appear to be required at different stages of nodulation, with their concentration highly regulated by the host plant. To achieve successful nodulation, a window of GA appears to be required temporally and spatially, with too much or too little being inhibitory to nodule development. High throughput RNA-seq identified a set of differentially expressed GA oxidase genes in soybean. *GmGA20ox a*, *GmGA3ox 1a*, and *GmGA2ox* were all up-regulated in soybean roots inoculated with compatible rhizobia, indicating a requirement for GA oxidase genes in nodulation; however, their precise roles in nodulation remain unclear. Our research aims to enhance the knowledge of GAs, and the individual GA oxidase genes, in soybean nodulation. Outcomes will also help to further understanding the physiological and genetic changes of soybean nodulation when GA is applied.

# P10

# Reduced night-time transpiration is a relevant breeding target for high water-use efficiency in grapevine

**<u>AUDE COUPEL-LEDRU</u>[1,3], ERIC LEBON[1], ANGELIQUE CHRISTOPHE[1], AGUSTINA GALLO[1], PILAR GAGO[2], FLORENT PANTIN[1], AGNÈS DOLIGEZ[3], THIERRY SIMONNEAU[1]**

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In the face of increasing water scarcity, breeding for higher transpiration efficiency (TE), that is, the biomass produced per unit of water transpired, has become crucial. This could be achieved by reducing plant transpiration through a better closure of the stomatal pores at the leaf surface. However, this strategy generally also lowers growth, as stomatal opening is necessary for the capture of atmospheric $CO_2$ that feeds daytime photosynthesis.

Here we tested whether reducing transpiration at night when photosynthesis is inactive could substantially reduce water loss without altering growth—a hypothesis that, to our knowledge, has never been genetically addressed in any species. We carried out a genetic analysis for night-time transpiration and TE in grapevine, a major crop in drought-prone areas. A 3-year experiment was conducted on the F1 progeny from a cross between Syrah and Grenache cultivars using a phenotyping platform coupled to a controlled-environment chamber, under well-watered and moderate soil water deficit scenarios. High genetic variability was found for night-time transpiration and 5 QTLs were detected. An experiment was also performed outdoors which confirmed the significance of this genetic variability. We further highlighted a major role of residual stomatal opening at night and a minor, yet significant contribution of the cuticle in determining this genetic variability. Strikingly, 4 of the QTLs detected for night-transpiration co-localized with QTLs for TE. Moreover, genotypes with favourable alleles on these common QTLs exhibited reduced night-time transpiration without altered growth. These original results (Coupel-Ledru et al., PNAS, 2016) open new horizons for breeding plants with lower water loss at night for higher TE.

# P11

# Potato yield and quality responses to partial root-zone drying and deficit irrigation under glasshouse conditions

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Deficit irrigation (DI) and partial root-zone drying (PRD) are water-saving irrigation methods based on stress physiology. DI irrigates the entire root-zone of the plant with an amount of water less than the maximum crop evapotranspiration. PRD, in some way, is an evolution of DI in which the root-zone is divided between two containers to alternate wetting and drying of the root-system. These strategies could enhance the quality and water-use efficiency (WUE) without reducing yield of the crop. In this work, both techniques were evaluated on potato (*Solanum tuberosum* L.) grown under glasshouse conditions. PRD and DI plants were irrigated according to transpiration demand for controls and the amount of water was reduced to 20%, 30% and 50% for both irrigation strategies. The results showed that the best and the only treatment that showed non-significant difference in yield compared to controls was PRD 20%. Tubers from water stressed plants presented higher contents of total sugars, dry matter and ash content than the well-watered plants. With the same amount of irrigation water, PRD technique showed advantage compared to DI particularly for moderate water restriction.

# P12

# Uncovering the volatile nature of bryophytes during dehydration and rehydration cycles

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Plants produce volatile organic compounds (VOCs) that have prominent roles in plant resistance to stresses and communication with other organisms, and may influence air quality, cloud dynamics, and global climate. While VOC production from angiosperms has been intensively characterized, and green algae are currently under scrutiny for their VOC profiles, it remains challenging to study VOCs in the closest relatives to the first land plants, the bryophytes. The phylogenetic and ecological importance[1] position of bryophytes as fundamental organisms is key to reveal VOC evolution and functions. The aim of this work was to investigate the impact of dehydration-hydration cycles on VOC profiles of desiccation sensitive (DS) and tolerant (DT) model species of bryophytes: *Porella platyphylla* (DT), *Pleurochaete squarrosa* (DT) and *Vessicularia dubyana* (DT). In particular, we hypothesized that, as in higher plants, VOCs might have played protective functions already in the first land plants. We combined imaging fluorescence, gas exchange measurements and headspace-solid phase microextraction approach for VOC quantification. The blend of VOC was different between (i) dehydration and hydration cycles and (ii) DS and DT bryophytes. It is suggested that volatile isoprenoids in the VOC blend might play an important photoprotective role, especially during the initial stages of dehydration, possibly in cooperation with other non-volatile isoprenoids and coupled with an enhanced contribution of photorespiration during the recovery. This work will be especially valuable under global warming scenario that may change the emission patterns in bryophytes with important

consequences for future plant communication and stress resistance, and in biosphere-atmosphere interactions.

References:
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**P13**

# Ectomycorrhizal ecology is imprinted in the genome of the dominant symbiotic fungus *Cenococcum geophilum*

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The most frequently encountered symbiont on tree roots is *Cenococcum geophilum*, the only mycorrhizal species within the largest fungal class Dothideomycetes.

As shown for other sequenced ectomycorrhizal (ECM) genomes, the *C. geophilum* genome contains a reduced number of plant cell wall-degrading enzymes and symbiosis-induced genes of unknown function. *C. geophilum* shows an increased genome size due to about 80% transposable elements. Transcript profiling of ectomycorrhiza and free-living mycelium revealed an up-regulation of membrane transporters, including water channels (AQPs) and sugar transporters, and mycorrhiza-induced small secreted proteins (MiSSPs) during symbiosis. Interestingly, the transcriptome of *C. geophilum* interacting with Pine or Poplar revealed similar sets of up-regulated MiSSPs, with only a few restricted to one host. By analyzing 15 re-sequenced *C. geophilum* strains, we found that MiSSPs are likely evolving through gene gain/loss. The high expression of water permeable AQPs in functioning ectomycorrhiza may be provoked by plant water demand upon the interaction. Plant water and nutrient transporters were more highly expressed in mycorrhizas of Pine interacting with *C. geophilum* compared to other ECM fungi, supporting a possible role of *C. geophilum* in drought tolerance of host trees.

# P14

# Reductions in tree performance during hotter droughts are minimized by shifts in nitrogen cycling

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Anthropogenic climate warming is projected to result in hotter droughts of unprecedented severity in this century. Such global-change-type droughts have been linked with massive tree mortality and data suggest warming interacts with drought to aggravate plant performance. Yet, how forest ecosystems will respond to hotter droughts remains unclear, as does the suite of mechanisms trees use to deal with hot droughts. Limited evidence and theory suggest that shifts in soil and plant processes, particularly via nutrient cycling processes, could mitigate the combined effects of warming and soil moisture limitations. Using mature trees exposed to multi-year temperature and precipitation manipulation, we found that while negative impacts on plant carbon and water balance are manifest after prolonged drought these performance reductions were not amplified by warmer temperatures. Rather, increased temperatures stimulated nitrogen (N) availability and altered tree N allocation, resulting in mitigation of hotter drought impacts. These findings suggest that adjustments in N cycling are likely after several years of warming conditions and that such changes may buffer reductions in tree performance during hotter droughts. The results also highlight our incomplete understanding of trees' ability to acclimate to climate change, raising fundamental questions about the resistance potential of forests to long-term, compound climatic stresses.

# P15

# Cadmium inhibits primary root growth by modulating auxin synthesis and transport in *Arabidopsis*

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The heavy metal cadmium (Cd) is a non-essential toxic metal and inhibits the primary root growth in plants. However, the underlying mechanism by which Cd participates in this inhibition remains to be further explored. In the present study, we demonstrated that Cd prevented the normal growth of primary root via diminishing the size of meristematic zone in *Arabidopsis* seedling. Cd-treated *Arabidopsis* plants exhibited a reduction in meristematic cell division and to some extent, stem cell niche activity as shown by *CYCB1;1::GUS* and *pSCR::YFP* transgenic *Arabidopsis* respectively. In addition, root cell length of elongation and differentiation zone was decreased, which was supported by reduced expressions of *EXP8* and *10* and enhanced ROS level. Moreover, auxin distribution was altered in response to Cd in *DR5rev::GFP* transgenic *Arabidopsis* plant, leading to an enhanced auxin level in elongation and meristem zones. Cd modulated expressions of genes involved in auxin biosynthesis, transport and signalling. Cd-induced auxin transport was associated with increased PIN1, PIN2 and AUX1 protein levels as well as enhanced *PIN3/4/7* and *ABCB4/14* transcript levels. Taken together, Cd inhibits the primary root growth by reducing cell division and elongation through modulating auxin synthesis, transport and signalling in *Arabidopsis*.

# P16

# Plant growth-promoting *Pseudomonas putida* KB-25 isolated from alfalfa rhizosphere increases seed germination and vigor index in alfalfa and cucumber

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Utilization of plant growth-promoting (PGP) rhizobacteria is a promising and environmentally-friendly alternative to existing conventional methods to improve crop production under diverse abiotic and biotic stress conditions. In this study, 25 bacterial strains were isolated from alfalfa rhizosphere grown in salt-stressed land in Jeddah, Saudi Arabia, and screened for PGP traits such as the in vitro ability to produce indole-3-acetic acid (IAA), 1-aminocyclopropane-1-carboxylic acid (ACC) deaminase, inorganic phosphate (Pi) solubilization activity, exopolysaccharides (EPS), ammonia ($NH_3$) and hydrogen cyanide (HCN). The most promising strain, KB-25, produced 19 $\mu g\ ml^{-1}$ IAA, 0.1 $\mu mol$ α-ketobutyrate $mg^{-1}\ h^{-1}$ ACC deaminase, Pi solubilization activity, and $NH_3$. KB-25 was able to grow in nutrient broth supplemented with 5% NaCl. The isolate was gram-negative, rod-shaped, motile, catalase and oxidase positive, and tentatively identified as a *Pseudomonas putida* strain based on phenotypic and biochemical characteristics and 16S rRNA gene phylogeny. Priming of alfalfa and cucumber seeds with KB-25 significantly increased seed germination rate and seedling vigor for both plants. A pot experiment is currently underway to evaluate the efficacy of this strain to alleviate salinity stress in alfalfa and cucumber. The present study indicated that *Pseudomonas putida* KB-25 has potential as an effective bioinoculant for sustainable agricultural practice.

Key words: Plant growth-promoting rhizobacteria (PGPR), ACC deaminase, IAA, *Pseudomonas*, alfalfa, cucumber.

# P17 Phenotyping plant abiotic-biotic interactions using non-invasive technologies

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Individual plants vary in their ability to respond to environmental changes. The plastic response of a plant enhances its ability to avoid environmental constraints, and hence supports growth and reproduction, and evolutionary and agricultural success.

Plant phenotyping can provide quantitative and novel above and below ground plant traits in response to dynamic changes in the environment. Identifying plant traits which are responsive dynamically, and beneficial in abiotic and biotic interactions, needs non-invasive measurements because phenotypic responses are continuous and mostly non-linear in space and time. Dynamic, plastic phenotypic traits cannot be captured with destructive measurements and therefore today's phenotyping technologies offer a large advantage over previous phenotyping methods. At IBG-2 we develop and provide non-invasive 2D and 3D imaging technologies for a holistic characterization of plant dynamic performance in controlled conditions and in the field. This includes specialised cultivation systems, precise environmental monitoring, and information technology for data management for large numbers of plants.

The presentation will include examples of phenotyping of plant plasticity, to provide evidence that non-invasive phenotyping technologies enable the investigation of plant responses to abiotic-biotic interactions to accelerate crop improvement in a modern crop management.

# P18 *Flora robotica*: biomechanical stimulation in plants bio-hybrids

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*Flora robotica* is a European Union project with objective to create and investigate the plants-robots societies. Bio-hybrids consist of electronic and organic components that interact with each other and form a self-organizing system. The natural plants provide growth structures showing embodied memory and sensation capability, robots provide extended sensing and decision making capabilities. Robots can be programmed in the way that enable to achieve desired architectural artifacts and living spaces by close cooperation with plants. In *flora robotica*, vibration motors, air flow, phytohormones, braids structures and RGB LED lights are being used for shaping plants. Physiology sensors provide information about plants fitness and reactions to robotic stimulation.

Example robots are nodes that determine action of Plants Binary Decision Wall (PBDW). The nodes create distributed system and influence a common bean growth with RGB and far-red LED. Evolving controllers for obtaining spatial targets by a bean’s tip are also presented. For growth regulation of bio hybrids structures a plant physiology inspired controller was developed, which is called Vascular Morphogenesis Controller (VMC). Braided structures were chosen as structural elements and tasks like creating braiding robots and braided robots are in progress.

# P19

# Root trait plasticity to maintain plant productivity under nutrient limitation in soil

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To combat soil nutrient limitation which is further strengthened by intense competition between plant and microorganisms, plants have developed complex adaptive responses in various root traits. Root hairs and root colonization by arbuscular mycorrhizal fungi (AMF) are two key traits for plant phosphorus (P) acquisition in P limited soil. Main objective of present study was to understand plants' P acquisition strategies with shifting root traits using two genotypes of maize characterized by presence (wild type) or absence (*roothairless3* mutant) of root hairs. We hypothesized that 1) in P limited soils, plants compensate for the lack of root hairs by shifting to root mycorrhizal colonization (functionally analogous to hairs) for P acquisition; 2) root mycorrhizal colonization decreases with P fertilization due to strong trade-off for C costs. The present study demonstrated that root hairs and AMF are crucial for plant P acquisition. Root hairs promoted P uptake most likely by increasing root surface area for absorption. Root hairs decreased the dependency of plants on root mycorrhizal colonization, thereby reducing C costs for P acquisition. However, smaller surface area for absorption in absence of root hairs can be counterbalanced by increased root mycorrhizal colonization. This alternative root trait for P uptake by exploring the soil volumes beyond root depletion zone is important for maintaining plant growth in absence of root hairs and under nutrient limitation.

# P20

# Interactions of allelochemicals with plant plasma membrane: a case study with alkaloids from barley

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Allelopathy is defined as ‘any direct or indirect harmful effect by one plant on another through production of chemical compounds that escape into the environment’ (Rice, 1974). This phenomenon is seen as a potential tool for weeds management within the framework of sustainable agriculture. While many studies investigated the mode of action of various allelochemicals (molecules emitted by allelopathic plants), little attention was given to their initial contact with the plant plasma membrane (PPM). In our work, this key step is explored for two alkaloids, gramine and hordenine, that are allelochemicals produced by barley. First, bioassays were carried out and gramine was shown to be more phytotoxic towards *Matricaria recutita* L. (a common weed in northern countries) than hordenine. Biophysical techniques were then used to detect and characterize interactions between these compounds and lipid bilayers that mimick PPM. Both alkaloids were able to induce subtle perturbations of lipid bilayers properties and a good correlation between phytotoxicity and ability to disturb lipid bilayers was found. It is thus suggested that interactions of these allelochemicals with PPM could be linked to their mode of action.

# P21

# Shifts in ectomycorrhizal and saprophytic fungal communities mediate litter and humus decay in response to chronic nitrogen enrichment

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There is evidence that anthropogenic nitrogen (N) deposition enhances carbon (C) sequestration in boreal forest soils. However, it is unclear how changes in ectomycorrhizal (EM) fungi in response to N enrichment impact soil C dynamics. Our aim was to investigate how microbial communities are impacted by N enrichment and to estimate whether these shifts influence litter decomposition and humus degradation. We conducted a long-term experiment (since 2004) in northern Sweden, consisting of ambient, low N addition (3, 6 and 12 kg N $ha^{-1}$ $yr^{-1}$) and high (50 kg N $ha^{-1}$ $yr^{-1}$) using root-trenching method and ingrowth bags. Our data showed that low N addition treatments had no effect on microbial structure, while high N addition rates decreased the abundance of fungal and bacterial biomasses, while it increased actinomycete biomass. Further, the declined of humus decay with N enrichment was primary mediated by EM fungi, while the decline of litter decomposition in response to N addition appeared to be mediated by saprotrophic organisms. These results suggest that current N deposition rates in the boreal region (≤ 12 kg N $ha^{-1}$ $yr^{-1}$) are likely to have minor impact on the soil microbial community and C dynamics.

# P22

# Year-round monitoring of non-structural carbohydrates in the stem sapwood and ectomycorrhized fine roots of two lowland hardwood species

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Non-structural carbohydrate (NSC) reserves play key roles in tree growth and provide substrates for metabolism and nutrition of associated ectomycorrhizal (ECM) fungi. Indeed, in exchange to carbon (C), ECM fungi mobilize nutrients from organic sources using enzymes. However, the relationships between temporal dynamics of NSC in tree tissues and functioning of associated ECM fungi remain poorly studied, in particular under different forestry practices. We proposed to monitor i) the seasonal variations of NSC in stem sapwood and fine roots of two trees species (*F. sylvatica* and *Q. petraea)* and ii) the enzymatic activities of associated ECM fungi in response to organic matter removal. Ionic chromatography and spectrometry assays revealed similar seasonal variations of NSC content between oak and beech trees. Nevertheless, specific NSC compositions strongly differed between the two species, with high content of trehalose in stem sapwood and fine roots of oak trees. Interestingly, organic matter removal impacted the NSC content of oak tree fine roots only, but no difference was measured for the enzymes activities of associated ECM fungi. Finally, potential links between forest management, soil fertility, NSC content in tree tissues and mycorrhizal community functioning will be discussed.

# P23 Degradation of plant litter by lignocellulolytic fungi: ecological and applied implications

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Plant litter provides the main carbon input in forest ecosystems, where substrate quality strongly influences microbial composition and activity in soils. Connecting microbial activity in ecosystems with potential applications in biotechnology has been little explored, but increased understanding of microbial functionality could provide great potential for harnessing natural capacity to degrade and detoxify compounds due to human impact. We isolated a total of 19 basidiomycetes associated with leaf litter layer from temperate forests of Argentina, with the objective of evaluating extracellular lignocellulolytic enzyme systems. We also evaluated the capacity of these strains to degrade in vitro leaf litter of two dominant plant species: the native *Celtis tala* and the exotic *Ligustrum lucidum*. Significant differences between the two litter types were found one strain, *Leratiomyces ceres*, with greater mass loss with the exotic litter, which was associated mainly with manganese peroxidase production and preferential degradation of alkyl and lignified carbon compounds. We additionally evaluated the combination of litter-lignolytic enzymes for its potential to degrade xenobiotic compounds. The exotic litter proved to be a good matrix for the immobilization of nonylphenol polyethoxylates, one of the most extensively employed non-ionic surfactants with demonstrated toxicity and harmful effects on numerous organisms. A more profound understanding of plant-microbial interactions provides insight for ecosystem functioning and the possibility of functional applications in bioremediation.

# P24

# Jasmonic acid signalling pathway alters the structuring of the root microbiome in Grey Poplar

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Tree roots are colonized rhizospheric/endophytic bacteria and fungi, including ectomycorrhizal (EcM) fungi. Molecular mechanisms shaping this microbiota are poorly known. In this study, we aim to determine how defence-signalling pathways regulate the root microbiome in Grey Poplar (*Populus tremula x P. alba*).

We surveyed the root microbiota from wild-type (WT) and lines constitutively expressing the symbiotic effector MiSSP7 released by the EcM fungus *Laccaria bicolor*. This protein is required for symbiosis establishment and act as a repressor of the jasmonic acid (JA)-related defence signalling pathway. We show here that fungal colonisation was >30-fold higher in MiSSP7-expressing roots than WT, suggesting that alteration of JA signalling by MiSSP7 facilitated fungal colonization. Metabarcoding sequencing revealed that the fungal community of MiSSP7-expressing roots is enriched in EcM fungi compared to WT, whereas the fungal community of WT is dominated by endophytic and pathogenic taxa. MiSSP7-expressing roots also accumulated higher levels of EcM-associated metabolites compared to WT. The heterologous expression of MiSSP7 in roots also impacted bacterial communities although in a lower extent than fungal communities.

In conclusion, MiSSP7 play a key role in the establishment of *L. bicolor*-poplar symbiosis, but also regulates the structuring of root-associated microbial communities.

# P25

# Meeting points between arbuscular- and ectomycorrhiza in climatic borderline forest ecosystems of Balkan Peninsula

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The dogma of the so called delimitation between ecto- and arbuscular mycorrhiza (ECM, AM) dominating ecosystems was challenged lately, when the next generation sequencing (NGS) based methods have been applied on symbiotic fungal communities in different ecosystems. Unexpectedly, typical ECM dominating forests in temperate and boreal regions appeared to host rich AM fungal (AMF) communities as well. In South European regions such topics have rarely been addressed. Through two independent experiments in selected regions of Balkan Peninsula (Slovenia and Serbia) we aimed to explore the gradients of natural grass field-transition zone-forest AMF communities, in order to determine diversity rates and composition differences caused by vegetation, climatic and soil parameters. For approaching AMF communities we have applied comparative 18S DNA NGS based analyses of sampled roots and spore morphology based analyses from soil samples taken from the rhizosphere. Investigated ecosystems were located in calcareous regions, where the soils were in weakly acidic-neutral-weakly alkaline gradient, depending on the level of influence of Mediterranean climate and altitude. Vegetation differences were significant, but the AMF diversity was surprisingly high in *Pinus* and *Tilia* forests dominated by typically ECM trees. We discuss obtained results comparing the investigated variables in different climate zones of the Balkan Peninsula.

## P26

# A receptor-like iron-binding protein IOS1/PDLP5 involved in modulation of iron deficiency in *Arabidopsis*

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Iron is an essential micronutrient and required for various cellular processes, such as photosynthesis and respiration in plants. Unfortunately, the mechanisms regulating iron sensing and up taking remain unexplored. Here, a gain-of-function mutant from *Arabidopsis thaliana* was isolated, which showed an *iron-deficiency overly sensitive* (designated, *ios1*-D) phenotype in root growth. The *ios1*-D mutant exhibited a reduced acidification of the rhizosphere and an enhanced sensitivity towards iron deficiency as compared to the wild type. The Arabidopsis genome contains another gene, *PDLP8*, which provides redundancy to *IOS1*. The double mutant (*ios1 pdlp8*) showed an iron tolerant phenotype. In addition, *IOS1* modulates the iron deficiency responses by transcriptional regulation of iron responsive genes such as $H^+$-ATPase (*AHA7*)*, FER-like iron-deficiency-induced transcription factor 1* (*FIT1*)*, ferric reductase oxidase 2* (*FRO2*), the *iron-regulated transporter 1* (*IRT1*) and *metal tolerance protein 8* (*MTP8*). IOS1 appears to act as one of components of the iron sensor, and under iron deficiency binds directly to $Fe^{3+}$; this binding affects the movement of iron-responsive transcription factors (e.g. POPEYE) between cells by regulation of callose deposition at plasmodesmata. In conclusion, our study reveals a new mechanism for the $Fe^{3+}$ transport through plasmodesmata (PD) between the cells that is mediated by IOS1/PDLP5 in *Arabidopsis*.

# P27 Enhancement of seed germination of wild plant species through priming

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Desertification is a serious problem affecting the survival of many plants endemic to arid regions. Revegetation is difficult because it is widely influenced by extreme climatic factors, disturbance, limited revegetation technology and importantly a lack of understanding of the biology and ecology of native plant species. Seeds are central to the revegetation of degraded lands, but poor seedling establishment limits our capacity to restore diverse plant communities. Priming is an effective method to enhance seed germination. The purpose of this study is to enhance seed germination of species adapted to arid regions using priming technology and hence assist in arid land restoration. A seed priming experiment was conducted on native plant species (Poaceae) from the Pilbara region (northern Western Australia) in an attempt to improve germination percentage and the seeds resistance to water stress. Some combinations of priming treatments significantly increased germination percentage for two Poaceae species (*Cymbopogon obtectus*, *Eriachne mucronata*) under water stress. Priming has a positive effect on germination parameters such as germination percentage and speed for seeds under certain water stress; however, this positive effect decreases when water stress is high (-1.0 MPa). This study assists in better understanding how to improve germination of native species from the arid Pilbara which will improve the success of revegetation programs.

## P28

## Prevalence of *Bacillus* in the interior tissues of *Monsonia burkeana* and other medicinal plants in South Africa

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This study was undertaken to isolate and identify endophytic bacteria in *Monsonia burkeana* and eight other medicinal plant species, namely, *Aloe aculeata*, *A. arborescens*, *A. chabaudii*, *Aloe spp., Athrixia phylicoides*, *Cotyledon orbiculata*, *Portulacaria afra* and *Sanseviera hyacinthoides.* Interior tissues of the nine medicinal plant species were sampled and endophytic bacteria were isolated under sterile conditions. The bacteria were grown on Luria Bertani agar and bacterial species identification was done by using MALDI-TOF. A wide range of bacteria represented by the genera *Acinetobacter*, *Anaerococcus*, *Arthrobacter*, *Bacillus*, *Bulkhoderia*, *Cellulosimicrobium*, *Clostridium*, *Enterobacter*, *Escherichia*, *Kocuria, Lactobacillus*, *Microbacterium, Pseudomonas*, *Staphylococcus*, *Streptomyces* and *Viridibacillus* were identified in the different plant species. *Bacillus* was the most prevalent bacterial genus found in three plant genera and in all tissues of *M. burkeana*. This study forms the basis for further research in cataloguing endophytes in medicinal plants.

# P29 Unlocking plant intercellular channels: lessons from cell wall molecular biophysics

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Plasmodesmata (PD) are intercellular membrane channels containing a central structure formed by the endoplasmic reticulum[1]. PD allow diffusion of small signalling molecules, large proteins and RNAs, which makes them essential for plant development. These channels are embedded within distinct cell wall regions enriched in the (1,3)-β-glucan polymer callose [2]. The physical and mechanical properties as well as the composition of surrounding cell walls are important for the regulation of PD function and permeability. However very little is known about this[3]. A combination of techniques including: Atomic Force Microscopy; Scanning Electron Microscopy, Nuclear Magnetic Resonance and Fourier Transformed Infrared Resonance spectroscopy were used to analyse structural-physical properties that characterize PD cell wall microdomains. In particular, β-1,3-glycan and cellulose blends were analysed to model PD physico-mechanical properties. Our data derived from hydrogel measurements show that callose ((1,3)-β-glucan) can act as a plasticizer increasing the toughness of cellulose mixtures[4]. Currently, we are analyzing mechanical properties of PD cell wall microdomains using whole tissue and cryo-section to allow direct measurement of mechanical properties. This will contribute to our understanding of the role of cell walls in the regulation of PD function, which might open new possibilities to manipulate the transport of mobile developmental regulators.

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# P30

# Interspecies variation in reproductive strategy of co-existing alpine gingers (*Roscoea purpurea* and *R. tumjensis*): implication for reproductive isolation and species integrity

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Two Himalayan alpine gingers, *Roscoea purpurea* and *R. tumjensis*, occur sympatrically in central Nepal and have such similar morphology that it is not clear whether or how they maintain a distinct identity. Our quantitative measurements of the components of reproductive isolation show that they are, in fact, completely isolated by a combination of phenological displacement of flowering and complete fidelity of visitation by different pollinator species, a long-tongued fly for *R. purpurea* and bumblebees for *R. tumjensis*. The disjunction of pollinators seems surprising until the floral traits are analysed from the pollinators' perspective. Models of both dipteran and hymenopteran colour vision indicate that flowers of the two species would be easily discriminable. Furthermore, the nectar of R. purpurea is less accessible, requiring deep probing from long-tongued flies, while the nectar of *R. tumjensis* flowers is available to the shorter-tongued bumblebees. Although current barriers need not reflect evolutionary history, two possible pathways to isolation seem likely depending on whether displacement of flowering time or novel floral signals arose first. These two sympatric Roscoea species add to accumulating evidence of the primacy of early acting, pollination traits in speciation among angiosperms even in the absence of post-zygotic incompatibility.

Key words: bumblebee, floral colour, long-tongued fly, pollination, speciation, sympatry

# P31

# Searching solution for *Picea abies* L. adaptation to drought stress using molecular approaches

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In recent years, drought has become a critical abiotic factor affected many regions at a global scale. Woody plant species as sessile organisms have to cope with a plethora of specific adaptations to dry environment. Therefore, several protective mechanisms are evoke in plants at the cellular and organ levels before serious damages occurred. Crucial role in plant adaptive processes play drought responsive genes and their mutual interactions. Even though coniferous species are characterized by large genomes with a lot of gene duplications, up to date many coding sequences related to drought stress are annotated and thus available for further study.

In the Czech Republic, Norway spruce (*Picea abies* L.) belongs to species seriously threaten by drought periods. Therefore, there is a high need to find a potential stress marker identifying the adaptation to changing environmental conditions in time. Our present work is focused on the search for candidate genes involved in responses to drought stress and characterization their relative gene expression patterns in samples of Norway spruce growing at localities with optimal and drought stress conditions. In addition, sequencing method will be used for determination of possible variation in coding region of the selected genes. We assume that molecular approaches could be efficient tool for understanding the mechanism of plant adaptation to drought in forest tree species.

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# P32

# Catch the rhythm: An interplay of the clock and sugars with gibberellin biosynthesis

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Plant growth shows rhythmic behavior during day/night cycles and is highly dependent on environmental conditions. Gibberellin (GA) plays a key role in growth control. However, a lot remains unclear regarding how GAs interplay with light, sugar availability and the circadian clock, which are major inputs for plant growth. Therefore, this study explores the interplay between GA and these factors to create a mechanistic understanding of growth control via GAs. First, we identified GA biosynthetic and signaling machinery that showed rhythmic transcriptional behaviour throughout the day in adult Arabidopsis rosettes. Of these, KAURENE SYNTHASE (KS/GA2) was the only GA biosynthesis gene that retained rhythmicity under continuous light conditions. However, GA20OX1 (GA5) and GA3OX1 (GA4), the final enzymatic steps of GA biosynthesis, were affected by inhibiting photosynthesis and changes in the light regime. It seems that daytime sugar production and gating mechanism control the production of GA precursors, which are metabolized to bioactive GA during the night. Our results thus point to three prime candidates that are responsible for integrating sugar availability with GA biosynthesis, and simultaneously contribute to plant rhythmicity. Future work will validate their role in rhythmic hormone dynamics and their effect on growth rates during the day and night period.

# P33 Functional traits of tropical nickel hyperaccumulator plants: comparing the leaf economics spectrum with co-occurring species

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Metal hyperaccumulation is a plant functional trait. Some theories have been proposed to explain evolutionary advantages of this trait (since protection from herbivory to adaptation to drought). However, possible trade-offs between hyperaccumulation and other leaf traits related to resource capture or nutrient conservation are not clear. In order to explore these relations, we have performed a field study on 15 species (with leaf Ni concentrations ranging between 4.5 and 24000 µg $g^{-1}$) growing in sympatry on an ultramafic area in Kinabalu Park (N of Borneo, Sabah, Malaysia). Different morphological (LDMC, SLA) and chemical traits (leaf concentrations of Ca, Co, Cr, Cu, Fe, K, Mg, N, Na, Ni, P, S, Si, Zn and C isotopic signature) involved in leaf economy spectrum have been measured in several plants per species. Differences in measured variables between Ni hyperaccumulators (leaf [Ni] > 1 mg $g^{-1}$, 5 species) and non hyperaccumulators (10 species) has been assessed by nested one-way ANOVA. Linear correlations between foliar Ni concentration and other variables have been computed.

Irrespective of species type (H or NH), a nutrient-conservative strategy (i.e. low SLA) seems to be the most performant in tropical ultramafic habitats. Apart from Ni, differences between species type occurred only for leaf concentrations of K (17 mg $g^{-1}$ in H vs. 9 mg $g^{-1}$ in NH) and the trace elements Co and Zn (25 and 128 µg $g^{-1}$ in H vs. 1 and 16 µg $g^{-1}$ in NH). Ni foliar concentration was positively correlated with leaf P, S, Co, Mn and Zn. Our results indicate that the main benefits of hyperaccumulation would not be related to drought resistance but to more efficient mechanisms for nutrient uptake.

# P34 Roles of Malectin-like kinases FERONIA and HERK1 in plant immunity

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Plants detect pathogens through receptors present either at the cell surface or within the plant cell. Surface receptors are typically membrane-embedded receptor proteins or receptor kinases (RK), whereas intracellular recognition is mediated by NB-LRR receptors. Diverse pathogens secrete effector proteins to modulate host physiology to their benefit. We are interested in the role of the RK FERONIA (FER) and HERCULES1 (HERK1) in host-pathogen interactions. FER is the receptor of plant and fungal RALF peptides and is involved in plant development, pathogen responses, hormone and sugar signalling. In particular, plants lacking FER are hypersensitive to ABA treatments. We found that one effector from the bacterium *Pseudomonas syringae*, AvrPtoB, interacts with FER and HERK1 kinase domains and is able to suppress RALF responses. We found that FER and HERK1 are necessary for early responses triggered by bacterial PAMPs and fungal RALF. We are now testing whether FER and/or HERK1 are able to influence sugar signalling within the plant. Lastly, because HERK1 kinase domain is strongly homologous to Pto kinase, a receptor that recognises AvrPtoB together with the NB-LRR protein Prf, we are testing if these pathways interact.

# P35 Metabolomic profiling of non-model plants as a tool to investigate plant-environment interactions

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Phytochemicals play critical roles in diverse physiological and pathological processes by participating in biological reactions that are necessary for proper biological functions and plant environment interactions. Under increasingly stressful conditions, plants experience progressively more impaired cellular and whole-plant processes until the limiting conditions for survival are reached. In brief, plants respond to environmental conditions with changes in the pattern of expression of genes that encode proteins that furthermore control the biosynthesis of metabolites involved in interactions between a given plant and its environment. Phytochemicals present in the plants which are more resistant to the unpleasant environmental condition may help us in the explanation of the processes how plants can cope with situation such as climate changes. Therefore, metabolomics as an important sector of post-genome science can show us how plants respond to environment. In the present work we will show metabolomic data (GC-MS, LC-QToF and MALDI Imaging) for two non-model plants which are attributed with good adaptation to environmental condition. First is early whisk fern *Psilotum nudum* (L.) P. Beauv or so called "living fossils" whose metabolic processes could help in understanding plant adaptations through evolution. Second plant is kale (*Brassica oleracea* L. var. *acephala*), which is highly resistant to low temperature and whose metabolite profile could help us in the understanding the molecular mechanisms contributing to the plant's low temperature tolerance.

## P36

# Stomatal conductance variability of four garlic (*Allium sativum* L.) cultivars in response to soil volumetric water content and vapor pressure deficit

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Stomatal control of water loss is critical for the acclimation and adaptation of crops to fluctuating environmental conditions, especially with regards to aridity gradients. Therefore, stomatal conductance (gs) is particularly sensitive to vapor pressure deficit (VPD) and soil water content. Evaluation of potential intraspecific variability in the stomatal response pattern to these factors can provide insight on the vulnerability and adaptive potential of crops to future environmental scenarios. Garlic is an important crop worldwide, especially in Mediterranean climates, where water availability is an increasingly limiting factor. In this study, the response of gs to soil volumetric water content (VWCs) and VPD was studied in four garlic cultivars, Gardacho (GAR); Morado de Pedroñeras (PED); Violet Spring (VSP) and White Spring (WSP) . Multiple lineal regression models were analyzed separately for each variety where gs was expressed as a function of VWCs and VPD (). The studied cultivars significantly differed in gs and its response to both VWCs and VPD. The results confirm that garlic's gs is sensitive to soil water content and VPD and interestingly that the stomatal response pattern to this factors varies across cultivars. Further analysis will be carried out to test whether the observed inter-cultivar variability in the stomatal response patterns can be related with inter-cultivar variation in drought resistance.

# P37

# A thermotolerant variant of Rubisco activase from a wild relative improves growth and seed yield in rice under heat stress

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There is an increase in frequency and severity of heat waves due to climate change and how crops can tolerate this increase in heat load is of major interest to the scientific and general community. It is well known that the photosynthesis protein Rubisco activase (Rca) is heat-labile and a main contributor to limited rates of photosynthesis at supra-optimal temperatures. We have recently established that a wild relative of rice, *Oryza australiensis*, has a variant of Rca which is more tolerant to higher temperatures when compared to domesticated rice (http://dx.doi.org/10.1111/nph.13963). We have transformed this Rca variant from the wild relative into domestic rice (*Oryza sativa*) and observed enhanced growth and development when rice is exposed to heat stress throughout the vegetative life-cycle. This improvement culminated in a 2.5-fold relative increase in seed number for the transgenic line with highest recombinant Rca protein abundance. To our knowledge this is the first time an improvement in crop productivity during heat stress due to the thermostability of Rca has been established. We believe these findings can contribute to food security in a warmer future.

# P38

# Role of the long noncoding RNAs in plant reproductive development

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Long non-coding RNA (lncRNAs) are transcripts over 200 base pairs in length with no discernible protein coding potential. Multiple lines of evidence point to lncRNAs as master regulators, controlling the expression of protein-coding genes. Studies in plants and animals consistently show high expression of lncRNAs in reproductive organs.

In plants lncRNAs appear to play essential roles in key processes associated with sexual reproduction including floral transition, meiotic progression, anther and pollen development. Here we report development and use of an algorithm for genome wide discovery of sexual reproduction associated genes in rice. The classification has been performed on the rice genome re-annotated using deep sequencing transcriptomic data from reproduction-associated tissues/cell types and 2,115 protein coding and 658 lincRNA genes were predicted to be involved in sexual reproduction. The male reproductive tissues of rice and rice gametes show higher lncRNA expression than in any other tissue, suggesting that lncRNAs have particular sperm-specific functions.

## P39

# Translating mechanisms of biological nitrogen response from *Brachypodium* to cereal crops

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The challenge of increasing nitrogen use efficiency (NUE) in crops is a global issue which is particularly marked in India: fertiliser is government-subsidised and often over-applied leading to significant pollution. Thus, the need to feed a growing population of 1.2 billion people requires a combined strategy of both reducing N-input and increasing yield output. The Cambridge-India Network for Translational Research in Nitrogen (CINTRIN) aims to deliver a translational pipeline for production of new crop ideotypes to optimise NUE in agriculture, bringing both environmental and socioeconomic benefits.

Previously, studies in *Arabidopsis thaliana* have shown that nutritional nitrate availability affects the developmental process of axillary shoot branching1 and also existence of contrasting nitrate sensitive and insensitive accessions in *Arabidopsis*. Following a screen to determine N response in *Brachypodium*, a RIL mapping experiment is being performed in a cross between two *Brachypodium* parental accessions displaying contrasting nitrate sensitivities to identify the genomic loci associated with N-related branching responses. Additionally, CRISPR/Cas9 gene editing is being currently tested in *Brachypodium* on several targets known to be involved in *Arabidopsis* shoot branching. Replication of branching phenotypes in *Brachypodium* could represent a promising first step to using CRISPR/Cas9 to engineer crops for increased NUE in the future.

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# P40

# Understanding the mechanism of decoding of calcium signatures regulating transcript and protein expression in *Arabidopsis thaliana*

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It is known that different stimuli, and indeed different magnitudes of the same stimulus, lead to different kinetics of cytosolic calcium response, termed ‘calcium signatures’. We have previously shown that in *Arabidopsis* different calcium signatures can indeed induce very different transcriptomic profiles, suggesting that plant cells can ‘decode’ the signatures. Additionally, we have identified 4 potential transcription factor families (CAMTAs, ABFs, CBF/DREB2 and TCP) which are calcium-regulated. We have started to identify the mechanisms by which one such family of transcription factors (CAMTAs) can decode specific-calcium signatures. Our data also indicates that different transcription factors are regulated differentially by different calcium signatures. We present work aimed at testing this hypothesis using specific reporters in planta which report the activity of one of the 4 calcium-regulated transcription factors. Finally, we are adopting a proteomic approach to understanding how specificity through calcium signatures might regulate the *Arabidopsis* proteome. By comparison with our existing work on the calcium-regulated transcriptome, we hope to identify novel posttranslational regulation of proteins by specific calcium signatures.

# P41 Using synchrotron light to illuminate the origins of wood

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The evolution of wood was fundamental to the early diversification of vascular plants, giving rise to progymnosperm trees by the end of the Devonian (ca 370 Ma), however wood first evolved in plants of small-stature during the early Devonian (407–397 Ma). Here we develop an approach based on synchrotron analyses to investigate the wall structure and chemical composition of the tracheids in the earliest fossil wood. Axes of *Armoricaphyton chateaupannense* (Armorican Massif, France) were preserved as compressions and 3D permineralizations. They were imaged using propagation phase contrast X-ray synchrotron microtomography. Synchrotron-based scanning transmission X-ray microscopy, coupled with X-ray absorption near edge structure spectroscopy, was also used on focused ion beam ultrathin sections to document the chemical nature of the tracheids.
Tomography enables digital visualization of cell walls in unprecedented detail for the specimen preserved in 3D revealing structures similar to those observed in extant lignified cells. Spectrometry shows that organic carbon from both samples has a similar spectrum, but quite different from modern lignin. This indicates that the preserved organic matter has been altered and is not original. The synchrotron-based microscopy, coupled with spectroscopy, shows that both compressed and 3D-preserved fossils can be used in terms of chemical analyses.

# P42

# The origin of corolla neck in *Torenia fournieri*

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Nectar flowers have to face the dilemma of making pollinators easily access to their nectars meanwhile keeping the raindrops away from them. One of the strategies that many Lamiales species have evolved is to specify the flower structures including generating a neck above the nectar container. This trait has been documented for long; however, the molecular control of the corolla neck remains unsettled. Here, we studied *Torenia fournieri*, whose corolla tube differentiates into a neck in the base. By performing expressional analysis and functional studies, we discovered the first gene, *TfNECK*, involving in the formation of corolla neck. *TfNECK* was specifically expressed in the flower buds and RNA *in-situ* hybridization indicated that its mRNA was abundant in the epidermal cells of the neck regions. In the wild-type of *Torenia fournieri*, the neck epidermal cells from late stages expanded larger than non-neck regions, while in the loss-of-function *TfNECK*-Cas9 lines, epidermal cells on the neck regions showed no difference compared with the non-neck regions, whose flower normally developed but without a corolla neck. We finally observed that water could easily enter the nectar container without the corolla neck. Altogether, our study reported the first factor controlling the differentiation of corolla neck.

# P43 A prophage tail-like protein is deployed by *Burkholderia* bacteria to feed on fungi

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Bacteria are considered as one of the simplest living organisms with capacity to rapidly multiply and evolve. Several bacteria demonstrate anti-fungal properties by producing anti-fungal metabolites, chitinolytic enzymes, siderophores, toxins. However, some of them are capable of growing and multiplying at the cost of living fungal biomass by utilizing fungal biomass as source of nutrient/energy. Such fungal eating phenomenon is known as bacterial mycophagy. Furthermore, being equipped to kill and feed upon fungi, the mycophagous bacteria could serve as an experimental tool box to facilitate discovery of novel anti-fungal molecules. We have recently isolated a bacterium (*Burkholderia gladioli* strain NGJ1) from the rice seedlings. It demonstrates broad spectrum anti-fungal activities on various phytopathogenic fungi, including *Rhizoctonia solani* (causal agent of sheath blight disease in rice). Moreover we demonstrated that the bacteria NGJ1 deploys a prophage tail like protein (Bg_9562) to feed over fungi in a T3SS dependant manner. Furthermore we observed that Bg_9562 has a broad spectrum antifungal activity on *Rhizoctonia solani* as well as various phytopathogenic fungi. This opens up a new biotechnological application of this prophage tail like protein in controlling fungal diseases in rice as well as in other plants.

## P44

# FORGETTER2 protein phosphatase interacts with a phospholipase to modulate lipid dynamics underlying heat stress memory in *Arabidopsis*

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In *Arabidopsis,* it is known that exposure to mild heat stress (HS) enables seedlings to survive more severe HS, a physiological process known as acquired thermotolerance or 'HS priming'. Understanding of how plants get primed is well described, but less is known about the maintenance of this state over time. We have characterized the function of *FORGETTER2* (*FGT2*), a protein phosphatase that belongs to the type 2C protein-phosphatase family (PP2C). Mutants in the *FGT2* gene can be primed after an acclimatizing HS, but fail in sustaining this state over time when compared to WT, thus indicating that *FGT2* plays a positive and specific role in the maintenance of the acquired thermotolerance (HS memory) in *A. thaliana*. FGT2 interacts at the plasma membrane with a phospholipase, an enzyme involved in phospholipid metabolism. Mutants in this enzyme are able to acquire thermotolerance as WT, but display an impaired HS memory, hence supporting the interaction with FGT2. Profiling of membrane lipids upon HS revealed that both mutants displayed an altered metabolism of glycerolipids of the PC, DGDG and MGDG classes in comparison to WT. This work suggests that signaling associated to PA upregulation and membrane fluidity are two processes relevant for HS memory.

# P45 A framework for genomics-informed biophysical modeling of *Brassica rapa*

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One challenge in utilizing biophysical models to study plant time-series responses to environmental drivers lies in the selection of appropriate values for input parameters needed to constrain simulations. While ideally these parameters are directly observable, practical barriers limit empirical assessment for many difficult-to-measure traits. Literature values from previous experiments can often provide acceptable proxies at species- or genus-level. However, this approach may be unsuitable when models are used to dissect intra-specific response variation, where parameters reflect differences at genotype-level. Here, we propose a framework for leveraging genomic information to inform parameters of a biophysical model in *Brassica rapa*. We develop a vegetative growth model with the objective to test whether its parameters are predictable using genome-wide Single Nucleotide Polymorphism (SNP) information. This growth module interacts dynamically with hydraulic and metabolic processes through exchange of resources as part the biophysical process model, Terrestrial Regional Ecosystem Exchange Simulator (TREES). Preliminary results indicate that genomic prediction has the potential to yield genotype-specific input parameters. This framework will be useful to enable research on the interaction of natural genetic variation with environment-modulated plant response, especially as evaluations expand from small panels of non-related conspecifics to large bi-parental Recombinant Inbred Line (RIL) populations.

# P46

# Transcriptome-metabolome co-analysis reveals temperature- and air humidity-related heat components and novel networks in drought-heat scenarios

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Elevated temperature and reduced water availability are frequently linked abiotic stresses that may provoke distinct as well as interacting molecular responses. This study aimed at a data-driven elucidation of relationships between drought and heat scenarios based on non-targeted metabolomic and transcriptomic datasets from Arabidopsis rosettes.

We first decomposed the response to a combined stress scenario relative to single stresses. Additive combinations of independent drought and heat effects could be distinguished from responses indicating interaction effects in combined stress.

Applying heat stress with and without supplemented air humidity allowed separating temperature- and air humidity-related components of a heat scenario. The ‘dry air’ component of heat specifically comprises JA- and ABA-related responses to water deprivation previously associated with ‘heat’ stress. Remarkably, the ‘dry air’ effect seems to be the primary trigger of the metabolomic response to heat, whereas the transcriptomic response is dominated by the temperature component. Canonical correlation analysis and network mining of transcriptomic and metabolomic changes across all stress experiments predicted novel, highly correlated metabolite/gene networks.

Hypotheses based on these results will assist mechanistic studies on the relationship between transcripts and metabolites, the annotation of previously uncharacterized features and the analysis of putative, new drought- and heat stress-related pathways.

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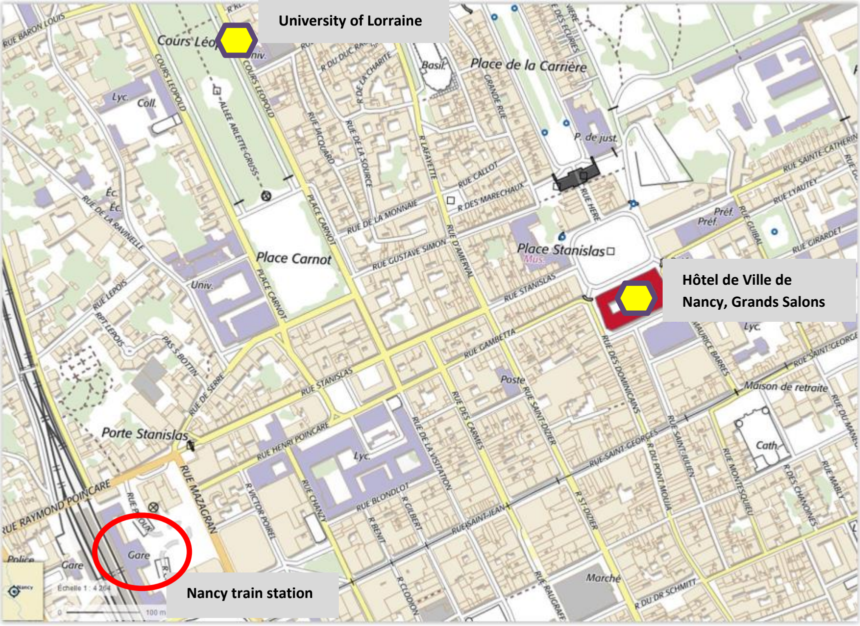
# Map of Nancy centre



**Symposium location**
University of Lorraine
Présidence/Headquarters
34 Cours Léopold, 54000 NANCY

**Symposium dinner on Wednesday 11 April (and Marc-André Selosse public lecture Friday 13 April):**
Hôtel de Ville de Nancy, Grands Salons
1 Place Stanislas, 54000 NANCY

**Taxis are available from Nancy train station**
2 Place de la République, 54000 NANCY
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