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SwissPLANT 2025

Symposium 'Plant Science Research'

33nd edition

Scientific Program Committee
Julia Santiago, Christiane Nawrath, Sebastian Soyk,
Mateusz Majda, John Pannell and Philippe Reymond
University of Lausanne

SwissPLANT 2025

15 – 17 January 2025
Les Diablerets, Switzerland

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Venue
The Glacier Hotel (ex - Eurotel Victoria)
Chemin du Vernex 3, 1865 Les Diablerets

Scientific Program Committee
Julia Santiago, Christiane Nawrath, Sebastian Soyk, Mateusz Majda, John Pannell and Philippe Reymond
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Conference Organization
Swiss Society of Plant Biology / Swiss Plant Science Web
swissplantscienceweb.ch

We gratefully acknowledge Syngenta’s financial support of the conference

Swiss Society of Plant Biology, Annual Report & SwissPLANT 2025

In 2024, the committee of the Swiss Society of Plant Biology (SSPB) held two meetings to discuss ongoing topics, and, in January, we had our General Assembly. We are running again as a regular society with contacts with the Swiss Academy of Sciences (SCNAT) and its Biology Platform. We were particularly pleased to get SCNAT's support for the Early Career Meeting (ECM) that we started in 2023. This allowed us to organise this exciting event just before the 2025 edition of our annual SwissPLANT symposium.

The Early Career Meeting was a great success in 2024. Our young colleagues had lively and exciting scientific discussions together but in addition they brought their enthusiasm to SwissPLANT 2024 where they contributed to a lively poster session and two selected talks.

Given that our society is part of the Federation of European Societies of Plant Biology (FESPB), which organizes a meeting every 2 years, I would like to announce that in 2025 "Plant Biology Europe" will take place in Budapest from June 25 to 28. More details can be found here https://pbe2025-budapest.org/. I also take this opportunity to thank SCNAT for covering our FESPB membership. For those more interested by Arabidopsis, ICAR 2025 will take place in Gent from June 16 to 20.

I would like to congratulate Domitille Coq-Etchegaray (UniZH) who obtained 15'000.- from the Rübel Fund of SCNAT for her exciting project on genetic diversity in Swiss beech trees and how this may affect their survival with increasing temperatures.

In December 2024, the Society had 101 members. We keep encouraging all Swiss Plant Science Web (SPSW) members to join. SPSW will continue to be our window on the internet for academic research in plant biology at Swiss universities.

We note that as a group we had troubles in obtaining funding in large initiatives such as NCCRs. We would like to discuss possible strategies during the General Assembly. We also count on you to propose new ideas and initiatives to develop our society at this occasion.

I would like to thank the members of our board, Kirsten Bomblies, Thomas Boller, Cyril Zipfel and Klaus Schläppi with whom I had the pleasure working for the past 3 years. A new board and presidency will be elected during our General Assembly and as indicated earlier this year I'll step down from the presidency.

I cordially thank Julia Santiago, Christiane Nawrath, Sebastian Soyk, Mateusz Majda, John Pannell and Philippe Reymond for organizing the SwissPLANT 2025 conference, as well as Maria V. Aparicio Chacon and Noel Blanco Tourinan for organizing the Early Career Meeting.

Christian **Fankhauser**, President of the Swiss Society of Plant Biology

The Swiss Society of Plant Biology and its portal – the Swiss Plant Science Web – serve as an information platform for academic plant biology in Switzerland. The network enhances the visibility of plant biology and the achievements of plant science research for society. By joining forces, the society advances research and education efforts in Switzerland.

PROGRAM

Wednesday, 15 January 2025

15:45 Swiss Society of Plant Biology, General Assembly 2024 (all welcome)

17:00 Welcome aperitif

17:50 Welcome by Christian Fankhauser, President of the Swiss Society of Plant Biology

17:55 Opening remarks by Philippe Reymond, chair of the Program Committee

Session I, chair: Philippe Reymond

18:00 **Didier Reinhardt** | University of Fribourg
How *Medicago truncatula* sanctions ineffective rhizobial endosymbionts (*Sinorhizobium meliloti*)

18:20 **Cyril Zipfel** | University of Zürich
Receptors and ligands at the cell wall-plasma membrane continuum and their roles in immunity

18:40 **Heike Lindner** | University of Bern
Crassulaceae MUTE drives asymmetric divisions to form stomatal subsidiary cells in succulents

19:00 **Christian Parisod** | University of Fribourg
Dynamics of centromeric transposable elements and their consequences for chromosomal evolution

19:30 Dinner, afterwards discussion at the bar

Thursday, 16 January 2025

07:00 *Breakfast*

Session II, chair: Julia Santiago

08:00 **Sara Simonini** | University of Zürich
A class of chromatin readers control cell fate establishment in the Arabidopsis embryo

08:20 **Sebastian Soyk** | University of Lausanne
Repairing deleterious mutations by precision genome editing in tomato

08:40 **Michael Hothorn** | University of Geneva
Kelch phosphatases as key cell cycle regulators in plants

09:00 **Fabrizio Menardo** | University of Zürich
Population genomics and molecular epidemiology of wheat powdery mildew in Europe

09:20 **Priya Ramakrishna** | EPFL
Unveiling salinity stress at the subcellular scale by elemental cryo-imaging

09:40 *Coffee break*

Session III, chair: Mateusz Majda

10:30 Early Career Meeting | **Talk 1**
Selected candidate from preceding Early Career Meeting

10:50 **Christiane Nawrath** | University of Lausanne
Lipids or phenylpropanoids? Diversity of protective barriers in the apoplast of Arabidopsis root tissues

11:10 **Matthias Erb** | University of Bern
Leaf volatile uptake, perception and response

11:30 **Thomas Wicker** | University of Zürich
A reference metagenome sequence of the False Reindeer Lichen *Cladonia rangiformis*

11:50 *Leisure time (lunch on your own, skiing and other activities)*

Session IV, chair: Sebastian Soyk

17:30 Early Career Meeting | **Talk 2**
Selected candidate from preceding Early Career Meeting

17:50 **Kentaro Shimizu** | University of Zürich
10+ genomes and pan-transcriptome projects of hexaploid bread wheat highlighted the pattern of selection and yellow rust resistance in Asian landraces

18:10 **Mateusz Majda**| University of Lausanne
How endoreduplication impacts multiscale growth coordination in plants

18:30 **Ueli Grossniklaus**| University of Zurich
The synergid cell forms a peritubular membrane to accommodate the pollen tube for double fertilization

19:00 *Dinner*

20:30 Poster Session (2 h, drinks will be served)

Friday, 17 January 2025

07:00 *Breakfast*

Session V, chair: John Pannell

08:20 **Katalin Csilléry** | WSL
Next generation citizen scientists run experiments: when research meets the needs of forestry facing climate change

08:40 **Klaus Schlaeppi** | University of Basel
Root immune components mediate microbiome feedbacks in Arabidopsis

09:00 **Samuel Zeeman** | ETHZ
Structural proteins define the sites of starch granule initiation and control granule growth

09:20 **Thomas Badet**| University of Neuchâtel
Loss of transposon control has contrasted effects on fungal genome evolution

09:40 *Coffee break*

Session VI, chair: Christiane Nawrath

10:30 **John Pannell** | University of Lausanne
A dialectic on the costs of plant reproduction

10:50 **Meredith Schuman** | University of Zürich
Remotely sensing plant genetic resources and their consequences for ecosystems

11:10 **Shanmugabalaji Venkatasalam** | University of Neuchâtel
ABA orchestrates chloroplast protein import pathways and chloroplast biogenesis during the seed-to-seedling transition

11:30 Closing remarks by Philippe Reymond

TALK

Loss of transposon control has contrasted effects on fungal genome evolution

Thomas Badet[1], Daniel Croll[1]

[1]Laboratory of Evolutionary Genetics, Institute of Biology, University of Neuchâtel, Neuchâtel, Switzerland
E-mail: thomas.badet@unine.ch

Genomic diversity driven by transposable elements (TEs) plays a pivotal role in the rapid adaptation of plant pathogens. In fungi, genome size varies over 100-fold, largely due to the proliferation of repetitive sequences such as TEs, which are the primary contributors to genome expansion. To counteract this, fungi have evolved repeat-induced point mutation (RIP), a genomic defense mechanism that targets TE copies by mutating repeated sequences. Understanding the interplay between TEs and genomic defenses is critical for unraveling fungal genome evolution. Despite its significance, the prevalence of RIP and its influence on genome architecture remain poorly understood. To address this, we developed a screening method to detect mutational signatures specific to repetitive sequences across the fungal kingdom. Our results revealed that enrichment of these mutational signatures at non-coding and repetitive sequences is restricted to Pezizomycota, indicating a phylogenetically limited distribution of RIP-like defenses. We further quantified mutational signatures to identify phylogenetic links to gene functions, uncovering a zinc-finger protein as the strongest candidate for a novel genome defense mechanism. Additionally, we demonstrated that the loss of RIP components drove an ~80% (~30 Mb) increase in genome size in a major group of plant pathogens. These findings highlight the intricate relationship between TE defense mechanisms and genome size evolution, illustrating how localized processes can shape genome architecture across deep evolutionary timescales.

TALK

Next generation citizen scientists run experiments: when research meets the needs of forestry facing climate change

Katalin Csilléry, Daniella Schweizer, Marjorie Bison, Nicole Ponta

Evolutionary Genetics Group, Biodiversity and Conservation Biology Unit Swiss Federal Research Institute WSL
E-mail: katalin.csillery@wsl.ch

Finding generality in nature has been a perpetual goal of biologists. Meta-analysis of numerous local studies has been a common way to search for nature's "laws", nevertheless, issues of data harmonization arise. Citizen science (CS) is an emerging as a tool to increase the scale of ecological experiments as global changes trigger citizen engagement in environmental issues. However, the true potential of CS has not yet been exploited. Through a compilation of CS projects, we found that most global CS projects use extremely simple protocols, thereby providing correlative evidence or, at best, detecting temporal changes. In contrast, a few emerging CS projects target a public with specialized knowledge, who can follow a complex protocol or even conduct experiments. These projects have a high potential to create new knowledge. In this talk I describe the design and recruitment strategy of the CS project, MyGardenOfTrees, aimed at revealing major environmental and genetic drivers of adaptation at a broadleaf and conifer forest tree species using a continent-wide transplant experiment. The project recruited over 300 foresters across Europe who have now completed their first year of observations. How was it possible to make a transplant experiment of this scale happen? What compromises we have to make due to the CS nature of the project? I summarize the lessons learned three years into the project.

TALK

Leaf volatile uptake, perception and response

Matthias Erb

University of Bern
E-mail: matthias.erb@unibe.ch

Plant leaves respond to stress volatiles from their environment. However, how they take up and perceive these volatiles is poorly understood. Over the last years, we have explored plant volatile interactions in maize by studying how maize and rice leaves respond to stress volatiles that are induced by herbivory. Maize leaves respond to green leaf volatiles and indole through direct induction and defense priming. The two types of volatiles act synergistically to strengthen jasmonate-dependent defenses and herbivore resistance. We find that the defense responses of leaves include a clocking component that combines both priming and induction for maximal responses the day after the onset of attack. Younger maize leaves are significantly more sensitive to volatiles and thus act as transient volatile perception organs. Our current work also sheds light on the relative importance of stomata and the cuticle in volatile uptake, and we are in the process of identifying novel genetic factors that are required for the responsiveness of maize to herbivory induced volatiles.

TALK

The synergid cell forms a peritubular membrane to accommodate the pollen tube for double fertilization

Nicholas Desnoyer, Marta Belloli, Stefano Bencivenga, Hannes Vogler, **Ueli Grossniklaus**

Department of Plant and Microbial Biology & Zurich-Basel Plant Science Center, University of Zurich, Zurich, Switzerland
E-mail: grossnik@botinst.uzh.ch

One of the research foci in our laboratory is the molecular dissection of cell-cell communication during double fertilization. Successful fertilization depends on the proper reception of the pollen tube by one of the synergid cells, which are situated at the micropylar pole of the embryo sac where the pollen tube enters. Receptor kinases of the *Cr*RLK1L subfamily play an important role in this process, with FERONIA and related receptor kinases acting in the synergids to mediate proper pollen tube reception. Using an improved live-imaging approach combined with genetically encoded biosensors, we could investigate the different stages of pollen tube reception in great detail and found that second messengers calcium (Ca^{2+}) and reactive oxygen species (ROS) show distinct developmental dynamics. Surprisingly, upon arrival at the micropyle, the pollen tube gradually deforms the filliform apparatus, an area rich in membrane invaginations, before rapidly growing into the receptive synergid. This phase is characterized by a strong ROS burst in the synergid cell. Upon penetration, the membrane of the receptive synergid is pushed inside and envelopes the pollen tube in a newly discovered structure that we termed the 'peritubular membrane'. The formation of the peritubular membrane is associated with a Ca^{2+} spike of high amplitude in the pollen tube. Mutants disrupting the Ca^{2+} pump encoded by the *AUTOINHIBITED Ca^{2+} ATPASE9 (ACA9)* gene frequently fail to penetrate the synergid and no peritubular membrane is found. Collectively, these findings suggest that synergid penetration and the non-cell autonomous control of pollen tube rupture are distinct steps of pollen tube reception required for double fertilization.

TALK

Kelch phosphatases as key cell cycle regulators in plants

Michael Hothorn

Structural Plant Biology Laboratory, Department of Plant Sciences, University of Geneva
E-mail: michael.hothorn@unige.ch

Plant-unique protein phosphatases with N-terminal Kelch domains have previously been characterized as tyrosine phosphatases in brassinosteroid signaling (BRI1 SUPPRESSOR 1, BSU1) and stomatal patterning. I will present structural, quantitative biochemical, and genetic evidence suggesting that BSU1 is a bona fide Ser/Thr phosphatase with no apparent function in brassinosteroid signaling. Instead, BSU1 and its BSL homologs share significant structural homology with animal cell cycle-specific PP1 phosphatases. Strikingly, the eukaryotic CDK1 - cyclin B1 - CKS1 (CCC) complex phosphorylates the BSU1/BSL C-terminus in vivo and in vitro, thereby inhibiting its phosphatase activity. CRISPR/Cas deletion of the only Kelch phosphatase in *Marchantia polymorpha* results in severe cell cycle defects and associated growth phenotypes. Transcriptomic and phosphoprotein analyses of the *Marchantia* mutant reveal that plant Kelch phosphatases act on a wide variety of substrates, many of which are involved in the control of the plant cell cycle.

TALK

Crassulaceae MUTE drives asymmetric divisions to form stomatal subsidiary cells in succulents

Heike Lindner[1,3,*,§], Xin Cheng[1,2,*], Lidia Hoffmann[1], Antonio Aristides Nunes Gomes Filho[1,3], Paola Ruiz Duarte[1], Yigit Berkay Gündogmus[2], Jessica Pritchard[4], Susanna F. Boxall[4], Miro Läderach[1], James Hartwell[4], Michael T. Raissig[1,3,§]

[1]Institute of Plant Sciences, University of Bern, Switzerland
[2]Centre for Organismal Studies Heidelberg, Heidelberg University, Germany
[3]Oeschger Centre for Climate Change Research, University of Bern, Switzerland
[4]Department of Functional and Comparative Genomics, Institute of Integrative Biology, University of Liverpool, United Kingdom

*these authors contributed equally
[§]E-mail: heike.lindner@unibe.ch; michael.raissig@unibe.ch

Anatomical, metabolic, and physiological innovations allowed succulents to thrive in harsh, water-scarce environments. Amongst these innovations falls CAM photosynthesis, which temporally uncouples plant-atmosphere gas exchange and carbon fixation involving stomata that consist of two guard cells (GCs) surrounded by three putative subsidiary cells (SCs). Here, we used the emerging leaf succulent model plant *Kalanchoë laxiflora* to decipher how succulents build their innovative stomatal morphology. We could show that K^+ ions shuffle between the GCs and SCs during stomatal opening and closing, respectively, thus suggesting an active role of SCs in stomatal movement in succulents. Using gene-editing, reporter constructs, and overexpression lines, we showed that the duplicated bHLH transcription factors *KlaxMUTE1* and *KlaxMUTE2* enabled additional rounds of asymmetric cell divisions to form succulent SCs. This was supported by the upregulation of specific cell-cycle programs associated with asymmetric rather than symmetric cell divisions in *KlaxMUTE1* overexpression lines. This is opposite to *Arabidopsis thaliana*, where *MUTE* stops rather than induces asymmetric cell divisions during stomatal development. Together, our work indicated that MUTE adopted a novel role in the leaf succulent *K. laxiflora* to facilitate SC formation, much like in the distantly related grasses. Furthermore, *K. laxiflora* establishes a genetically tractable, succulent model system to mechanistically dissect the development of diverse anatomical and morphological innovations required for the water-use-efficient CAM lifestyle.

TALK

How endoreduplication impacts multiscale growth coordination in plants

Mateusz Majda

Department of Plant Molecular Biology, University of Lausanne
E-mail: mateusz.majda@unil.ch

Plant cells are tightly connected by rigid cell walls, which prevent them from moving. This requires coordinated growth across tissues to maintain structural integrity and ensure proper development. Growth coordination is regulated by the cell cycle: cyclins and cyclin-dependent kinases (CDKs), which drive mitotic divisions, while suppressors like SIAMESE (SIM) and SIAMESE-RELATED (SMRs) inhibit mitosis and promote endoreduplication. Endoreduplication, a modified cell cycle that increases nuclear and cell size without division, is crucial for plant growth, but its role in regulating cell wall extensibility and coordinating growth across scales remains unclear. To investigate this, we used cell cycle suppressor lines to manipulate cell division and expansion in etiolated Arabidopsis hypocotyls, which naturally undergo endoreduplication and extensive cell expansion with minimal division. Expression analysis showed that *SIM*, *SMR1*, and *SMR2* are highly expressed in hypocotyls. The *sim smr1* double mutant displayed reduced ploidy levels, smaller and more numerous cells, slower growth, and thinner hypocotyls compared to wild type. In contrast, overexpression of *SIM* or *SMR1* led to increased ploidy, longer cells, faster growth, and thicker hypocotyls. Biophysical analyses revealed that smaller cells in the mutant had stiffer cell walls, suggesting changes in cell wall composition. Preliminary cell wall analyses pointed to potential downstream regulators involved in modifying xyloglucan and pectin composition, indicating a link between endoreduplication and changes in cell wall properties. Altogether, we propose that differences in endoreduplication levels across tissues drive variations in cell size, division rates, and mechanical properties, which are essential for coordinating growth across scales. Our findings suggest that endoreduplication fine-tunes cell wall stiffness and expansion by regulating genes involved in cell wall biosynthesis and modification, which has direct consequences for organ growth.

TALK

Population genomics and molecular epidemiology of wheat powdery mildew in Europe

Jigisha, **Fabrizio Menardo**

Department of Plant and Microbial Biology, University of Zurich.
E-mail: fabrizio.menardo@uzh.ch

Agricultural diseases are a major threat to sustainable food production. Yet, for many pathogens we know exceptionally little about their epidemiological and population dynamics. Here we study the population genomics and molecular epidemiology of wheat powdery mildew, a disease caused by the biotrophic fungus *Blumeria graminis* f.sp. *tritici* (Bgt). We sampled Bgt for two consecutive years, 2022 and 2023, from 22 countries in Europe and surrounding regions, and compiled a genomic dataset of 415 Bgt isolates. We found one single epidemic unit in the north of Europe, consisting of a highly homogeneous population. Conversely, the south of Europe hosts smaller local populations which are less interconnected. In addition, we show that the population structure can be largely predicted by the prevalent wind patterns. We identified several loci that were under selection in the recent past, including fungicide targets and avirulence genes. We reconstructed the evolutionary history of one of these loci, *AvrPm17*, coding for an effector recognized by the wheat receptor Pm17. We found evidence for a soft sweep on standing genetic variation. Multiple *AvrPm17* haplotypes, which can partially escape recognition by Pm17, spread rapidly throughout the continent upon its introduction in the early 2000s. Overall, we highlight the potential of genomic surveillance in resolving the evolutionary and epidemiological dynamics of agricultural pathogens, as well as in guiding control strategies.

TALK

Lipids or phenylpropanoids? Diversity of protective barriers in the apoplast of Arabidopsis root tissues

Christiane Nawrath[1], Alice Berhin[1], Kay Gully[1], Nasim Farahani Zayas[1], Aurore Guerault[1], Damien deBellis[1,2]
[1]Department of Plant Molecular Biology, University of Lausanne
[2]Electron Microscopy Facility, University of Lausanne
E-mail: christiane.nawrath@unil.ch

Evolution of land plants is tightly associated with the formation of apoplastic barriers protecting plants against aversive environmental conditions. Both aromatic as well as aliphatic polymers have evolved for cell wall strengthening and impregnation.

Plants show a high diversity of cell wall modifications that change in composition between organs, tissues and developmental stages. The cell type-specific expression patterns of the members of the glycerol-3-phosphate acyltransferases (GPAT) family indicate a high diversity in lipidic cell wall modifications of Arabidopsis root tissues. GPATs are bifunctional enzymes having an acyltransferase and phosphatase domain and synthesize monoacylglycerols or lysophosphatidic acids dependent on the activity of the phosphatase domain. In contrast to earlier assumptions that cutin, the structural polyester of the cuticle, is synthesized by monoacylglycerols and suberin by lysophosphatidic acids we recently revealed that GPATs of both activities contribute to the formation of suberin lamellae and the root cap cuticle contributing specific compositional and/or structural features to the lipid polymers. Furthermore, we revealed a phenylpropanoid-derived cell wall modification in the outer cell wall of the root epidermis, in addition to these of the endodermis and vasculature. Lipid-derived cell wall modifications were however under detection limit in the root epidermis. Assessment of the physical properties of the different modified cell walls will be necessary to better understand the diversity of cell wall modifications and their functions.

TALK

A dialectic on the costs of plant reproduction

John Pannell

Departement of Ecology and Evolution, University of Lausanne
E-mail: john.pannell@unil.ch

In this presentation, I will address a number of related questions concerning the optimization of reproductive and life-history strategies in plants, drawing on evolutionary theory, observations and experiments, and decades of personal musing. To what extent does it make sense to invoke differential costs of reproduction between males and females of dioecious species? If females pay the higher price for reproduction (as often supposed), why should they have evolved to do so, and who benefits? How might costs of reproduction affect evolutionary transitions between dioecy and hermaphroditism, and why should hermaphrodites pay a higher price in producing seeds and fruits than in making and dispersing pollen (as often supposed)? I will end with the surprising demonstration that the relative costs of reproduction to male versus female function should influence whether the males or the females are more likely to be the heterogametic sex when separate sexes evolve.

TALK

Dynamics of centromeric transposable elements and their consequences for chromosomal evolution

Manuel Poretti[1], Rimjhim Choudhury[1], Yile Huang[2], Hussein Anani[2], Terezie Mandakova[2], Martin Lysák[2], **Christian Parisod**[1]

[1]Department of Biology, University of Fribourg, Fribourg, Switzerland
[2]CEITEC Masaryk University, Brno, Czech Republic
E-mail: christian.parisod@unifr.ch

Beyond their fundamental importance for the segregation of chromosomes, centromeres and their evolution remain elusive. In plants, flanking (pericentromeric) segments are characterized by low recombination and chiefly constituted of gypsy retrotransposons. Although such distribution expectedly results from an equilibrium between the insertion of new copies and their removal by purifying selection in high-recombining segments away from the centromere, empirical evidence remains scarce. Chromosome-scale assemblies characterizing the gene space and repetitive fraction of three diploids within the highly-polymorphic species *Biscutella leavigata* and one outgroup species were used to assess the evolution of retrotransposons around centromeres. Despite high synteny within the species, we find large variability in the non-coding part of the genome and particularly high sequence turnover among pericentromeric segments of the genome from the population mostly affected by genetic drift due to its relatively small size. By comparing retrotransposons actively targeting pericentromeric regions such as CRM elements to similarly-distributed retrotransposons that are unknown to present biased insertion such as ATHILA elements, we infer their dynamics of transposition vs deletion and highlight the role of specialized retrotransposons during a centromere shift. We further show that they disperse towards the distal part of nucleolar chromosomes and invade intervening gene-rich regions, increasing the methylation of nearby gene and decreasing their expression. Accordingly, bursts of retrotransposon activity associated with the rapid evolution of centromeres are not only affecting the formation and maintenance of heterochromatin and chromocenters, but also result in considerable changes across the gene space.

TALK

Unveiling salinity stress at the subcellular scale by elemental cryo-imaging

Priya Ramakrishna[1,2], Etienne Bellani[2], Cristina Martin Olmos[1,3], Stephane Escrig[1], Damien De Bellis[2,4], Christel Genoud[4,5], Niko Geldner[2], Anders Meibom[1,3]

[1]Laboratory for Biological Geochemistry, EPFL
[2]Department of Plant Molecular Biology, University of Lausanne
[3]Center for Advanced Surface Analysis, University of Lausanne
[4]Electron Microscopy Facility, University of Lausanne
[5]Life Sciences, EPFL
E-mail: priya.ramakrishna@epfl.ch

Salinity is a major environmental stress that affects plant growth and development. Plants avoid salt (primarily sodium) toxicity through subcellular compartmentation by intricate processes that involves a high level of elemental interdependence. Current technologies to visualize sodium together with other elements, are either indirect or lack in resolution. I will describe the newly developed cryo nanoscale secondary ion mass spectrometry (CryoNanoSIMS) ion microprobe, which allows high-resolution elemental imaging of cryo-preserved samples and reveals the subcellular distributions of key macronutrients and micronutrients in root meristem cells of Arabidopsis and rice. I will further talk about the unexpected, concentration-dependent switch in sodium accumulation in the cells from low to stressful salinity concentrations. A new role for the classic sodium antiporter SALT OVERLY SENSITIVE 1 (SOS1)/ Na^+/H^+ family antiporter 7 (NHX7) in sodium sequesteration identified with a combination of genetics and cryo-elemental imaging approach. The potential the cryo-elemental imaging holds to understand salinity stress in plants and other biological processes.

TALK

How *Medicago truncatula* sanctions ineffective rhizobial endosymbionts (*Sinorhizobium meliloti*)

Min Chen[1], Axelle Raisin[1], Nathalie Judkins[1], Pierre-Marie Allard[1], Emmanuel Défossez[1], Michael Stumpe[1], Inmaculada Yruela[2], Manuel Becana[2], **Didier Reinhardt**[1]

[1]Department of Biology, University of Fribourg, Chemin du Musée 10, 1700 Fribourg, Switzerland
[2]Department of Plant Biology, Estación Experimental de Aula Dei, CSIC, Zaragoza, Spain
E-mail: didier.reinhardt@unifr.ch

In symbiotic plant-microbe interactions, the host invests considerable amounts of resources in the microbial partner. If the microbe does not reciprocate with a comparable symbiotic benefit, the interaction represents a parasitic relationship. This is thought to trigger negative feedback mechanisms (sanctions) from the plant against such microbial cheaters to prevent the resulting selective disadvantage of being parasitized. Indeed, sanctioning of bad mutualists has been observed in interactions such as arbuscular mycorrhiza and legume-rhizobium symbioses. Here, we study sanctioning by manipulating the exchange of resources between the model legume *Medicago truncatula* and its bacterial partner *Sinorhizobium meliloti* in three ways: i.) by using mutant rhizobia defective in nitrogenase, ii.) by replacing nitrogen in the atmosphere with argon gas, and, iii.) by supplying high nitrate to the host. We follow the consequences of these manipulations by examining the metabolome, proteome, and phosphopro-teome of nodules. We find that cheating conditions result in sanctioning of the bacterial partner at different levels. In particular, we observe induction of defense markers, repression of essential symbiotic functions, and changes in central metabolism that may be relevant for microbial fitness and that could therefore contribute to sanctioning.

TALK

Root immune components mediate microbiome feedbacks in Arabidopsis

Klaus Schlaeppi

Department of Environmental Sciences, University of Basel
E-mail: klaus.schlaeppi@unibas.ch

It becomes more and more established that different soil microbiomes affect growth and health of plants growing in complex soils. While the ecological impact of such microbiome feedbacks are well described, how plants perceive soil microbiomes and how they modulate their performance in response to microbiome feedbacks remains largely unknown. We have established a model system with *Arabidopsis thaliana* to investigate the mechanisms of plant feedbacks to differential soil microbiomes. We find microbial feedbacks where Arabidopsis plants with larger rosette growth showed enhanced defense signatures in roots and shoot and that they were more resistant to the fungal pathogen *Botrytis cinerea*. We found evidence that this simultaneous increase of growth and defense is mediated by priming of the immune processes. Furthermore, these microbiome feedbacks coincided with differential communities of root bacteria. Based on natural variation among Arabidopsis accessions and searching for genome-wide associations, we found a toll-interleukin receptor nucleotide-binding site leucine-rich repeat (TNL) gene, termed Mediator of Microbiome Feedbacks 1 (MMF1), to be associated with microbiome feedbacks. Mutants of mmf1 lack the microbiome feedbacks, the shifts in root bacterial communities, and defense-related transcriptome signature observed in wildtype plants. Overall, our results indicate that root immune components, particularly the TNL receptor MMF1, are important determinants of microbiome feedbacks in Arabidopsis

TALK

Remotely sensing plant genetic resources and their consequences for ecosystems

Meredith C. Schuman

Departments of Geography and Chemistry, University of Zürich
E-mail: meredithchristine.schuman@uzh.ch

Plants feed much of life on earth, cultivate and secure soil, fix carbon and exhale oxygen. Volatile organic compounds in Earth's atmosphere originate primarily from plants (Schuman, 2023), with each plant having its own fluctuating body odor as a result of its particular genetic make-up interacting with its environment over time (Schuman, Valim, et al., 2016). Trees can be smelled from a distance and seen or even counted from the air or from space (Schuman, 2023; Schuman et al., 2024). Differences in the spectral reflectance of sunlight off tree canopies can reveal important information about their functional diversity and performance, as well as their genetic differentiation (Schuman et al., 2024). Scalable tools, such as those that allow us to sample chemistry over forest canopies and to record their spectral reflectance of sunlight, allow us to map different aspects of forest biodiversity and functioning, and to study changes over time in response to human interventions and other factors. The Spatial Genetics group at the University of Zurich works to map molecular differences that matter for the responses of plant populations, species, and their ecosystems to the environment, including the variation within and among plants that is critical for acclimation and adaptation. I will present examples from our recent work, and future directions, with a focus on Eurasian beech as a study system.

TALK

ABA orchestrates chloroplast protein import pathways and chloroplast biogenesis during the seed-to-seedling transition

Maryam Forough[1], Thomas Badet[2], Barbara Pfister[3], Etienne Delannoy[4], Felix Kessler[1], **Venkatasalam Shanmugabalaji**[1]

[1]Laboratory of Plant Physiology, University of Neuchâtel, 2000 Neuchâtel, Switzerland
[2]Laboratory of cell and molecular biology, University of Neuchâtel, 2000 Neuchâtel, Switzerland
[3]Plant Biochemistry, ETH Zurich, Switzerland
[4]Institute of Plant Sciences Paris-Saclay (IPS2) Orsay, France
E-mail: shanmugabalaji.venkatasalam@unine.ch

Chloroplast biogenesis describes the transition of non-photosynthetic proplastids to photosynthetically active chloroplasts in the embryonic cells of germinating seeds. It is the key to photoautotrophic growth in plants. Chloroplast biogenesis requires the import of thousands of nuclear-encoded preproteins. It depends on the essential import receptor TOC159, which is needed to import photosynthesis-associated proteins, and the mutation of which results in non-photosynthetic albino plants. Seed germination is negatively regulated by the plant hormone abscisic acid (ABA). However, there is still a lack of understanding of how ABA influences the protein import machinery and chloroplast biogenesis at this early developmental stage. Our transcriptomics and proteomics data suggest the remodeling of translocon complexes and the chloroplast proteome under ABA. Photosynthesis-associated genes are downregulated, stress-related genes are upregulated via transcriptional regulation, and the corresponding proteins behave accordingly. Under the same conditions, photosynthesis-associated translocon were downregulated, and stress-associated translocions were upregulated via post-transcriptional regulation. This included the activity of SP1, a chloroplast outer membrane E3 ubiquitin ligase, and degradation by the ubiquitin-proteasome system (UPS). Subsequently, stress-related proteins are imported mostly via stress-associated translocon. The results indicate transcriptional and post-transcriptional mechanisms remodeling the chloroplast protein import machinery and chloroplast biogenesis under ABA. Our data provide new insight into the ABA-dependent regulation of chloroplast protein import pathway and the synchronization of chloroplast biogenesis with plant development.

TALK

10+ genomes and pan-transcriptome projects of hexaploid bread wheat highlighted the pattern of selection and yellow rust resistance in Asian landraces

Kentaro K. Shimizu[1,4], Gwyneth Halstead-Nussloch[1], Georg Haberer[2], Thomas Laux[2], A S M Faridul Islam[3], Moeko Okada[1,4,5], Masaomi Hatakeyama[1,6], Roman Briskine[1,7], Ben White[8], Anthony Hall[8], Curtis Pozniak[9], 10+ Wheat Genome Project, Manuel Spannagl[2], Timothy Paape[1,10,11], Katharina Jung[1], Reiko Akiyama[1], Jilu Nie[12], Miyuki Nitta[12], Naoto-Benjamin Hamaya[1], Naeela Qureshi[13], Sridhar Bhavani[13,14], Thomas Wicker[15], Beat Keller[15], Masahiro Kishii[13,16], Shuhei Nasuda[12]

[1]Department of Evolutionary Biology and Environmental Studies, University of Zurich, Switzerland.
[2]Helmholtz Zentrum München, Germany.
[3]Institute for Advancing Health through Agriculture, Texas A&M, USA.
[4]Kihara Institute for Biological Research, Yokohama City University, Japan.
[5]Niigata University, Japan
[6]Functional Genomics Center Zurich, Switzerland
[7]Science IT, University of Zurich, Switzerland
[8]Earlham Institute, UK
[9]Crop Development Centre and Department of Plant Sciences, University of Saskatchewan, Canada
[10]USDA-ARS Responsive Agriculture Food Systems Research Unit, USA
[11]Department of Soil and Crop Sciences, Texas A&M, USA
[12]Graduate School of Agriculture, Kyoto University, Japan
[13]CIMMYT, El Batán, Mexico
[14]CIMMYT, Nairobi, Kenya
[15]Department of Plant and Microbial Biology, University of Zurich, Switzerland
[16]Japan International Research Center for Agricultural Sciences (JIRCAS), Japan.
E-mail: kentaro.shimizu@uzh.ch

Complex and large genomes of allopolyploid species have been an obstacle to studying their genome-wide variation. Bread wheat is an allohexaploid species with a genome size of ~15 Gb. In the 10+ Wheat Genome Project, my group sequenced the Japanese variety Norin 61 and reported unique variations in Asia. In the second phase of the project, pan-transcriptomic analysis and high-quality *de novo* annotation are being conducted. First, we analyzed the genome-wide pattern of purifying selection by integrating genomic and transcriptomic data. Despite potential functional redundancy of duplicated homeologs, purifying selection was observed, consistent with the efficacy of hybrid breeding in wheat. Interestingly, strong purifying selection was observed in genes that are highly expressed in root tissues and are in the D subgenome, which is consistent with adaptation to broader environments by the acquisition of the D subgenome. Second, to exploit underutilized Asian wheat, 1,000 lines of nested association mapping (NAM) population between Norin 61 and 13 Asian landraces/cultivars were grown. We found known and novel loci of yellow rust resistance from near-Himalayan region, which is thought to be the origin place of its fungal pathogen. The broad geographic distribution of a QTL on chromosome 5B across regions with high disease pressure suggests it may serve as a durable source of resistance, and highlights the potential of Asian wheat germplasm.

TALK

A class of chromatin readers control cell fate establishment in the *Arabidopsis* embryo

Sara Simonini, Yixuan Fu, Janik Scotton, Edouard Tourdot

Institute of Plant and Microbial Biology, University of Zurich
E-mail: sara.simonini@botinst.uzh.ch

Multicellular organisms contain cells with identical genetic information, yet these cells differentiate into various types with unique properties and functions. This diversity arises primarily through changes in gene expression, enabling cells to adopt distinct identities, perform specialized functions, and respond to environmental and internal stimuli. Mechanisms that regulate gene expression without altering DNA sequences are termed “epigenetic.” Among these, histone post-translational modifications, such as methylation, acetylation, and phosphorylation, play pivotal roles. The specific effects of these modifications depend on the targeted amino acid residues. These modifications are established by “writer” complexes and interpreted by “reader” proteins, which mediate downstream effects by for instance recruiting transcription factors or transcriptional machinery. We have characterized a plant-specific family of reader of the histone modification H3K4me3, a mark associated with active gene expression. Our research demonstrates that reading the H3K4me3 mark is essential for early embryogenesis in *Arabidopsis*. Disruption of these H3K4me3 readers function results in severe patterning defects during zygote division and early embryo development. These phentotypes are driven by misexpression of gene important for embryo and suspensor identity, which ultimately lead to seed abortion. These findings demonstrate an essential role for H3K4me3 in the zygote for directing cell fate acquisition and establishing proper embryonic development.

TALK

Repairing deleterious mutations by precision genome editing in tomato

Sebastian Soyk

[1]Department of Plant Molecular Biology, University of Lausanne
E-mail: sebastian.soyk@unil.ch

The intense selection during domestication shaped plant genomes to adapt their traits to human preferences. However, domestication also caused an accumulation of potentially harmful mutation that are deleterious for gene function, a process often referred to as the “cost of domestication”. Advances in genome editing offer opportunities to repair deleterious mutations, however, experimental demonstration has been lacking. In this study, we computed the load of deleterious mutations along the domestication history of tomato. We identified potentially deleterious mutations in flowering time genes and functionally characterized a deleterious variant in the transcription factor gene *SUPPRESSOR OF SP2* (*SSP2*) that was enriched during domestication. The deleterious variant reduces the function of the floral regulator by compromising its DNA-binding ability at genome-wide targets. Intriguingly, reduced *SSP2* activity caused a loss of redundancy with its paralog *SSP* and allowed the utilization of *ssp* mutations in breeding, illustrating how deleterious variants can become adaptive in domestic environments. Finally, we applied base editing to directly repair the deleterious variant and obtained plants with compact growth and early fruit yield. Our findings suggest that deleterious variants sensitized modern genotypes for phenotypic tuning and demonstrate the potential of genome editing to repair deleterious mutations for predictable crop improvement.

TALK

A reference metagenome sequence of the False Reindeer Lichen *Cladonia rangiformis*

Thomas Wicker[1], Matthias Heuberger1, Carlotta Marie Wehrkamp[1], Alina Pfammatter[1], Manuel Poretti[2], Johannes Peter Graf[1], Aline Herger[1], Jonatan Isaksson[1], Edith Schlagenhauf[1], Rosmarie Honegger[1], Alexandros G. Sotiropoulos[3]

[1]Department of Plant and Microbial Biology, University of Zurich
[2]Institute of Plant Sciences, University of Bern
[3]University of Queensland, Australia
E-mail: wicker@botinst.uzh.ch

Lichens are an ancient symbiosis comprising the thalli of lichen-forming fungi, their photoautotrophic partners and their microbiome. So far they were poorly studied at the genome sequence level. Here, we present a reference metagenome for the holobiont of *Cladonia rangiformis*. Using long read sequences from an entire symbiotic complex, plus short read libraries from 28 additional diverse European lichen samples, we were able to separate genome sequences of 20 individual species. We constructed chromosome-scale assemblies of the *C. rangiformis* fungus and its trebouxioid green algal photobiont *Asterochloris mediterranea*. The genome of the fungus comprises ~40% transposable elements and is highly compartmentalized into genic regions and large TE-derived segments which show extensive signatures of repeat-induced point mutations (RIP). We found that centromeres are predominantly derived from two interacting retrotransposon families. We also identified strong candidates for genes that were horizontally transferred from bacteria to both alga and fungus. Furthermore, we isolated 18 near-complete bacterial genomes, of which 13 are enriched in the lichen compared to surrounding soil. Our study revealed that the thalli of *C. rangiformis* have a highly complex microbiome, comprising a mix of species that may include opportunists, ecologically obligate symbionts and possibly even lichen-beneficial bacteria.

TALK

Structural proteins define the sites of starch granule initiation and control granule growth

Samuel C. Zeeman, Mayank Sharma

Institute of Molecular Plant Biology, ETH Zurich, Zurich
E-mail: szeeman@ethz.ch

Starch, the key reserve carbohydrate in plants, occurs as insoluble granules in plastids. In Arabidopsis chloroplasts, the granules always form between the thylakoid membranes. We previously used a set of complementary microscopy approaches (electron tomography, isotope labelling and NanoSIMS imaging) to visualize how starch granules initiate and subsequently grow. In parallel, we identified proteins controlling granule initiation, two of which (MFP1 and MRC) are structural proteins containing long coiled-col motifs, enabling protein-protein interactions. MFP1 is membrane anchored and assembles into discrete patches on the thylakoids, where it co-localises other factors to determine initiation sites. Re-localizing MFP1 to the inner chloroplast envelope re-directs starch granules formation to the envelope. MRC is soluble but also localizes to puncta within the chloroplast stroma. Recent data suggest that MRC influences anisotropic granule growth; overexpression disrupts the growth pattern, yielding highly distorted granules. We suggest MRC helps localize the rest of the starch biosynthetic machinery at the granule surface, the testing of which is ongoing. These studies into the cell biological aspects of starch biosynthesis offer new targets with which to influence starch biosynthesis in crops, which could improve both crop yield and properties.

TALK

Receptors and ligands at the cell wall-plasma membrane continuum and their roles in immunity

Cyril Zipfel[1,2]

[1]Department of Plant and Microbial Biology, Zurich-Basel Plant Science Center, University of Zurich
[2]The Sainsbury Laboratory, University of East Anglia, Norwich Research Park, Norwich, UK
E-mail: cyril.zipfel@botinst.uzh.ch

The cellular interface represented by the plasma membrane-cell wall continuum is a major sensory landscape determining how plants can adapt to their external environment, including biotic stresses. In this context, it has become recently increasingly apparent that receptors at the plasma membrane of plant cells are critical for the initial detection of pathogen-derived molecules, but also endogenous signals that are released during the first phases of the encounter between would-be pathogens and the plant. Yet, the exact molecular mechanisms underlying the perception of these signals are mostly unclear. Here, we will present our recent work on receptor kinases and corresponding ligands proposed to act at the plasma membrane-cell wall continuum and their regulation of plant immune signaling.

POSTER

Unveiling TOC and TIC: Evidence for independent functioning of the chloroplast protein import machinery

Gent Ballabani, Venkatasalam Shanmugabalaji, Felix Kessler

Plant Physiology Laboratory, University of Neuchâtel, Neuchâtel, Switzerland
E-mail: gent.ballabani@unine.ch

Chloroplasts are the organelles essential for photosynthesis and energy production in plants. A key component of chloroplast development and functionality is efficiently importing nuclear-encoded proteins. The chloroplast translocons, TOC (Translocon at the Outer Chloroplast membrane), and TIC (Translocon at the Inner Chloroplast membrane) are the entry points of the pre-protein. The trimeric core of the TOC complex is composed of the GTP-binding proteins TOC34 and TOC159. The C-terminus of TOC159 forms a hybrid β barrel channel together with TOC75. The GTP-binding proteins are known pre-protein receptors of the TOC complex, whereas the TOC159/TOC75 hybrid channel allows preprotein translocation across the outer envelope. Understanding the configuration and mechanism of those components would help us better understand the chloroplast protein import mechanism. In our study, we isolated native active forms of the TOC complex from *Pisum sativum*. The proteomics data revealed a substoichiometric relation between TOC and TIC, suggesting that the TOC complex can function independently of the TIC complex. Our results also suggested the existence of different forms of the TOC complex varying in the composition of the GTP-binding proteins. In the future, we aim to reconstitute the TOC complex into proteo-liposomes and to conduct structural studies and modeling to provide further insight into the protein import mechanism of chloroplasts.

POSTER

Secrets of a gene body: The brassinosteroid receptor gene *BRI1* safeguards cell-autonomous brassinosteroid signaling across tissues

Noel Blanco-Touriñán[1], Surbhi Rana[1], Trevor M. Nolan[2,3], Kunkun Li[1], Nemanja Vukašinović[4,5], Che-Wei Hsu[2,3], Eugenia Russinova[4,5], Christian S. Hardtke[1]

[1]Department of Plant Molecular Biology, University of Lausanne, Lausanne, Switzerland
[2]Department of Biology, Duke University, Durham, NC, USA.
[3]Howard Hughes Medical Institute, Duke University, Durham, NC, USA.
[4]Department of Plant Biotechnology and Bioinformatics, Ghent University, 9052 Ghent, Belgium.
[5]Center for Plant Systems Biology, VIB, Ghent, Belgium.
E-mail: noel.blancotourinan@unil.ch

Brassinosteroid signaling is essential for plant growth as exemplified by the dwarf phenotype of loss-of-function mutants in *BRASSINOSTEROID INSENSITIVE 1* (*BRI1*), a ubiquitously expressed Arabidopsis brassinosteroid receptor gene. Complementation of brassinosteroid-blind triple receptor mutants by *BRI1* expression with various tissue specific promoters implied that local brassinosteroid signaling may instruct growth non-cell-autonomously. Here we performed such rescues with a panel of receptor variants and promoters, in combination with tissue-specific transgene knockouts. Our experiments demonstrate that brassinosteroid receptor expression in several tissues is necessary but not sufficient for rescue. Moreover, such rescues do not occur with a recoded *BRI1* gene although it produces an identical and functional BRI1 protein. Thus, complementation with tissue-specific promoters requires the genuine *BRI1* gene body sequence, because it confers ubiquitous expression of trace BRI1 receptor amounts that are sufficient to promote brassinosteroid-dependent root growth. Our data, therefore, argue for a largely cell-autonomous action of brassinosteroid receptors, although brassinosteroid itself may instruct growth non-cell-autonomously through its targeted biosynthesis, transport and distribution.

POSTER

UniProt knowledgebase: A comprehensive reference for plant protein sequences and functions

Emmanuel Boutet, the Swiss-Prot group

Swiss-Prot Group, Swiss Institute of Bioinformatics
E-mail: emmanuel.boutet@sib.swiss

The UniProt knowledgebase (UniProtKB, www.uniprot.org) is a reference resource of protein sequences and functional annotations frequently used for proteomic, transcriptomic and genomic analyses. The expertly managed UniProtKB/Swiss-Prot core comprises around 580,000 sequences, of which around 42,000 are from plants (as of January 2025), supplemented by information from the scientific literature. UniProtKB's range of applications is extended to include chemical data through the curation of enzyme and transporter functions using Rhea, an expert-curated knowledge base of biochemical reactions (www.rhea-db.org), leveraging the ChEBI small molecule ontology (www.ebi.ac.uk/chebi/). ChEBI is also used to annotate ligand binding sites and post-translational modifications (PTMs) to improve the representation of small molecule data. The structured and high-quality information provided by UniProtKB is accessible to both humans and machines, enhancing interoperability with other data and knowledge resources and providing enhanced support for metabolic modeling, multi-omics data integration and analysis, and the use of advanced machine learning approaches to predict enzyme function and biosynthetic pathways. The UniProt web portal (www.uniprot.org) provides access to a robust advanced search tool, programmatic interfaces, an identifier mapping tool encompassing over a hundred databases, as well as tools for sequence and structure searching, alignment and analysis. All data can be downloaded without any restrictions.

POSTER

MYB's & MYB's: Endodermal suberin regulation

Maria Beatriz Capitão[1], Laura Pérez Martín[1], Kevin Robe[1], Fabienne Cléard[1], Vinay Shukla[1,2], Marie Barberon[1]

[1]Department of Botany and Plant Biology, University of Geneva, Geneva, Switzerland
[2]Department of Biology, University of Oxford, Oxford, England
E-mail: Maria.Capitao@unige.ch

Suberin is a hydrophobic biopolymer present in endodermal cells protecting the plant vasculature against stresses and controlling water and nutrient acquisition. Endodermal suberization is highly plastic being regulated by environmental and developmental cues. Previous work reported increased endodermal suberization in presence of ABA and an ethylene-mediated decreased suberization. Although suberin plasticity appears to be a hallmark of endodermal suberization, the molecular players involved remain largely unknown. Our recent work enlightened the involvement of four MYB transcription factors associated with endodermal suberization. A simultaneous mutation of *MYB41*, *MYB53*, *MYB92* and *MYB93* leads to a drastic reduction in endodermal suberization and almost no suberin induction by ABA. Although severely diminished, suberin is still present in some endodermal cells of this quadruple mutant, suggesting that more factors are involved. In this context, we used TRAP (Translating Ribosome Affinity Purification) to identify genes induced by ABA in the endodermis and/or coregulated with previously characterized suberin genes. Amongst these we identified 33 additional MYBs, previously uncharacterized in the context of endodermal suberization. We are currently characterizing in detail 4 of these additional MYBs according to their expression, functionality and positioning regarding the previously published MYB transcription factors. The ongoing characterization led to the identification of 2 positive regulators of endodermal suberin likely upstream of the transcription factors previously characterized as well as 2 negative regulators.

POSTER

Germination and survival of *Abies* and *Fagus* provenances sown across Europe

Justine Charlet de Sauvage, Katalin Csilléry

Evolutionary Genetics Group, Biodiversity and Conservation Biology, Swiss Federal Research Institute WSL, Switzerland
E-mail: justine.charlet@wsl.ch

Strong selection during early life stages could foster local adaptation in forest trees. However, due to the stochastic nature of spring environmental conditions, selection might favor plasticity. We studied the phenotypic plasticity of germination and early survival in two forest tree genera represented by 13 (*Abies*) and 10 (*Fagus*) provenances using 18 common gardens established directly under the forest canopy. Additionally, all provenances were tested in climate chambers. We considered environmental factors known to affect the germination and spring phenology in trees, such as chilling, precipitation and temperature. Germination rates of different provenances ranged from 0 to 70%. For *Abies* and *Fagus*, respectively, on average, 10.9 and 6.7% of the seeds sown in the gardens germinated, 2% and 1.8% were still alive in the second year, and 0.7% and 0.6% in the third year. Some provenances appeared to be generalists and showed similar germination rates across environments while some others germinated preferentially under specific environmental conditions (e.g., wetter conditions than at the site of seed origin). Higher precipitation in spring was associated with higher germination rates for most provenances. Longer chilling reduced the growing degree-days necessary for germination. Forest regeneration is a key step in forest adaptation to climate change and our results bring novel information about the germination potential of various provenances from two major genera in European forests.

POSTER

Natural variation of UV-B photoprotection in Arabidopsis

Emilie Demarsy, Charlotte Grometto, Roman Ulm

Department of Plant Sciences, University of Geneva
E-mail: emilie.demarsy@unige.ch

To get new insights into photoprotection against UV-B, we studied the UV-B tolerance of 151 different natural accessions (ecotypes) of *Arabidopsis thaliana*. We revealed a large variation in UV-B tolerance and the absence of a trade-off with growth and development. Using the most tolerant and sensitive accessions, we now examine the underlying molecular mechanisms that explain the variations. In parallel, candidate genes were selected based on GWAS analyses and we are now generating corresponding mutants and characterizing the potential function of these genes in UV-B photoprotection.

POSTER

Lignin patterning and evolutionary transitions in explosive fruit

Aurélia Emonet[1,2], Angela Hay[1]

[1]Max Planck Institute for Plant Breeding Research, Köln, Germany
[2]Institute of Plant Sciences, University of Bern, Bern, Switzerland
E-mail: aurelia.emonet@unibe.ch

Adaptations for seed dispersal can be found all around us – from the fleshy fruit you eat, to the dandelions you blow on. Cardamine species spread their seeds by explosive dispersal, a trait innovation that distinguishes this genus from the rest of the Brassicaceae family. Explosive dispersal relies on a unique pattern of lignin that is deposited asymmetrically in a single cell layer found on the adaxial side of the fruit valve called the endocarp *b*. Genetic analysis in *Cardamine hirsuta*, together with mathematical modelling and phylogenetic comparisons, have shown that this specific lignin pattern is necessary for seed pods to explode and is strictly associated with the evolution of this trait. To investigate the genetic basis of polar lignin patterning and whether such genes play a role in evolutionary transitions between non-explosive and explosive fruit, we developed *Cardamine chenopodiifolia* as a novel experimental system. *C. chenopodiifolia* is amphicarpic: above ground it bears explosive fruit with polar lignin deposition, while underground it develops non-explosive fruit with uniform lignification. We use this comparative system to identify differentially expressed transcripts between explosive and non-explosive fruit and potential gene functions in the evolution and development of explosive fruit.

POSTER

Quantifying reproductive isolation and gene flow across a clade of *Phlox* wildflowers

Anna Feller[1,2], Felix Wu[2], Manuel Marty[1], Robin Hopkins[2]

[1]Department of Environmental Systems Science, ETH Zurich, Zurich, Switzerland
[2]Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, USA
E-mail: annafell@ethz.ch

As independent lineages diverge, they evolve barriers that prevent them from reproducing with each other, and thus form species. Even after decades of research on the evolution of reproductive isolation, questions remain about which barriers are the most important, and if barriers quantified in the lab correspond to measurable variation in gene flow between species. Here, we performed a large crossing experiment and analyzed publicly available occurrence data to quantify reproductive barriers in eight species of closely related *Phlox* wildflowers. Additionally, we use a combination of ddRAD and long read whole genome sequencing data to infer patterns of gene flow among the eight species. We find strong reproductive isolation between the species, with later acting barriers tending to have larger effects than earlier acting barriers. From our genomic data we infer that the species are well-differentiated with relatively sparse evidence for gene flow. Ongoing genomic analyses will show if the species differ in structural features of the genome. Our work highlights the importance of integrating comparative genomics and experimental investigations when studying the processes that generate and maintain species diversity.

POSTER

Dual functionality of pathogenesis-related proteins: Defense in plants versus immunosuppression in pathogens

Zhu Han, Yi-Fang Xie, Yangyang Qin, Roger Schneiter

Department of of Biology, University of Fribourg, Chemin du Musée 10, 1700 Fribourg, Switzerland
E-mail: zhu.han@unifr.ch

Plants defend against pathogen invasion by activating Pathogenesis-Related (PR) proteins, a diverse group categorized into 17 families (PR1–PR17). These proteins, predominantly secreted into the apoplast, often exhibit direct antimicrobial activity. Intriguingly, recent studies reveal that phytopathogens can secrete PR-like proteins (PR1-Ls) to enhance their virulence and suppress plant immunity. This paradox raises a fundamental question: how can conserved PR-like proteins act as antimicrobial agents when produced by plants but serve as virulence factors when expressed by pathogens? To address this question, we investigated the role of pathogen-derived PR1-like proteins (PR1-Ls) in plant-pathogen interactions. Using host-induced gene silencing (HIGS), we demonstrated that two of the four identified PR1-L proteins from *Botrytis cinerea* (BcPR1-Ls) are required for full fungal virulence. In contrast, knockout of two PR1-L homologs from *Pseudomonas syringae* pv. tomato (Pst) did not affect bacterial growth or virulence, suggesting functional divergence between fungal and bacterial PR1-Ls. Preliminary structural predictions using AlphaFold, combined with yeast two-hybrid assays, revealed that BcPR1-Ls interact with plant PR proteins, including Arabidopsis thaliana PR1, PR5, and PR14. These plant PR proteins form homodimers or heterodimers, which enhance resistance, suggesting that pathogen-derived PR1-Ls may interfere with these defense-related interactions to suppress plant immunity. This study sheds light on the dual functionality of PR-like proteins, highlighting their complex roles in plant-pathogen dynamics and offering new perspectives on the molecular mechanisms underlying plant immunity and pathogen virulence.

POSTER

Conditional photosynthesis mutants *abc1k1* and *var2* accumulate partially processed thylakoid preproteins and are defective in chloroplast biogenesis

Joy Collombat[1], Manfredo Quadroni[2], Fiamma Longoni[1], **Felix Kessler**[1]

[1]Institute of biology, Plant Physiology Laboratory, Université de Neuchâtel, Neuchâtel, Switzerland
[2]Protein Analysis Facility (PAF), Université de Lausanne, Lausanne, Switzerland
E-mail: felix.kessler@unine.ch

During biogenesis, chloroplasts import most proteins via the TOC-TIC pathway. But some of them must be transported further across the photosynthetic thylakoid membrane into its lumen. This requires evolutionarily conserved SEC (Secretory) and TAT (Twin Arginine Translocation) pathways. These are energized by ATP and the trans-thylakoid proton gradient, respectively. Most luminal proteins are synthesized in the cytoplasm with bi-partite, cleavable targeting sequences (first for the chloroplast envelope, second for the thylakoid membrane). Two-stage cleavage of these peptides is a critical step of chloroplast biogenesis. Here, we present two mutants (*var2* and *abc1k1)* in which photosynthesis can be reversibly disrupted by red light. Red light arrests chloroplast biogenesis and accumulation of higher molecular mass protein bands can be observed. Deep quantitative proteomics reveal that the higher molecular mass bands belong to a specific module of proteins extrinsically associated with luminal side of Photosystems I and II and correspond to rarely observed partially processed intermediates. These still possess the targeting sequences for the thylakoid SEC and TAT machineries. The results show that the processing of a specific module of Photosystem-associated proteins and concomitantly progression of chloroplast biogenesis depend on active photosynthesis early in plant development.

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POSTER

Environmental control of shoot architecture in Arabidopsis

Cindy Chen, **Martina Legris**

Institute of Biology, University of Neuchâtel
E-mail: martina.legris@unine.ch

Shoot architecture is a plastic trait determined by the number, position and shape of leaves and branches, and it is a key determinant of reproductive success. In this project we aim at evaluating the regulation of branch development by light and temperature signals using Arabidopsis as a model. Branches develop in the axils of leaves, where an axillary meristem produces a small bud, that can remain dormant or be activated to form a branch. Shade light signals arising from neighboring plants inhibit bud outgrowth. This response is triggered by the light receptor phytochrome B (phyB) which regulates PHYTOCHROME INTERACTING FACTOR 4 (PIF4) and PIF5, and the branching regulator BRANCHED 1 (BRC1). These factors modulate auxin and ABA to inhibit bud outgrowth. However, in recent years it has become evident that other PIFs have a stronger role regulating shade avoidance responses. Moreover, the temporal and spatial regulation of this response remains unexplored. Finally, phyB and PIFs are also key factors regulating temperature responses, but how temperature regulates branching, and whether these factors have a role in the process remains unknown. Our preliminary experiments identified new putative branching regulators in Arabidopsis, and novel phenotypes of phyB mutants regarding the spatio-temporal development of axillary buds.

POSTER

Phototropism regulated through PKS – BPM interaction?

Lucius Muthert, Christian Fankhauser

Center for Integrative Genomics, University of Lausanne, Lausanne, Switzerland
E-mail: lucius.muthert@unil.ch

Plants show various responses to uneven light environment in order to increase the amount of light they capture. Phototropism is one of these responses, and known to rely on the blue light photoreceptors called phototropins. While it is known that in the end auxin asymmetry leads to hypocotyl bending, the links between phototropins and auxin are missing. The intrinsically disordered PHYTOCHROME KINASE SUBSTRATE (PKS) proteins interact with the phototropins and are critical for normal bending towards blue light. While their exact role is not known, it is clear that their function in phototropism is mediated through one specific conserved motif. We have found several BTB/POZ-MATH (BPM) proteins to interact with this motif, and several higher order *BPM* mutants have altered phototropism. Especially in phototropism under true shade conditions, certain *BPM* mutants exhibit strongly enhanced bending. Given their role as substrate adaptors for E3 ubiquitin ligases, it is seems likely that the effect of BPM proteins on phototropism is exerted through control of PKS protein levels. Understanding this interaction would give us insight on how plants manage to adapt a single response – phototropism – to various different conditions, including shade.

POSTER

GPAT2 acts non-redundantly with GPAT4/8 in the formation of the cutin of the *Arabidopsis* root cap cuticle

Alice Berhin[1], Aurore Guerault[1], Damien de Bellis[1,2], **Christiane Nawrath**[1]

[1]Department of Plant Molecular Biology, University of Lausanne, Lausanne, Switzerland
[2]Electron Microscopy Facility, University of Lausanne, Lausanne, Switzerland
E-mail: christiane.nawrath@unil.ch

During embryogenesis, a cuticle is formed that surrounds the entire embryo. The embryonal cuticle is present at the surface of the root cap of the seedling during the first days after germination protecting the root meristem in the altered environmental conditions. The cutin of the root cap cuticle (RCC) of Arabidopsis has an unusual composition, not only being rich in oxygenated fatty acids, but also in saturated and monounsaturated C26 and C28 unsubstituted fatty acids. The biosynthesis of the cutin in the RCC depends on the redundantly acting glycerol-3-phosphate acyltransferases GPAT4 and GPAT8 as well as on DEFECTIVE IN CUTICULAR RIDGES (DCR) and BODYGUARD (BDG). Strikingly, only oxygenated fatty acids are reduced in the *gpat4gpat8* double mutant. Here we show that GPAT2 is necessary for the incorporation of very long-chain fatty acids in the RCC and plays only a minor role in the incorporation of oxygenated fatty acids. The *gpat2* mutant exhibits ultrastructural changes of the RCC, increased RCC permeability, and higher sensitivity to abiotic stress conditions. This resembles the *gpat4gpat8* mutant highlighting the non-redundant functions of GPAT2 and GPAT4/8. Furthermore, we identified a role of the long-chain acyl-CoA transferase LACS2 in the incorporation of exclusively oxygenated fatty acids in the cutin of the RCC. The findings suggest two largely separated pathways for the early steps in cutin biosynthesis.

POSTER

RNA regulation in warm conditions

Jingmin Hua, Dominique Vuarambon, Shitij Gupta, Dolly Mehta, Lázara Simões, **Rodrigo S. Reis**

Institute of Plant Sciences, University of Bern
E-mail: rodrigo.reis@unibe.ch

Warmer temperatures can cause various physiological and phenotypic changes in plants, many of which with detrimental consequences, and theses processes are regulated by a diverse set of molecular mechanisms. Temperature is also a major parameter for RNA structure formation and stability, and the plant cell's environment, with its constant shifts in temperature, might have created ideal conditions for RNA structures to be selected and genetically transmitted as an adaptive mechanism to temperature increases. We have identified several genes post-transcriptionally regulated in Arabidopsis seedlings exposed to minutes or days to warm temperature. Our current data provides new insights into plant perception and acclimation to warmth, and indicates a regulatory role for temperature-sensitive RNA structures.

The phosphatase PP2C12 is a negative player in LRX-RALF-FER-mediated cell wall integrity sensing

Xiaoyu Hou, Kyle Bender, Cyril Zipfel, **Christoph Ringli**

Department of Plant and Microbial Biology, University of Zurich
E-mail: chringli@botinst.uzh.ch

Plants have evolved an elaborate cell wall integrity (CWI) sensing system to monitor and modify cell wall formation. LRR-extensins (LRXs) are cell wall-anchored proteins that bind RAPID ALKALINIZATION FACTOR (RALF) peptide hormones and induce compaction of cell wall structures. At the same time, LRXs form a signaling platform with RALFs and the transmembrane receptor kinase FERONIA (FER) as a means to relay changes in CWI to the protoplast. *LRX1* of *Arabidopsis thaliana* is predominantly expressed in root hairs and *lrx1* mutants develop defective root hairs. Here, we identify a regulator of LRX1-RALF-FER signaling as a suppressor of the *lrx1* root hair phenotype. The *repressor of lrx1_23* (*rol23*) gene encodes PP2C12, a type 2C phosphatase of clade H that interacts with FER and dephosphorylates Thr696 in the FER activation loop *in vitro*. The LRX1-related function of PP2Cs appears clade H-specific and was not observed for other PP2Cs investigated. Collectively, our data suggest that LRX1 acts upstream of the RALF1-FER signaling module and PP2C12 has an inhibitory activity via modulating FER activity to fine-tune CWI signaling.

POSTER

Revealing cryptic modifiers that affect inflorescence architecture in tomato

Gwen Swinnen[1,2], Stéphanie Afonso[2], Sebastian Soyk[1,2]

[1]Department of Plant Molecular Biology, University of Lausanne, Lausanne, Switzerland
[2]Center for Integrative Genomics, University of Lausanne, Lausanne, Switzerland
E-mail: gwen.swinnen@unil.ch

A major goal in genetics is to uncover the genes and variants that underlie phenotypic diversity. However, the effect of individual variants is often modified by genetic interactions with additional loci, which limits our ability to link genotypes to phenotypes and thus presents a barrier for crop improvement. In domesticated tomato (*Solanum lycopersicum*), the *compound inflorescence 2* (*s2*) mutant develops strongly branched inflorescences, leading to a reduction in fruit yield. However, inflorescence branching is suppressed when *s2* mutations are introduced into the genome of the wild tomato progenitor species *S. pimpinellifolium*. This example of a cryptic genetic modification was recently mapped to a ~9 Mbp locus on chromosome 2 and designated *suppressor of branching 2* (*sb2*) but the causative gene variant(s) that underlie *sb2* remained unknown. Here, we fine-map the *sb2* locus to *ANANTHA*, a homolog of Arabidopsis *UNUSUAL FLORAL ORGANS* and a key regulator of tomato inflorescence development. With no coding sequence variation present in *ANANTHA*, we utilize genome editing of cis-regulatory regions to investigate how changes in *ANANTHA* expression can explain variation in inflorescence branching between wild and domesticated tomato. Understanding how genetic interactions and cryptic variation contributed to crop domestication can allow a better prediction of phenotypes from genotypes and offer potential strategies for fine-tuning flower number in crop breeding.

LIST OF PARTICIPANTS

Family Name	First Name	Affiliation
Aurangzeb	Wajid	Tuscia U.
Badet	Thomas	UNINE
Ballabani	Gent	UNINE
Barberon	Marie	UNIGE
Baroux	Celia	UNIZH
Blanco-Touriñán	Noel	UNIL
Boller	Thomas	UNIBA
Bomblies	Kirsten	ETHZ
Boutet	Emmanuel	UNIGE
Capitão	Maria Beatriz	UNIGE
Charlet de Sauvage	Justine	WSL
Csilléry	Katalin	WSL
Demarsy	Emilie	UNIGE
Emonet	Aurélia	UNIBE
Erb	Matthias	UNIBE
Fankhauser	Christian	UNIL
Feller	Anna	ETHZ
Geldner	Niko	UNIL
Grossniklaus	Ueli	UNIZH
Han	Zhu	UNIFR
Hothorn	Michael	UNIGE
Hyvärinen	Lena	UNINE
Jullien	Pauline	UNIBE
Kalmbach	Lothar	UNINE
Kessler	Felix	UNINE
Legris	Martina	UNINE
Lindner	Heike	UNIBE
Lopez-Molina	Luis	UNIGE
Majda	Mateusz	UNIL
Marín	Macarena	UNIL
Menardo	Fabrizio	UNIZH
Muthert	Lucius	UNIL
Naciri	Yamama	UNIGE
Nawrath	Christiane	UNIL
Pannell	John	UNIL
Parisod	Christian	UNIFR
Poirier	Yves	UNIL
Qin	Yangyang	UNIFR
Raissig	Michael	UNIBE
Ramakrishna	Priya	EPFL
Reinhardt	Didier	UNIFR
Reis	Rodrigo	UNIBE
Rentsch	Doris	UNIBE
Reymond	Philippe	UNIL
Ringli	Christoph	UNIZH
Roulin	Anne	Agroscope
Santiago	Julia	UNIL
Schlaeppi	Klaus	UNIBA
Schuman	Meredith	UNIZH
Shimizu	Kentaro	UNIZH
Simonini	Sara	UNIZH
Soyk	Sebastian	UNIL
Swinnen	Gwen	UNIL
Ulm	Roman	UNIGE
Venkatasalam	Shanmugabalaji	UNINE
Vermeer	Joop	UNINE
Wicker	Thomas	UNIZH
Zeeman	Samuel	ETHZ
Zipfel	Cyril	UNIZH
Züst	Tobias	UNIZH