SwissPLANT 2026

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Symposium “Plant Science Research’

34th edition

Organizing committee
Martina Legris, Lena Hyvärinen, Felix Kessler, Daniel Croll, Lothar Kalmbach and Joop Vermeer
University of Neuchâtel

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SwissPLANT 2026

14 – 16 January 2026
Les Diablerets, Switzerland

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Venue

The Glacier Hotel
Chemin du Vernex 3, 1865 Les Diablerets

Organizing committee

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Swiss Society of Plant Biology, Annual Report & SwissPLANT 2026

In 2025, 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 just before SwissPLANT2025. We elected our new board and presidency for 2025-2027. We welcomed Prof. Marie Barberon as new board member joining Profs Kirsten Bomblies, Klaus Schlaeppi, Thomas Boller, Cyril Zipfel and Christian Fankhauser. We started a new rolling presidency system with Christian Fankhauser serving for his last year as president in 2025, then Cyril Zipfel for 2026 and Kirsten Bomblies for 2027. Starting in 2026 we will have administrative support from Luisa Last who is also working at the Zurich-Basel Plant Science Center. We are hopeful that this will allow us to improve communication within our society and beyond. Specifically, we plan to implement a new web site dedicated to the Swiss Society of Plant Biology.

We were particularly pleased to obtain SCNAT's support for the Early Career Meeting (ECM) that we started in 2023. This allowed us to organise this exciting event for the 4th time just before the 2026 edition of our annual SwissPLANT symposium.

In December 2025, the Society had 109 members. We keep encouraging all Swiss Plant Science Web (SPSW) members to join.

We note that recent changes in available funds at the Swiss National Science Foundation and the way the grants are evaluated led to an alarmingly high rejection rate amongst members of our society. We would like to discuss what can be done regarding these developments 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, Marie Barberon, Kirsten Bomblies, Thomas Boller, Cyril Zipfel and Klaus Schläppi with whom I had the pleasure working in 2025. I will gladly stay in the board and wish the best of luck to its new president Cyril Zipfel.

I cordially thank Martina Legris, Lothar Kalmbach, Lena Hyvärinen, Daniel Croll, Felix Kessler and Joop Vermeer for organizing the SwissPLANT 2026 conference, and Matina and Lothar for also organizing the Early Career Meeting.

Christian Fankhauser, President of the Swiss Society for Plant Biology Christian Fankhauser, President of the Swiss Society for 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, 14 January 2026

15:45 Swiss Society of Plant Biology, General Assembly 2025 (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 Joop Vermeer, chair of the Organizing Committee

Gentiana alpina Session, chair: Joop Vermeer

18:00 **Tonni Grube Andersen** | University of Zürich
We will block you: the interplay between physical and chemical root barriers

18:20 **Heike Lindner** | University of Bern
Stay hydrated – Deciphering the development and physiology of leaf succulence

18:40 **Quint Rusman** | University of Zürich
Coevolution in a warming world: an experimental test of the geographic mosaic of coevolution

19:00 **Klaus Schlaeppi** | University of Basel
Soil iron and root immune components mediate microbiome feedbacks in Arabidopsis

19:30 Dinner, afterwards discussion at the bar

Thursday, 15 January 2026

07:00 Breakfast

Viola cenisia Session, chair: Martina Legris

08:00 **Cyril Zipfel** | University of Zürich
Solving the puzzle of early cell-surface immune signaling, one piece at a time

8:20 **Anne C. Roulin** | Agroscope
Polygenic architecture of flowering time and its relationship with local environments in the grass *Brachypodium distachyon*

08:40 **Philippe Reymond** | University of Lausanne
The glutamate receptor-like GLR2.7 modulates insect egg-induced defense responses in Arabidopsis

09:00 **Tobias Züst** | University of Zürich
Evidence for synergistic interactions between chemical and physical defences in a recently derived plant lineage

09:20 **Rodrigo S. Reis** | University of Bern
RNA turnover mediates the plant growth-defense tradeoff at warm temperatures

09:40 Coffee break

Androsace alpina Session, chair: Lena Hyvärinen

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

10:50 **Daniel Croll** | University of Neuchâtel
Tracking plant pathogen emergence using thousand-genome panels

11:10 **Ewumi Azeez Folorunso** | Zurich University of Applied Sciences
The potential of indigenous microbial isolates of soilless systems as biocontrol agents and growth promoters

11:30 **Nathalie Wuyts** | Agroscope / SPPN Coordinator
The Swiss Plant Phenotyping Network (SPPN)

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

Dryas octopetala Session, chair: Lothar Kalmbach

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

17:50 **Elisabeth Truernit** | ETH Zürich
OPS Family Genes Integrate Phloem Differentiation and Meristematic Activity in Arabidopsis Roots

18:10 **Emmanuel Boutet** | SIB - Swiss Institute of Bioinformatics
Updates to plant protein sequences and annotations in UniProtKB

18:30 **Niko Geldner** | University of Lausanne
The basis of receptor signaling specificity

19:00 Dinner

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

Friday, 16 January 2026

07:00 *Breakfast*

Sempervivum montanum Session, chair: Daniel Croll

8:00 **Federica Schranz** | Getting attached to seaweed: ecological impact of cultivated sugar kelp and its associated microbiota in the North Sea

8:20 **Christian Fankhauser** | University of Lausanne
Internal sugar allocation in response to a shade signal is regulated by concerted action of auxin and sucrose

8:40 **Lothar Kalmbach** | University of Neuchâtel
Development Under High Pressure – Cell Walls in the Phloem

9:00 **Doris Rentsch** | University of Bern
Transporters are main drivers for organic nitrogen use efficiency

9:20 **Christian Parisod** | University of Fribourg
The role of whole-genome duplication vs post-polyploidy evolution in adaptation to environmental changes

9:40 *Coffee break*

Leontopodium alpinum Session, chair: Felix Kessler

10:30 **Julia Santiago** | University of Lausanne
Glycan recognition by a plant sentinel immune receptor

10:50 **Christian S. Hardtke** | University of Lausanne
The Genetics of Paradoxes – an alternative history of the BRX story

11:10 **Marie Barberon** | University of Geneva
GWAs reveals SUBER GENE1-mediated suberization via Type One Phosphatases

11:30 Closing remarks by Joop Vermeer

We will block you: the interplay between physical and chemical root barriers

Tonni Grube Andersen

Affiliation(s) University of Zurich, Department of Plant and Microbial Biology, Zurich, Switzerland Max Planck Institute for Plant Breeding, Cologne, Germany
Email: Tonni.andersen@uzh.ch

Arabidopsis roots are widely used as a model for developmental biology, but most studies stop before day 10, overlooking the onset of periderm development. This secondary barrier tissue is poorly understood, particularly in soils that resemble agricultural conditions. In this talk, I will present work on a mutant with a dysfunctional periderm, combining spatially resolved -omics, exudates and microbial community profiling to connect responses with root axial developmental patterns. Our results show that periderm-based physical barriers are tightly linked to chemical defense mechanisms, and that this integration has major consequences for root performance and survival in complex, microbially active soils.

Stay hydrated – Deciphering the development and physiology of leaf succulence

Antonio Aristides Pereira Gomes Filho[1,2], Alexander Betekhtin[3], **Heike Lindner[1,2]**

[1]Institute of Plant Sciences, University of Bern, Switzerland
[2]Oeschger Centre for Climate Change Research, University of Bern, Switzerland
[3]Institute of Biology, Biotechnology and Environmental Protection, University of Silesia in Katowice, Poland
Email: heike.lindner@unibe.ch

Succulent plants have evolved anatomical and physiological characteristics that enabled their expansion into arid environments. Specialized succulent tissues store- and remobilize water during water-scarce growth periods, and the most water-use efficient mode of photosynthesis, Crassulacean Acid Metabolism (CAM), allows for an advantageous flexibility in hot and dry environments. However, whether succulent anatomy is required for efficient CAM photosynthesis and how its development is regulated remain largely unknown.

Here, we use the leaf succulent *Kalanchoë laxiflora*, a constitutive CAM plant with a developmental transition from C_3 photosynthesis in young leaves to CAM photosynthesis in mature leaves. This transition enabled the detailed description of anatomical, physiological, and metabolic differences between C_3 and CAM leaves within a single plant individual. We observed increasing succulent anatomy accompanied by a gradual transition from C_3 to CAM photosynthesis, where succulent anatomy development preceded CAM physiology. This indicates that succulent anatomy not only enables water-storing capacity but might also be required for efficient CAM photosynthesis. We will now use single-nucleus transcriptomics, gene editing, and forward genetics to identify developmental modules required for leaf succulence. Through the manipulation of distinct anatomical leaf traits, we will be able to experimentally link anatomical aspects of leaf succulence to CAM physiology and, with that, understand strategies of succulents to survive prolonged drought periods.

Coevolution in a warming world: an experimental test of the geographic mosaic of coevolution

Quint Rusman, Tyler Figueira, Juan Traine, Florain P. Schiestl

Department of Evolutionary and Systematic Botany, University of Zurich
Email: quint.rusman@syst.bot.uzh.ch

According to the geographic mosaic theory of coevolution (GMTC), coevolution varies with abiotic and biotic environmental factors. We assessed this hypothesis using experimental plant-butterfly coevolution and by testing the effects of temperature and the presence of mutualistic bumblebees on co-divergence during six generations of selection. Butterflies are mutualistic by pollinating plants and antagonistic by ovipositing on plants from which caterpillars feed. We found unique plant-butterfly coevolutionary trajectories in response to abiotic and biotic factors: plants evolved strong herbivore resistance when exposed to either bumblebee presence or elevated temperatures, while their combination led to less strong plant-resistance evolution and the evolution of flower-advertisement and butterfly-foraging traits. We provide experimental proof for the GCMT and show rapid divergent coevolution to the combination of local abiotic and biotic conditions. Global warming will likely have profound impact on the geographic mosaic of coevolution and lead to new coevolutionary trajectories.

Soil iron and root immune components mediate microbiome feedbacks in Arabidopsis

Klaus Schlaeppi and TEAM

University of Basel
Email: klaus.schlaeppi@unibas.ch

The compositions of soil microbiomes affect growth and health of plants growing in complex soils. While the (agro-)ecological impact of such microbiome feedbacks is well established, their very high variability by soil context and plant varieties remains a major unresolved issue. We have established a model system with *Arabidopsis thaliana* to investigate the mechanisms of plant feedbacks to differential soil microbiomes. We also find the microbial feedbacks of Arabidopsis plants to vary strongly with soil batches and plant genotype. Using multivariate, correlation and modelling approaches and including additional data from field experiments, we identified plant-available iron to explain the variation of microbiome feedbacks on plants. We demonstrate that beneficial microbiome feedbacks occur mainly at low levels of plant-available iron, i.e. when plants grow in suboptimal soil. The main usage of our system however, is to investigate how plants perceive soil microbiomes and how they modulate their performance in response to microbiome feedbacks. Based on natural variation among Arabidopsis accessions and a screen for genome-wide associations, we found several gene candidates to be associated with microbiome feedbacks. Most advanced is our work on a TNL receptor termed Mediator of Microbiome Feedbacks 1 (MMF1). An update on recent results that point towards the importance of root immune components as genetic determinants for microbiome feedbacks in Arabidopsis will be presented.

Solving the puzzle of early cell-surface immune signaling, one piece at a time

Cyril Zipfel[1,2]
[1]*Institute of Plant and Microbial Biology, Zurich-Basel Plant Science Center, University of Zurich, Zurich, Switzerland.*
[2]*The Sainsbury Laboratory, University of East Anglia, Norwich Research Park, Norwich, United Kingdom.*
Email: Cyril.Zipfel@botinst.uzh.ch

Plant immunity relies on cell-surface pattern recognition receptors (PRRs) that mediate cellular signaling outputs upon perception of their ligands (pathogen-associated molecular patterns, damage-associated molecular patterns, or phytocytokines), as part of pattern-triggered immunity. These signaling events include rapid fluxes of Ca^{2+} and other ions, reactive oxygen species production and distinct phosphorylation cascades. Many plant PRRs are receptor kinases or are part of receptor kinase-containing complexes. An important question has been how ligand-activated PRR complexes induce intracellular signaling events. I will present our biochemical and genetic efforts to address this question; mostly through the identification and characterization of substrates of the plasma-associated receptor-like cytoplasmic kinase BIK1 that acts downstream of multiple PRR complexes to orchestrate immune signaling.

The Swiss Plant Phenotyping Network (SPPN)

Nathalie Wuyts

SPPN Coordinator, Agroscope, Plant Production Systems, Cultivation Techniques and Varieties in Arable Farming, Nyon
Email: nathalie.wuyts@agroscope.admin.ch

The Swiss Plant Phenotyping Network (SPPN) is set to become recognized as a national node of EMPHASIS, the European infrastructure for plant phenotyping. EMPHASIS aims to provide access to high-quality research infrastructure across its member nodes. Further services in the field of plant phenotyping will include across-EMPHASIS development of FAIR data management and standards, as well as the provision of education and training and the dissemination of advances in plant phenotyping technology and data processing. The SPPN will facilitate the involvement of Swiss researchers in delivering and using EMPHASIS services.

The SPPN has recently grown to include members from beyond its two founding institutions, AGROSCOPE and ETH Zurich, encompassing the wider scientific community, industry and non-profit organizations. Our research themes span the broad range from fundamental research in ecology and biology using model plants and crops to applied research in field and orchard crops. Research is conducted at scales ranging from the landscape level to the individual plant and organ level.

The SPPN organizational framework involves a top-down approach, whereby the EMPHASIS functional units, i.e. the executive bodies responsible for delivering services, are matched by key topic groups in SPPN. This enables efficient and decisive interaction with EMPHASIS. Conversely, SPPN members use a bottom-up approach based on working groups to define topics of particular concern to the national community.

The glutamate receptor-like GLR2.7 modulates insect egg-induced defense responses in Arabidopsis

Maria Mineiro[1], Raphael Groux[1], Caroline Gouhier-Darimont[1], Pierre Mateo[2], Christelle Aurelie Maud Robert[2] and **Philippe Reymond[1]**

[1]Department of Plant Molecular Biology, University of Lausanne, Lausanne
[2]Institute of Plant Sciences, University of Bern, Bern
Email: philippe.reymond@unil.ch

Insect eggs activate an immune response that culminates in cell death in *Arabidopsis thaliana*. While inducing this defense can subsequently impact egg survival, the molecular mechanisms are poorly understood. Through a genome-wide association study (GWAS), we identified the amino acid-gated calcium channel GLUTAMATE-LIKE RECEPTOR2.7 (GLR2.7) as an important factor controlling the extent of cell death and accumulation of salicylic acid (SA) in response to egg extract of *Pieris brassicae*. Analysis of natural polymorphisms revealed two major haplotypes that segregate at the species-wide, probably via balancing selection at this locus. Insect oviposition triggered a long-lasting and localized cytosolic calcium accumulation that depended on GLR2.7 and was linked with egg-associated glutamate (Glu) and glutathione (GSH). We propose that Glu/GSH-activated GLR2.7 is involved in egg perception and early immune responses.

Evidence for synergistic interactions between chemical and physical defences in a recently derived plant lineage

Tobias Züst

Department of Systematic and Evolutionary Botany
Email: tobias.zuest@systbot.uzh.ch

The evolution of novel defensive traits can reshape plant–herbivore interactions, yet how newly gained defences integrate with other defensive traits remains unclear. *Erysimum cheiranthoides* (Brassicaceae) recently evolved the ability to produce cardenolide toxins in addition to ancestral glucosinolates, and the genus is further characterized by unusually dense trichomes that differ from those of its closest non-*Erysimum* relatives. To dissect the individual and combined contributions of these defences, we used CRISPR–Cas9 to generate factorial knockouts of cardenolide biosynthesis and trichome development. We then quantified feeding behavior and short-term performance of two specialist herbivores, *Pieris rapae* and *Plutella xylostella*. *P. rapae* strongly rejected cardenolide-producing plants and experienced high levels of mortality. When cardenolides were absent, caterpillars consumed leaf tissue but still lost mass, indicating an additional constraint on performance. Positive growth occurred only on plants lacking both cardenolides and trichomes. In contrast, *P. xylostella* did not avoid cardenolides, yet growth was lowest on wild-type plants and highest on double knockouts. Together, these results reveal synergistic interactions between two independently derived defences and demonstrate how recent molecular innovations can integrate to generate emergent ecological effects.

RNA turnover mediates the plant growth-defense tradeoff at warm temperatures

Dominique Jacques-Vuarambon[1], Borys Alexander León Alcivar[1,2], Jingmin Hua[1], Dolly Mehta[1], Lázara Aline Simoes Silva[1,3], **Rodrigo S. Reis**[1]

[1]Institute of Plant Sciences, University of Bern, Switzerland
[2]Department of Biochemistry and Molecular Biology, Federal University of Viçosa, Brazil
[3]Department of Plant Biology, Federal University of Viçosa, Brazil
Email: rodrigo.reis@unibe.ch

Plant response to warm temperatures involves coordinated morphological changes, including hypocotyl, root, and petiole elongation. This developmental reprogramming is a conserved acclimatisation mechanism to warming conditions in plants, with various negative impact on crop yield, food quality, and disease resistance. Here, we show that warm temperatures trigger selective, organ-specific changes in RNA turnover. We found that mutants in decay pathway genes are affected in plant response to warm temperature, showing that RNA turnover is critical in this process. Transcriptome-wide analysis revealed that defense-related mRNAs (SA, JA, and glucosinolate pathways) are selectively destabilised by increased temperatures. Consistently, *DCP5* mutant, which is partially impaired in cytoplasmic RNA degradation and storage, including defence-related mRNAs, displays enhanced resistance to bacterial infection. Collectively, our work identifies RNA turnover as a central regulatory mechanism that suppresses immunity to prioritize growth under warming conditions.

Tracking plant pathogen emergence using thousand-genome panels

Daniel Croll

Institute of Biology, University of Neuchatel
Email: daniel.croll@unine.ch

Adaptation of plant pathogens proceeds at speeds that easily overwhelm the rate of resistant cultivar deployment and fungicide development. Low cultivar diversity and the application of single fungicides can exacerbate these dynamics. Understanding the molecular basis of pathogen adaptation is critical to define more sustainable containment strategies. Emerging traits such as virulence on resistant cultivars or fungicide resistance often appear in a geographically structured manner. Such geographic mosaics can be determined by regional variation in selection pressures or as a consequence of the pathogen's population history. I will introduce the use of very large panels of pathogen genomes from the same species. Such genome panels can recapitulate historic colonization patterns and reveal constraints on pathogen genetic diversity. In combination with phenotyping assays, large genome panels enable the tracking of fungicide resistance mutations across continents and reveal how effector gene loci are undergoing adaptive sequence rearrangements. Recent research has pointed to selfish elements (i.e. transposable elements) as key factors in pathogen evolution, facilitating adaptation to biotic and abiotic factors in their environment. Selfish elements, by nature, can also impact the integrity of genomes and lead to deleterious dynamics for the pathogen. In conclusion, large-scale genomic investigations of individual pathogen species unravel essential mechanisms of pathogen adaptation.

The potential of indigenous microbial isolates of soilless systems as biocontrol agents and growth promoters

Ewumi Azeez Folorunso[1,3], Glory Hartmann[1], Felix Kuebutornye[1], Andrea Bohata

[1]Faculty of Fisheries and Protection of Waters, University of South Bohemia in České Budějovice, South Bohemian Research Center of Aquaculture and Biodiversity of Hydrocenoses, Institute of Aquaculture and Protection of Waters, České Budějovice, Czech Republic
[2]Department of Plant Protection, Faculty of Agriculture and Technology, University of South Bohemia in Ceske Budejovice, České Budějovice, Czech Republic
[3]Environmental Genomics and Systems Biology Research Group, Institute of Natural Resource Sciences, Zurich University of Applied Sciences, Wädenswil, Switzerland
Email: Efolorunso@frov.jcu.cz

Aquaponics integrate fish culture and hydroponic plant cultivation, enabling nutrient recycling and water conservation. However, because both plants and fish share the same water-loop, there is an essential challenge associated with managing plant pests and pathogens, as chemical treatments may be toxic to fish and beneficial microbes within the system. This study examined the potential of microbes originating from soilless systems as biocontrol agents and plant growth promoters. Pure strains were isolated from the root of lettuce (*Lactuca sativa*) and basil (*Ocimum basilicum*) grown for 7 weeks in hydroponics and aquaponics. The isolates were screened for antagonistic activity against *Fusarium oxysporum, Sclerotinia sclerotiorum*, and *Rhizoctonia solani,* using dual culture methods. Phosphorus solubility potential was assessed by growing the isolates in Pikosvkaya's media, while iron solubility potential was tested using CAS assay. The result showed that isolates APB1B1 (~50%) and APB21 (~36%) demonstrated efficient suppression of *R. solani* and *S. sclerotium*, respectively, whilst isolate HPB1B1 had the highest inhibition against *F. oxysporum* (72.44%). In the phosphorus solubility result, isolate APB2B showed the highest phosphorus solubilisation index at 1.21, showing a significant potential of increasing the biological availability of the nutrient to plants. This study shows that microbial isolates from soilless systems possess the potential to act as biocontrol agents as well as plant-growth promoters.

Polygenic architecture of flowering time and its relationship with local environments in the grass Brachypodium distachyon

Nikolaos Minadakis, **Anne C. Roulin**

Agroscope – Wadenswil
Email: anne.roulin@agroscope.admin.ch

Synchronizing reproductive timing with environmental conditions is crucial for annual plants in the wild. Among the mechanisms they use to sense their environment, cold-mediated vernalization is a major process that prevents flowering during winter. In many annual species, including crops, both long and short vernalization requirements occur within the same species, producing early- (spring) and late- (winter) flowering genotypes. Here, I present how we used *Brachypodium distachyon* to explore the links between flowering-time traits, environmental variation, and genetic diversity at flowering-time loci by combining greenhouse and outdoor experiments. These experiments confirmed that natural *B. distachyon* accessions exhibit substantial variation in vernalization requirements and consequently in flowering time. We also highlight significant, though quantitative, effects of current environmental conditions on these traits. Although disentangling the confounding role of population structure on flowering-time variation remains challenging, population genomics analyses suggest that well-characterized flowering-time genes contribute quantitatively to phenotypic variation and exhibit signatures of polygenic selection. Together, our work advances the understanding of the polygenic architecture of flowering time in a natural grass system and opens new avenues for investigating the gene-by-environment interactions underlying this key adaptive trait.

OPS Family Genes Integrate Phloem Differentiation and Meristematic Activity in Arabidopsis Roots

Simona Crivelli, Kai Bartusch, M. Aguila Ruiz-Sola, Mario Coiro, Signe Schmidt Kjølner Hansen, **Elisabeth Truernit**

Institute of Molecular Plant Biology, ETH Zürich
Email: etruerni@ethz.ch

Roots act as classic sink organs, relying on the phloem to deliver carbohydrates produced through photosynthesis in source tissues. Sugars synthesized mainly in mature leaves move through the metaphloem sieve elements during long-distance transport. As they approach the root apex, they are redirected into the protophloem sieve elements and subsequently unloaded into neighboring tissues. Our earlier work identified *OCTOPUS* (*OPS*), a gene expressed specifically in the phloem, together with its more broadly expressed homolog *OPS-LIKE 2* (*OPL2*), as regulators of protophloem and metaphloem differentiation in the root. More recently, we examined the roles of the remaining three *OPS* homologs in the Arabidopsis genome, *OPL1*, *OPL3*, and *OPL4,* and found that, although they do not influence phloem development, their loss further compromises root growth beyond the defects observed in the *ops opl2* background. These findings point to a direct role for the examined *OPL* genes in sustaining meristematic activity. Moreover, they indicate that balanced expression of these genes across root cell files is crucial for optimal root growth, with *OPS* and the phloem domain contributing most prominently. This highlights the phloem's essential function as a growth organizer, extending beyond its physiological responsibility for solute transport. Nonetheless, separating this organizational capacity from its transport role remains difficult.

Updates to plant protein sequences and annotations in UniProtKB

Emmanuel Boutet, the Swiss-Prot group

Swiss-Prot Group, SIB - Swiss Institute of Bioinformatics
Email: emmanuel.boutet@sib.swiss

I will cover recent updates to the UniProtKB knowledgebase (www.uniprot.org) affecting plant proteome users, including: 1) the *Arabidopsis thaliana* proteome update with the new genome assembly, and 2) changes to UniProtKB protein contents from the new Reference Proteome selection pipeline.

UniProtKB is a central resource for protein sequences and functional annotations used across proteomic, transcriptomic, and genomic research. Its expertly curated UniProtKB/Swiss-Prot section offers comprehensive, experimentally supported information on proteins, including those from key plant models such as *A. thaliana* and *Oryza sativa*. In parallel, UniProtKB/TrEMBL provides programmatically generated entries derived largely from complete proteomes produced by genome sequencing efforts.

A. thaliana remains a foundational plant model. A collaborative effort coordinated by The Arabidopsis Information Resource (TAIR) and involving UniProtKB/Swiss-Prot is contributing to the Columbia cultivar genome assembly. The updated assembly is expected to be released publicly in 2026, and protein sequences predicted from coding sequences will be integrated into UniProtKB to enhance available knowledge for plant biology.

Rapid growth in sequencing output has increased redundancy within UniProtKB/TrEMBL, complicating data management and generating noise in sequence analysis workflows. To address these challenges, we are redesigning our Reference Proteome selection pipeline to improve species biodiversity representation while reducing unnecessary redundancy. Going forward, UniProtKB will include only sequences belonging to a designated reference proteome, alongside all expert-reviewed UniProtKB/Swiss-Prot entries. Deprecated proteomes will remain accessible through UniParc, ensuring continued traceability and data continuity.

The basis of receptor signaling specificity

Niko Geldner

DBMV, University of Lausanne
Email: Niko.Geldner@unil.ch

We have generated a genetic background allowing stimulation of two LRR receptor kinases, FLS2 and SGN3, in a single cell type, the differentiating Arabidopsis root endodermis. Using this system, we have been able to demonstrate that, even at saturating receptor stimulation, distinct RNA profiles are generated, leading to distinct cellular differentiation outcomes, such as the growth and closure of CASPARIAN STRIP MEMBRANE DOMAIN PROTEIN (CASP) microdomains, which is only occurring upon SGN3 stimulation [1]. This signaling specificity can be explained by the differential effects that MKKs and MPKs exert on the transcription factor MYB36, a central regulator of Casparian strip formation, but which specific MKKs/MPKs are activated by FLS2 vs. SGN3 stimulation and how this is achieved remains obscure. We now show that fully distinct sets of membrane-localized RLCKVII-type kinase (PBLs) are used for FLS2 vs. SGN3 signaling. These kinases are known to be direct targets of activated receptor complexes and can account for the distinct patterns of cytosolic calcium and ROS accumulation that we observe after receptor stimulation using genetically-encoded live read-outs. Our data suggests that early signalling specificity is encoded in the differential activity of PBL kinases and translated into different calcium and ROS dynamics. How this is translated into differential activation of MKKs and MPKs in the nucleus remains an open question.

1. Ma, Y. *et al.* Comparisons of two receptor-MAPK pathways in a single cell-type reveal mechanisms of signalling specificity. *Nat. Plants* **10**, 1343–1362 (2024).

Getting attached to seaweed: ecological impact of cultivated sugar kelp and its associated microbiota in the North Sea

Federica R. Schanz[1], Tijs Ketelaar[2], Detmer Sipkema[1]

[1] Laboratory of Microbiology, Wageningen University and Research (WUR), The Netherlands
[2] Laboratory of Cell and Developmental Biology, WUR, The Netherlands
Email : federica.schanz@wur.nl

The European seaweed cultivation sector is receiving growing attention, with sugar kelp (*Saccharina latissima*) being a widely cultivated species, used for food, cosmetics and bioremediation applications. Its biphasic life cycle alternates between microscopic gametophyte and macroscopic sporophyte stages. Direct seeding cultivation involves gluing gametophytes and young sporophytes to ropes, where they attach by rhizoids and mature into harvestable adult sporophytes. However, >90 % of the seeded material fails to attach, posing two upscaling constraints, the understudied ecological impact of the sugar kelp and its associated microbiota, and the considerable economic risks. The Dutch SEASEEDS project addresses these risks. We quantified the viability and sinking rates of detached sugar kelp seeding material. Although its viability declines over time, material persists for over a month. In collaboration with Deltares, we incorporated the sinking rate into hydrodynamic dispersal models for detached seeding material from the novel commercial-scale offshore North Sea Farm #1. The model indicates rapid sinking within the site footprint and limited long-distance transport. As the viability indicates potential for local settlement, we characterized sugar kelp-associated microbiota via 16S rRNA gene amplicon sequencing. We ran a full cultivation cycle monitoring approach at the nearshore Oosterschelde site in comparison with selected NSF1 samples. Our research supports the European seaweed cultivation upscaling, promoting both economic viability and ecological sustainability.

Internal sugar allocation in response to a shade signal is regulated by concerted action of auxin and sucrose

Sandi Paulišić[1], Blanca Jazmin Reyes-Hernández[2], Yetkin Çaka Ince[1], Jade Heinel[1], **Christian Fankhauser[1]** and Johanna Krahmer[2]

[1] Center for Integrative Genomics, University of Lausanne, Switzerland
[2] Department of Plant and Environmental Sciences, University of Copenhagen, Denmark
Email: christian.fankhauser@unil.ch

Plants detect proximity to neighboring vegetation by light spectral signatures which are sensed by phytochrome photoreceptors. As a response, many species grow taller to out-compete their neighbors. In seedlings, the rapid elongation of hypocotyls requires enhanced supply of carbon resources from the cotyledons, transported as sucrose. The mechanisms of how phytochrome signaling regulates carbon allocation are unknown. We show that sucrose biosynthesis, particularly the step catalyzed by sucrose phosphate synthase (SPS), is a key determinant of hypocotyl elongation. Moreover, we demonstrate that auxin is responsible for directing resource allocation to the elongating hypocotyl, and increased sucrose availability promotes elongation only when sufficient auxin is present, revealing an interdependence between sugar supply and auxin. In contrast, our data reveal that reduced sucrose availability does not impair neighbor-proximity-induced auxin synthesis and signaling. Our findings shed light on the regulation of carbon allocation — a process which is poorly understood, despite its importance for crop yield.

Development Under High Pressure – Cell Walls in the Phloem

Lothar Kalmbach[1], Ambre Dalle[1], Leon-Samuel Icking[1]

[1] Institute of Biology, University of Neuchâtel, Rue Emile-Argand 11, 2000 Neuchâtel, Switzerland
Email : lothar.kalmbach@unine.ch

The phloem is the sugar-transporting part of the plant vascular system. Its conductive cells, the sieve elements display extraordinary forms of cellular differentiation. Among the key features are the thick and strong cell walls to withstand the internal pressure, and large cellular connections between neighboring sieve elements, the so-called sieve pores to ensure high transport rates from source tissues (i.e. photosynthetically active leaves) to sinks (roots, fruits, and buds).

We previously demonstrated a necessity for polarly localized CALLOSE SYNTHASE 7 (CALS7) in sieve pores and activity of the pectin-degrading PECTATE LYASE LIKE 12 (PLL12) during sieve pore maturation to ensure sustained phloem transport as plants grow.

Our current works aims at understanding cell wall remodeling in the developing sieve elements. Recent results suggest that CALS7 has a dual role in sieve pore development and putatively adaptive callose deposition that are functionally distinct. We further expect pectin breakdown products, generated through phloem-specific PLL12-activity, to relay critical information during phloem development and, more broadly, organ growth.

Transporters are main drivers for organic nitrogen use efficiency

Robin Bautzmann[1], Viona Ernst[1], Adriana Vega Fernandez[1], Nicolas Maier[2], Marc Mialet[1], Ahmed F. Elfarargi[3], Michaela Freihart[1], Kirsten Schröder[1], Jerome Bechtold[1], Paolo Favaro[2], Thomas E. Juenger[3], **Doris Rentsch**[1]

[1]Institute of Plant Sciences, University of Bern, Bern, Switzerland
[2]Institute for Computer Science, University of Bern, Bern, Switzerland
[3]Department of Integrative Biology, University of Texas at Austin, Austin, USA
Email: doris.rentsch@unibe.ch

The uptake of nitrogen (N) from the soil, its assimilation, and the subsequent reallocation are key processes that drive plant productivity. The efficiency with which N is acquired depends not only on its availability in the soil, but also on the plant's preference for certain forms of N. While inorganic N represents the largest pool of soluble N in many fertilised soils, organic N forms, including amino acids, peptides and proteins, often dominate in natural ecosystems. In agriculture, the application of N in fertilisers is essential for achieving high crop productivity and yield. However, excess application can cause environmental pollution through runoff and volatilisation. Therefore, improving N use efficiency is key to achieving more sustainable agriculture.

By exploring the natural genetic diversity of Arabidopsis, we found that the utilisation of organic N – measured as growth – differed considerably between accessions. Using recombinant Arabidopsis inbred lines with dipeptides as the sole source of N, we identified the peptide transporter PTR1 as a major QTL. Furthermore, a genome-wide association study (GWAS) revealed that the amino acid permease AAP1 was associated with growth on amino acids. These results emphasise the importance of transport systems, however, the underlying mechanisms still need to be fully resolved, and further research is required to demonstrate the significance of these variants in natural ecosystems and crop breeding.

The role of whole-genome duplication vs post-polyploidy evolution in adaptation to environmental changes

Christian Parisod

Department of Biology, University of Fribourg, Switzerland
Email: Christian.parisod@unifr.ch

Whole-genome duplication (WGD) is a major driver of plant evolution, although it remains unclear whether WGD per se fosters adaptive phenotypes and promotes response to selection. Using the *Biscutella laevigata* species complex whose diploids underwent a WGD event that generated autotetraploids some 25 KY ago, we address to what extent WGD promotes adaptation to environmental heterogeneity. We first assessed how populations from both ploidal levels have adapted to contrasted elevation using whole-genome sequence data and transplant experiments. Consistent with a post-WGD enhancement of their adaptive potential, tetraploids showed genetically based fitness variation, whereas diploids maintained considerable fitness homeostasis across elevation. To conclusively quantify the contribution of WGD per se vs post-WGD evolution, we assessed phenotypic and transcriptomic responses of diploids, synthetic tetraploids and established tetraploids to stable vs changing environmental conditions. Although WGD induced immediate phenotypic changes, transcriptional changes were only driven by post-WGD evolution that also reverted traits toward diploid-like values or elaborated them. In particular, WGD reduced fitness and was mitigated by post-WGD evolution that resulted in tetraploids with higher fitness than diploids under changing environments. WGD hence appears as a driver of reproductive isolation, supporting the accumulation of genomic variation in tetraploids and promoting their adaptive evolution under harsh environments.

Glycan recognition by a plant sentinel immune receptor

Pedro Jiménez-Sandoval[1], Caroline Broyart[1†], Owen Kentish[1†], Hyun Kyung Lee[1†], Klara Culjak[2,3], Uwe Osswald[4], Meriem Aitouguinane[2], Emanuele Tettamanti[1], Manon Schmidli[1], Lu Zhang[5,6], Charles Roussin-Lévéillée[7], Diego José Berlanga[2,3,6], Marina Martin-Dacal[2,3], Miguel Angel Torres[2,3,6], Varun Kumar[2], Patricia Fernández-Calvo[2], José M. Jimenez-Gomez[2], Alberto P. Macho[5,6], Fabian Pfrengle[4], Lucía Jordá[2,3,6], Antonio Molina[2,3,6], **Julia Santiago[1]***

The Plant Signaling Mechanisms Laboratory, Department of Plant Molecular Biology, University of Lausanne, 1015, Lausanne, Switzerland.
Email: Julia.santiago@unil.ch

Pathogens target and degrade the extracellular matrix surrounding plant cells. A central question is how cell wall–derived damage-associated molecular patterns (DAMPs) are recognized and integrated to trigger immune responses. We address this question by determining the structure of the multidomain receptor IGP1 in both apo form and bound to the cellulose-derived DAMP cellotriose. Structural analyses reveal that constitutive Leucine Rich Repeat–malectin interactions preconfigure IGP1 for ligand recognition and that the receptor features a highly specific sugar-binding pocket in the LRR domain capable of distinguishing fine variations in glycan structures. By directly sensing cello-oligomers, IGP1 acts as a cell wall sentinel that links pathogen-induced wall degradation to immune alerting, equipping plants to mount rapid and robust defense responses.

The Genetics of Paradoxes – an alternative history of the BRX story

Christian S. Hardtke

Department of Plant Molecular Biology
University of Lausanne
Biophore Building, DBMV
CH-1015 Lausanne
Email: christian.hardtke@unil.ch

Efficient vascular systems were the evolutionary innovation that enabled plants to colonize land and reshape the surface of our planet. The ontogenesis of the primary protophloem vasculature can be traced along a spatiotemporal gradient in the Arabidopsis root meristem, observable at subcellular and molecular resolution. In this context our research uncovered a molecular-genetic network that is essential for precise initiation of the protophloem sieve elements and their timely differentiation. A critical component of this network is a molecular rheostat which modulates auxin flux. It antagonizes an autocrine CLE peptide sensing receptor kinase pathway whose hyperactivity inhibits phloem formation. While it was unclear whether the rheostat antagonizes CLE signaling directly or indirectly, we recently found that it directly interferes with the activity of downstream CLE signal transducers, thereby dampening signaling output. Phloem-specific CLE signaling is further antagonized by the brassinosteroid pathway, which acts in parallel to the rheostat, although it remains unclear how. Using a custom Synthetic Biology tool, we found that this quantitative antagonism occurs at the level of shared transcriptional targets. This insight now enables indirect identification of the elusive downstream effectors that drive protophloem precursor maturation. Our data further explain the frequently paradoxical genetic interactions within the network, revealing that an intricate quantitative interplay between distinct and antagonistic CLE signaling pathways steers phloem formation in the Arabidopsis root.

GWAs reveals SUBER GENE1-mediated suberization via Type One Phosphatases.

Jian-Pu Han[1], Linnka Lefebvre-Legendre[1], Jun Yu[2], Maria Beatriz Capitão[1], Chloé Beaulieu[3], Kay Gully[4], Vinay Shukla[1,6], Yibo Wu[5,7], Andreas Boland[2], Christiane Nawrath[4], **Marie Barberon[1]**

[1]Department of Plant Sciences, University of Geneva, 1205 Geneva, Switzerland.
[2]Department of Molecular and Cellular Biology, University of Geneva, 1205 Geneva, Switzerland.
[3]MARBEC, Univ Montpellier, CNRS, Ifremer, IRD, 34200 Sète, France.
[4]Department of Plant Molecular Biology, University of Lausanne, 1015 Lausanne, Switzerland.[5]Chemical Biology Mass Spectrometry Platform, Faculty of Sciences, University of Geneva, 1205 Geneva, Switzerland.
[6]Current address: Department of Biology, University of Oxford, Oxford OX1 3RB, United Kingdom.
[7]Current address: Department of Biomedical Sciences University of Lausanne, 1011 Lausanne, Switzerland.
Email : marie.barberon@unige.ch

Suberin deposition in the root endodermis is critical for plant nutrient acquisition and environmental adaptation. Here, we used an unbiased forward genetic approach based on natural variation across 284 *Arabidopsis thaliana* accessions to identify novel regulators of endodermal suberization. This screen revealed striking diversity in suberin levels and patterns, uncovering broader roles for suberin beyond those observed in the reference accession Col-0. A genome-wide association study pinpointed *SUBER GENE1* (*SBG1*), a previously uncharacterized gene encoding a 129-amino acid protein, as a key regulator of suberin deposition. SBG1 acts through physical interaction with type one protein phosphatases (TOPPs) via conserved SILK and RVxF motifs. Disrupting this interaction abolishes SBG1 function, while *topp* mutants exhibit enhanced endodermal suberization, mirroring *SBG1* overexpression. Our findings uncover a previously unknown regulatory module linking suberin formation to TOPP activity and ABA signaling and provide a framework for improving plant stress resilience through targeted manipulation of root barrier properties.

Excess endoreduplication correlates with cellular defects in neo- autopolyploid Arabidopsis arenosa that are remedied in established polyploids

Meschichi, Anis1; Dukić, Marinela1; Schmid Lars1; Bachmann, Andreas1; Tan, Hui San1; Bomblies, Kirsten1

1 Institute of Molecular Plant Biology, Department of Biology, ETH Zürich, Zürich, Switzerland
Email: kirsten.bomblies@biol.ethz.ch

Whole-genome duplication (WGD) is common in plants and can lead to both fertility problems and compromised tissue integrity due to larger, softer cells. Endopolyploidy is where specific somatic cells undergo extra genome duplications and is also linked to increased cell size and wall softening. However, it has been unclear whether or why reducing endopolyploidy in organismal polyploids is important.
We thus hypothesized that endopolyploidy might compound cellular defects of neo-polyploids. We test this by comparing neo-tetraploid (created from diploids) and established (naturally evolved) autotetraploids of Arabidopsis arenosa.
We find neo-tetraploids have more endoreduplication and reach higher ploidy levels than established ones, and this associates with morphological defects including very large cells, aberrant root hairs, fragile cell walls, and sometimes cell death, which are absent from the established tetraploid lineage.
Using tetraploid populations segregating ancestral diploid and derived tetraploid alleles of the cell cycle regulator CYCD3;2, which shows signatures of directional selection in A. arenosa tetraploids, we demonstrate that tetraploid plants homozygous for the diploid allele phenocopy neo-tetraploids, with high endopolyploidy levels, and cellular structure defects.

Plants homozygous for the tetraploid allele undergo less endopolyploidy, which correlates with restored cellular robustness. Our results suggest that limiting endopolyploidy during polyploid evolution, in part through a novel allele of CyclinD3;2, is intimately linked with restored cellular integrity.

Targeted cryo-electron tomography of plant cell walls through improved cryo-CLEM workflow

Etienne Bellani [1], Jean Daraspe [2], Damien De Bellis [2], Christel Genoud [2], Niko Geldner [1].
1- Department of Plant Molecular Biology, University of Lausanne, Lausanne, Switzerland
2- Electron Microscopy Facility, University of Lausanne, Lausanne, Switzerland

etienne.bellani@unil.ch

Understanding plant cell wall architecture at the nanoscale has long been hindered by technical limitations. Here, we introduce major improvements to cryo-correlative light and electron microscopy (cryo-CLEM) and cryo-focused ion beam scanning electron microscopy (cryo-FIBSEM) workflows that enable routine, high-precision targeting and preparation of cryo-lamellae from complex tissues such as those found in plants.
By extending cryo-FIBSEM operational stability, simplifying lift-out procedures through the use of silver-plated manipulation tools, and achieving high three-dimensional targeting accuracy, this approach allows reproducible access to rare, cell-type-specific structures deep within intact organs.
Applied to *Arabidopsis thaliana* roots, the method enables cryo-electron tomography (cryo-ET) imaging of Casparian strips, suberin lamellae, and xylem cell walls in a near-native, fully hydrated state. These advances overcome long-standing barriers that previously restricted cryo-ET largely to thin samples and open new research avenues for plant biologists. The ability to visualize cell wall polymers, membrane–wall interfaces, and secretion-related structures without chemical fixation or heavy metal staining provides a powerful framework to investigate cell wall assembly, barrier formation, transport regulation, and stress adaptation at molecular resolution. More broadly, this workflow establishes cryo-ET as a transformative tool for structural plant biology.

NAD(P)H Dehydrogenase C1 (NDC1) is involved in prenylquinone metabolism and plastoquinone homeostasis

Ségolène Bressoud[1], Venkatasalam Shanmugabalaji[1], Michel Havaux[2], Felix Kessler[1]
1 Laboratoire de Physiologie Végétale, University of Neuchâtel
2 CEA Cadarache, Cité des Energies

Photosynthesis relies on an electron transport chain in the thylakoid membrane of the chloroplast. There, plastoquinone (PQ-9) is an essential photosynthetic electron carrier (photoactive PQ-9 pool). At the same time, PQ-9 functions as a critical antioxidant that is consumed during photosynthesis and must be replaced constantly. A reservoir of plastoquinone is found in the plastoglobule (PG) (non-photoactive PQ-9 pool). PGs are thylakoid-associated lipid droplets that are continuous with the thylakoid leaflet, allowing exchange of molecules between the two compartments. PG contains proteins that are involved in plastoquinone metabolism and can therefore be considered as a metabolic hub for PQ-9 metabolism, providing fresh PQ-9 to the thylakoid membrane to assure plastoquinone homeostasis. NAD(P)H Dehydrogenase C1 (NDC1) is a plastoglobular type II NAD(P)H dehydrogenase functioning as PQ reductase. *ndc1* mutants accumulate higher and more oxidized levels of PQ-9 compared to the WT. Therefore, NDC1 is essential for maintaining a reduced redox state of plastoquinone. We showed that the overaccumulation of plastoquinone in *ndc1* is independent of PQ-9 related gene expression, and it has been proposed that PQ-9 itself acts as a redox signal for plastoquinone production. Finally, the non-photoactive PQ-9 pool in *ndc1* is increased, suggesting that the reduction of plastoquinone in the plastoglobule is essential for its allocation to the thylakoid membrane, highlighting NDC1 key role in plastoquinone homeostasis.

How seeds know when to germinate: the role of DOG1 in seed dormancy

Christophe Buser [1], Urszula Piskurewicz [1], Mayumi Iwasaki [1].

1- Department of Plant Sciences, University of Geneva, Switzerland

christophe.buser@unige.ch

In *Arabidopsis thaliana*, newly produced seeds are both dry and dormant. Dormancy is a trait that prevents germination upon seed imbibition in water, thereby preventing germination out-of-season. Remarkably, however, while remaining dry, seeds become non-dormant over a period called after-ripening, therefore enabling germination.

A physiological process, referred to as the 'dry seed mechanism', must take place in the dry seed state to mediate this transition. While still uncharacterized, this mechanism is thought to involve accumulation of oxidative events in dry seeds. A potential protein involved in the dry seed mechanism is DOG1, a seed-specific protein of unclear molecular function that is essential to control dormancy.

In our studies, we found that DOG1 promotes abscisic acid (ABA) production in the endosperm, respectively a hormone and a seed tissue that are both important to block germination. We also found that DOG1 undergoes structural changes while the seed is still in a dry state. More precisely, seed after-ripening promotes dimerization of DOG1, and current evidence indicates that it is likely due to oxidation-dependent cysteine disulfide bond formation. By combining genetic, biochemical, and genomic approaches, our recent findings suggest that DOG1's ability to promote ABA production is mediated by its interaction with other proteins and that these interactions depend on DOG1's oxidative state.

Soil Microbiome-induced DNA Methylation Mediating Feedbacks on Plant Growth

Hilal Civelek[1], Henry Janse van Rensburg[1], Jan Wälchli[1], Rahim H. Goulamhoussen[2], Pauline E. Jullien[2], Klaus Schlaeppi[1]

[1] Department of Environmental Sciences, University of Basel, Switzerland: [2] Institute of Molecular Plant Biology, University of Strasbourg, France

E-mail: h.civelek@unibas.ch

Soil microbiomes modulate plant performance through plant-soil feedbacks (PSFs). While microbiome feedbacks are well established, how plants perceive and mediate these feedbacks remains largely unknown. To differentially condition soils, we use maize lines that differ in exudation of benzoxazinoids (BXs), which are multifunctional plant secondary metabolites that also structure microbiomes. We then study how the model plant *Arabidopsis thaliana* perceives and responds to differential soil microbiomes. Better growth and enhanced defence were found for the reference genotype Columbia-0 when grown on BX-conditioned soil microbiomes. However, we found that *Arabidopsis* accessions, different naturally occurring genotypes, revealed very high phenotypic variation in their growth responses to BX-conditioned soil microbiomes. Through genome-wide association analysis, we identified several candidate genes involved in PSFs. Among these was a *Tudor-domain-containing* gene, which pointed to a possible involvement of epigenetics. A *tudor* mutant lost the beneficial feedback to BX-conditioned soil microbiomes and also displayed an altered transcriptional response compared to wild type. These results highlight an essential role of *Tudor* in microbiome feedbacks. Further, preliminary results from whole-genome bisulfite sequencing revealed distinct DNA methylation in wild-type *Arabidopsis* after growth on the different soil microbiomes. Currently, we try to understand whether *Tudor* mediates these soil microbiome-induced epigenetic changes. Taken together, our study provides evidence that microbiome–epigenetic interactions could mediate the differential growth responses.

Green leaf volatiles (GLVs) are essential for volatile-mediated defense activation in maize

Tristan M. Cofer (tristan.cofer@unibe.ch)[1], Matthias Erb (matthias.erb@unibe.ch)[1]

[1]Institute of Plant Sciences, University of Bern

Plants attacked by insect herbivores emit volatile organic compounds that activate and prime defense responses in neighboring plants. However, the specific volatiles responsible for the direct activation of defenses remain poorly characterized. Although green leaf volatiles (GLVs) are well established as defense inducers, their contribution within complex, herbivore-induced volatile blends is unclear. Here, we genetically manipulated volatile emissions in planta and show that herbivore-induced volatiles from maize stimulate neighboring plants to rapidly release their own characteristic blend of stress-related volatiles. Genetic disruption of indole and terpene biosynthesis in wounded plants did not affect this response, indicating that these compounds are not required for the direct induction of volatile emissions in neighbors. In contrast, mutants deficient in GLV production failed to induce volatile emissions in neighboring plants, whereas mutants that produced GLVs but lacked most other herbivore-induced volatiles retained this ability. Together, these findings identify GLVs as the key airborne signals driving direct volatile-mediated defense activation in maize.

A Hidden Layer of Translation: Evidence for tRNA Import into Chloroplasts

Andrea Fontana, Eleonore Abbt, Samuel C. Zeeman, and Barbara Pfister

Institute of Molecular Plant Biology, ETH Zürich, Switzerland

andrea.fontana@biol.ethz.ch

tRNA genes are among the few genes still harboured in the plastid genome. tRNA import from the cytosol into plastids is thought to be restricted to the few species in which plastidial tRNA gene losses must be compensated. Our recent findings, however, provide evidence that this phenomenon may be more widespread—even occurring in species with a seemingly complete plastidial tRNA gene set, such as Arabidopsis and tobacco. Using next-generation tRNA sequencing, we identified the same, selective nuclear-encoded arginine-tRNAs in highly pure chloroplasts from Arabidopsis and tobacco. Accumulation of these tRNAs in chloroplast isolates was confirmed by northern blots. RNase treatment of intact chloroplasts did not degrade these tRNAs, suggesting that they are located inside the organelles. Comparison with the prokaryotic tRNA setup suggests that the two arginine codons read by the imported tRNAs may be poorly recognized by the endogenous plastidial tRNA pool. Among the proteins encoded in the chloroplast genome, these arginine codons are furthermore specifically enriched in ribosomal proteins. Together, our findings suggest that selective tRNA import may support plastidial translation. In addition, it may provide an additional layer of nuclear control over plastidial translation. We are currently testing the necessity of these imported tRNAs using *in-vitro* chloroplast translation assays with tRNA pools depleted for these tRNAs and by CRISPR-mediated knockout of corresponding nuclear tRNA genes.

Climate resilience in soybean: Root plasticity confers flooding tolerance

Jeoffrey George[1,5], Heng Ye[2], Maureen Hummel[1], Lijuan Zhou[2], Li Song[2], Chengjun Wu[3], Pengyin Chen[4], Henry T. Nguyen[2], Julia Bailey-Serres[1]

1- Center for Plant Cell Biology, Botany and Plant Sciences Department, University of California, Riverside, CA, USA
2- Division of Plant Sciences, University of Missouri, Columbia, MO, USA.
3- Department of Crop, Soil, and Environmental Sciences, University of Arkansas, Fayetteville, AR, USA
4- Division of Plant Sciences, University of Missouri Fisher Delta Research Center, Portageville, MO, USA
5- Present address: Department of Biology, University of Fribourg, Fribourg, Switzerland.

jeoffrey.george@unifr.ch

As climate change intensifies, flooding increasingly disrupts crop production by depriving roots of oxygen and limiting nutrient acquisition. Identifying natural genetic variation that confers tolerance to soil flooding (waterlogging) in soybean offers a promising strategy to enhance yield stability. Using genome-wide association studies and recombinant inbred lines, we identified genomic regions associated with flooding resilience and discovered functional polymorphisms in a gene we named *WATERLOGGING TOLERANCE 1* (*WLT1*). Introgression of the semi-dominant tolerant allele, *WLT1-1*, into an elite soybean background significantly increased yield under field conditions following 7 or 14 days of waterlogging. Mechanistically, *WLT1-1* promotes a plastic root architecture characterized by enhanced lateral and adventitious root formation. Although promoter polymorphisms do not affect *WLT1* transcript abundance or pericycle-specific localization, allelic variation within the 5′ untranslated region regulates translational efficiency of the coding sequence (mORF). We propose a model in which elevated WLT1 protein abundance in the pericycle drives adaptive root architectural remodeling during flooding stress. Together, these findings demonstrate the potential of leveraging natural genetic variation to improve flood tolerance in soybean and provide valuable insights for future breeding efforts.

Identifying the Regulation and Functional Consequences of PIF7 Localization

Yoëlle Hilbers[1], Geoffrey Cobb[1], Laure Allenbach Petrolati[1], Karen Thulasi Devendrakumar[1], Christian Fankhauser[1]

1- Center for Integrative Genomics, University of Lausanne, Switzerland

Yoelle.Hilbers@unil.ch

Shade-avoiding species such as *Arabidopsis thaliana* detect neighboring plants through low red:far-red light ratios (LRFR), caused by reflected FR-light from surrounding vegetation. This cue initiates the neighbor-proximity response, enabling plants to outgrow their competitors and prevent the risk of being shaded in the future. Crucial in the regulation of this shade avoidance response is the photoreceptor PHYTOCHROME B (PhyB), and its downstream signaling components, the PHYTOCHROME INTERACTING FACTORs (PIFs), among which PIF7 is the key mediator under LRFR conditions. Despite its importance, the regulation of PIF7 remains poorly understood. In this study, we investigated the distinct localization of PIF7 in nuclear condensates. Using mutant PIF7 lines, we show that these nuclear bodies are stabilized when PIF7 dimerization and DNA binding are inhibited, and that the PIF7 Active PhyB Binding (APB) domain is crucial for their formation. Furthermore, we investigated the asymmetry in PIF7 expression between the adaxial (upper) and abaxial (lower) side of young leaves and cotyledons, and its relevance in the LRFR response.

Microbiome-Mediated Immune Modulation: Stable Root Exudation Under Chronic Exposure to Immune-Eliciting Peptides in the Presence of Root Microbiota

Charlotte Joller[1], Joelle Schlaepfer[2], Klaus Schlaeppi[1]

1 Department of Environmental Sciences, University of Basel

2 Molecular Ecology, Methods Development and Analytics, Agroscope, Reckenholz

charlotte.joller@unibas.ch

Plants recognise the presence of microbes via conserved non-self and damaged-self molecular patterns. The recognition of these patterns induces a suite of basal plant immune responses that restrict the growth of opportunistic pathogens and prevent microbiome dysbiosis, but, at the same time, are also needed to establish interactions with some beneficial microbes. How immune activation affects root exudation, the first point of contact between plant roots and surrounding microbes, and how that relates to root microbiome structure is not known. Here, we show that, under axenic conditions, chronic basal immune activation leads to extensive changes in exudate blends that encompass both primary and secondary metabolites. However, while inoculation with different commensal microbiota results in convergent exudate profiles that partially overlap with immune responses under axenic conditions, they are not affected by the application of immune-activating molecular patterns. We show that microbial immune modulation is a capacity of single strains but that it also represents a synergistic property of the root-associated microbial community as a whole. Collectively, this study highlights extensive root exudate reshuffling in response to non-self and damaged-self recognition and microbial interference therewith.

How light reprograms plant cells: impact on the 3D organisation of transcription

Filippo Maria MIRASOLE[1] Clara BOURBOUSSE[2], Fredy BARNECHE[2], Célia BAROUX[1]

1- Department of Plant and Microbial Biology Zürich-Basel Plant Science Center University of Zürich, Zollikerstrasse 107, 8008 Zürich, Switzerland

2- Plant Nuclear Dynamics & Signaling, Department of Development Adaptation and Ageing, IBPS-CNRS-Sorbonne Université-INSERM, Paris, France

filippo.mirasole@botinst.uzh.ch

Light is essential for plants as a source of energy for photosynthesis and as a source of information to adapt their physiology and development to environmental conditions. During seedling establishment, light induces rapid and large-scale changes of the transcriptional and epigenomic status in the cotyledon embryonic leaves, which include increased nuclear size and heterochromatin reorganization [1, 2]. Here, we first investigated whether the 3D patterns of transcriptional responses are organ or tissue-specific. To address this, we used a live transcriptional reporter of RNA Polymerase II activity [3] to quantify light-induced transcriptional activity in cotyledon nuclei, specifically comparing epidermis and mesophyll tissues on both adaxial and abaxial sides. We then did a kinetic analysis of transcriptional and chromatin changes to determine whether these processes occur synchronously or are uncoupled. Finally, we screened a series of light-signaling and light-response mutants to understand their quantitative impact on transcriptional and chromatin dynamics. The results and future investigations will be presented and discussed.

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Functional insights and emerging roles of plant METALLOTHIONEINS

Carlota Montells[1,2], Christoph Ringli[1], Eva Freisinger[2]

[1] Institute of Plant and Microbial Biology, University of Zürich, Switzerland
[2] Department of Chemistry, University of Zürich, Switzerland

carlota.montells@chem.uzh.ch

Metallothioneins (MTs) are low-molecular-weight, cysteine-rich proteins that are present across all domains of life. Their most outstanding characteristic is their ability to coordinate metal ions, including Zn(II), Cu(I) and Cd(II), through the thiol groups of the cysteines, which also confer strong antioxidant capacity. Hence, MTs are associated with roles in metal ion homeostasis, as well as protection against metal toxicity and oxidative stress. *Arabidopsis thaliana* encodes 7 known functional MTs, and their expression is tissue-specific and under developmental control, and it is also induced by different abiotic and biotic stresses.

To better understand the molecular role of plant MTs, we generated a CRISPR/Cas9 *Arabidopsis* mutant lacking five MTs, which shows reduced growth under standard growing conditions and increased sensitivity to cadmium stress. Additionally, through IP-MS and validation via Co-IP and Split-Luc assays, we found that AtMT2a and AtMT4b can interact *in vivo* with various proteins. These findings suggest that MTs participate in different protein networks, influencing cellular processes and plant development. Further studies aim to investigate the molecular basis and biological significance of these interactions.

Elucidation of a perception mechanism for cell wall-derived oligogalacturonides in *Arabidopsis thaliana*

Jana Ordon [*1], Klara Culjak [*2,3], Owen Kendish [*4], Marina Martín-Dacal [2,3], Miguel Angel Torres [2,3,5], Meriem Aitouguinane [2], Vicente Ramírez [6], Lu Zhang [5,7], Diego José Berlanga [2,3,5], Gemma López [2], Kyle Bender [1], Alberto Macho [5,7], Markus Pauly [6], Lucía Jordá [2,3,5], Julia Santiago [#4], Antonio Molina [#2,3,5], Cyril Zipfel [#1,8]

1- Institute of Plant and Microbial Biology, University of Zürich, 8008 Zürich, Switzerland
2- Centro de Biotecnología y Genómica de Plantas (CBGP), Universidad Politécnica de Madrid (UPM)-Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA)/Consejo Superior de Investigaciones Científicas (CSIC), 28223 Pozuelo de Alarcón (Madrid), Spain
3- Departamento de Biotecnología-Biología Vegetal, Escuela Técnica Superior de Ingeniería Agronómica, Alimentaria y de Biosistemas, Universidad Politécnica de Madrid, 28040 Madrid, Spain
4- Department of Plant Molecular Biology, University of Lausanne, 1015 Lausanne, Switzerland
5- Center of Excellence for Plant-Environment Interactions (CEPEI), CBGP-CEMPS
6- Institute of Plant Cell Biology and Biotechnology, Heinrich Heine University, 40225 Düsseldorf, Germany
7- Shanghai Center for Plant Stress Biology, CAS Center for Excellence in Molecular Plant Sciences (CEMPS), Chinese Academy of Sciences (CAS), 201602 Shanghai, China
8- The Sainsbury Laboratory, University of East Anglia, Norwich Research Park, NR47UH Norwich, UK
*- equally contributed
corresponding authors

jana.ordon@botinst.uzh.ch

Oligogalacturonides (OGs) are released from pectin, a major component of plant cell walls, during pathogen infection and act as damage-associated molecular patterns activating plant immune responses. Pectin-binding receptor kinases of the WALL-ASSOCIATED KINASE (WAK) family were previously proposed to function as OG receptors. However, we recently showed that an *Arabidopsis thaliana* mutant lacking all five *WAK* genes exhibits wild type-like hallmarks of immune responses upon OG treatment. Thus, *bona fide* OG receptors remain still to be identified. Here we report that the Arabidopsis receptor kinase REDUCED SENSITIVITY TO OGs 1 (RSO1) is required for OG-triggered responses. *rso1* mutants display impaired OG-induced Ca^{2+} influx, mitogen-associated protein kinase activation, and transcriptional reprogramming, while their responses to other immunogenic ligands such as chitin or flg22 were similar to wild-type plants. Purified OGs with different degrees of polymerization (DP) elicited immune responses in both RSO1-dependent and -independent manners, indicating that OGs with different DPs are perceived by distinct receptors. Notably, incubation of pectin with the phytopathogenic fungus *Plectosphaerella cucumerina* produced OG fractions that triggered RSO1-dependent immune responses. Moreover, *rso1* mutants exhibited enhanced susceptibility to pathogens such as *Plectosphaerella cucumerina*, *Pseudomonas syringae* pv. *tomato* and *Ralstonia solanacearum*. Collectively, these findings indicate that RSO1 is a key sensor of OGs released during pathogen-induced pectin degradation, underscoring its central role in glycan-triggered immune responses.

Unveiling the Role of Pathogenesis-Related 1-Like Proteins in Botrytis cinerea-Nicotiana benthamiana Interactions

Yangyang Qin[1] Linping Wang[1] Roger Schneiter[1]

[1]Department of biology, University of Fribourg

yangyang.qin@unifr.ch

The Cysteine-rich secretory protein, Antigen 5, and Pathogenesis-related protein 1 (CAP) superfamily protein PATHOGENESIS-RELATED

PROTEIN 1-LIKE PROTEIN (BcPR1-L) plays an important role in the pathogenicity of *Botrytis cinerea* in plants. Despite their importance, the molecular mechanisms underlying BcPR1-L protein functions remain elusive. This study utilizes the *B. cinerea-Nicotiana benthamiana* pathosystem to investigate the role of BcPR1-L proteins in plant-fungus interactions and unravel the mechanisms driving their activity. Bioinformatics analyses identified four BcPR1-L proteins, two of which showed significant induction under various biotic and abiotic stress conditions. Using host-induced gene silencing (HIGS) and knockout

mutants (*ΔBcPR1-L*), we demonstrated BcPR1-L proteins are required for the full virulence of *B. cinerea*. Further functional analyses, including yeast two-hybrid and colocalization assays, revealed that these BcPR1-L proteins interact with *Arabidopsis thaliana* PR proteins. These findings highlight the dual role of BcPR1-L proteins in host-pathogen interactions, suggesting their involvement in subverting plant defense mechanisms by potentially interfering with host PR1 protein function. This work provides new insights into the molecular dynamics of PR1-L proteins and underscores their significance as potential targets for improving plant resistance to fungal pathogens.

Tomato fruit skin: how transporters control cuticle integrity

Yifat Quan[1], Aurore Guerault[1], Damien de Bellis[1, 2], John Perrin[1] and Christiane Nawrath[1]

[1]*University of Lausanne, DBMV, Lausanne, Switzerland*
[2]*University of Lausanne, EMF, Lausanne, Switzerland*
E-mail: yifat.quan@unil.ch

The plant cuticle is a continuous hydrophobic layer of the apoplast that covers the aerial surfaces of plants, acting as a barrier such as regulating evapotranspiration and limiting pathogen entry. Beyond its protective function, the cuticle plays a key role in plant development and provides biomechanical support to fruit integrity. This barrier is mainly composed of cutin, an insoluble polyester predominantly constituted by oxygenated fatty acids. ATP-binding cassette of the G family (ABCG) are transporters involved in the export of cutin precursors, such as tomato SlABCG36 and SlABGC42. However, the precise roles of SlABCG36 and SlABGC42 in cuticle composition and properties remain unclear.

Here, we show that in tomato fruits of the Micro-Tom and Sweet-100 cultivars, SlABCG36 and SlABGC42 transporters are required to form a thick and well-structured cuticle. Interestingly, only in the double *slabcg36alabcg42* knockout of Sweet-100, which has a tender pericarp, we found an increased resistance to fruit cracking compared with the wild-type, possibly suggesting enhanced extensibility of the cell wall-cuticle continuum. Our results indicate that ABCG transporters impact cuticle morphology and properties in both tomato cultivars differently. Further assessment of the chemical structure of cutin and the mechanical properties of the resulting cuticle-cell wall continuum in distinct tomato varieties will be necessary to better understand their intricate diversity and functions.

Plant Kelch phosphatases are Ser/Thr phosphatases involved in cell cycle regulation

***Felix Rico-Resendiz*[1]*, Oded Pri-tal*[1]*, Pierre Raia*[1]*, Andrea Moretti*[1]*, Houming Chen*[1]*, Andreas Boland*[2] *and Michael Hothorn*[1]

[1]Structural Plant Biology Laboratory, Department of Plant Sciences, University of Geneva, Geneva, Switzerland [2]Department of Molecular and Cellular Biology, University of Geneva, Geneva, Switzerland

Brassinosteroids (BRs) are plant hormones essential for growth and development. The Kelch phosphatase BSU1 has been previously shown to dephosphorylate the GSK3 kinase BIN2 at Tyr200, enabling BES1/BZR1 transcription factors to induce gene expression in BR signaling. Here, we found that BSU1 phosphatase domain shares strong structural homology with the human Ser/Thr phosphatase PP1 and fails to dephosphorylate BIN2 at Tyr200 *in vitro*. Consistent with earlier reports, overexpressing BSU1 supress the growth defects of the weak BR receptor allele *bri1-5*. The isolated catalytic phosphatase domain, but not the Kelch domain, is able to rescue *bri1-5* plants. Strikingly, a phosphatase-dead version also rescues the mutant phenotype, indicating that BSU1 phosphatase activity is not required for BR signaling. Over-expressed BSU1 interacts strongly with is homologs BSL1-3 via its RVxL substrate-binding motif. Disrupting this motif prevents both BSLs interaction and *bri1-5* rescue. However, higher-order *bsu1 bsl* knockout mutants show no detectable BR defects, suggesting that BSU1 acts as a neomorph in *bri1-5* and functions as scaffold protein recruiting other Kelch phosphatases. Structural studies revealed the BSU1 C-terminus to be phosphorylated by the CDK-CKS-CYCB1 complex. The phosphorylated tail folds into the active site to block substrate access, linking BSU1 to the cell cycle. In *Marchantia polymorpha*, loss of the sole BSU1 homolog (*bslm*^{ge1}) causes excessive cell proliferation, abnormal morphogenesis, and tissue disorganization. Transcriptomic analyses, EdU incorporation, and cyclin D reporter assays confirm widespread cell cycle activation. These findings establish plant Kelch phosphatases as conserved cell cycle regulators, mechanistically analogous to yeast and human PP1.

Unravelling the spatiotemporal component of carrier-mediated nutrient transport in *Arabidopsis thaliana* roots.

Kévin ROBE[1], Linnka LEGENDRE[1], Marie BARBERON[1].

[1]- *BIVEG, University of Geneva, Geneva, Switzerland*

kevin.robe@unige.ch

Plant roots uptake nutrients and water from the soil. Within the roots, nutrients and water are transported from the epidermis to the vasculature, which involved crossing different cell layers. Among these layers, two (the epidermis and the endodermis) are particularly crucial for mineral uptake and transport. Using a combination of physiology studies, ionomic profiling and genetic analysis, we have identified and characterized several new metal carriers in the epidermis. Using translatomic and cell biology approaches, we have also localized several new nutrient carriers in the endodermis. We demonstrated that the endodermis can function in mineral uptake, reinforcing the importance of apoplast in mineral nutrition. Finally, because little is known about how suberin deposition in the root endodermis affects nutrient carrier localization and activity, we are currently investigating this interaction. Interestingly, most of the nutrient carriers studied are no longer detected in the suberized endodermis. We are now further exploring the role of suberin in nutrient transport, aiming to modulate transporter accumulation by controlling endodermal suberization. The data obtained in this project will help redefine our models of nutrient transport in roots.

Polycomb-Mediated Epigenetic Control of Cell Fate: Insights from Early Embryogenesis to Stomatal Lineage

Max Schwarze[1], Sara Simonini[1]

[1]Institute of Plant and Microbial Biology and Zurich-Basel Plant Science Center, University of Zurich, CH-8008 Zurich, Switzerland
max.schwarze@botinst.uzh.ch

Precise regulation of gene expression during embryogenesis is essential for the establishment of cell identity. In multicellular organisms such as animal and plants, the Polycomb Repressive Complex 2 (PRC2) mediates deposition of the H3K27me3 histone mark, silencing key pluripotency and developmental genes, particularly during embryogenesis. Errors in the addition or removal of this modification can lead to severe developmental defects, including severe morphological abnormalities and embryo abortion. Despite its importance, how the dynamics of histone modifications coordinate chromatin state changes and cell fate acquisition along embryogenesis remains unclear.

Using the embryo of *Arabidopsis thaliana*, we investigate the role of PRC2 in histone methylation dynamics, focusing on stomatal lineage genes as a model for cell fate transitions. We profile H3K27me3 and chromatin accessibility across critical embryonic stages (globular to late heart) in both wild-type and in the PRC2 mutant *mea* using CUT&Tag. Loss of MEA (and thus PRC2) activity disrupt stomatal lineage patterning, suggesting that MEA-PRC2 represses stomatal fate during early embryogenesis. By combining genome-wide epigenetic profiling, functional genetics, advanced live imaging, pharmacological treatments and allele-specific analyses, we propose a model where PRC2 activity and gene expression interact dynamically to regulate lineage-specific gene repression during early development. Our findings advance our understanding of epigenetic regulation in plant development and of the molecuar mechanisms underlying developmental plasticity in multicellular organisms.

Leveraging AI-based structural modeling to characterize the interaction interfaces of LRR receptor complexes

Simon Snoeck1, Lisha Zhang2, Valentin Studer1, Gijeong Kim1, Álvaro D. Fernández-Fernández1, Thorsten Nürnberger2, and Cyril Zipfel1,3

1Institute of Plant and Microbial Biology, Zurich-Basel Plant Science Center, University of Zurich, Zurich, Switzerland.

2Center of Plant Molecular Biology (ZMBP), University of Tübingen, Tübingen, Germany.

3The Sainsbury Laboratory, University of East Anglia, Norwich Research Park, Norwich, United Kingdom.

Leucine-rich repeat (LRR) receptor kinases (RKs) and receptor proteins (RPs) are important classes of plant pattern recognition receptors (PRRs) activating pattern-triggered immunity. While classical and AI-based structural approaches have recently provided crucial insights into ligand-LRR-RK binding mechanisms, little is known about how ligands are perceived by LRR-RPs. In contrast to LRR-RKs, many LRR-RPs typically embed one or more loopout regions in their extracellular domains that are crucial for functionality. We here used an AI-based approach to reveal a ligand-binding mechanism shared by the Arabidopsis LRR-RPs RLP23 and RLP42 – the PRRs for the short peptide ligands nlp20 and pg13, derived from NECROSIS- AND ETHYLENE-INDUCING PEPTIDE 1-like proteins (NLPs) and fungal endopolygalacturonases (PGs), respectively. This mechanism relies on a β-strand interaction with the N-terminal part of the island domain (ID) loopout, which adopts an anti-parallel β-sheet conformation. Additionally, we investigated the binding interface of RLP32 – the PRR for proteobacterial TRANSLATION INITIATION FACTOR 1, a folded protein ligand that requires its tertiary structure for recognition. Finally, we describe a mechanistic role of the ID for co-receptor recruitment conserved across LRR-RPs. Together, our results shed light on the ligand-binding mechanisms and receptor complex formation of LRR-RPs, opening avenues for their engineering for crop disease resistance.

Investigating effects of whole genome duplication on pollen tube growth

Zihan Song[1], Thanvi Srikant[1], Kirsten Bomblies[1]

1 Institute of Molecular Plant Biology, Department of Biology, ETH Zürich

Polyploidy, arising from whole-genome duplication, is common in plants and can generate novel traits useful for adaptation and crop improvement. However, newly formed polyploids (neopolyploids) often have fertility problems. Understanding these defects—and how they were resolved in established polyploids—can clarify the evolutionary processes that restore fertility. Although recent work has identified pollen tube growth as a key challenge in polyploid fertility, the specific factors that make pollen tube growth challenging for neopolyploids, and how evolution subsequently fixes these defects, remain unclear.

Here, we study this question using *Arabidopsis arenosa* diploids, colchicine induced neotetraploids (Neo-4X) and established tetraploids (Est-4X). Immunostaining shows that Neo-4X pollen tube tips have elevated levels of methyl-esterified pectin, whereas diploid and Est-4X tubes exhibit similar lower levels. Consistently, Neo-4X tubes contain reduced demethyl-esterified pectin in the shank compared to the other cytotypes. These patterns suggest that Neo-4X pollen tubes may have softer cell walls, potentially explaining their impaired growth. Pollen tube RNA-seq results indicate that PMEI5 expression is upregulated both in Neo-4X and Est-4X, potentially contributing to Neo-4X wall softening while indicating indirect compensation in Est-4X. We will next develop mathematical models to elucidate the causes of NEO-4X pollen tube defects and investigate the roles of pollen genes under selection in Est-4X adaptation.

Epigenomic and transcriptomic diversity in diploid and autotetraploid *Arabidopsis arenosa* populations

Thanvi Srikant[1], Kirsten Bomblies[2]

[1]Institute of Molecular Plant Biology, Department of Biology, ETH Zürich, Zürich, Switzerland thanvi.srikant@biol.ethz.ch

Whole genome duplication (WGD) events give rise to polyploidy, which increases genome complexity, phenotypic novelty and adaptive potential in plants. But how does WGD impact the epigenome and transcriptome? Do these features change during the intraspecific diversification of polyploids? To answer these questions, we use *Arabidopsis arenosa* as a model plant system, where natural diploid and autotetraploid populations have been characterized, and new tetraploids can be generated experimentally. Autotetraploid *A. arenosa* populations also show genetic signatures of selection in multiple chromatin remodelling and transcriptional machinery genes, and have expanded their climatic niche relative to diploids.

Using ATAC-seq on leaf tissues from 10 populations, we found that differentially accessible chromatin regions (dACRs) between diploids are strongly enriched near transposable elements, whereas tetraploid dACRs are enriched in gene-rich regions. RNA-seq analysis of the same plants revealed that differentially expressed genes between diploids and tetraploids are largely involved in biotic and abiotic stress response. At the genome-wide scale, both chromatin accessibility and expression profiles partially reflect the underlying genetic architecture of different populations. When examining all populations together, we find that genes involved in RNA metabolism show strong correlations between accessibility and expression levels, suggesting coordinated regulatory evolution. Taken together, our results provide new insights into the interplay between the genome, epigenome and transcriptome during adaptation to polyploidy and local environments.

Characterizing the role of APB and lysine-rich motifs on function and stability of Arabidopsis Phytochrome Interacting Factor 4

Karen Thulasi Devendrakumar [1], Geoffrey Cobb[1], Christian Fankhauser[1]

1- Centre for Integrative Genomics, Faculty of Biology and Medicine, Génopode Building, University of Lausanne, 1015 Lausanne, Switzerland.

karen.thulasi@unil.ch

Phytochrome interacting factor 4 (PIF4) is a growth promoting transcription factor that mediates responses to shade and high temperature. Under normal light and temperature conditions, PIF4 interacts with the red and far-red light photoreceptor phytochrome B (phyB) via its Active Phytochrome Binding (APB) motif. This interaction results in suppression of PIF4 activity by its sequestration and phyB-mediated degradation. Since the APB-phyB interaction negatively affects PIF4 activity, theoretically, mutations affecting this interaction should result in increased activity. However, we found that plants expressing PIF4 APB mutant respond less to high temperature and shade conditions when compared to wild-type (WT) PIF4 expressing plants. We also identified a novel lysine-rich (KR) motif in PIF4 that is evolutionarily conserved in a subset of PIFs. Mutating this motif resulted in PIF4 that is more stable in tested light and temperature conditions. Further, when compared to WT PIF4 expressing plants, ones expressing PIF4 KR motif mutant responded stronger to low-blue light condition. PIFs have been shown to co-degrade phyB in continuous red light. PIF4 KR motif mutant displayed high stability in red light and the plants also displayed reduced phyB co-degradation. Further experiments are underway for characterization of these motifs to understand their role in PIF4 function, PIF4 and phyB protein stability, and explore how these motifs might interact with each other and regulate PIF4 activity.

Meiosis Adaptation to temperature in Diploid *Arabidopsis arenosa* Populations

Jing Wang, Marinela Dukic, Kirsten Bomblies

Plant Evolutionary Genetics, Institute of Molecular Plant Biology, ETH Zürich

As agriculture confronts mounting pressures from climate change, understanding how heat stress disrupts plant reproduction is increasingly urgent. Meiosis, the specialized division that produces haploid spores, is highly temperature sensitive, yet the basis of this sensitivity remains largely unknown. Nature, however, offers a path forward: many lineages have already adapted to warmer habitats, providing natural experiments we can analyze.

A diploid lineage of *Arabidopsis arenosa* from the warm Pannonian Basin maintains higher pollen viability and fertility about eight days after a 48-hour exposure to 34 °C compared with plants from cooler regions. These Pannonian plants also show fewer univalents at the end of prophase I and reduced chromosome lagging during segregation after heat stress. Preliminary data further indicate that several key components of meiotic prophase I, the kinetochore, and the spindle assembly checkpoint experienced selective sweeps in this lineage.

These findings support the hypothesis that genes acting at different meiotic stages have been selected to enhance heat tolerance. My aim is to uncover how heat stress disrupts meiosis at the mechanistic level and to determine whether, and how, naturally selected alleles of meiosis-related proteins mitigate the detrimental effects of high temperature.

Developing Potyvirus Resistance in Tomato and Potato by Targeting Susceptibility Factors with CRISPR-Cas9

Linping Wang [1,3], Caroline Lebaron [2], Katrin Artola [1]. Jean-Luc Gallois [2], Kristiina Mäkinen [1] Roger Schneiter [3]

[1.] Department of Agriculture Science, University of Helsinki, 00014 Helsinki, Finland
[2.] Improvement of Fruit and Vegetables (GAFL), INRAE, 84143 Montfavet, France
[3.] Department of Biology, University of Fribourg,00170 Fribourg, Switzerland
linping.wang@unifr.ch

Viral diseases in crops present an escalating global threat to food security, with potyviruses being particularly problematic. Genome editing offers new opportunities to introduce genetic resistance in crops of interest, and while the eukaryotic translation initiation factor 4E (eIF4E) is commonly studied for enhancing virus resistance in crop breeding, there is an urgent need for novel targets. Our research investigates the VARICOSE (VCS) gene, a susceptibility factor with a proviral effect for potyvirus infection. Our findings indicated that VCS facilitates systemic viral spread and particle formation by associating with the viral helper component proteinase (HCPro). As such, VCS could be a new target to develop genetic resistances. However its inactivation is likely to cause strong developmental defects, which would jeopardize its use in plant breeding.

Here, we aim at taking advantage of the presence of two VCS genes in tomato and potato to find a trade-off between resistance to potyviruses and plant development. Using CRISPR-Cas9 genome editing, we are generating single and double *VCS* knockouts and assessing their effects on both virus resistance and plant growth. In parallel, we aimed to combine *VCS* knockouts with *eIF4E*-based resistance to enhance durability and broaden the resistance spectrum. This study is expected to provide valuable insights into potyvirus resistance mechanisms and some information to guide future strategies for durable crop protection.

Orientation matters: MAP70-2 Directs Division Orientation in Lateral Root Formation

Zsófia Winter[1], Dorothee Stöckle[2], Milica Nenadić[1], Sophie Marc-Martin[1], Mark Roosjen [3], Dolf Weijers [3] and Joop EM Vermeer [1]

[1] Laboratory of Cell and Molecular Biology, Institute of Biology, University of Neuchâtel, Switzerland

[2] Department of Plant and Molecular Biology, University of Zürich, Switzerland

[3] Wageningen University, Netherlands

Lateral root (LR) initiation begins with anticlinal, asymmetric cell divisions in the inner primary root. Although division plane orientation is key for tissue architecture, the mechanisms enabling three-dimensional differential growth deep within tissues remain unclear. Emerging evidence indicates that cytoskeletal reorganization, regulated by specific MICROTUBULE-ASSOCIATED PROTEINS (MAPs), is essential for defining division plane orientation and position.

We previously identified MAP70-5, a member of the MAP70 family, as essential for LR development and for establishing spatially distinct cortical microtubule (CMT) domains in the endodermis. Proper LR formation requires an isotropic arrangement of CMTs within the LR primordia and adjacent endodermal cells. Here, we characterize MAP70-2, predominantly expressed in the pericycle and LR primordia. MAP70-2 displays a dynamic localization that marks early division sites during all stages of LR development. MAP70-2 loss-of-function mutants displayed deformed LRPs and misaligned division site angles, only in lateral root primordia. We propose that MAP70-2 integrates biochemical and mechanical cues to establish correct division plane orientation. Using TurboID-based proximity ligation, we further identified BASIC PROLINE-RICH PROTEIN 1 (BPP1) as a putative interactor of both MAP70-2 and MAP70-5. Preliminary results show that BPP1 shows a similar localization pattern as MAP70-2 and a *bpp125* triple mutant shows altered plant development.

Post-transcriptional regulation via calcium-modulated ribonucleotide structures

Chen Xiao[1], Dolly Mehta[1], Rodrigo S. Reis[1]

1- Institute of Plant Sciences, University of Bern
chen.xiao@unibe.ch

Ca^{2+} acts as a key second messenger in plant immunity, characterized by rapid and transient cytosolic Ca^{2+} influx upon pathogen perception. While Ca^{2+} is known to exert its functions through binding to protein sensors, recent studies in mammals revealed that Ca^{2+} influx can trigger RNA G-quadruplex assembly, indicating that cytosolic increases in Ca^{2+} concentration might alter RNA structure. However, whether cytosolic Ca^{2+} influx can directly affect RNA structure in vivo and contributes to post-transcriptional regulation remains unknown in plants.

Here, we demonstrated that Ca^{2+} plays a critical role in post-transcriptional regulation during pattern-triggered immunity (PTI) in plants. By combining in vivo and in vitro RNA probing analyses (DMS-MaP), we showed that Ca^{2+} directly binds to RNA and induces widespread changes in RNA structure. Integration of RNA structure profiling with RNA decay analyses revealed that Ca^{2+}-dependent structural remodeling is associated with altered RNA stability in a subset of stress-responsive genes. Functional analyses further showed that mutants of these genes fail to exhibit the flg22-induced root growth inhibition, indicating their essential roles in PTI responses. Our current data uncover a previously unrecognized layer of Ca^{2+} signaling in plant immunity, extending its function from protein-mediated signal transduction to RNA structure–dependent post-transcriptional regulation.

LIST OF PARTICIPANTS:

First name	Family name	Institution
Tonni	Andersen	UZH
Marie	Barberon	UNIGE
Emmanuel	Boutet	SIB
Daniel	Croll	UNINE
Christian	Fankhauser	UNIL
Ewumi Azeez	Folorunso	ZHAW
Andrea	Fontana	ETHZ
Niko	Geldner	UNIL
Christian	Hardtke	UNIL
Michael	Hothorn	UNIGE
Lothar	Kalmbach	UNINE
Heike	Lindner	UNIBE
Mateusz	Majda	UNIL
Christian	Parisod	UNIFRI
Yifat	Quan	UNIL
Rodrigo	Reis	UNIBE
Doris	Rentsch	UNIBE
Philippe	Reymond	UNIL
Quint	Rusman	UZH
Julia	Santiago	UNIL
Federica R.	Schanz	WUR
Klaus	Schläppi	UNIBAS
Kentaro	Shimizu	UZH
Thanvi	Srikant	ETHZ
Elisabeth	Truernit	ETHZ
Linping	Wang	UNIFRI
Zsofia	Winter	UNINE
Cyril	Zipfel	UZH
Tobias	Züst	UZH
Hilal	Civelek	UNIBAS
Jeoffrey	George	UNIFRI
Felix	Kessler	UNINE
Yangyang	Qin	UNIFRI
Christoph	Ringli	UZH
Zihan	Song	ETHZ
Karen	Thulasi Devendrakumar	UNIL

List of participants

First name	Family name	Institution
Jing	Wang	ETHZ
Chen	XIAO	UNIBE
Thomas	Boller	UNIBAS
Ségolène	Bressoud	UNINE
Christophe	Buser	UIGE
Tristan	Cofer	UNIBE
Emilie	Demarsy	UNIGE
Marinela	Dukic	ETHZ
Yoëlle	Hilbers	UNIL
Charlotte	Joller	UNIBAS
Luisa	Last	ETHZ
Martina	Legris	UNINE
Luis	Lopez-Molina	UNIGE
Macarena	Marin Arancibia	UNIL
Anis	Meschichi	ETHZ
Filippo Maria	Mirasole	UZH
Jana	Ordon	UZH
Yves	Poirier	UNIL
Michael	Raissig	UNIBE
Priya	Ramakrishna	EPFL
Christelle	Robert	UNIBE
Max	Schwarze	UZH
Sara	Simonini	UZH
Simon	Snoeck	UZH
Sebastian	Soyk	UNIL
Roman	Ulm	UNIGE
Joop	Vermeer	UNINE
Samuel	Zeeman	ETHZ
Kévin	Robe	UNIGE
Felix	Rico-Resendiz	UNIGE
Etienne	Bellani	UNIL
Lena	Hyvärinen	UNINE
Christiane	Nawrath	UNIL
Nathalie	Wuyts	Agroscope