



# SwissPLANT 2023

## Symposium Plant Science Research in Switzerland

### Scientific Program Committee

Klaus Schläppi, Thomas Boller,  
Jurriaan de Vos, Ben Engel, Pascale Flury,  
Günter Hoch, Sabine Rumpf  
University of Basel

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**23–25 January 2023**  
**Les Diablerets, Switzerland**



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We gratefully acknowledge Syngenta's financial support of the conference.



# SwissPLANT 2023

**Swiss Plant Symposium 2023**  
**23–25 January 2023**

**Les Diablerets, Switzerland**

## **Venue**

Eurotel Victoria, Chemin du Vernex 3, 1865 Les Diablerets, Switzerland

## **Scientific Program Committee**

Klaus Schläppi, Thomas Boller, Jurriaan de Vos, Ben Engel, Pascale Flury,  
Günter Hoch, Sabine Rumpf  
University of Basel

## **Conference Organization**

Swiss Society of Plant Biology / Swiss Plant Science Web  
Sylvia Martínez, University of Basel

**[swissplantsciencweb.ch](https://swissplantsciencweb.ch)**

## Swiss Society of Plant Biology Annual Report & SwissPLANT 2023

In 2022 the committee of the Swiss Society of Plant Biology (SSPB) held two meetings to discuss ongoing topics, and in June its General Assembly. Basically, 2022 has been a year of renewal for the society. In order to become operational again, we were in close contact with SCNAT and its Biology Platform. They both welcome the reactivated society and are happy to include it as a member society. A new core activity of our society is the promotion of young talents. At the end of SwissPLANT 2022, held in June, the society awarded eight prizes to young participants for their presentations.

In addition, the proposal to hold an Early Career Meeting (ECM) before SwissPLANT received great approval at the 2022 SSPB General Assembly. This new meeting addresses PhD students approaching the end of their project and postdoc scholars. Topics cover plant biology from ecology, evolution to molecular mechanisms. Overall, the ECM is an event for young researchers organized by young researchers. Two senior members attend as mentors. Thanks to special funding we obtained from SCNAT, the attendees of this “pilot” meeting can participate free of charge in 2023. It is a one-day event immediately preceding the SwissPLANT 2023 conference that participants are strongly encouraged to attend as well.

The call was so successful that it forced the committee to select amongst the applicants. Selected early career plant scientists present and discuss their latest findings with peer young researchers in a supportive atmosphere. The participants of the Early Career Meeting will select two speakers from the group to give an oral presentation at the following SwissPLANT Conference and in addition, all ECM participants will present a poster. If we obtain positive feedback from the community, we will organize such an event in the coming years.

In December 2022, the Society had 88 members. We keep encouraging all SPSW members to join. The Swiss Plant Science Web will continue to be our window on the internet for academic research in plant biology at Swiss universities. We are also counting on you to propose new ideas and initiatives to develop our society and looking forward to discussing them at our next General Assembly. This is important in order to develop a vibrant plant biology community, within our society but also in collaboration with colleagues from other societies including the Swiss Societies of Agronomy, Botany and Microbiology.

I cordially thank Klaus Schläppi and colleagues from the University of Basel (Thomas Boller, Jurriaan de Vos, Pascale Flury, Ben Engel, Günter Hoch, Sabine Rumpf and Sylvia Martinez) for organizing our core SwissPLANT conference.

Henry Janse van Rensburg and Wojciech Wietrzynski (both University of Basel) did not hesitate for a moment to seize the opportunity and organize the Early Career Meeting. A big thank you goes out to them as well!

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

### Monday, 23 January 2023

15:45	Swiss Society of Plant Biology, General Assembly 2023
17:00	<i>Welcome apéro</i>
17:50	Welcome by Christian Fankhauser, president Swiss Society of Plant Biology
17:55	Opening remarks by Klaus Schläppi, chair Program Committee
<b>Session I</b> , chair: Thomas Boller	
18:00	<u>Bruno Studer</u>   ETH Zurich The molecular basis of self-incompatibility in grasses
18:20	<u>Ben Engel</u>   U Basel Exploring the molecular architecture of photosynthesis and carbon fixation with cryo-electron tomography
18:40	<u>Thomas Badet</u>   U Neuchâtel Transposon activity shapes short-term evolution of a fungal pathogen
19:00	<u>Christiane Nawrath</u>   U Lausanne GPAT4, GPAT6, and GPAT8 are required for suberin deposition in <i>Arabidopsis</i> roots with non-redundant functions to GPAT5 and GPAT7
19:20	<i>Dinner, afterwards discussion at the bar</i>

## Tuesday, 24 January 2023

07:00 Breakfast

### Session II, chair: Jurriaan de Vos

08:00 Simon Bull | ETH Zurich

Translational research for crop improvement: A study of cassava

08:20 Charlotte Grossiord | EPFL & WSL

Adverse and mitigating impacts of warming on tree carbon cycling

08:40 Pascale Flury | U Basel

The secret lives of plant-beneficial rhizobacteria: unraveling their ecological versatility

09:00 Marie Barberon | U Geneva

Radial transport of nutrients in roots

09:20 Daniel Croll | U Neuchâtel

A thousand-genome panel retraces the global spread and climatic adaptation of a major crop pathogen

09:40 Coffee Break

### Session III, chair: Ben Engel

10:10 Early Career Meeting | Talk 1

Selected candidate from preceding Early Career Meeting will give a presentation

10:30 Sabine Rumpf | U Basel

The alpine flora in times of global change

10:50 Michael Raissig | U Bern

Decoding the developmental blueprint and form-function relationship of grass stomata

11:10 Lothar Kalmbach | U Lausanne

Cellular adaptations for long-distance transport through the phloem

11:30 Emilie Demarsy | U Geneva

UV-B photoprotection requires UVR8-mediated accumulation of sinapate esters in *Arabidopsis*

11:50 Leisure time (Lunch on your own, skiing, snowshoeing, hiking, swimming, sightseeing...)

**Session IV, chair: Sabine Rumpf**

- 17:30 Mateusz Majda | U Lausanne  
How mechanical forces control plant posture
- 17:50 Günter Hoch | U Basel  
How strictly controlled is carbon storage in trees?
- 18:10 Yasuhiro Sato | U Zürich  
Keystone genotype pairs increase population-level resistance to herbivory
- 18:30 *Dinner*
- 20:30 **Poster session** (c. 2h, drinks will be served)

## Wednesday, 25 January 2023

07:00 Breakfast

### Session V, chair: Günter Hoch

- 08:00 Rodrigo Reis | U Bern  
RNA structure discovery and function in plant adaptation to elevated temperatures
- 08:20 Beat Keller | U Zürich  
Molecular diversity in the resistance interactions of wheat and its fungal pathogens
- 08:40 Tsu-Hao Yang | U Lausanne  
Potential roles of vascular proton pumps in touch-induced electrical signaling
- 09:00 Didier Reinhardt | U Fribourg  
Does *Medicago truncatula* select its rhizobial partner based on efficient N-fixation during nodulation?
- 09:20 Philippe Reymond | U Lausanne  
How *Arabidopsis* perceive and respond to insect eggs
- 09:40 Coffee Break

### Session VI, chair: Pascale Flury

- 10:10 Early Career Meeting | Talk 2  
Selected candidate from preceding Early Career Meeting will give a presentation
- 10:30 Sofia van Moorsel | U Zürich  
Intraspecific trait variation of beech seedlings (*Fagus sylvatica*) in a common garden experiment
- 10:50 Christoph Ringli | U Zürich  
PP2C-type phosphatases influence LRX/FER/RALF signaling module
- 11:10 Tom Walker | ETH Zurich  
The plant metabolome as a vast repository of novel plant functional traits
- 11:30 Yves Poirier | U Lausanne  
A DOMON domain-cytochrome b561 protein acts as a ferric reductase in iron homeostasis and impacts primary root growth under phosphate deficiency
- 11:50 Closing remarks



## Transposon activity shapes short-term evolution of a fungal pathogen

**Thomas Badet**<sup>1,3</sup>, Ursula Oggenfuss<sup>1</sup>, Simone Fouché<sup>1,2</sup>, Marcello Zala<sup>2</sup>, Bruce A. McDonald<sup>2</sup> & Daniel Croll<sup>1</sup>

<sup>1</sup>Laboratory of Evolutionary Genetics, Institute of Biology, University of Neuchâtel

<sup>2</sup>Plant Pathology, Institute of Integrative Biology, ETH Zürich

<sup>3</sup>Laboratory of Molecular and Cellular Biology, Institute of Biology, University of Neuchâtel

Structural variation is a common source of intraspecific genetic variation. Human diseases, crop improvement traits and pesticide resistance have all been associated with such structural rearrangements. Understanding the mechanisms promoting genomic instability is therefore essential for the study of rapid evolution. In this work, we show that transposable elements are major drivers of the pangenome architecture of the fungal wheat pathogen *Zymoseptoria tritici*. We find that specific transposon families and chromosomal sequence characteristics are tightly correlated with the occurrence of specific genomic rearrangements. Using machine-learning, we were able to predict the emergence of spontaneous insertion-deletion variants produced during meiosis in a four-generations pedigree. Some of the most expansive structural variants generated in the pedigree were tied to a single highly active transposon. Retracing the activity of the element in the *Zymoseptoria* genus, we identified multiple independent reactivation events generating a complex set of transposon copies. Within the focal species *Z. tritici*, we identified recent reactivation of the transposon with a geographically localized rapid expansion in copy numbers. Our results retrace the recent origin of a transposon that successfully evaded host control to promote major structural rearrangements within a species.

## Radial transport of nutrients in roots

**Marie Barberon**

Department of Botany and Plant Biology, University of Geneva

Plant roots forage the soil to acquire water and nutrients for growth and development. This function is closely linked to their anatomy: water and nutrients move radially through the concentric layers of epidermis, cortex, and endodermis before entering the vasculature. This arrangement allows for three uptake scenarios: the “symplastic pathway”, where the outer cells actively take up nutrients, which are then transported from cell to cell through plasmodesmata; the “apoplastic pathway”, where nutrients are transported in the apoplast and blocked by the endodermal apoplastic barrier (Casparian strips); and the “coupled trans-cellular pathway”, where nutrients are transported sequentially from one cell to another by polarized influx and efflux carriers and are barred by the endodermal diffusion barrier (suberin lamellae). My group aims to functionally characterize these pathways by a combination of physiology, genomic, cell biology and developmental approaches. We are particularly interested in suberin and plasmodesmata functions and their regulations for nutrient acquisition.

## Translational research for crop improvement: A study of cassava

Christina J. Mueller<sup>1</sup>, Sophia Hedinger<sup>1</sup>, Nina Lergster<sup>1</sup>,  
Ravi B. Anjanappa<sup>1</sup>, Samuel C. Zeeman<sup>1</sup>, **Simon E. Bull**<sup>1,2</sup>

<sup>1</sup> Plant Biochemistry, Institute of Molecular Plant Biology, ETH Zurich

<sup>2</sup> Molecular Plant Breeding, Institute of Agricultural Sciences, ETH Zurich

Crop improvement programmes rely on a vast array of tools and expanding knowledge to ensure the crops for tomorrow are better suited to human demands and climate change than those grown today. Among the many globally important crops is the Euphorbiaceae plant, cassava (*Manihot esculenta* Crantz). The large, starch-rich storage roots of cassava provide a source of calories for nearly one billion people, mostly living in sub-Saharan Africa. Cassava is vegetatively propagated, and sexual reproduction is hampered by flowering capacity and weak fertility (a consequence of domestication) meaning conventional breeding is a lengthy and resource-consuming process. Here, I present how learnings about starch biosynthesis and starch granule formation in the model plant, *Arabidopsis*, and other plant species are informing our research in cassava. For example, through implementation of the CRISPR-Cas system coupled with an inducer of flowering, we were able to produce transgene-free, genome-edited cassava plants that produce a 'waxy' starch favourable for food and industry. Our advancing understanding of starch biosynthesis in cassava and translational research will contribute to the development of novel cassava cultivars with starch quality-traits and increased root yield. Ultimately these cultivars could benefit small-holder farmers in Africa.

## A thousand-genome panel retraces the global spread and climatic adaptation of a major crop pathogen

Daniel Croll

Laboratory of Evolutionary Genetics, Institute of Biology, University of Neuchâtel

Human activity impacts the evolutionary trajectories of many species worldwide. Global trade of agricultural goods contributes to the dispersal of pathogens reshaping their genetic makeup and providing opportunities for virulence gains. Understanding how pathogens surmount control strategies and cope with new climates is crucial to predicting the future impact of crop pathogens. Here, we address this by assembling a global thousand-genome panel of *Zymoseptoria tritici*, a major fungal pathogen of wheat reported in all production areas worldwide. We identify the global invasion routes and ongoing genetic exchange of the pathogen among wheat-growing regions. We find that the global expansion was accompanied by increased activity of transposable elements and weakened genomic defenses. Finally, we find significant standing variation for adaptation to new climates encountered during the global spread. Our work shows how large population genomic panels enable deep insights into the evolutionary trajectory of a major crop pathogen.

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## UV-B photoprotection requires UVR8-mediated accumulation of sinapate esters in *Arabidopsis*

Manuela Leonardelli<sup>1</sup>, Gaétan Glauser<sup>2</sup>, Roman Ulm<sup>1</sup>,  
Emilie Demarsy<sup>1</sup>

<sup>1</sup> Department of Plant Sciences, University of Geneva

<sup>2</sup> Neuchâtel Platform of Analytical Chemistry,  
University of Neuchâtel

Light fuels photosynthesis and affects plant growth, development, and metabolism throughout their life cycle. Sunlight can also constitute an environmental stress, when in excess, overwhelming the photosynthetic capacity, as well as due to intrinsic, potentially damaging ultraviolet-B radiation (UV-B). Plants evolved a specific photoreceptor, UVR8, that perceives and responds to UV-B. UVR8 signaling leads to transcriptional reprogramming and consequent physiological changes. For instance, UVR8 signaling has been shown to promote photomorphogenesis (e.g. hypocotyl growth inhibition and cotyledon expansion), can modulate flowering time, and induces photoprotective mechanisms by increasing the expression of DNA repair enzymes and accumulation of secondary metabolites having potential role as antioxidants and sunscreens. It was previously reported that UVR8 activation enhances the expression of phenylpropanoid pathway enzymes and accumulation of flavonoids and anthocyanins. Here we show that UVR8 also increases the expression of enzymes involved in sinapates derivatives, another branch of the phenylpropanoid pathway. Our physiological (photosynthesis parameters, and survival assays) and targeted metabolite profiling demonstrate that UVR8-mediated accumulation of the sinapates esters plays a major role in plant UV-B photoprotection.

## Exploring the molecular architecture of photosynthesis and carbon fixation with cryo-electron tomography

Ben Engel

Biozentrum, University of Basel

Cells accomplish the biochemical reactions of life by concentrating their proteins into a variety of subcellular compartments called organelles. Our group explores the relationship between the form of the organelle and the function of its resident macromolecules. How does organelle architecture direct molecular function, and reciprocally, how do macromolecules sculpt and shape organelles? To investigate these questions, we use focused ion beam (FIB) milling of frozen cells followed by cryo-electron tomography to image macromolecules within their native cellular environment. Through a combination of nanometer-precision localization and high-resolution structural analysis, we aim to chart the molecular landscapes of organelles.

In this talk, we will explore the molecular architecture of light-harvesting thylakoid membranes in cyanobacteria, green algae, and plants (Rast et al., 2019; Wietrzynski et al., 2020).

I will also describe our recent work on VIPP1, a conserved membrane-remodeling protein that is required for thylakoid biogenesis and maintenance (Gupta et al., 2021). We will then journey through to the pyrenoid, a carbon-fixing subcompartment of the chloroplast that is formed by liquid-liquid phase separation (Freeman Rosenzweig et al., 2017; He et al., 2020). Finally, will look at a highly efficient method of CO<sub>2</sub> capture in anaerobic bacteria, where HDCR electrical nanowires couple hydrogen splitting to carbon fixation (Dietrich et al. 2022).

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## The secret lives of plant-beneficial rhizobacteria: unraveling their ecological versatility

Pascale Flury

University of Basel, Department of Environmental Sciences, Plant Microbe Interactions

Root-colonizing *Pseudomonas* have been intensively studied for their various plant-beneficial activities, such as the suppression of soilborne diseases. The species *Pseudomonas chlororaphis* and *Pseudomonas protegens*, in addition, exhibit insecticidal activity. To interact with plants, plant-pathogens, and insects, they harbor a toolbox of genes, which are differentially expressed in a host-dependent manner, making them adapted to a multi-host lifestyle. Because of their antifungal and insecticidal properties, *Pseudomonas* are interesting for biocontrol of diseases and pests. However, not every fluorescent *Pseudomonas* exhibits these activities in every context, a phenomenon that is well-known for biocontrol microorganisms. The outcome of the interaction with insects, for instance, varies depending on the insect species. We found that *P. protegens* does not always cause lethal infections, but in certain insects persists throughout different developmental stages and potentially uses the insect as a vector for dispersal to a new host plant. This shows that manifold interactions of *Pseudomonas* with plants and insects are possible and there is increasing evidence that such multi-host lifestyles are also common for other plant-beneficial rhizobacteria. In my research team, we study the ecology and biocontrol activity of plant-beneficial rhizobacteria, in particular *Pseudomonas* and compost microbial communities, and we want to understand their interactions with plant and insect hosts, pathogenic microbes, and the environment.

## Adverse and mitigating impacts of warming on tree carbon cycling

Charlotte Grossiord<sup>1,2</sup>

<sup>1</sup>Plant Ecology Research Laboratory, EPFL

<sup>2</sup>Functional Plant Ecology Group, WSL

Recent decades have been characterized by increasing temperatures worldwide, resulting in an exponential climb in vapor pressure deficit (VPD). Heat and VPD has been identified as an increasingly important driver of plant functioning in terrestrial biomes and is a significant contributor to recent drought-induced tree mortality independent of other drivers associated with climate change. Despite this, few studies have isolated the physiological response of plant functioning to high VPD, heat, and soil drought, thus limiting our understanding and ability to predict future impacts on terrestrial ecosystems. In this presentation, I will discuss recent findings suggesting that high temperature and VPD can lead to a cascade of impacts, including reduced photosynthesis and growth as well as higher risks of carbon starvation and hydraulic failure, independently of soil moisture changes. I will further show how compensation mechanisms associated with shifts in phenology and species interactions may mitigate the negative impacts of rising temperature.



## How strictly controlled is carbon storage in trees?

**Günter Hoch**, Raphael Weber, Cedric Zahnd,  
Ansgar Kahmen

Department of Environmental Sciences – Botany,  
University of Basel

Trees store most of their carbon (C) reserves in the living parenchyma cells of stems and roots. These reserves exhibit characteristic variations with phenology, growth and environmental stress. Up to date, it is largely unknown how the formation and re-mobilization of stored C in sapwood is regulated and synchronized over tissues in trees. Mechanistic concepts of C storage therefore often assume simple bucket-models, where the amount of stored C equals the net-balance between C assimilation and the sum of all C sink activities (e.g., respiration and growth).

Here, we summarize results from previous experimental and observational studies in our group, that tested the reaction of non-structural carbohydrate reserve pools in trees to situations of limited photosynthetic C supply. Overall, these studies suggested that C reserve concentrations in sapwood follow abrupt changes of the net C-source-sink balance in the short-term and at severe C starvation, but they consistently reach homeostatic levels that are very similar across different C-source-sink conditions over longer time periods. According to our findings, we propose that C reserve pool sizes in tree sapwood are determined and closely controlled rather than the simple net-result of C source vs. -sink activities of a tree. With respect to mechanistic C models of trees we therefore suggest that C reserve formation should be regarded as a determined C-sink parameter.

## Cellular adaptations for long-distance transport through the phloem

Lothar Kalmbach<sup>1,\*</sup>, Ykä Helariutta<sup>1,2</sup>

<sup>1</sup> Sainsbury Laboratory, University of Cambridge, UK

<sup>2</sup> Institute of Biotechnology, University of Helsinki, FIN

\* Present address: Department of Plant Molecular Biology, University of Lausanne, CH

Sieve elements are the conductive cells of the phloem. During development, sieve elements acquire thick cell walls and elongate considerably. Adjacent sieve elements are separated through sieve plates – thick cell walls, which are dotted with large perforations, the so-called sieve pores. Like plasmodesmata, sieve pores are symplastic connections between neighboring cells. Unlike plasmodesmata, however, they need to allow for considerable hydraulic conductivity for long-distance transport from source (leaves) to sink tissues (roots, fruits, and buds).

Despite their physiological importance, the profound cell wall modifications occurring during phloem differentiation are poorly understood on the molecular and genetic level. Callose accumulates both rapidly and reversibly to regulate symplastic transport. In *Arabidopsis*, callose is deposited around the developing sieve pores by CALLOSE SYNTHASE 7 and is required for high transport capacities along the sieve tube. Additional cell wall modifications during sieve element differentiation involve pectin remodeling in a spatially restricted region, mediated through PECTATE LYASE LIKE 12 for sustained phloem transport.

While providing a model how pectin and callose metabolism may interact during formation of the sieve plate, open questions remain with respect to the evolution and cell biology of such tissue-specific cell wall remodeling and their consequences for phloem function.

## Molecular diversity in the resistance interactions of wheat and its fungal pathogens

**Beat Keller, Javier Sanchez-Martin**

Department of Plant and Microbial Biology, University of Zürich

We recently contributed to the establishment of high-quality reference genomes of wheat and its fungal pathogen powdery mildew. These resources provide the basis for the identification of genes involved in host-pathogen interactions and the establishment of a wheat resistance gene atlas, including the proteins specifically recognized in the pathogens. Novel and diverse genes were identified in wheat using genomics. There is a surprising diversity in the proteins determining race-specific resistance in wheat against powdery mildew and leaf rust pathogens. One of the identified proteins is proposed to act as an executor protein specifically induced by avirulent pathogen isolates. We propose that identification and monitoring of avirulence gene diversity in pathogen populations becomes an integral part of introgression breeding to ensure effective and durable resistance in wheat. Thus, the knowledge of the wheat-fungal pathogen “interactome” promises to support breeding strategies for increased durability of resistance. The molecular basis of non-NLR based race-specific resistance remains to be explored and provides a rich field of research expected to identify novel types of mechanisms involved in plant immunity.

## How mechanical forces control plant posture

Mateusz Majda

Department of Plant Molecular Biology, University of Lausanne

Upright growth was a crucial evolutionary innovation that allowed plants to develop complex structures and colonize land. It is associated with a change in cellular geometry and elastic stiffness, which is achieved through developmental gradients of different tissues and cell types. Shoots actively control their posture by regulating primary and secondary growth and adjust their thickness to elongate over growth. From a physical perspective, upright growth is achieved by a proper balancing between stiffness and elasticity, which reacts to the compressive force increasing over development. Interestingly, many non-woody plant species such as *Arabidopsis* are not able to support their own weight, and this leads to instability and buckling.

In order to understand why plants fail to maintain their upright growth, we undertake multiscale studies from cell wall properties and cell geometry to tissue patterning and organ shape. We use interdisciplinary approaches by combining genetics and developmental biology with biomechanics and mathematical modeling. We are performing genetic screens to identify new players controlling local mechanical heterogeneities, which translate to changes seen at the cellular-, tissue and organ levels. We employ image processing software to quantify cell geometrical parameters and use custom biophysical tools such as micro-indentation and extensometer to access the stiffness at different

scales. The future experimental outcomes will be integrated into computational simulations for testing how they sustain upright plant growth. More broadly, our research will address how mechanical heterogeneities emerge and control robust plant structures, which in turn will improve our understanding of the lodging in crop species or toppling in young trees.

MNOPQRSTUVWXYZ

## GPAT4, GPAT6, and GPAT8 are required for suberin deposition in *Arabidopsis* roots with non-redundant functions to GPAT5 and GPAT7

Kay Gully<sup>1</sup>, Alice Berhin<sup>1</sup>, Damien De Bellis<sup>1,2</sup> and Christiane Nawrath<sup>1</sup>

<sup>1</sup> Department of Plant Molecular Biology, University of Lausanne

<sup>2</sup> Electron Microscopy Facility, University of Lausanne

Lipid polymers, such as cutin and suberin, strengthen the diffusion barrier properties of the cell wall in specific cell types and are essential for the water relations, mineral nutrition, and stress protection of plants.

A family of closely related land plant-specific glycerol-3-phosphate acyltransferases (GPATs) are essential for the biosynthesis of cutin and suberin precursors. GPATs also have a phosphatase domain. The GPAT4/6/8 clade, in which the phosphatase activity is conserved was associated with cutin formation, while the GPAT5/GPAT7 clade without phosphatase activity was associated with suberin formation, respectively.

Using knockout mutants of the different *GPAT* clades we were able to revise this view by identifying specific roles of both *GPAT* clades in suberin formation of *Arabidopsis* roots. The *GPAT4/6/8* clade plays a crucial role in endodermal suberin formation of unstressed plants. The *GPAT5/7* clade is essential for adaptive suberin formation in response to stresses. The activity of phosphatase domain plays a critical role in these processes. The phosphatase activity of GPAT4/6/GPAT8 is important for suberization of the endodermis. The loss of phosphatase activity is essential for the formation of the typical suberin ultrastructure in form of lamellae.

Our studies provide therefore not only novel insights into the mechanism of how plants form suberin lamellae, but also into the evolution and specialization of lipid-rich diffusion barriers in land plants.

## A DOMON domain-cytochrome b561 protein acts as a ferric reductase in iron homeostasis and impacts primary root growth under phosphate deficiency

Joaquín Clúa, Jonatan Montpetit, Yves Poirier

Department of Plant Molecular Biology, University of Lausanne

Several interactions between iron (Fe) and phosphate (Pi) homeostasis have been described, such as the Fe-dependent inhibition of primary root growth under Pi deficiency. This response involves the formation of apoplastic Fe<sup>+3</sup>-malate complexes in the root meristem which implicates the oxidation of Fe<sup>+2</sup> by the LPR1 ferroxidase. However, how the reduced Fe<sup>+2</sup> is generated in the root meristem is unknown.

increased uptake and translocation of Fe to the shoot and resulted in plants highly sensitive to Fe excess toxicity. This study reveals a biological role for CYBDOM proteins in plants.

We have identified a gene in *Arabidopsis*, named *CRR*, that is implicated in primary root growth under Pi deficiency. Under low-Pi conditions, the *crr* mutant showed an enhanced reduction of primary root growth associated with increased accumulation of apoplastic Fe in the root meristem. Conversely, CRR overexpression rendered primary root growth insensitive to low-Pi inhibition, reduced root apoplastic Fe deposition, and impacted the expression of genes involved in Fe and redox homeostasis. CRR is a member of an uncharacterized CYBDOM protein family possessing a cytochrome b561 (CYB561) with an N-terminal DOMON domain. We demonstrated that CRR localizes to the plasma membrane and possesses ascorbate-dependent ferric reductase activity. The *crr* mutant showed increased tolerance to high-Fe stress upon germination and seedling growth. In contrast, CRR overexpression was associated with

## Decoding the developmental blueprint and form-function relationship of grass stomata

Roxane P Spiegelhalder<sup>1,2</sup>, Lea S Berg<sup>1,2</sup>, Dan Zhang<sup>2</sup>,  
Tiago DG Nunes<sup>2</sup>, Kim N Janssen<sup>1,2</sup>, Xin Cheng<sup>1,2</sup>, Paola  
Ruiz Duarte<sup>2</sup>, Gabriel Deslandes<sup>1</sup>, Heike Lindner<sup>1</sup>,  
**Michael T Raissig<sup>1</sup>**

<sup>1</sup> Institute of Plant Sciences, University of Bern,  
Switzerland

<sup>2</sup> Centre for Organismal Studies Heidelberg, Heidelberg  
University, Germany

Stomata are microscopic “breathing pores” on land plants that balance photosynthetic carbon dioxide uptake with water vapor loss. Plant fossils suggest that the ancestral stomatal morphology consisted of two kidney-shaped guard cells (GCs) surrounding the central pore and most extant land plants still form kidney-shaped GCs. Grasses, however, form derived stomatal complexes consisting of two dumbbell-shaped GCs flanked by two lateral subsidiary cells (SCs). This “graminoid” morphology is linked to faster stomatal kinetics and higher water-use efficiency.

We use the model grass *Brachypodium distachyon* to decipher (1) how SCs are recruited and formed, (2) how grass GCs morph into dumbbell-shaped cells (3) and how stomatal form affects function. The grass stomatal lineage presents an ideal developmental system with a solid base-to-tip developmental gradient and highly stereotypic patterning. We have identified the key transcription factors establishing both the GC and SC lineages, different polarity genes that regulate asymmetric cell divisions, and novel players

involved in GC differentiation and morphogenesis. Finally, we employed single-cell RNA-sequencing to build a cell atlas of the developing grass leaf at single-cell resolution. Together, we attempt to comprehensively identify all relevant developmental modules and their cellular roles in the making of the most innovative stomatal morphology in the plant kingdom to understand how the graminoid form improves function.

## Does *Medicago truncatula* select its rhizobial partner based on efficient N-fixation during nodulation?

Min Chen, Axelle Raisin, Maro Widmer, Natalie Judkins, Laurent Falquet, Daniel Wegmann, **Didier Reinhardt**

Department of Biology, University of Fribourg

Nodule symbiosis between legumes (Fabaceae) and nitrogen-fixing bacteria (rhizobia) exhibits highly asymmetrical dynamics. Individual plant hosts acquire single bacterial cells that amplify in the host to populations of approximately  $10^8$  bacterial cells. During this process, non-fixing bacterial clones (cheaters) are likely to arise by spontaneous mutations, which are predicted to have a selective advantage relative to their N-fixing kin, because they can profit from host benefits (carbon) without an investment in the extremely energy-intensive N-fixation reaction that requires large amounts of reduction equivalents and ATP. Hence, it has been predicted that nodule symbiosis should be prone to erosion and transition to parasitism. However, nodule symbiosis has persisted for >50 million years, suggesting that the host can assess and enforce adequate bacterial service, either by preferentially rewarding good N-fixers, or by sanctioning cheaters. Although experimental evidence revealed signs of selection, the involved mechanisms remain elusive.

We take a combinatorial approach to assess signatures of selection and sanctioning at the genomic level in the rhizobia, and by proteomic and metabolomic analysis in both partners (*Medicago truncatula* and *Sinorhizobium meliloti*). We find that life style affects genome sequence diversity in the bacterial partner in a locus-specific manner, and that cheating results in a global transition of symbiotic status in the host, with a general induction of defense markers and suppression of symbiotic functions.



## RNA structure discovery and function in plant adaptation to elevated temperatures

Rodrigo Reis

Institute of Plant Sciences, University of Bern

Rises in global average temperature is a major consequence of climate change, with significant impact on plant development, growth, and defence. However, our understanding of how plants perceive and adapt to elevated temperatures is still recent and far from complete. Although temperature is a major parameter for RNA structure, the biological role of temperature modulation of RNA structure has not been thoroughly explored in biology yet. Plants are not homeotherms and their cell's environment, with constant shifts in temperature, likely have created ideal conditions for RNA structures to be selected and genetically transmitted as an adaptive mechanism to elevated temperatures.

The main topic in my newly formed research group is to understand how the plant model *Arabidopsis thaliana* adapts to elevated temperatures, focused on the conformational changes of secondary structures in the transcriptome. For this, we will identify and study the conserved RNA structures that have evolved to perceive elevated temperatures with critical role in plant adaptation. We will apply cutting-edge high-throughput approaches to study RNA structural dynamics in vivo, and a suite of approaches to dissect conserved structures that are critical for plant adaptation.

## How *Arabidopsis* perceive and respond to insect eggs

Philippe Reymond

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Insect eggs from the Large White butterfly *Pieris brassicae* release phosphatidylcholines (PCs) that trigger innate immunity in *Arabidopsis*, including salicylic acid accumulation, defense gene expression and localized cell death. These responses are mediated by candidate cell-surface Lectin Receptor Kinases (LecRK-I.1 and LecRK-I.8) and calcium channels. However, whether PCs directly bind LecRKs is under investigation. In addition, oviposition inhibits growth of pathogens through the establishment of an intra- and interplant systemic acquired resistance. The biological relevance of this striking phenomenon will be discussed.

## PP2C-type phosphatases influence LRX/FER/RALF signaling module

Christoph Ringli, Xiaoyu Hou, Siby Gupta, Gabor Kadler

Department of Plant and Microbial Biology, University of Zürich

The controlled growth of plant cells requires the coordinated development of the wall surrounding each cell. To this end, plants have evolved a cell wall integrity (CWI) sensing machinery encompassing a number of cell wall-localized proteins and transmembrane receptors. These sense alterations in the cell wall and can induce changes in cell-wall properties and -composition to coordinate growth processes including the regulated expansion of the cell wall surface. LRR-extensins, LRXs, are cell wall-anchored proteins that act as high-affinity binding sites of RALF peptide hormones and signal via the FERONIA receptor kinase to adjust wall development, cell growth and responses to stress conditions such as salt stress.

Our group is interested in the understanding of the signaling process of LRX proteins. The *lrx1* mutant of *Arabidopsis*, develops a root hair-developmental defect, and a suppressor mutant, *rol23* (*repressor of lrx1*) was identified that alleviates the *lrx1*-induced aberrant root hair phenotype. ROL23 is part of a three-member subfamily of PP2C phosphatases that have so far not been characterized. Complementation experiments showed that the three members of this subfamily are functionally redundant as they all complement the *lrx1 rol23* mutant, resulting in transgenic plants developing the *lrx1* root hair phenotype. By contrast, several *PP2C* genes from

other subgroups of the *PP2C* phosphatases fail to complement the *rol23* mutation, suggesting a specific function of the ROL23-type PP2Cs in the LRX1-related process. Double- and triple mutants of the *ROL23*-type PP2C genes are being established to investigate the importance of this subgroup for plant development. Ultimately, we aim to identify substrate proteins of the PP2C to shed light on the function of these proteins in the LRX/FER/RALF regulated process and the mechanism by which the *rol23* mutation suppresses the *lrx1* root hair phenotype.

## The alpine flora in times of global change

**Sabine Rumpf**

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of Basel

Mountain regions are warming faster than the global average while being additionally affected by land use changes, non-native species introductions, and nitrogen emissions in the lowlands. Yet, these ecosystems are comparatively pristine, harbor disproportionately high levels of biodiversity and provide fundamental contributions to people. Predicting future responses of alpine plant species to global change is therefore crucial to conserve global biodiversity and ensure ecosystem integrity with immediate relevance to humankind. For accurately predicting the future it is, however, inevitable to first understand already occurred changes of species performance and distributions as well as community composition. Here, I will summarize recent trends in the phenology, growth and re-distribution of alpine plant species in Europe.

## Keystone genotype pairs increase population-level resistance to herbivory

**Yasuhiro Sato**<sup>1</sup>, Rie Shimizu-Inatsugi<sup>1</sup>, Kazuya Takeda<sup>2</sup>,  
Atsushi J. Nagano<sup>2</sup>, Kentaro K. Shimizu<sup>1</sup>

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<sup>2</sup> Faculty of Agriculture, Ryukoku University, Japan

Plant genotypic diversity alters population-level ecological processes, such as resistance to natural enemies. Although those genotypes are expected to have non-additive and unequal contributions to the ecological process, identification of keystone pairs remains difficult. To predict genotype pairs that exert positive effects of mixed planting on anti-herbivore resistance, we used genome-wide polymorphisms of the plant species *Arabidopsis thaliana*. By setting randomized mixtures of 199 genotypes in two field sites, we first uncovered plant genomic basis that could reduce herbivore damage among neighboring genotypes. We then planted key genotype pairs under mixture and monoculture conditions, and indeed found significant reduction in herbivore damage in the mixture over monocultures. These results demonstrate the relevance of keystone genotype pairs in population-level resistance, enlightening an avenue to control biodiversity effects by within-species mixed planting.

## The molecular basis of self-incompatibility in grasses

Marius Rohner<sup>1</sup>, Chloé Manzanares<sup>1</sup>, Steven Yates<sup>1</sup>, Daniel Thorogood<sup>2</sup>, Thomas Lübberstedt<sup>3</sup>, Torben Asp<sup>4</sup> and **Bruno Studer**<sup>1</sup>

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Self-incompatibility (SI) is a genetic mechanism of hermaphroditic plants to prevent inbreeding. Allogamous species of the Poaceae family exhibit a unique gametophytic SI system controlled by two multi-allelic and independent loci, S and Z. Despite intense research efforts in the last decades, the genes that determine the initial SI recognition mechanism are yet to be identified. We used fine-mapping in perennial ryegrass

(*Lolium perenne* L.) and comparative genomic analyses within the Poaceae family to describe the genes underlying SI in detail. This revealed the S- and the Z-locus to be similar: at both loci, the pollen and stigma components are determined by two genes encoding DUF247 domain proteins and a gene encoding for a secreted short stigmatic peptide, respectively. They exhibited high allelic diversity as well as tissue-specific gene expression, matching the expected characteristics of SI determinants known from other systems. We propose a model for the action of these components in the SI response and provide evidence for a duplicated origin of the two-locus SI system of grasses. Our

study provides new insights into the origin and evolutionary history of the unique gametophytic SI system in one of the largest and economically most important plant families.

## Intraspecific trait variation of beech seedlings (*Fagus sylvatica*) in a common garden experiment

**Sofia J. van Moorsel**, Meredith C. Schuman,  
Ewa A. Czyz, Aboubakr Mouradi, Katia Pfister,  
Mike Werfeli, Marylaure De la Harpe,  
Carmen Meiller, Andreas Huehni, Felix Morsdorf,  
Michael E. Schaepman

Department of Geography, University of Zurich

Intraspecific diversity is the basis for adaptation to new environmental conditions. However, the interactions between genotypic contribution to intraspecific trait diversity and plasticity are still largely unknown. Beech (*Fagus sylvatica*) is common in Europe and commercially and culturally important. However, climate change, including droughts and heatwaves, is likely to change the distribution of beech in Europe and lead to local population declines. For beech to persist, it relies on intraspecific phenotypic and genetic diversity.

We conducted a common garden experiment with 200 beech seedlings from 16 European beech populations with known population genetic structure. Once placed in the common environment, we determined intraspecific trait variation that remained and its association with genetic variation.

We found strong signals of beech tree origin on the plant phenotype for plant height, stem diameter, growth rates and phenology. For example, the length of the growing season decreased with increasing altitude of the source site but increased with increasing temperature. Other traits, such as leaf spectra, were also highly variable between trees but lacked an origin-specific signal. The intraspecific trait variation will be assessed over several years to find out if variation decreases or increases with tree age. Our study aims to provide a window into the mechanisms underlying the link between intraspecific genetic diversity and trait variation to support efforts to help Beech persist.

## The plant metabolome as a vast repository of novel plant functional traits

**Tom W. N. Walker**<sup>1,2</sup>, Franziska Schrodtr<sup>3</sup>, Pierre-Marie Allard<sup>4</sup>, Emmanuel Defosse<sup>2</sup>, Vincent E. J. Jassey<sup>5</sup>, Jake M. Alexander<sup>1</sup>, Oliver Baines<sup>4</sup>, Virginie Baldy<sup>6</sup>, Richard D. Bardgett<sup>7</sup>, Pol Capdevila<sup>8,9</sup>, Phyllis D. Coley<sup>10</sup>, Nicole M. van Dam<sup>11,12</sup>, Bruno David<sup>13</sup>, Patrice Descombes<sup>1,23</sup>, Maria-Jose Endara<sup>10</sup>, Catherine Fernandez<sup>6</sup>, Dale Forrister<sup>10</sup>, Albert Gargallo-Garriga<sup>14,15</sup>, Gaëtan Gauser<sup>2</sup>, Sue Marr<sup>11,12,17</sup>, Steffen Neumann<sup>11,17</sup>, Loïc Pellissier<sup>1,23</sup>, Kristian Peters<sup>11,17,18</sup>, Sergio Rasmann<sup>2</sup>, Ute Roessner<sup>19</sup>, Roberto Salguero-Gómez<sup>3</sup>, Jordi Sardans<sup>14,15</sup>, Meredith C. Schuman<sup>20</sup>, Jean-Luc Wolfender<sup>4</sup>, Wolfram Weckwerth<sup>21,22</sup> & Josep Peñuelas<sup>14,15</sup>

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<sup>6</sup> Aix Marseille Université, Avignon U, CNRS, IRD, IMBE

<sup>7</sup> Dept of Earth & Environmental Sciences, The University of Manchester

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<sup>10</sup> School of Biological Sciences, U of Utah

<sup>11</sup> German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig

<sup>12</sup> Institute of Biodiversity, Friedrich Schiller U Jena

<sup>13</sup> Green Mission Pierre Fabre, Institut de Recherche Pierre Fabre

<sup>14</sup> CSIC, Global Ecology Unit CREAL-CSIC-UAB

<sup>15</sup> CREAL

<sup>17</sup> Leibniz Institute of Plant Biochemistry, Bioinformatics and Scientific Data

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<sup>23</sup> Landscape Ecology, Swiss Federal Institute for Forest, Snow and Landscape Research (WSL)

Plants produce a staggering diversity of metabolites (>1'000'000 throughout the plant kingdom) that are the biochemical foundations of plant form and function (collectively, “the metabolome”). The diversity of the plant metabolome is well known to human society, being the source of most foods and medicines. Yet, although evolutionary and ecological forces have constrained plant physiology to a limited number of successful life history strategies, we know little about how the plant metabolome varies systematically across the plant kingdom. Here, we draw on the ecological framework of the plant functional trait concept to interpret leaf metabolome variation among 457 tropical and 405 temperate species. We find that distilling metabolite chemistry into five metabolomic functional traits reveals that plants vary on two axes of metabolomic specialisation – a leaf chemical defence spectrum (carbon bond saturation, polarity) and leaf longevity (structural complexity, intermolecular interactions). Axes are similar for tropical and temperate species, with many trait combinations yielding successful life-history strategies. However, metabolomic traits vary orthogonally to life-history strategies described by widely used plant functional traits. The metabolome thus describes unique dimensions of plant form and function that are missed by existing functional traits, and offers clear capacity to enhance the plant functional trait concept.



## Potential roles of vascular proton pumps in touch-induced electrical signaling

**Tsu-Hao Yang** and Edward E. Farmer

Department of Plant Molecular Biology, University of Lausanne

The activation of the jasmonate (JA) biosynthesis pathway depends on membrane depolarization in vascular tissues. Wound-induced electrical signals propagate from wounded leaves through the vascular tissues to activate the JA pathway in undamaged distal leaves. But the mechanism of initiation of touch- and wound-induced electrical signals is unclear. Are mechanostimulation-induced pressure changes in the vascular tissues associated with the initiation of electrical signalling? Or does the initiation of the electrical signal only require damage-associated molecular patterns released from wounds? To investigate such questions, I characterized mechanostimulation-induced electrical signals in leaves of *Arabidopsis thaliana*. This signal propagated through the midvein bi-directionally with a velocity similar to wound-associated electrical signals. Furthermore, the signals in the vascular tissues were investigated using the electrical penetration graph system, i.e., using aphids as living electrodes. We found the mechanostimulation-induced electrical signal was likely associated with the activity of *Arabidopsis* H<sup>+</sup>-ATPase (AHA) proton pumps. This was confirmed using CRISPR-Cas9 mutation.

## UniProtKB maintains its garden

**Emmanuel Boutet**, Damien Lieberherr, Sylvain Poux,  
Nicole Redaschi, Alan Bridge, and the Swiss-Prot group

Swiss-Prot Group – SIB Swiss Institute of Bio-  
informatics, Geneva

The UniProt Knowledgebase (UniProtKB, <https://www.uniprot.org>) is a comprehensive, high quality and freely accessible resource of protein sequences and functional information. UniProtKB includes 600 plant proteomes and 41,500 expert curated plant proteins annotated with over 24,600 publications. Expert curation of plant proteins is a major focus of our work, as plants are key to global food security and the source of an incredible variety of natural products including medicines, pesticides, and biofuels, which we now describe using the Rhea knowledgebase of biochemical reactions ([www.rhea-db.org](http://www.rhea-db.org)). In this work, we will highlight how plants and their proteins interact with their environment and ourselves using examples from UniProtKB/Swiss-Prot – from proteins that repel attacks by herbivores, to those that attract friendly pollinators or symbiotic nitrogen-fixing bacteria, to those that produce drugs for the war on cancer – and how we capture that knowledge in forms that are FAIR.

**B**CDEFGHIJKLMNOPQRSTUVWXYZ

## A receptor protein mediates soil microbial feedbacks on *Arabidopsis*

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Plants exude a diverse array of compounds into the soil and thereby they condition the surrounding soil and its microbiome. Such soil conditioning results in microbial feedbacks on the performance of the next plant generation. Benzoxazinoids (BXs) are abundant bioactive compounds in the root exudates of important crops like maize and they selectively structure the rhizosphere microbiota of maize. *Arabidopsis thaliana* expresses positive growth feedbacks when grown on BX conditioned soil. While the ecology and the agronomic impact of plant-soil feedbacks are well described, little is known about the underlying mechanisms of plant responses to soil microbiomes. Using a Genome Wide Association Study performed on 410 *Arabidopsis* accessions, we identified an uncharacterized toll-interleukin (TIR) nucleotide-binding site (NBS)-leucine-rich repeat (LRR) receptor, possibly involved in plant defense responses. A particular allele variant of this receptor locus was associated with accessions

that expressed a positive growth feedback on BX conditioned soils, while other variants associated with negative growth feedbacks. Mutants of the receptor have lost the strong positive growth feedback on BX-conditioned soil, confirming the involvement of the identified receptor in microbiome-driven growth feedbacks. We have identified a novel receptor gene mediating responsiveness to microbial feedbacks and our results suggest a growth-defense trade-off during plant-soil feedbacks.

## PGR6/ABC1K1: a connection between proton gradient regulation and chloroplast biogenesis?

Joy Collombat, Fiamma Longoni and **Felix Kessler**

Institute of Biology, University of Neuchâtel

ABC1K1 is an atypical kinase located in plastoglobules which are thylakoid-associated lipid droplets. It was originally identified as PGR6 and the *pgr6* mutant has a conditional high fluorescence phenotype (1). Due to its localization at plastoglobules, the role of ABC1K1 in photosynthesis is not obvious. However, plastoglobules contain large amounts of non-photoactive plastoquinone and we have shown that ABC1K1 is required to replenish and maintain the photoactive plastoquinone pool presumably from the plastoglobule source ("plastoquinone homeostasis") (2). This provides explanations for the *pgr6* phenotype. Moreover, *pgr6/abc1k1* is hypersensitive to red light resulting in an albino seedling phenotype when germinated under this condition. This negatively impacts expression of photosynthesis-associated nuclear genes but the proximate defects are unclear. Here we show that *pgr6/abc1k1* disrupts the assembly of Photosystem II. We propose that this defect triggers retrograde signaling to downregulate photosynthesis-associated genes which ultimately unravels chloroplast biogenesis.

- 1) Pralon, T. et al. (2019) Plastoquinone homeostasis by *Arabidopsis* Proton Gradient Regulation 6 is essential for photosynthetic efficiency. *Comms. Biol.*, 2, 220
- 2) Pralon, T. et al. (2020) Front. Plant Sci., Mutation of the Atypical Kinase ABC1K3 Partially Rescues the PROTON GRADIENT REGULATION 6 Phenotype in *Arabidopsis thaliana*. <https://doi.org/10.3389/fpls.2020.00337>

KLMNOPQRSTUVWXYZ

## Cell-surface receptors in plant-microbe interactions

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Freising, Germany

My lab studies the dynamic interaction between plant hosts and bacteria at the molecular, cellular and physiological level. A major aspect of this work is a mechanistic understanding of how plant receptors sense and control microbial colonisation. Pattern-recognition receptors at the cell-surface sense so-called microbe-associated molecular patterns and activate broad-spectrum pattern-triggered immunity. We identified the receptor kinase LORE (LIPOOLIGOSACCHARIDE-SPECIFIC REDUCED ELICITATION) in *Arabidopsis thaliana* as pattern-recognition receptor that senses 3-hydroxy fatty acid metabolites, such as 3-hydroxydecanoic acid (3-HDA), released by Gram-negative bacteria (1,2). LORE alias SD1-29 belongs to the class of S-domain-1 (SD1) receptor kinases. How S-domain receptor kinases are activated and trigger downstream signalling is largely unknown. To unravel the mechanism of 3-HDA sensing by LORE and activation of downstream immune signalling at the molecular level, we apply a combination of biochemistry, genetics, computational modelling, and natural diversity screening. I will present an overview of our current and planned work on LORE signalling.

- 1) Ranf S, et al. (2015) A lectin S-domain receptor kinase mediates lipopolysaccharide sensing in *Arabidopsis thaliana*. *Nature Immunology* 16: 426-433
- 2) Kutschera A, et al. (2019) Bacterial medium-chain 3-hydroxy fatty acid metabolites trigger immunity in *Arabidopsis* plants. *Science* 364, 178-181

ABCDEFGHIJKLMNOPQRSTUVWXYZR

## Investigating the complex relationship between phloem development and sink organ growth

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Our lab has identified *OCTOPUS (OPS)* and its homolog *OPS-LIKE 2 (OPL2)* as important regulators of *Arabidopsis* root phloem development. In the developing root protophloem files, loss of function of *OPS* leads to the appearance of cells that do not adopt protophloem cell identity. These so-called “gap cells” interrupt the integrity of the phloem, and we can show that phloem transport of mobile dyes is impaired in the roots of these plants. Thus, it does not come as a surprise that root growth is negatively affected in *ops*. A knock-out of *OPL2* in the *ops* background further enhances phloem and root growth defects. Also shoot growth is impaired more in *ops opl2* than in *ops*. To better understand the contribution of the root and the shoot to the observed phenotypes, we recently started grafting experiments. In these, we were able to show that *ops opl2* roots have a negative impact on the growth of wild-type shoots, while wild-type shoots cannot rescue *ops opl2* root growth. Thus, these experiments enable us to investigate how impaired phloem development in sink tissues influences the growth of source organs. We have performed a series of experiments to achieve a better understanding of these processes. Results from these investigations will be presented.

## Architecture and maintenance of thylakoid membranes visualized by Cryo-electron Tomography

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Chloroplasts of vascular plants contain extensive network of thylakoids – flat cisternae that scaffold photosynthetic complexes that work in chain to harness light energy. Visualization of thylakoids at molecular level, in native conditions has been a major challenge due to a difficulty to preserve a fine interaction between proteins and their membranous support. We use cryo-Electron Tomography (Cryo-ET) and AI-assisted approaches to detect and map the native molecular landscapes of thylakoid membranes in variety of species, from: cyanobacteria, green algae to vascular plants. Here we show tomograms detailing membrane organization of Spinach chloroplasts. We are able to detect individual complexes embedded in the membrane and provide insights into molecular forces that drive protein separation and thylakoid stacking. We reveal the distribution of photosynthetic complexes in appressed and non-appressed membrane domains as a universal phenomenon of eukaryotic green lineage.

## Early Career Meeting SwissPLANT 2023

### Poster contributions by junior researchers

- 1 **Non-cell autonomous RNA silencing restricts Turnip Yellow Virus (TuYV) spread in *Arabidopsis thaliana***  
Daniele Albertini, Olivier Voinnet  
 > Department of Biology, Institute of Molecular Plant Biology, ETH Zürich
  
- 2 **Effects of biodegradable micro- and macroplastic on *Zea mays* L. growth, transcriptome and the associated root and soil microbiome**  
Robin Bautzmann<sup>1</sup>, Jan Wächli<sup>2</sup>, Klaus Schläppi<sup>2</sup>, Doris Rentsch<sup>1</sup>  
 > <sup>1</sup>Institute of Plant Sciences, University of Bern  
 > <sup>2</sup>Department of Environmental Sciences, University of Basel
  
- 3 **Conserved developmental trajectories channelling lateral root primordium morphogenesis**  
 Cristovao De Jesus Vieira Teixeira<sup>1</sup>, Kevin Bellande<sup>1</sup>, Thomas Badet<sup>1</sup>, Anne C. Roulin<sup>2</sup>, Joop E.M Vermeer<sup>1,3</sup>  
 > <sup>1</sup>Laboratory of Cell and Molecular Biology, Institute of Biology, University of Neuchâtel  
 > <sup>2</sup>Department of Plant and Microbial Biology, University of Zurich
  
- 4 **Functional organization of plant immune receptor kinase complexes**  
Kyle W. Bender, Cyril Zipfel  
 > Department of Plant and Microbial Biology, University of Zürich
  
- 5 **Bacterial engineering of symbionts of entomopathogenic nematodes to enhance biological control on the western corn rootworm in maize crops**  
Anja Boss<sup>1</sup>, Szabolcs Tóth<sup>2</sup>, Stefan Toepfer<sup>2,3</sup>, Matthias Erb<sup>1</sup>, Ricardo Machado<sup>4</sup>  
 > <sup>1</sup>Institute of Plant Sciences, University of Bern  
 > <sup>2</sup>Plant Protection Institute, Szent Istvan University, Hungary  
 > <sup>3</sup>CABI, Delémont  
 > <sup>4</sup>Institute of Biology, University of Neuchâtel
  
- 6 **A cytochrome-containing protein plays a dual role in phosphate starvation responses and iron homeostasis**  
Joaquín Clúa, Jonatan Montpetit and Yves Poirier  
 > Department of Plant Molecular Biology, University of Lausanne
  
- 7 **A lignin-like polymer is deposited in the outer cell wall of the *Arabidopsis* root epidermis**  
Nasim Farahani Zayas<sup>1</sup>, Damien De Bellis<sup>1,2</sup>, Christiane Nawrath<sup>1</sup>  
 > <sup>1</sup>Department of Plant Molecular Biology, University of Lausanne  
 > <sup>2</sup>Electron Microscopy Facility, University of Lausanne
  
- 8 **Harnessing genetic interactions driving inflorescence complexity in tomato**  
Natalia Gaarslev, Sebastian Soyk  
 > Center for Integrative Genomics, University of Lausanne



- 9 **The *Arabidopsis* PP2Cs regulate LRX1-mediated cell wall integrity sensing**  
Xiaoyu Hou, Garbor Kadler, Shibu Gupta, Amandine Guérin, Caroline Levasseur and Christoph Ringli  
> Institute of Plant and Microbial Biology, University of Zurich
- 10 **Temperature plasticity of a seed coat apoplastic barrier promotes seed dormancy in *Arabidopsis thaliana***  
Lena Hyvärinen<sup>1</sup>, Anne Utz-Pugin<sup>1</sup>, Christelle Fuchs<sup>1</sup>, Kay Gully<sup>2</sup>, Christiane Nawrath<sup>2</sup>, Sylvain Loubéry<sup>1</sup> and Luis Lopez-Molina<sup>1</sup>  
> <sup>1</sup>Department of Plant Sciences, University of Geneva  
<sup>2</sup>Department of Plant Molecular Biology, University of Lausanne
- 11 **Insight into the molecular mechanisms of the AvrPm3-SvrPm3 effector protein interactions derived from the wheat powdery mildew pathogen**  
Jonatan Isaksson, Matthias Heuberger, Milena Amhof, Lukas Kunz, Kaitlin McNally, Beat Keller  
> Institute of Plant and Microbial Biology, University of Zurich
- 12 **Symplastic connections in differentiated *Arabidopsis* roots**  
Léa Jacquier, Linnka Legendre Lefebvre, Marie Barberon  
> Department of Plant Sciences, University of Geneva
- 13 **A receptor protein mediates soil microbial feedbacks on *Arabidopsis***  
Henry Janse van Rensburg<sup>1</sup>, Niklas Schandry<sup>2</sup>, Claude Becker<sup>2</sup>, Klaus Schlaeppi<sup>1</sup>  
> <sup>1</sup>Plant Microbe Interactions, Department of Environmental Sciences, University of Basel  
<sup>2</sup>Faculty of Biology, Institute of Genetics, Ludwig Maximilian University of Munich
- 14 **Phylogenetic resolution of deep nodes of the Ophioglossaceae ferns**  
Darina Koubínová<sup>1</sup>, Li-Yaung Kuo<sup>2</sup> and Jason R. Grant<sup>1</sup>  
> <sup>1</sup>Institute of Biology, University of Neuchâtel, Neuchâtel, Switzerland  
<sup>2</sup>Institute of Molecular & Cellular Biology, National Tsing Hua University, Hsinchu City, Taiwan
- 15 **NEW: Cross-talk between biotic and abiotic stress: *Arabidopsis* response to phosphate starvation and *Botrytis cinerea* infection**  
Aïme Jaskolowski, Yves Poirier  
> Department of Plant Molecular Biology, University of Lausanne
- 16 **Efficient monitoring of plant genetic diversity changes in multispecies meadows**  
Miguel Loera-Sánchez, Bruno Studer, Roland Kölliker  
> Molecular Plant Breeding, Institute of Agricultural Sciences, ETH Zurich

- 17 **The wheat zinc finger protein TaZF acts as third component in the NLR-mediated powdery mildew effector recognition**  
Beatrice Manser, Stephanie Bräunlich, Jonatan Isaksson, Thomas Wicker, Beat Keller  
> Department of Plant and Microbial Biology, University of Zurich
- 18 **Functional Variation of Naturally Evolved Plant Meiotic Axis Protein ASY1**  
Aditya Nayak, Kirsten Bomblies  
> Institute of Molecular Plant Biology, ETH Zurich
- 19 **Shade induced changes of chromatin architecture in *Arabidopsis thaliana***  
Sandi Paulisic, Alessandra Boccaccini, Christian Fankhauser  
> Center for Integrative Genomics, University of Lausanne
- 20 **Linker histone H1 as a facilitator of transcriptomic reprogramming during diurnal rhythm**  
Kinga Rutowicz<sup>1</sup>, Diana Zörner<sup>1</sup>, Marc Schmidt<sup>1</sup>, Maciej Kotliński<sup>2</sup>, Tomasz Bieluszewski<sup>3</sup> and Célia Baroux<sup>1</sup>  
> <sup>1</sup>Department of Plant and Microbial Biology, University of Zürich, Switzerland  
<sup>2</sup>Institute of Biochemistry and Biophysics, Polish Academy of Sciences, Warsaw, Poland  
<sup>3</sup>Institute of Molecular Biology and Biotechnology, Adam Mickiewicz University, Poland
- 21 **MAR-binding filament protein-1 determines the location of starch granule initiation in chloroplasts**  
Mayank Sharma, Melanie R. Abt, Simona Eicke, Chun Liu, Theresa Ilse, Barbara Pfister, Samuel C. Zeeman  
> Institute of Molecular Plant Biology, Department of Biology, ETH Zurich
- 22 **Investigate the functional role of 3D chromosome folding in nuclear defense systems and molecular actors involved using reverse ChIP approach**  
Edouard Tourdot, Stefan Grob  
> Department of Plant and Microbial Biology, University of Zürich
- 23 **Investigating post-translational control and trafficking of *Arabidopsis* PHOSPHATE1 (AtPHO1)**  
Pallavi Vetal and Yves Poirier  
> Department of Plant Molecular Biology, University of Lausanne
- 24 **Investigating mitochondrial molecular organization across photosynthetic organisms using cryo-electron tomography**  
Florent Waltz, Benjamin D. Engel  
> Biozentrum, University of Basel
- 25 **Immature leaves are the volatile sensing organs of maize**  
Lei Wang, Simon Jäggi, Jamie Waterman, Mario Walthert, Matthias Erb  
> Institute of Plant Sciences, University of Bern
- 26 **Architecture and maintenance of thylakoid membranes visualized by Cryo-electron Tomography**  
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