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SwissPLANT 2024

Symposium ‘Plant Science Research’
32nd Edition

Scientific Program Committee
Simon Aeschbacher, Florian Schiestl, Rie Shimizu-Inatsugi, Sara Simonini,
Sofia van Moorsel, Tobias Züst, and Cyril Zipfel
University of Zurich

SwissPLANT 2024

17 – 19 January 2024
Les Diablerets, Switzerland

Table of content

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

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Conference Organization
Swiss Society of Plant Biology / Swiss Plant Science Web
swissplantscienceweb.ch

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

Swiss Society of Plant Biology, Annual Report & SwissPLANT 2024

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

The Early Career Meeting was a great success in 2023. Our young colleagues had lively and exciting scientific discussions together but in addition they brought a great spirit to SwissPLANT 2023 where they contributed to a great poster session and two selected talks. I am very optimistic that, in 2024, this experience will be similarly positive.

In July, I attended Plant Biology Europe 2023 in Marseille, a meeting organised every 2 years by the Federation of European Societies of Plant Biology (FESPB). It was an excellent meeting for people interested in the great diversity of plant biology fields and topics. Clearly a meeting to consider for those looking for more 'local' alternatives. The next edition will happen in Budapest in 2025. I also take this opportunity to thank SCNAT for covering our FESPB membership.

I would also like to congratulate Sofia van Moorsel (UZH) who obtained 15'000.- from the Rübel Fund of SCNAT for her exciting project on genetic diversity in Swiss aquatic plants.

Finally, I would like to thank Sylvia Martinez for her invaluable support in re-launching our society and for her constant invaluable support in the organization of SwissPLANT over the years. Sylvia is now retired, and I must admit that I miss her dearly. We are currently looking into possibilities to obtain some administrative support.

In December 2023, the Society had 95 members. We keep encouraging all Swiss Plant Science Web (SPSW) members to join. SPSW will continue to be our window on the internet for academic research in plant biology at Swiss universities. We are also counting on you to propose new ideas and initiatives to develop our society and are looking forward to discussing them at our next General Assembly. This is important 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 Cyril Zipfel and colleagues from the University of Zurich (Simon Aeschbacher, Florian Schiestl, Rie Shimizu-Inatsugi, Sara Simonini, Sofia van Moorsel, and Tobias Züst) for organizing our core SwissPLANT 2024 conference, as well as Narjes Yousefi and Kyle Bender for organizing the Early Career Meeting.

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, 17 January 2024

15:45 Swiss Society of Plant Biology, General Assembly 2023 (all welcome)

17:00 Welcome apéro

17:50 Welcome by Christian Fankhauser, President Swiss Society of Plant Biology
17:55 Opening remarks by Cyril Zipfel, chair Program Committee

Session I, chair: Tobias Züst

18:00 Simon Aeschbacher | University of Zurich
Herbarium genomes shed light on the ancestry and flavour of early European tomatoes

18:20 Célia Baroux | University of Zurich
Spotlight on the nuclear periphery: super-resolution microscopy reveals a radial distribution of transcription factories

18:40 Niko Geldner | University of Lausanne
The importance of nutrient restriction in shaping root microbial colonisation

19:00 Natasha Glover | Swiss Institute of Bioinformatics
Advancing Plant Science with the OMA Knowledgebase

19:30 Dinner, afterwards discussion at the bar

Thursday, 18 January 2024

07:00 *Breakfast*

Session II, chair: Sara Simonini

08:00 Ora Hazak | University of Fribourg
Peptide-Receptor-dependent module controls phloem patterning in tomato

08:20 Michael Hothorn | University of Geneva
Plant steroid receptor kinases sense a wide range of brassinosteroid generated by a complex biosynthetic network

08:40 Felix Kessler | University of Neuchatel
Photosynthesis drives pre-protein processing and progression of chloroplast biogenesis

09:00 Macarena Marín | University of Lausanne
A nodule's armour: How legumes protect their nitrogen-fixing partners

09:20 Mark Mescher | ETH Zurich
Bumblebee leaf-damaging behavior and its effects on plant flowering

09:40 *Coffee Break*

Session III, chair: Simon Aeschbacher

10:10 Early Career Meeting | Talk 1
Selected candidate from preceding Early Career Meeting will give a presentation

10:30 John Pannell | University of Lausanne
Evolution of sex chromosomes in the iconic South African genus Leucadendron

10:50 Christian Parisod | University of Fribourg
Whole genome duplications provide genomic substrate for ecological radiation

11:10 Michael Raissig | University of Bern
Getting into shape - a grass-specific factor guides morphogenesis and pore formation in the grass stomatal complex

11:30 Joelle Schläpfer | University of Zurich
Complex metabolic responses to biotic interactions in Arabidopsis

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

Session IV, chair: Florian Schiestl

17:30 Philippe Reymond | University of Lausanne
Egg phospholipids induce PTI in Arabidopsis

17:50 Christoph Ringli | University of Zurich
Tissue-specific specialization of the family of LRX proteins in Arabidopsis

18:10 Kentaro Shimizu | University of Zurich
Inherited epigenetic regulation in polyploid species: transgenic restoration of self-incompatibility of allopolyploid *Arabidopsis kamchatica*

18:45 Dinner

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

Friday, 19 January 2024

07:00 *Breakfast*

Session V, chair: Sofia van Moorsel

08:00 Florian Schiestl | University of Zurich
Experimental evolution of plant ecotypes

08:20 Klaus Schlaeppi | University of Basel
Tolerance and metabolization of plant secondary metabolites by the maize root microbiome

08:40 Stefanie Ranf | University of Fribourg
LORE-mediated immunity in Brassicaceae: from natural diversity to mechanisms

09:00 Julia Santiago | University of Lausanne
A new connection with the matrix: Structural role of RALF peptides to sustain pollen tube expansion

09:20 Rie Shimizu-Inatsugi | University of Zurich
How does environmental condition contribute to diverging DNA methylation patterns in the early stage of polyploidy?

09:40 Coffee Break

Session VI, chair: Rie Shimizu-Inatsugi

10:10 Early Career Meeting | Talk 2
Selected candidate from preceding Early Career Meeting will give a presentation

10:30 Joop Vermeer | University of Neuchatel
Channelling organ growth via intercellular communication

10:50 Thomas Wicker | University of Zurich
Chromosome-scale assemblies of 76 barley genomes reveal fast-evolving hot spots for gene copy number variation

11:10 Narjes Yousefi | University of Zurich
Comparative genomics elucidates the convergent origins of heterostyly across Primulaceae

11:30 Tobias Züst | University of Zurich
Key genes regulate qualitative variation in a novel chemical defence of *Erysimum cheiranthoides*

11:50 Closing remarks by Cyril Zipfel

TALK

Herbarium genomes shed light on the ancestry and flavour of early European tomatoes

Thomas Grubinger[1], Gülfirde Akgül[2], Alessia Guggisberg[3], Reto Nyffeler[4], Jurriaan M. de Vos[5], Verena J. Schuenemann[2,5,6], and **Simon Aeschbacher[1]**

[1] Department of Evolutionary Biology and Environmental Studies, University of Zurich
[2] Institute of Evolutionary Medicine, University of Zurich
[3] Department of Environmental Systems Science, ETH Zurich
[4] Department of Systematic and Evolutionary Botany, University of Zurich
[5] Department of Environmental Sciences, University of Basel
[6] Department of Evolutionary Anthropology, University of Vienna

The first cultivated tomatoes (*Solanum lycopersicum* L.) introduced to Europe in the 16th century showed large phenotypic variation, but their geographic origins and fruit flavour remain unknown. We sequenced 21 European herbarium tomatoes collected between 1596 and 1915, and we included published sequences from 166 20th-century Latin American tomato varieties and low-coverage data from the 16th-century "En Tibi" tomato. All historical specimens were found to be most closely related to either large-fruited or cherry-sized cultivars from Mexico. Variation at 119 genes related to fruit yield and flavour revealed haplotypes private to subsets of historical specimens at 13.3% of the flavour genes, but only at 5.7% of the fruit-yield genes. Across putative causal variants underlying fruit size and flavour, specimens with more fruit-size increasing alleles tended to have fewer alleles associated with favourable flavour. Sequence variation at the *LIN5* gene suggested higher sugar levels in both historical and modern cherry-sized tomatoes than in large-fruited tomatoes. In contrast, variation at the *ALMT9* gene controlling malic acid levels implied that historical large-fruited tomatoes tasted better than modern ones. Our results suggest Mexico as the origin of European tomatoes, are consistent with large variation in fruit size reported in historical records, and compatible with a genetic trade-off between fruit size and flavour. Overall, herbarium genomics allowed us to explore hidden stages of tomato domestication.

TALK

Spotlight on the nuclear periphery: super-resolution microscopy reveals a radial distribution of transcription factories

Randall R, **Baroux C.**

Department of Plant and Microbial Biology, University of Zürich, Switzerland

Plant cells show remarkably rapid transcriptional responses to various environmental cues, such as light, temperature or the presence of pathogens, enabling them to engage efficient cellular adaption. Transcriptional reprogramming is a result of epigenetic and molecular processes in the nucleus redistributing RNA Polymerase II along the genome. Whether the transcribed regions are randomly distributed in the nuclear space or follows a functional pattern is not known. Probing such spatial organisation of functional domains in the plant cell's nucleus is very challenging but becomes accessible with the development super-resolution imaging and image processing solutions. Using 3D STED imaging and a customized, image analysis workflow, we found that light induced transcriptional reprogramming involves a redistribution of transcription factories, along a radial pattern, involving prominent nanoscale domains at the nuclear periphery.

Dumur et al. (2019) Probing the 3D architecture of the plant nucleus with microscopy approaches: challenges and solutions. Nucleus, 10:1, doi: 10.1080/19491034.2019.1644592

Randall et al. (2022) Image analysis workflows to reveal the spatial organization of cell nuclei and chromosomes. Nucleus 13(1), doi: 10.1080/19491034.2022.2144013

TALK

The importance of nutrient restriction in shaping root microbial colonisation

Niko Geldner

University of Lausanne

To absorb essential nutrients and prevent the absorption of harmful compounds, plants rely on a specialized cell layer in the roots called the endodermis, which surrounds the central vascular system. During their differentiation, the extracellular space between endodermal cells is sealed off by a ring-like cell wall impregnation, the Casparian strip. Our recent work indicates that Casparian strips are not allowing for selective uptake of water and nutrients, but are also crucial to avoid leakage of photoassimilates to the rhizosphere. We found a strong increase in bacterial attraction to – and colonization of - the root of endodermal barrier mutants. MetabRoot exudate analysis indicates that amino acids may be the factor driving enhanced bacterial colonization of the mutant. Our findings suggest that restricted nutrient provision by CS formation could underlie the spatial pattern of bacterial colonization in wild-type plants, where enhanced colonization of bacteria co-incides with sites where endodermal barriers are naturally broken, or not yet formed. Intriguingly, a Pseudomonas protegens mutant unable to perceive amino acids, showed a clearly impaired attraction towards lateral root emergence sites, strongly supporting this idea.

TALK

Advancing Plant Science with the OMA Knowledgebase

Natasha M Glover[1,2], Irene Julca[2,1], Silvia Prieto Baños[2,1], Alex Warwick Vesztrocy[2,1], Stefano Pascarelli[2,3,1], David Moi[2,1], Yannis Nevers[2,1], Sina Majidian[2,1], Adrian M Altenhoff[1,3], Christophe Dessimoz[1,2]

[1] SIB Swiss Institute of Bioinformatics, 1015 Lausanne, Switzerland
[2] Department of Computational Biology, University of Lausanne, 1015 Lausanne, Switzerland
[3] ETH Zurich, Computer Science, Universitätstr. 6, 8092 Zurich, Switzerland

The OMA (Orthologous MAtrix) Browser offers a robust method and database for discerning homologous relationships across species. With 85 diverse plant species among its 2851 total species across the tree of life, OMA is a key resource for gene family exploration and understanding plant genome evolution. Our presentation will discuss how OMA can be used to study gene families, with applications in functional annotation and comparative genomics.

OMA's Hierarchical Orthologous Groups are instrumental in constructing phylogenetic trees and deciphering the evolutionary dynamics of gene duplication, gain, and loss. Furthermore, the ability to annotate Gene Ontology (GO) functions for both current and ancestral plant genomes, paired with easy-to-use GO enrichment tools, allows for in-depth analysis of the functions and the evolutionary history of gene families.

We will also highlight the adaptability of OMA's algorithms, including FastOMA, which offers users the ability to infer orthology and paralogy on newly sequenced, custom genomes. Plant scientists are invited to harness the comprehensive tools and data OMA provides at https://omabrowser.org, a gateway to a wealth of genomic knowledge which will help to advance the field of plant genomics.

TALK

Peptide-Receptor-dependent module controls phloem patterning in tomato

Samy Carbonnel, Abdellatif Essahibi, Salves Cornelis, Sara Vimercati and Ora Hazak

Department of Biology, University of Fribourg

In vascular plants, phloem tissue plays a key role in supporting meristems, by unloading photoassimilates and hormones to the actively dividing cells. In Arabidopsis root tip, two phloem poles, containing functional protophloem sieve elements, unload the phloem sap in the meristematic region. The formation of protophloem tissue is regulated by multiple factors, such as hormone gradients, DOF transcription factors, memebrane-localized proteins BREVIX RADIX (BRX) and OCTOPUS (OPS), and peptide-receptor modules.

Beyond Arabidopsis, we still lack the knowledge on the molecular mechanisms of phloem formation in other angiosperm species. It is not yet clear, to what extend the genetic circuits uncovered in Arabidopsis are conserved in other plant species. We recently identified an uncharacterized *CLE33* gene in Arabidopsis that encodes for an active CLE33 peptide, which acts as a repressor of phloem differentiation via autocrine and paracrine signaling. CLE33 functions in concert with CLE45 via BAM3 receptor in inhibiting differentiation of the sieve element cells and the surrounding cells. Interestingly, *CLE33* gene has the orthologs in all angiosperm species, including tomato, whereas *CLE45* orthologs are found only in *Brassicales*, suggesting a recent gene duplication event giving rise to *CLE45*.

To elucidate if a similar peptide-receptor-dependent pathway exists and functions in tomato phloem, we performed a phylogenetic analysis of *CLE33* and *BAM3* genes. We identified two orthologs of *CLE33* and two orthologs of *BAM3* in the tomato genome. To study the role of these peptide-receptor modules in protophloem development, we first, established a protocol of visualization of sieve element differentiation in wild type tomato roots. Like in Arabidopsis, in tomato roots two phloem poles unload phloem sap into the meristematic region. By analyzing the corresponding tomato receptor mutants we found, that one phloem-expressed *BAM3* ortholog plays a key role in root phloem patterning, whereas the second ortholog has a smaller impact. Remarkably, in comparison to Arabidopsis, it appears that phloem CLE signaling in tomato plays a more significant role in phloem patterning and overall plant growth. Strikingly, we found that the loss-of-function of phloem receptors phenocopies the loss-of-function of phloem CLE ligands, supporting the idea that these ligands and receptors act in the same pathway. I will present the genetic data, combined with expression analysis and plant physiology assays that together pinpoint on the discovery of a key tomato peptide-receptor module controlling phloem patterning and plant growth.

TALK

Plant steroid receptor kinases sense a wide range of brassinosteroid generated by a complex biosynthetic network.

Alberto Caregnato[1], Houming Chen[1], Miroslav Kvasnica[2], Jana Oklestkova[2], Miroslav Strnad[2], **Michael Hothorn**[1]

[1] Department of Plant Sciences, University of Geneva, CH
[2] Palacky University, Olomouc, CZ

The model plant Arabidopsis contains the membrane-integral steroid receptor kinases BRI1, BRL1 and BRL3. Brassinolide is considered the physiological ligand for BRI1, but in planta chemically diverse brassinosteroids are synthesised by a complex and non-linear biosynthetic pathway. Using a sensor-based quantitative binding assay, we have characterised the ligand binding specificities of BRI1, BRL1 and BRL3 in vitro. We find that chemically diverse brassinosteroids that accumulate in Arabidopsis can be detected with high affinity. A complete structural and mutational analysis of the BRI1 steroid binding pocket defines key determinants of ligand selectivity and enables the design of novel receptor agonists and antagonists. Our structural, quantitative biochemical and physiological experiments define three biochemically redundant steroid receptors in Arabidopsis capable of sensing a broad spectrum of bioactive brassinosteroids in vivo.

TALK

Photosynthesis drives pre-protein processing and progression of chloroplast biogenesis

Joy Collombat[1], Manfredo Quadroni[2], Véronique Douet[1], Rosa Pipitone[3], Fiamma Longoni[1] and **Felix Kessler**[1]

[1] Institute of biology, Plant Physiology Laboratory, Université de Neuchâtel
[2] Protein Analysis Facility (PAF), Université de Lausanne
[3] Thermo Fisher, 39 rue d'Armagnac, 33800 Bordeaux, France

Proteins of many organelles are synthesized in the cytosol as pre-proteins with cleavable N-terminal targeting sequences. Some chloroplast pre-proteins have special bi-partite targeting sequences enabling sequential translocation across the envelope followed by the photosynthetic thylakoid membrane [1]. But due to tight regulation [2] and rapid cleavage of targeting sequences, unprocessed chloroplast pre-proteins are normally undetectable. Using proteome-wide targeting peptide mapping, we report on the accumulation of a module of five partially processed, essential pre-proteins of the oxygen evolving complex and the plastocyanin docking site (PsbO, -P, -Q and PsaF, -N) that is linked to conditional albino mutations (*abc1k1* and *var2*). These block photosynthesis at the level of the Photosystem II reaction center and also arrest chloroplast biogenesis. Under permissive conditions when photosynthesis resumes, pre-protein processing as well as chloroplast biogenesis progress normally, consistent with the requirement for photosynthetic activity to complete these processes [3].

[1] Ballabani et al. 2023 10.3389/fphys.2023.1213866

[2] Venkatasalam et al. Current Biol. 28, 2616-2623 (2018)

[3] Pipitone et al. eLife 2021;10:e62709.

TALK

A nodule's armour: How legumes protect their nitrogen-fixing partners

Roberta Portararo[1], Rafael E. Venado[1], Marta Martín Rivero[1], and **Macarena Marín A.**[1,2]

[1] Genetics, Faculty of Biology – LMU Munich
[2] Department of Plant Molecular Biology – University of Lausanne

Legumes establish a mutually beneficial endosymbiotic relationship with nitrogen-fixing rhizobia bacteria. They host them within specialized root organs known as nodules and provide them with carbon and other nutrients in exchange for ammonia. Nodules possess adaptations that facilitate the accommodation and protection of high rhizobia numbers within their cells. A critical protective mechanism involves a suberized cell layer, acting as a diffusion barrier in the periphery of nodules. This barrier restricts oxygen's penetration—an inhibiting factor for the nitrogenase, the enzyme responsible for nitrogen fixation.

We've identified genes required for the formation of this barrier. These genes encode enzymes crucial in lipid polyester biosynthesis. They exhibit strong upregulation in infected nodules, particularly in their periphery. Mutant lines lacking one of these genes demonstrate impaired suberization of tissues, resulting in elevated oxygen concentrations within the nodules. Consequently, this leads to decreased nitrogenase activity and compromised plant growth under symbiotic conditions (1).

We will discuss the advancements in understanding the regulation of suberin deposition in nodules and its broader implications for nodule colonization, not only by rhizobia but also by commensals and pathogens.

(1) R. E. Venado, L. E. Wange, D. Shen, F. Pinnau, T. G. Andersen, W. Enard W, M. Marín. (2022) Proc Natl Acad Sci U S A. 119, e2206291119

TALK

Bumblebee leaf-damaging behavior and its effects on plant flowering

Mark Mescher, Consuelo De Moraes

Department of Environmentals Systems Sciences – ETH Zürich

Maintenance of temporal synchrony between flowering plants and pollinators is a key ecological process, particularly in the context of ongoing environmental change. Recently, we reported that bumblebee (*Bombus terrestris*) workers respond to pollen scarcity by damaging plant leaves and that the damage inflicted can accelerate plant flowering. However, the broader ecological and adaptive significance of bumblebee leaf-damaging behavior remains uncertain. In this talk we present new findings which show that leaf-damaging behavior is widespread among bumblebee species and that bees damage plant leaves in natural settings. In addition, we discuss ecological factors that influence damaging behavior, behavioral preferences of bees for particular plant species and plant parts, and potential implications for plant and bee fitness.

TALK

Evolution of sex chromosomes in the iconic South African genus *Leucadendron*

Mathias Scharmann and John R. Pannell

Department of Ecology and Evolution, University of Lausanne

The question of how suppressed recombination evolves is the major gap in our understanding of sex chromosomes and other supergenes. The diverse hypotheses regarding the drivers of recombination suppression include sexually antagonistic selection, ancestral lack of recombination, as well as neutral evolution. The mutations that suppress recombination are often thought to be inversions. Here, we present empirical results from the iconic South African plant genus *Leucadendron*, which is fully dioecious and includes some of the most sexually dimorphic of all flowering plants. We found that the non-recombining Y-linked region of *Leucadendron* evolved predominantly by segmental duplications rather than by incremental recombination suppression or inversions along ancestral, collinear chromosomes. Furthermore, comparative analysis of the Y-linked regions from 25 *Leucadendron* species suggests that their gene content turns over rapidly, except for two 'core' genes. Turnover appears to be driven by inserted duplications from elsewhere in the genome, as well via sex chromosome degeneration. Finally, we observe an unexpectedly high incidence of repeated acquisition of the same genes in the Y-linked region in distinct lineages, as well as a positive association between gene content and the degree of sexual dimorphism. Our study indicates that sex-chromosome evolution in *Leucadendron* is largely characterised by the duplication of previously autosomal and pseudo-autosomal genes and their insertion into the sex-determining region.

TALK

Whole genome duplications provide genomic substrate for ecological radiation

Christian Parisod, Marc Beringer, Sandra Grünig, Manuel Poretti, Rimjhim Roy Choudhury

Department of Biology, University of Fribourg, Switzerland

To what extent whole-genome duplication (WGD) promotes adaptation to environmental changes is poorly understood. The genus *Biscutella* offers promising assets to address such long-standing questions, as it radiated from Mediterranean to alpine biomes following recurrent WGD events. Assembly of the genome of *Biscutella laevigata* coupled with RNAseq showed that WGD and subsequent fractionation over the last 10 million years led to the retention of environment-responsive duplicates and promoted modular transcriptional responses to ecological changes. A range-wide phylogeography of the species confirmed WGD out of a diploid population from the Southern Alps some 25'000 years ago at the origin of widespread autotetraploids having expended across the Alps following the retreat of ice sheets. Population genomics and transplant experiments among pairs of populations from both ploidal levels and contrasted elevations in a factorial design highlighted that, despite evidence of high phenotypic plasticity and genetically-based adaptation to elevation, diploids present higher homeostasis and adaptation to elevation through fewer, tightly linked loci than autotetraploids presenting signature of highly multigenic adaptation. Genomic patterns left by recurrent WGDs in Buckler Mustards thus appear consistent with the retention of environment-responding duplicates supporting increased stress tolerance and promoting effective mobilization of such adaptive variation under changing environments.

TALK

Getting into shape - a grass-specific factor guides morphogenesis and pore formation in the grass stomatal complex

Roxane P. Spiegelhalder[1], Anakine Prizins[2] , Dan Zhang[2], Heike Lindner[1], **Michael T. Raissig**[1]

[1] Institute for plant science (IPS), University of Bern, 3012 Bern, Switzerland
[2] Centre for Organismal Studies (COS), Heidelberg University, Im Neuenheimer Feld 230, 69120 Heidelberg, Germany

Stomata are epidermal valves at the leaf surface that open and close to absorb photosynthetic carbon dioxide and restrict water loss through transpiration. Grasses form morphologically innovative stomata, consisting of two dumbbell-shaped GCs flanked by two lateral subsidiary cells (SCs). This “graminoid” morphology is associated with faster stomatal movements and contributes to more water use-efficient gas exchange. Yet, the developmental programs that shape GC morphogenesis and/or pore formation are completely unknown. A forward genetic screen identified a mutant phenotype that showed stocky and undifferentiated (“pouty”) or collapsed GCs (“thin-lipped”). We mapped the mutation to a grass-specific gene of unknown function and were able to reproduce the “thin-lipped and pouty” (*tlp*) phenotype using CRISPR/Cas9. In developing GCs, fluorescently tagged TLP reporter proteins accumulated in a highly polarized manner to the apical and basal ends of the newly formed guard cell wall. Careful 3D microscopy of the *tlp* phenotype revealed impaired pore formation and aberrant morphogenesis of the dumbbell-shaped grass GCs. Finally, disrupting polarized localization of TLP in the developing GCs and forcing TLP equally to the whole plasma membrane showed strong dominant negative effects with misformed pores and aberrant GC shapes. In conclusion, a grass-specific, polarized factor shapes the unique morphogenesis of the dumbbell-shaped GCs and guides pore formation in grasses.

TALK

LORE-mediated immunity in Brassicaceae: from natural diversity to mechanisms

Stefanie Ranf[1,2]

[1] University of Fribourg, Department of Biology, Fribourg, Switzerland
[2] Technical University of Munich, Phytopathology, Freising, Germany

The immune receptor LORE (LIPOOLIGOSACCHARIDE-SPECIFIC REDUCED ELICITATION) in *Arabidopsis thaliana* and other *Brassicaceae* senses 3-hydroxy fatty acid metabolites released by Gram-negative bacteria, such as 3-hydroxydecanoic acid (3-HDA) and activates pattern-triggered immunity. LORE alias SD1-29 belongs to the class of S-domain-1 (SD1) receptor kinases, the second largest class of cell surface 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. This provided mechanistic insights into how the 3-HDA ligand binds to the ectodomain of LORE, and how the LORE receptor complex is formed and activated. Transfer of LORE to 3-HDA-insensitive tomatoes confers 3-HDA-sensitivity. LORE-transgenic tomatoes show increased antibacterial immunity and 3-HDA application to the roots induces resistance against major tomato pathogens.

TALK

Egg phospholipids induce PTI in Arabidopsis

Elia Stahl, Léonie Mottet, Marion Bréchet, and **Philippe Reymond**

Department of Plant Molecular Biology, University of Lausanne

Arabidopsis responds to insect egg-derived phosphatidylcholine (PC) and triggers a PTI response, including ROS burst, salicylic acid accumulation, defense gene expression and localized cell death. The plasma membrane-localized LecRK-I.1 and LecRK-I.8 have been shown to participate in egg-induced PTI. We have now found that PC is converted to phosphatidic acid (PA) in the apoplast by a plant phospholipase D. PA directly binds to LecRK-I.1 and I.8 and is able to activate PTI responses when applied exogenously. We thus provide an example of unusual extracellular modification of a non-self molecule to trigger defenses.

TALK

Tissue-specific specialization of the family of LRX proteins in Arabidopsis

Christoph Ringli, Aline Herger, Amandine Guérin, Xiaoyu Hu

IPMB, University of Zurich

For cell growth to take place, a coordinated expansion of the protoplast and the surrounding cell wall is a requirement. The structure of the cell wall is constantly being reorganized, a process that also involves LRX proteins. LRXs have an LRR- domain as high-affinity binding site for RALF peptide hormones, and an extensin domain that helps anchoring the protein in the cell wall.
Extensins are highly repetitive, glycosylated, structural cell wall proteins that are not well characterized on the functional level. The extensin domains of the different LRXs are quite diverse both in length and in sequence. Here, we investigated whether this diversification represents a functional specialization. This is potentially necessary as the cell wall-interacting extensin domains of the LRXs might be adapted to the cell wall of their respective tissue of expression. We addressed this question by complementation experiments with domain-swap constructs. Extensin domains were tested for their activity in tissues/cell types they are normally not expressed in compared to in "tissue of origin".
Extensins are mainly *O*-glycosylated with Galactose at Ser and several Arabinoses at Hyp (Hydroxyproline) residues by corresponding glycosyltransferases. We have mutagenized the genes encoding these enzymes in genetic backgrounds containing cmyc-tagged versions of LRX1 to assess the importance of these *O*-glycosylations for the LRX1 extensin domain.

TALK

A new connection with the matrix: Structural role of RALF peptides to sustain pollen tube expansion

Steven Moussu[1†‡], Hyun Kyung Lee[1†], Kalina T. Haas[2], Caroline Broyart[1], Ursina Rathgeb,[3] Damien De Bellis[4,3], Thomas Levasseur[5], Sébastjen Schoenaers[2,6], Gorka S. Fernandez[7], Ueli Grossniklaus[7], Estelle Bonnin[5], Eric Hosy[8], Kris Vissenberg[6,9], Niko Geldner[3], Bernard Cathala[5], Herman Höfte[2]*, Julia Santiago[1]*

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A central question in plant biology is how cell wall polymers assemble into specific mesoscale patterns, conferring to the walls their physico-chemical properties that allow growth and development. A complex of RAPID ALKALINIZATION FACTOR4 (RALF4) and its cell wall-anchored LEUCINE-RICH REPEAT-EXTENSIN8 (LRX8) interacting protein is crucial for cell-wall integrity during pollen tube growth, but their molecular connection with the cell wall is unknown. Our results uncover that LRX8-RALF4 complexes adopt a heterotetrametric configuration in vivo, displaying a dendritic distribution along the pollen tube shank. The LRX8-RALF4 complex specifically interacts with demethylesterified pectins in a charge-dependent manner through a newly generated RALF4's polycationic surface upon binding to LRX proteins. The LRX8-RALF4-pectin interaction exerts a condensing effect, patterning the cell-wall pectin into a reticulated network essential for cell wall integrity and expansion. Our work uncovers the unique dual structural and signaling role for RALF4 in shaping cell wall assembly during pollen tube expansion and morphogenesis and may provide inspiration to uncover additional roles for protein-polysaccharide interactions in defining cell wall architecture and properties.

TALK

Experimental evolution of plant ecotypes

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Adaptation to local ecological conditions can lead to the evolution of ecotypes in organisms. Sometime these ecotypes have higher fitness in their local environment as compared to foreign ecotypes, a phenomenon called local adaptation. Local adaptation can be associated to reproductive isolation, thus being a first step towards speciation. In plants, adaptation to pollinators, herbivores, soil type, and climate are common phenomena, however, which of these (combinations of) factors are the main driver of diversification, and which traits and genes diverge first, is little understood. In my research I have been using experimental evolution with fast cycling *Brassica rapa* plants as a model system, to investigate the importance of different ecological factors as well as their interactions in driving the formation of ecotypes. These experiments have shown that adaptation to different pollinators causes the rapid evolution of divergent phenotypes. Interactions of different ecological factors also have rapid and strong effects on plant evolution. Plants under herbivores attack evolve to be less attractive to pollinators, than plants without herbivory, demonstrating a trade-off between reproduction and defense. Plants that evolve on different soil types rapidly form ecotypes, but only when they are pollinated by bees, rather than by hand. Only when plants interact with both bees and herbivores, local adaptation to soil types evolved in our experiments, and this was caused by genes with opposite fitness effects in different soil types (i.e. antagonistic pleiotropy). My conclusion is that 1) biotic interactions play a decisive role in plant diversification and 2) rapid adaptation is likely common and should be integrated more into the “purely” ecological sciences.

TALK

Tolerance and metabolization of plant secondary metabolites by the Maize root microbiome

Klaus Schlaeppi and team

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Plant root exudates can have many functions including to act as semiochemicals for the recruitment, to serve as carbon substrates for microbial growth, or to structure the composition of the microbiome. Mechanistically however, relatively little is known how root microbes deal and cope with specialized plant exudates. We have built a culture collection of maize root bacteria to study toxicity, tolerance, and metabolization of plant-derived Benzoxazinoids, a group of bioactive and antimicrobial secondary metabolites of grasses including crops such as maize. Benzoxazinoids inhibited bacterial growth in a strain- and compound-dependent manner, which largely explained strain abundance on maize roots. We found a specific enrichment of bacteria that metabolise the major compound accumulating in the maize rhizosphere. Combining comparative genomics and transcriptomics, we identified an N-acyl homoserine lactonase in *Microbacteria* that mediates the key step in benzoxazinoid metabolization. Interestingly, we found the native root bacteria (isolated from maize) to tolerate and metabolise the benzoxazinoids better compared to non-host Arabidopsis bacteria, suggesting adaptation to the specialized metabolites of their host plant. Our work reveals that tolerance and metabolization of plant specialized metabolites are important competence determinants for root colonization.

TALK

Complex metabolic responses to biotic interactions in *Arabidopsis*

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Plants produce a plethora of compounds, some of which are ubiquitously present, others are produced in response to environmental stimuli. The latter, secondary metabolites, function as toxins against pathogens, and in attracting beneficials. Thus, plant responses to pathogenic or beneficial microbes mostly focused on these specialized compounds. However, how and when the more general primary metabolites change in response to biotic interactions remains unclear.
Here, we investigate shifts in *Arabidopsis thaliana* metabolic profiles in tissues and exudates in a time-resolved manner. We inoculate with microbial elicitors, beneficial or pathogenic strains, or with a synthetic community, investigating plant metabolic responses. We find complex changes depending on the timepoint and chemical class, and interesting phenotypic and metabolic changes in co-inoculation experiments.

TALK

Inherited epigenetic regulation in polyploid species: transgenic restoration of self-incompatibility of allopolyploid *Arabidopsis kamchatica*

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Allopolyploid species are widespread among natural and crop plant species and tend to be self-compatible. However, it was unclear how self-compatibility evolved by overcoming the redundancy of duplicated genes. In *Arabidopsis* relatives, the self-incompatibility system is characterized by epigenetic dominance modifiers, among which small RNAs suppress the expression of a recessive *SCR/SP11* haplogroup. Here, using three transgenic experiments of the allotetraploid *A. kamchatica*, we show that redundancy was overcome by dominance. First, when dominant *SCR-B* was repaired by removing a single loss-of-function mutation through a transposable element insertion, self-incompatibility was restored. Second, a recessive *SCR* construct could not restore self-incompatibility. Third, the same construct restored self-incompatibility in an accession that lacks the small RNA. Dominant self-compatibility supports the prediction that mutations that increase the selfing rate are dominant to pass through the Haldane's sieve. The inter-subgenomic suppression suggests the importance of inherited epigenetic regulation, which is distinct from novel epigenetic mutations at polyploidization called genome shock.

TALK

How does environmental condition contribute to diverging DNA methylation patterns in the early stage of polyploidy?

Rie Shimizu-Inatsugi, Kentaro K. Shimizu, Stefan Milosavljevic, Kenji Yip Ton

Department of Evolutionary Biology and Environmental Sciences, University of Zurich

Polyploidization is a major evolutionary force in plants and other lineages. Among many studies reporting the ecological advantages of polyploid species, the underlying molecular mechanisms behind their success and prevalence are reported in some examples. In contrast, the adaptation process at the early stage of polyploids has not been explored yet. However, it should have played a key role in achieving the ecological advantages of polyploids in the current habitat. Since the genetic change is slow and might not be effective in a short time in changing the transcriptome and phenome, epigenetic changes would play an important role in adaptation. This study focuses on the epigenetic evolution of new polyploid individuals with the same genetic background at multiple environmental conditions and how transcriptome follows this change.
We artificially crossed *Arabidopsis halleri and A. lyrata* to synthesize a tetraploid mimicking a natural tetraploid species *A. kamchatica.* The synthetic individuals were kept in two conditions (mild and hot) for up to eight generations to answer the following questions: 1) How much of the DNA methylation is affected by polyploidization? 2) How does the pattern change/maintain in subsequent generations? 3) To what extent does the environmental condition affect the change? and 4) How is the methylation pattern related to gene expression patterns?

TALK

Channelling organ growth via intercellular communication

Joop EM Vermeer

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Lateral root (LR) formation requires the establishment of differential growth within a tissue consisting out of non-motile, interconnected, and pressurized cells. To emerge, LRs need to overcome the mechanical constraints provided by the surrounding tissues. Although it is known that mechanical properties of overlying tissues are important this process, we still lack mechanistic insights into how plants can re-establish differential growth deep within a tissue. In Arabidopsis, overlying endodermal cells need to actively accommodate the expansion growth of the LR. Failure to do so results in a block of LR formation. We have shown that cytoskeleton dynamics, both in the pericycle and endodermis, are required to channel LR morphogenesis. We have identified a plant-specific family of microtubule associated proteins, MAP70, as potential integrators of mechanical signals during development. In parallel, we are investigating to which extend the developmental trajectories underlying LR morphogenesis are conserved in different plant species. To this end we are also investigating LR formation in *Brachypodium distachyon.* Using improved tissue clearing techniques, we have constructed a LR developmental atlas of this wild grass species. We have recently also use snRNAseq to get an insight into the gene regulatory network underlying LR development in Brachypodium.

TALK

Chromosome-scale assemblies of 76 barley genomes reveal fast-evolving hot spots for gene copy number variation

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A main problem in assemblies of large genomes was that arrays of large tandem repeated sequences were usually “collapsed” (i.e. adjacent repeat units were assembled into a single sequence, thus hiding the complexity of a given locus). With recent technologies, such “complex loci” can finally be resolved. Here, we studied 173 gene-containing complex loci in the barley genome. They range in size between 40 kb and 2.2. Mb and contain between 2 and 74 tandem repeated genes. Interestingly, 50 of the loci contain agriculturally important genes (e.g. NLRs, F-box, RLKs or Thionins). Comparative analysis of the 173 loci across 76 newly sequenced barley accessions revealed that they are hot spots for copy number variation, most extreme being a Thionin locus where copy numbers vary between 3 and 74. Because individual tandem repeat units differ from each other by dozens or hundreds of SNPs (depending on age and length of the duplications), complex loci constitute a large reservoir of gene variants.
We propose that the tandem repeat structure of the loci drives their rapid evolution, as neighboring tandem repeats can serve as templates for unequal recombination, leading to rapid expansion or contraction of the loci. Indeed, molecular dating indicates that the duplications are very young with 63 loci having duplications that occurred less than 10,000 years ago, after domestication of barley.

TALK

Comparative genomics elucidates the convergent origins of heterostyly across Primulaceae

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The repeated origins of the same phenotypic trait (i.e., convergence) is one of the key topics in evolutionary biology. One of the most famous examples of convergence in plants is heterostyly, a type of floral heteromorphism that evolved multiple times to promote outcrossing. Ever since Darwin's seminal studies, Primulaceae provided the prime model for heterostyly, which evolved three times independently in the family: once in the *Primula* clade, once in *Hottonia palustris,* and once in *Androsace vitaliana*. Heterostyly is known to be controlled by the S-locus supergene (a cluster of five tightly linked genes in a region of 280kb) in *Primula veris* and *P. vulgaris*, but equivalent knowledge is not available in *Androsace* and *Hottonia*. Here, we generated a high-quality reference genome of the endangered plant *Hottonia palustris* (diploid, genome size of 820Mb, n=10) using PacBio HiFi reads (31x coverage per allele) to compare the sequence and architecture of the heterostyly supergene with those of *Primula* and *Androsace*. With these comparative genomic analyses, we aim to address the following key question: Are the three independent origins of heterostyly in Primulaceae characterized by the same architecture of the heterostyly supergene? Our analyses suggests that S-locus in *H. palustris* has a different architecture to that of *P. veris* and *A. vitaliana*, indicating different genomic architecture controlling the same phenotypic trait across Primulaceae.

TALK

Key genes regulate qualitative variation in a novel chemical defence of *Erysimum cheiranthoides*

Tobias Züst

Department of Systematic and Evolutionary Botany, University of Zürich

The Brassicaceae plant *Erysimum cheiranthoides* produces two distinct types of chemical defences against herbivorous insects, ancestrally conserved glucosinolates and evolutionary novel cardenolides. In an extensive screening of the natural variation among populations and individuals of *E. cheiranthoides*, we found substantial qualitative variation in cardenolide defences, whereas all plants shared a single glucosinolate phenotype. By crossing chemically distinct plants, we could demonstrate that cardenolide diversity is primarily controlled by a few major-effect genetic loci which follow Mendelian inheritance, suggesting repeated gains-of-function in cardenolide-modifying enzymes. While the adaptive benefits of these traits are still unclear, these results shed light on the origin of phytochemical diversity in a newly evolved defensive trait.

POSTER

Towards a quantitative, in vivo understanding of receptor kinase mediated signaling

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Timely and adaptive cellular responses to external stimuli are governed at the molecular level by signal transduction networks. In this context, endogenous and exogenous signals are perceived by receptors that activate cytosolic signaling cascades which regulate the activity of downstream effectors – transcription factors, metabolic enzymes, etc. – that reprogram the cell to an adaptive state. In plants, the receptor function is fulfilled primarily by plasma membrane-localized receptor kinases (RKs) that perceive molecular signals and activate signal transduction through cytosolic protein kinase domains. While considerable effort has been made to understand how RK-mediated signaling is regulated, a quantitative understanding of RK organization and regulation in living cells is lacking. To address this knowledge gap, we adopted a quantitative affinity proteomics approach and characterized a suite of immune-related RKs under steady-state and ligand-stimulated conditions. Our analysis reveals three previously unappreciated facets of RK signaling: 1) Ligand perception has little effect on RK complex composition – only co-receptors are recruited to ligand-bound receptors; 2) Activated RK complexes are likely present at relatively low stoichiometries; and 3) RKs associate in functionally related receptor clusters. Collectively, our results provide novel insights into RK signaling in an *in vivo* context and provide a framework to better understand critical questions in RK biology, including a path forward to understand mechanisms governing signaling specificity in RK-activated pathways.

POSTER

UniProt Knowledgebase

Emmanuel Boutet[1], the Swiss-Prot group.

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The UniProt Knowledgebase (UniProtKB, https://www.uniprot.org) is a comprehensive, high-quality, and freely accessible resource of protein sequences and functional information. The expert curated core UniProtKB/Swiss-Prot includes about 580,000 sequences of which around 42'000 are of plant origin (January 2024), enriched with curated knowledge from the scientific literature.
UniProtKB provides structured and high-quality knowledge that is readable by both humans and machines, using ontologies such as the Gene Ontology (https://geneontology.org/) and the chemical ontology ChEBI (https://www.ebi.ac.uk/chebi/init.do). UniProtKB has a broad range of applications, which include teaching AI methods to understand protein sequences and use them to predict protein structures and functions (e.g. PubMeds: 35896542, 36702895, 37188731 and DOI: 10.1101/2023.10.31.564943).
We also use human-in-the-loop AI methods to help triage literature and extract knowledge from it to help scale expert curation in UniProtKB. The UniProt web portal (www.uniprot.org) provides access to a powerful advanced search tool, programmatic interfaces, an ID mapping tool that includes over one hundred databases, and tools for sequence and structure search, alignment, and analysis. All data is available to freely download without restriction.
In this presentation we will highlight recent improvements in UniProt data coverage and quality, including recent genome reannotation efforts for model plants, and will showcase a range of methods to access UniProtKB data using the website and APIs that you can adapt to your needs.

POSTER

TITLE

Ségolène Bressoud

POSTER

Tuning meiosis: the effect of habitat on temperature-induced recombination plasticity in *Arabidopsis arenosa*

Marinela Dukić[1], Ursula Abad[1], Kirsten Bomblies[1]

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Meiotic crossover recombination, a fundamental feature of sexual reproduction, involves the reciprocal exchange of genetic information between homologous chromosomes. The number and location of recombination events impact the accuracy of chromosome segregation, directly influencing individual fitness. At the population level, meiotic recombination promotes genetic diversity and contributes to adaptive potential. Importantly, recombination rates can vary across levels and conditions, but the evolutionary significance and underlying molecular mechanisms of this variation remain largely unknown. We focus on understanding how recombination rate changes in response to environmental factors, particularly temperature, as this plasticity may play an important role in challenging environments.

We are studying genetic lineages of *Arabidopsis arenosa* inhabiting adjacent yet thermally distinct regions: Pannonian Basin and Carpathian Mountains. Using a genome scan approach, we identified several meiotic genes that show signatures of diversifying selection in the Pannonian populations, suggesting ecologically driven selection on meiotic processes. Assessment of crossover recombination in plants from both regions exposed to six different temperatures revealed temperature-induced variation in recombination rates in all populations, particularly at higher temperatures. However, the response curves differed significantly between populations. Complementary fertility assays following heat treatment provided additional insight into the relationship between meiotic recombination, stability and fitness. Overall, this study offers a rare perspective on how recombination rates may change as organisms evolve to adapt to varying environments.

POSTER

Adaptation of plant architecture during domestication

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Shoot architecture has been a recurrent target of human selection during crop domestication and remains a main target for crop improvement. Shoot architecture is controlled by the rate at which meristems transition from vegetative to reproductive growth. In flowering plants, the conserved flowering hormone, florigen, and its antagonist, anti-florigen, interact with basic leucine zipper (bZIP) transcription factors to regulate meristem transition. We identified a paralog of the tomato bZIP transcription factor *SUPPRESSOR OF SP* (*SSP*), which we named *SSP2* and contains a non-synonymous mutation in domesticated accessions. To characterize the effect of this mutation on plant architecture, we applied CRISPR-Cas9 base editing to repair the mutation in domesticated tomato. Additionally, we modelled the ancestral and domesticated SSP2 to assess how the domestication mutation influences the DNA binding-affinity of the bZIP transcription factor. To investigate a potential redundancy between SSP and SSP2 on the *cis*-regulatory regions of target genes, we performed DNA affinity purification sequencing (DAP-seq) on SSP, the ancestral and domesticated SSP2. Our results indicate that the domestication mutation in *SSP2* leads to a delay in meristem maturation, and that *SSP* and *SSP2* function redundantly to regulate specific aspects of shoot and inflorescence architecture. Additionally, we demonstrate the potential of precision genome editing in correcting deleterious mutations that arose during crop domestication.

POSTER

Understanding the Significance of Adaptive Suberin Plasticity

Jian-Pu Han and Marie Barberon

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Due to sessile living conditions, plants forage the soil to acquire nutrients necessary for their growth and development. In this process, the root endodermis forms a checkpoint controlling the transport of nutrients through two distinct differentiation states: Casparian strips, wood-like barriers blocking the apoplastic pathway, and suberin, a cork-like substance, coating endodermal cells controlling the transcellular pathway. With these two distinct barriers roots can fine-tune nutrient uptake and adjust nutrition to stress conditions. In particular suberin lamellae formation is highly in response to nutrient availability, biotic and abiotic stresses, but the function of this plasticity in plant adaptation remains unclear.

In order to decipher suberin function in plant adaptation we developed high-throughput suberin patterning analysis in roots in order to screen for suberin variations in Arabidopsis accessions. For this purpose, we collected 284 natural accessions of Arabidopsis from the 1001 genome projects and screened for suberin variants. Combined with ionomic quantification these analyses provide a large dataset allowing to uncover the correlations between adaptive suberization and nutrients uptake. Moreover, genome-wide association was studied to identify the associated polymorphisms which would further help us understand how adaptive suberization was achieved at the molecular level. Overall this analysis of natural variation for suberin will pave the way for deciphering suberin function in plant adaptation.

POSTER

Maize response to entomopathogenic nematodes: Consequences for tri-trophic interactions

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Multitrophic interactions between plants, herbivores and herbivore natural enemies are key components of ecosystem functioning, above- and belowground. However, the direct plant responses to natural enemies of herbivores, and its feedback in multitrophic interactions, remain poorly understood. In this study, we investigated the plant-mediated impact of entomopathogenic nematodes (EPNs) on the performance and behaviour of root- and leaf herbivores under laboratory and field conditions. A prior exposure of maize plants to EPNs altered the distribution of the stem borer *Ostrinia nubilalis*. This shift in population dynamic relied on changes in female oviposition site selection, but not on larval survival or performance. The cues modulating the female preference are under investigation. Contrastingly, maize exposure to EPNs did not affect the performance or behaviour of two root herbivores, *Diabrotica virgifera* and *D. balteata*. We discuss the potential adaptive value of the maize response to EPNs and how it may contribute to sustainable agricultural practices.

POSTER

Hydraulic constraints caused by low root temperature contribute to the upper distribution limits of temperate tree species

Yating Li[1] and Günter Hoch[1*]

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Low root zone temperatures might contribute to the species-specific limits of tree distribution via induced physiological water stress. Within a comprehensive experiment, we investigated the cold sensitivity of root water uptake and transport in seedlings of 16 European temperate tree species that differ in their natural high elevation distribution limits in the Swiss Alps within an over 1500 m altitudinal belt from lower montane areas to the alpine treeline (corresponding to a > 8K temperature difference at the species' upper range limits). We used ^{2}H-H_2O pulse-labelling of the source water in a hydroponic waterbath sysetm to quantify the water uptake and transport velocity from roots to leaves in tree seedlings exposed to 15, 7 or 2 °C root temperature, but identically warm abovground temperatures under controlled greenhouse conditions. In all species, low root temperatures significantly reduced the water transport speed accompanied by reduced stem water potentials and stomatal conductance. However, at 7 °C root temperature, the root water uptake rate, the plant water potential, and the stomatal conductance relative to 15 °C root temperature corelated positively with the species-specific upper elevation limit, indicating an increasingly higher sensitivity against lower root zone temperatures, the lower a species' natural elevational distribution limit. Conversely, 2 °C root temperature severely inhibited water uptake in all species, irrespective of the species' thermal elevational limits. We conclude that the observed hydraulic constraints at low root temperatures are contributing factors for the cold distribution limits of temperate tree species and a potential underlying physiological cause for low temperature growth restrictions of plants in general.

POSTER

Using Kmer-GWAS to explore the genetics of powdery mildew resistance in the Swiss Wheat collection.

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Wheat domestication and breeding led to genetic bottlenecks and consequently, commercial varieties have problems coping with biotic and abiotic stresses imposed by climate change and pathogen adaptation. Bread wheat landraces, compared to modern breeding material, have broader genetic diversity, likely to be important for adaptation. To exploit this untapped genetic diversity potential, a diverse collection of 500 Swiss bread wheat accessions has been assembled within the Activated GEnebank NeTwork (EU AGENT) project to identify sources of resistance against the wheat yield-reducing fungal disease powdery mildew caused by *Blumeria graminis* f. sp. *Tritici*.

The collection, genotyped using Dartseq technology, was phenotyped for seedling resistance against ten powdery mildew isolates. We observed strong variation in disease resistance. We developed a kmer-based GWAS approach that uses 12 wheat reference genomes. Such an approach maximizes the discovery of the resistance genes segregating in natural populations. On top of multiple known *Pm* genes (*Pm1*, *Pm2* and *Pm4b*), we also detected novel regions contributing to resistance on chromosomes 3D, 5D, 6A. The most promising candidates have been selected for further molecular characterization.

Compared with standard GWAS (e.g., SNP matrix), our method identifies associations with structural variations and regions that are absent in the reference genome. Our work highlights the relevance of landraces as a source of novel genetic variation.

POSTER

A defense protein mediates microbiome feedbacks in Arabidopsis

Henry Janse van Rensburg[1], Niklas Schandry[2], Claude Becker[2], Klaus Schlaeppi[1].

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Plants secrete a diverse array of compounds into the soil to condition the surrounding microbiome. Root exudation often results in plant soil feedbacks, that define the performance of the second plant generation. Benzoxazinoids (BXs) are plant toxins abundant in the root exudates of important crops like maize and wheat. The rhizosphere microbiota is selectively structured by the exudation of BXs, mediating growth and defense feedbacks on maize and rye. While the ecology and agronomic impact of plant-soil feedbacks in crop rotations are well described, little is known about the underlying mechanisms of plant responses to soil microbiomes. Natural *Arabidopsis thaliana* accessions show a tremendous diversity in their growth feedback when grown on a BX-conditioned microbiome. Using a Genome Wide Association study performed on 410 of these *Arabidopsis* accessions, we identified a gene that codes for a toll-interleukin receptor nucleotide-binding site leucine-rich repeat protein, called *mediator of microbiome feedbacks 1* (*MMF1*), to be associated with the BX microbiome-driven growth feedback. We showed that plants that lack a functional copy of this gene no longer show a positive growth feedback when grown on a BX-conditoned microbiome. Microbiome profiling revealed that mutant plants assembled a bacterial microbiome that is distinct from that of wild-type plants. These results suggest that *MMF1* acts as a regulator of BX-mediated microbiome feedbacks in Arabidopsis.

POSTER

Comparative transcriptomic analysis of land plants

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Gene expression data for Archaeplastida are accumulating exponentially, with more than 300,000 RNA-sequencing (RNA-seq) experiments available for hundreds of species. This amount of data gives us the possibility to study gene expression in a kingdom-wide manner. However, there are limitations such as missing or inconsistent metadata, and not uniform RNA-seq distribution across samples and lineages. To address this, we first annotated >4000 experiments using standardised sample names and generated gene expression atlases for various samples of 10 plant species comprising bryophytes, vascular plants, gymnosperms, and flowering plants. The analysis of this dataset identified hundreds of organ- and gamete-specific gene families, and revealed that most of the specific transcriptomes are significantly conserved. Interestingly, the appearance of organ-specific gene families does not coincide with the appearance of the corresponding organ, suggesting that co-option of existing genes is the main mechanism for evolving new organs. Although these datasets included different lineages of Archaeplastida, some groups, such as ferns, were underrepresented. For that, we are generating the data for different organs, including leafs, roots, and reproductive organs for 22 species, representing 22 families of Ferns. We envision that this dataset will help to understand the evolution of biological processes that are conserved across different plant lineages, as well as those that are unique to specific groups.

POSTER

High-throughput field phenotyping reveals that selection in breeding has affected the phenology and temperature response of wheat in the stem elongation phase

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Crop growth and phenology are driven by seasonal changes in environmental variables, with temperature as one important factor. However, knowledge about genotype-specific temperature response and its influence on phenology is limited. Such information is elementary to improve crop models and adapt selection strategies. We measured the height development of 352 European winter wheat varieties in four years to quantify phenology, and fitted an asymptotic temperature response model. The model used hourly fluctuations in temperature to parameterize the base temperature (T_{min}), the temperature optimum (r_{max}), and the steepness (*lrc*) of growth responses. Our results show that higher T_{min} and *lrc* relate to an earlier start and end of stem elongation. A higher r_{max} relates to an increased final height. Both final height and r_{max} decreased for varieties originating from the continental east of Europe towards the maritime west. A GWAS indicated a quantitative inheritance and a large degree of independence among loci. Nevertheless, genomic prediction accuracies (GBLUPs) for T_{min} and *lrc* were low ($r \leq 0.32$) compared to other traits ($r \geq 0.59$). Besides known, major genes related to vernalization, photoperiod, or dwarfing, the GWAS indicated additional, yet unknown loci that dominate the temperature response.

POSTER

Herbarium genomics traces *Phytophthora infestans* strain that caused the Irish Potato Famine into 20th-century Europe

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Plant pathogens have influenced human societies since the cultivation of crop plants. A notable example is *Phytophthora infestans*, an oomycete that induces late blight in potato and tomato. Introduced to Europe in the 1840s, *P. infestans* led to severe epidemic outbreaks throughout Europe, including the Irish Potato Famine. Since preventing future *P. infestans* outbreaks requires a better understanding of this fast evolving pathogen, we have extracted DNA from 26 infected European potato leaves dating between 1850 and 1982. We sequenced 19 mitochondrial genomes at 6- to 54-fold mean coverage and combined them with 33 published historical and modern sequences for phylogenetic analyses. We found that HERB-1, the strain previously identified as being responsible for the Irish Potato Famine, still existed in 17 European potato specimens collected during the 19th and 20th century. Our study suggests the persistence of HERB-1 into mid-20th century Europe and demonstrates the importance of herbarium genomics in biogeographic analyses of plant-pathosystems.

POSTER

Leveraging co-evolutionary insights and Alphafold-multimer to unravel receptor ligand binding mechanisms

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Plant secreted signaling peptides regulate growth, development, and stress responses. Nevertheless, specific steps in the evolution of these peptides and their receptors are not well understood. Recent studies reported the characterization of SERINE RICH ENDOGENOUS PEPTIDES (SCOOPs). SCOOPs were shown to be transcriptionally induced during stresses and perceived by the leucine-rich repeat receptor kinase MALE DISCOVERER 1-INTERACTING RECEPTOR-LIKE KINASE 2 (MIK2). *In silico* analysis of 350 plant genomes and subsequent functional validation reveal a strong conservation upon the gain of this novel function, the recognition of SCOOPs, within the Brassicales. We leveraged AlphaFold-Multimer MIK2/SCOOP predictions and comparative genomics to identify two conserved binding pockets across the Brassicales MIK2 homologues which interact with the 'SxS' motif of otherwise sequence-divergent SCOOPs. SCOOP12 ligand binding, SCOOP12-induced MIK2/BAK1 complex formation and SCOOP-induced ROS production were shown to be affected for MIK2 variants, confirming our *in silico* predictions of the binding pockets. Analysis of MIK2/SCOOP evolution and function provides a model for structure-function analysis of other plant receptors and their ligands.

POSTER

Chromatin accessibility and transcriptome dynamics during adaptation to polyploidy

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Whole genome duplication (WGD) events give rise to polyploidy, resulting in increased genome complexity, phenotypic novelty and adaptive potential. The immediate impact of WGD on cellular processes and how this may be stabilized over evolutionary time remains largely unknown. *Arabidopsis arenosa* is a powerful model system to answer these questions; natural populations of diploids and autotetraploids exist, while neo-tetraploids can be generated from diploids. Comparative studies of these cytotypes can identify perturbations that accompany WGD and also the evolved responses. Several genes involved in core transcriptional regulation and chromatin remodeling were previously found with genomic signatures of selection in autotetraploid *A. arenosa* populations, leading us to hypothesize that chromatin architecture and transcription may be particularly affected by WGD.
Using ATAC-seq on leaf and petal samples, we found over 10,000 differentially accessible chromatin regions (dACRs) between diploid, neo-tetraploid and evolved tetraploid populations, with various dACR groups exhibiting unique evolutionary trajectories. Furthermore, RNA-seq analyses revealed ~4000 differentially expressed genes (DEGs) across cytotypes, a majority of which were identified in a contrast between neo-tetraploids and evolved tetraploids. Interestingly, large changes in chromatin accessibility levels following WGD were significantly associated with the proximity of transposable elements and DEGs. Taken together, our results provide new insights on how epigenetic and transcriptional mechanisms contribute to genome stability during the evolution of polyploids.

POSTER

Maize root exudates modulate growth and defense of *Arabidopsis thaliana*

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Plants can alter their biotic soil environment through secretion of root exudates. Maize plants exude a class of secondary metabolites called benzoxazinoids (BXs) through their roots, which alters the surrounding soil microbiota and affects the performance of subsequently grown maize plants. To further investigate the mechanistics of these BX-driven plant soil feedbacks, we studied the response of *Arabidopsis thaliana* Col-0 (henceforth Arabidopsis) to BX-conditioned soils. We found that Arabidopsis responded robustly to BX-conditioning with bigger growth on soil conditioned with BX-exuding maize compared to the control soil conditioned with *bx1* mutant maize defective in BX biosynthesis. Furthermore, the Arabidopsis root bacterial community differed between BX-conditioned and control soil, while soil sterilization eliminated better growth on BX-conditioned soil. Arabidopsis was also better defended against a necrotrophic pathogen on BX-conditioned soil. This was also reflected in the shoot transcriptome, where gene clusters related to induced resistance were upregulated. Moreover, we found members of the GRF transcription factor family, which are known to be involved in the plant growth/defense trade-off, to be upregulated in roots grown on BX-conditioned soil, and the *grf1* and *grf3* mutants failed to show a BX-conditioning dependent growth response. Together, these findings imply that BX-conditioning can improve Arabidopsis growth and defense, and that BX-driven microbial soil legacies are translated to the root microbiota of next-generation Arabidopsis plants.

POSTER

Transport of Phytophthora virulence factors during infection

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Phytophthora species are devastating plant pathogens that belong to Oomycetes. One representant of this group, *P. infestans*, causes potato late blight that contributed to the Great Irish Famine in the 19th century.

The ability of Phytophthora to colonize host plants relies on its virulence factors (effectors), which are molecules produced and secreted during infection to suppress host immune response and favor processes supporting pathogen growth. They are divided into two classes: apoplastic effectors, functioning within the extracellular milieu, and symplastic effectors, which undergo translocation into the plant cell. Due to the controversy surrounding the mechanism of their transfection, symplastic effectors carrying RxLR motif (Arg-X-Leu-Arg) remain in the scientific spotlight.

With the confocal microscopy study of the *P. capsici- N. benthamiana* pathosystem, I provide strong evidence that both types of virulence factors are secreted even before haustoria are fully developed. In the range of *P. capsci* transformants I observed that apoplastic proteins are released into the extrahaustorial matrix, however RxLR effector Avr3 is targeted to the structure at haustoria neck. Furthermore, I demonstrate that the RxLR motif is not cleaved but stays an integral part of the effector, playing a crucial role in determining the localization of the effector during secretion and translocation to the host cell.

POSTER

Intraspecific variation of beech seedlings' responses to drought

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In Europe, climate change is intensifying and increasing the frequency of severe droughts. Beech (Fagus sylvatica L.), a drought-sensitive tree species, faces, therefore, heightened vulnerability during the seedling phase. Here, we assessed the intraspecific diversity of beech regarding drought tolerance. We conducted a common garden experiment with 184 2-year-old beech seedlings grown from seeds from 16 populations across the species range in Europe. We exposed the potted seedlings to two experimentally induced drought periods in June and July 2023 (two weeks each), with the appropriate controls.

We used leaf spectroscopy to assess the intraspecific differences in the response of beech seedlings to the droughts. We derived physiological, biochemical, and structural leaf traits based on spectral indices and the inverted PROSPECT-D radiative transfer model. This allowed us to capture a multitude of relevant physiological drought stress responses across beech tree genotypes.

The leaf spectra showed a clear signal of drought stress. The provenances showed a similar response to the induced drought treatment but, depending on the leaf spectral index, genotype was also a determinant of drought stress. The constituents derived from the inverse PROSPECT-D model yielded detailed information on beech seedling physiology under drought stress. Further research is needed to bridge leaf-to-canopy spectroscopy, facilitating methodology upscaling for larger nurseries or mature forests.

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