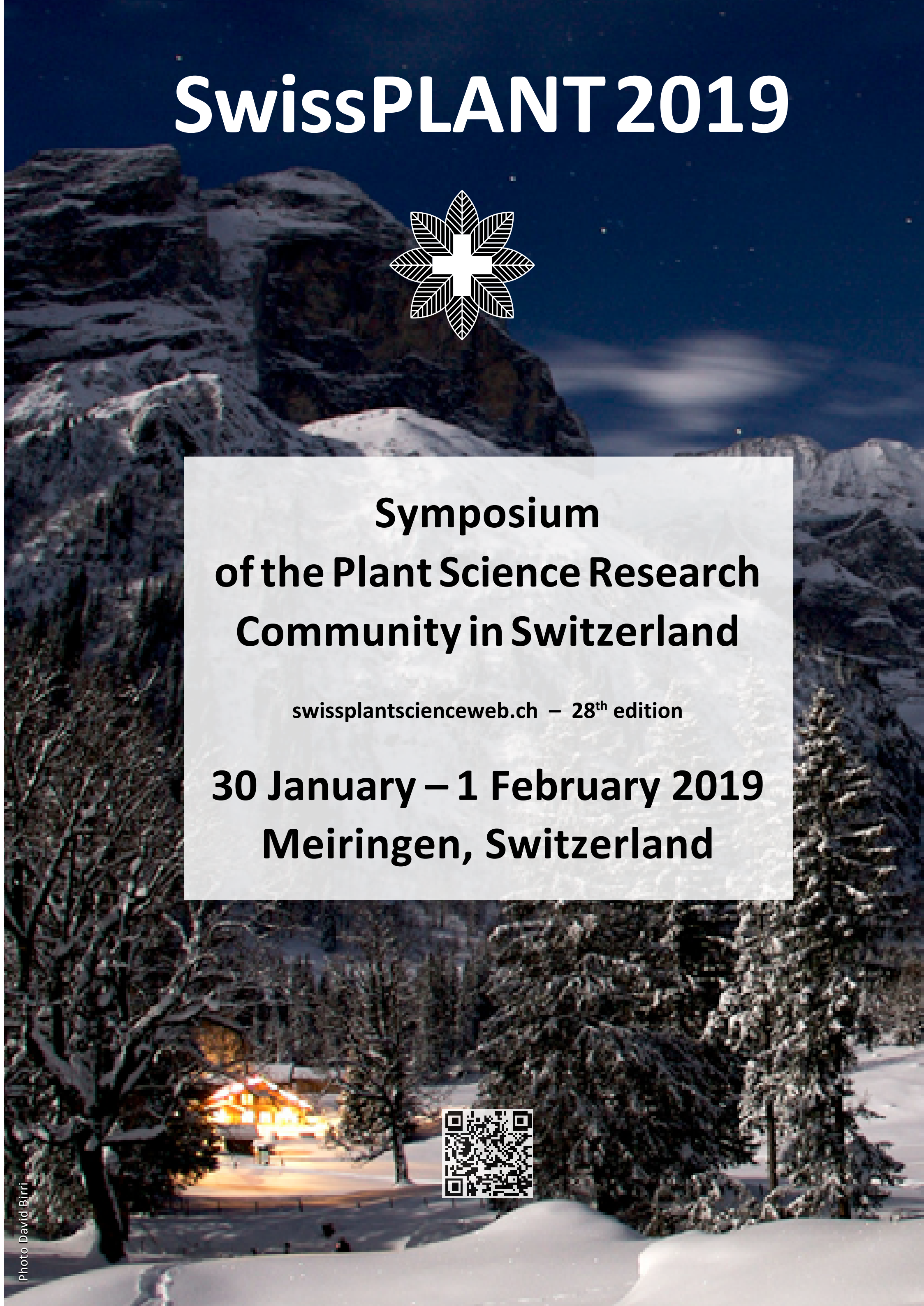
SwissPLANT 2019



Symposium of the Plant Science Research Community in Switzerland

swissplantscienceweb.ch – 28th edition

30 January – 1 February 2019
Meiringen, Switzerland

Photo David Birri

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SwissPLANT 2019

Symposium of the Swiss Plant Science Web
30 January – 1 February 2019
Meiringen, Switzerland

Venue

Parkhotel du Sauvage, Meiringen

Scientific Program Committee

Stefan Hörtensteiner, Kentaro Shimizu, Joop Vermeer, Cyril Zipfel
University of Zurich

Conference Organization

Swiss Plant Science Web
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SwissPLANT 2019 – Welcome by the president

This year's SwissPLANT Symposium represents the 9th annual meeting of the plant science research community in Switzerland, and already the 28th edition if we count from its inception as the "Swiss Plant Molecular and Cell Biology Conference" in 1992. When the Swiss Plant Science Web was founded 2009, the scope of this meeting was expanded to cover all of basic research in plant science, including ecology and evolution. The first meeting in this new format was held in Meiringen 2011. The mixing of different fields of plant science proved to be a success, so that we now meet already for the ninth time in this constellation, this time again in the cosy setting of Meiringen, to discuss current advances in plant science research "made in Switzerland".

As the organizers of this symposium, we aim to present research on form, function, genetics, ecology, and evolution of plants. We seek an integrative approach to increase the understanding of the complexity and diversity of the green world, and we want to spread the word that plants, as the fundamental components of the earth's biosystem, are at the center of "life sciences" and not at their periphery.

It is encouraging to see that talented scientists join the Swiss Plant Science Web community (SPSW) every year. I especially welcome all the newcomers. Your input and ideas will shape the long-term continuity of the Swiss Plant Science Web. The «SwissPLANT meeting» is the ideal place to start discussions on new collaborations.

This year's scientific conference committee is from the University of Zurich. I thank Elena Conti, Stefan Hörtensteiner, Kentaro Shimizu, Joop Vermeer, and Cyril Zipfel for setting up an exciting program. I am also very grateful to Sylvia Martínez, our SPSW coordinator, who took a big effort to organize the meeting and to make your stay inspirational and comfortable.

Enjoy the science and the leisure moments in Meiringen.

Thomas Boller, SPSW president

The Swiss Plant Science Web is the umbrella organization for plant science research and education at universities in Switzerland

Program

Wednesday, 30 January 2019

16h00	Swiss Plant Science Web strategic meeting for SPSW members
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17h40	Sylvain Bischof | U Zurich | page 8 Epigenetic regulation of gene expression
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18h00	Emmanuel Boutet | SIB | page 10 Enhanced plant enzyme annotation in UniProtKB supports integrated analyses and exploitation of protein and metabolite data
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	Session II: Physiology
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20h20	Felix Kessler | U Neuchâtel | page 18 Role for DELLA in early chloroplast biogenesis
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The kinase BIK1 orchestrates ion movements across the plasma membrane during plant immunity

08h20 Klaus Schläppi | U Bern | page 29
Plant root microbiome interactions: communication, traits and opportunities for smart farming

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Host specialization in fungal pathogens

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Discovering new signaling pathways in plant adaptation to changing environment

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Long-distance electrical signals in *Arabidopsis* leaves

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Impact of variation in nucleotides and transposable elements on linkage along chromosomes in natural populations of *Arabis alpina* (Brassicaceae)

10h50 Sergio Rasmann | U Neuchâtel | page 25
Micro- and macro-evolutionary trends in plant-herbivore-predator interaction along environmental gradients

11h10 Felix Gugerli | WSL | page 15
Environmental association analysis based on exome capture indicates candidate genes for adaptation to local site conditions in P*inus cembra*

11h30 Meredith Schuman | U Zurich | page 31
Towards remote sensing of intraspecific variation

11h50 Leisure time (lunch on your own, skiing, hiking, snowshoeing …)

17h00 Poster session (with apéro) | pages 37–41

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Specialized metabolites – a curse and a blessing for plants

20h40 Ted Turlings | U Neuchâtel | page 33
Insects may manipulate the release of plant volatiles to enhance the suitability of neighboring plants as host for their offspring

21h00 Laurent Zimmerli | National Taiwan U | page 35
FLAGELLIN SENSING2-ASSOCIATED KINASE1 regulates *Arabidopsis* abscisic acid-dependent stomatal immunity

Friday, 1 February 2019

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08h20	Simon Aeschbacher | U Zurich | page 7 Exploring speciation history through the joint inference of selection and gene flow
08h40	Yamama Naciri | U Geneva & CJB | page 21 Species delimitation in *Capurodendron* Aubrév. (Sapotaceae) using an integrative approach: patterns of diversification in an endemic genus of Madagascar
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09h20	Kentaro Shimizu | U Zurich | page 32 Advantages and disadvantages of polyploidy, revisited
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10h30	Joop Vermeer | U Zurich | page 34 Cytoskeleton dynamics shape lateral root formation in *Arabidopsis*
10h50	Antía Rodríguez-Villalon | ETH Zurich | page 26 Xylem differentiation and vacuolar loading: an intertwined road
11h10	Vinicius Costa Galvão | U Lausanne | page 11 PIF transcription factors link a neighbor threat cue to accelerated reproduction in *Arabidopsis*
11h30	Clara Sánchez Rodríguez | ETH Zurich | page 27 A Golgi-localized glycosyltransferase mediates the response of plant cells to cellulose perturbations
11h50	Closing remarks

TALK

Exploring speciation history through the joint inference of selection and gene flow

Simon Aeschbacher[1], Konrad Lohse[2]

[1] Department of Evolutionary Biology and Environmental Studies, University of Zurich
[2] Institute of Evolutionary Biology, University of Edinburgh, UK

Speciation involves a combination of gene flow and isolating mechanisms. How these two forces interact on the way to reproductive isolation remains unknown for many natural systems. To address this problem, we developed a population-genomic approach to inferring the amount and timing of gene flow as well as the strength of divergent selection acting among two incipient species. We used the block-wise distribution of pairwise inter- and intraspecific sequence differences to distinguish between continued gene flow and secondary contact among *Mimulus guttatus* and its selfing sister species *M. nasutus.* Focussing on an area of sympatry in the northern range oft the species' distributions in Western North America, we identified a strong signal of isolation after an initial split about 860,000 years ago, followed by recent secondary-contact gene flow from *M. nasutus* into *M. guttatus.* Moreover, we modelled the effective migration rate for genomic regions of varying recombination rates and exploited the observed relationship between the migration and recombination rate to estimate the strength of divergent selection. We found that a selection coefficient on the order of a few percent per megabase pair maintains the species barrier inspite of recent or on-going gene flow at a scaled rate of about 1.5 migrants per generation. Our results are consistent with previous phylogeographic and population-genomic studies in *Mimulus*. We have shown that the full distribution of sequence differences provides information to delineate alternative speciation scenarios.

TALK

Epigenetic regulation of gene expression

Sylvain Bischof

University of Zurich

The control of gene expression is of fundamental importance for cellular life. DNA not only serves as a repository for all genetic information but also constitutes a dynamic integration center. Condensation of the genome is primarily accomplished by wrapping DNA around nucleosomes, which consists of an octameric core of histone proteins. Histone deposition and occupancy directly impact chromatin stability and therefore regulate gene expression.

In a genetic screen designed to find new components of gene silencing, we identified mutations in ATRX (Alpha-thalassemia/mental retardation, X-linked) leading to the reactivation of a methylated reporter construct. ATRX is a highly conserved chromatin remodeler of the SWI/SNF family involved in the incorporation of the histone variant H3.3. In humans, mutations in ATRX result in mental retardation and alpha-thalassemia. However the molecular mechanisms by which defective ATRX lead to these syndromes are not yet fully explained. In plants, our data indicate that ATRX is part of a large protein complex that co-localizes genome-wide with H3.3 at genic promoters. Tethering ATRX to an active unmethylated locus using a zinc-finger fusion leads to its repression showing that ATRX can lead to transcriptional repression. Altogether, our data suggests that the mechanisms of plant and animal ATRX in histone H3.3 deposition and transcriptional regulation are conserved but that they operate through divergent molecular interactions.

TALK

How to tango with four: meiotic adaptation to whole genome duplication

Kirsten Bomblies

John Innes Centre, Norwich, UK

Whole genome duplication (WGD) has important implications for adaptation and speciation. However, doubling the number of homologs poses challenges to reliable chromosome segregation in meiosis. Newly formed polyploids commonly show meiotic defects such as multivalent associations among available homologs associated with reduced fertility. Nevertheless, many genome-duplicated (polyploid) species persist in nature; most have stable diploid-like chromosome segregation, indicating early problems can be overcome. We use *Arabidopsis arenosa,* an outcrossing relative of *A. thaliana* with extant diploid and autotetraploids, to understand the genic basis of adaptation to polyploidy. Autotetraploid *A. arenosa* has cytologically diploidized meiosis, while newly formed tetraploids have numerous multivalents in diakinesis and metaphase I. Reduction in multivalents in the established polyploid is associated with reduced crossover number per chromosome. We show from whole genome resequencing that there is strong ploidy-associated allelic differentiation in 18 loci with sharply elevated differentiation. Among these are six meiosis genes whose products are known to function together to coordinate chromosome pairing, synapsis, and the number and distribution of chiasmata. We show evidence for two interacting genes that the tetraploid alleles have a measurable functional consequence in polyploid meiosis. The two genes collaborate to reduce the number of crossovers, reduce the number of multivalent associations, and alter the placement of crossover sites to more distal locations. We hypothesize that these genes together represent a co-evolved polygenic solution to WGD-associated chromosome segregation challenges, likely through increased strength of crossover interference.

TALK

Enhanced plant enzyme annotation in UniProtKB supports integrated analyses and exploitation of protein and metabolite data

Emmanuel Boutet, Damien Lieberherr, Elisabeth Coudert, Anne Morgat, Kristian B. Axelsen, Sebastien Gehant, Edouard de Castro, Thierry Lombardot, Jerven Bolleman, Sylvain Poux, Nicole Redaschi, Ioannis Xenarios, Alan Bridge, and the Swiss-Prot group

Swiss-Prot Group, SIB – Swiss Institute of Bioinformatics, Geneva

The UniProt Knowledgbase (UniProtKB, https://www.uniprot.org) is a comprehensive, high-quality and freely accessible resource of protein sequences and functional information. The expert curated section UniProtKB/Swiss-Prot includes about 550,000 sequences; about 237,000 of these are enzymes, of which around 13,000 are of plant origin (release 2018_11).
Here we describe work on the enhancement of plant enzyme annotation using the Rhea resource of biochemical reactions (https://www.rhea-db.org). Rhea provides a structurally explicit and computationally tractable description of reaction chemistry using standard ontologies and cheminformatics standards. The use of Rhea will improve the usability, interoperability and consistency of enzyme annotation in UniProtKB. It will power enhanced search and identifier mapping services that integrate knowledge of small molecules and proteins, and will support the use of computational methods to mine UniProtKB data to study enzyme evolution or predict new pathways (to name but a few possibilities).

TALK

The whole-plant context of floral adaptation

Vinicius Costa Galvão and Christian Fankhauser

Center for Integrative Genomics, Faculty of Biology and Medicine, University of Lausanne

Changes in light quality indicative of competition for this essential resource influence plant growth and developmental transitions. Little is known about neighbor proximity-induced acceleration of reproduction. phytochrome B (phyB) senses light cues from plant competitors ultimately leading to the expression of the floral inducers *FLOWERING LOCUS (FT)* and *TWIN SISTER of FT (TSF).* We show that three PHYTOCHROME INTERACTING FACTOR (PIF) transcriptional regulators act directly downstream of phyB to promote expression of *FT* and *TSF.* Neighbor proximity enhances PIF accumulation towards the end of the day coinciding with enhanced floral inducer expression. We present evidence for direct PIF-mediated *TSF* expression. The relevance of our findings is illustrated by the prior identification of *FT, TSF* and *PIF4* as loci underlying flowering time regulation in nature.

> SPSW researcher portfolio:
https://swissplantscienceweb.unibas.ch/en/fankhauser

TALK

Specialized metabolites – a curse and a blessing for plants

Matthias Erb

Institute of Plant Sciences, University of Bern

Plants produce specialized metabolites that offer protection against pests and pathogens. At the same time, however, specialist natural enemies have evolved the capacity to misuse specialized metabolites for their own purposes, resulting in potential trade-offs in nature and agriculture. Over the last years, we have explored the genetics, biochemistry, chemistry and biology of benzoxazinoids, a major class of specialized metabolites in cereals, to understand their importance for plant performance and their role in protecting plants against insect pests. We find that benzoxazinoids act as within-plant signals, aphid resistance factors, microbiome modulators and siderophores. These different functions are reflected in tight spatiotemporal control of benzoxazinoid biosynthesis and release. At the same time, the western corn rootworm, a specialist maize pest, exploits benzoxazinoids as foraging cues, nutrients and protective agents against its own natural enemies. Thus, plant specialized metabolites are multifunctional, and this multifunctionality is exploited by both plants and their natural enemies.

> SPSW researcher portfolio:
https://swissplantscienceweb.unibas.ch/en/erb

TALK

Long-distance electrical signals in *Arabidopsis* leaves

Andrzej Kurenda and **Edward E. Farmer**

Plant Molecular Biology, University of Lausanne

Most organisms that feed on living meals extract their food stealthily. Many herbivorous insects do this by cutting tissues rapidly with sharp mandibles. However, during the feeding process, signals from leaf wounds escape into distal plant tissues where they initiate the synthesis of potent defense-response mediators called jasmonates (JAs). Leaf-to-leaf wound signalling is thought to be a two-phase process. Firstly, damage to the vasculature causes the transmission of signals through the xylem. This then activates the production of electrical signals known as slow wave potentials that in turn initiate JA synthesis. We combined surface electrophysiology and highly sensitive force probes to assess ion movements and leaf deformations in response to insect damage. We found that tissue deformation events and electrical signal architecture can be perturbed genetically. Our results reveal how the highly conserved architecture of the slow wave potential is likely to be maintained across the plant kingdom.

> SPSW researcher portfolio:
https://swissplantscienceweb.unibas.ch/en/farmer

TALK

Understanding cell-specific nutrient uptake and biotic Interactions in roots

Tonni Grube Andersen

University of Lausanne

> SPSW researcher portfolio:
https://swissplantscienceweb.unibas.ch/en/geldner

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TALK

Environmental association analysis based on exome capture indicates candidate genes for adaptation to local site conditions in *Pinus cembra*

Felix Gugerli, Christian Rellstab, Benjamin Dauphin

WSL Swiss Federal Research Institute Birmensdorf

Landscape genomics is an emerging research field that aims to identify environmental factors that shape adaptive genetic variation and to detect the gene variants that drive local adaptation. Here we use in-depth transcriptome sequencing to assemble a de novo transcriptome and design probes for exome capture in Swiss stone pine *(Pinus cembra),* a key conifer species of the timberline ecotone with an estimated genome size of 29.3 Gbp and no reference genome available. Our roughly 55,000 self-designed probes targeted 25,000 contigs which we applied to DNA pools of seven populations from the Swiss Alps (Pool-seq). We identified >140,000 SNPs in almost 13,000 contigs, and probes performed equally well in pools of the closely related species *Pinus sibirica*. However, a thorough analysis of individually sequenced *P. cembra* samples indicated that a majority of the contigs (63 %) represented multi-copy genes. Removing paralogous contigs based on heterozygote excess and deviation from allele balance led to allele frequencies of population pools which represented accurate estimates of individually determined allele frequencies. Using population genetic and landscape genomic methods, we show that inferences of neutral and adaptive genetic variation may be biased when not accounting for such multi-copy genes. In a next step, we tested for associations of allele frequencies with environmental descriptors in cohorts of *P. cembra* to test for spatial and temporal changes relative to site conditions at the time of establishment. This approach identifies candidate genes for location adaptation, which may be key in how populations are able respond to future climate change.

> SPSW researcher portfolio:
https://swissplantscienceweb.unibas.ch/en/gugerli

ABCDEFG

TALK

Discovering new signaling pathways in plant adaptation to changing environment

Ora Hazak

Department of Biology, University of Fribourg

Multicellular organisms cope with the challenge of maintaining efficient communication between different organs and tissues to coordinate growth and responses to the environment. Both, plants and animals produce biologically active compounds such as small peptides that move between cells through the vascular system or intercellular spaces and regulate plethora of developmental processes and stress responses. In plants, in addition to major hormones a myriad of secreted peptides orchestrate optimal growth and adaptation. CLAVATA3/EMBRYO SURROUNDING REGION (CLE) peptide family in *Arabidopsis* comprises of 32 genes encoding to pre-propeptides that undergo processing and glycosylation to create the biologically active CLE peptides. These genes are expressed within plant meristems and vascular tissues, but the biological role and the mode of action for most of them remains unknown. My previous research focused on the CLE45 signaling pathway. I found that the receptor-like protein CLAVATA 2 (CLV2) and the pseudokinase CORYNE (CRN) are necessary to act in the protophloem to fully sense root-active CLE peptides. Interestingly, at the optimal growth conditions most of the CLE peptides are not expressed in the developing phloem tissue. Therefore, the hypothesis is that at the specific stress conditions the CLE peptides can be rapidly produced to mediate specific responses. My new research group will perform a screen using CLE promoters and wide range of abiotic stresses to identify new signaling pathways mediating plant adaptation. In addition, we are interested to describe new CLE-dependent xylem-specific pathways. First, we will identify CLE-dependent pathways in *Arabidopsis* and later we will translate our knowledge into Tomato plants using mutants and specific markers collections as well as CRISPR-Cas9 technology. Later, designing modified CLE peptides or CLE receptors can contribute to increase the ability of tomato plants to adapt to certain abiotic stress and to avoid the yield loses.

TALK

Inositol pyrophosphate signaling networks – phosphate homeostasis and beyond

Michael Hothorn

Structural Plant Biology Laboratory, Department of Botany and Plant Biology, University of Geneva

Inositol pyrophosphates (PP-InsPs) are eukaryotic signaling molecules comprised of a fully phosphorylatyed inositol ring and featuring one ore several pyrophosphate groups. Litte is known about PP-InsP biosynthesis, signaling and perception in plants. I will describe our genetic and biochemical characterzation of two bifunctional kinase/phosphatase enzymes, which control the cellular levels of PP-InsPs in *Arabidopsis*. Deletion of both enzymes results in drastic growth and developmental phenotypes and in consitutive phosphate starvation responses. I will demonstrate that the phosphate starvation-related phenotypes are due to a misregulation of phosphate starvation transcription factors, which are normally controlled by PP-InsPs and their SPX receptor proteins (Wild et al., Science, 2016). Next, I will present a system-wide PP-InsP interaction screen which implicates PP-InsPs in plant development and light signaling. Integrating these findings with our genetic observations, we propose PP-InsPs as widely used signaling molcules in plants, conneting nutrient sensing with plant development.

> SPSW researcher portfolio:
https://swissplantscienceweb.unibas.ch/en/hothorn

TALK

Role for DELLA in early chloroplast biogenesis

Felix Kessler[1], Shanmugabalaji Venkatasalam[1], Hicham Chahtane[2], Luis Lopez-Molina[2]

[1] Laboratory of Plant Physiology, University of Neuchâtel
[2] Department of Plant Biology, University of Geneva

The rapid onset of photosynthesis and hence the biogenesis of functional chloroplasts is essential for survival of the seedling in natural habitats. In the laboratory, chloroplast biogenesis has mostly been studied as the transition from etioplasts (plastids in dark grown plants) to chloroplasts. Etioplasts can be considered partially differentiated organelles committed to become chloroplasts. By comparison, the seed embryo contains proplastids that are naive, undifferentiated plastids and potentially suitable to study the earliest events in chloroplast biogenesis. Despite their tiny size during the early hours of germination, biochemical studies in young seedlings are possible. Here, I will outline how the germination hormone gibberellin controls chloroplast biogenesis. When conditions are unfavorable for germination and gibberellin concentrations low, the chloroplast protein import receptor TOC159 interacts with the DELLA protein RGL2, targeting TOC159 for destruction by the ubiquitin proteasome system (UPS). The photosynthetic pre-protein cargo of TOC159 meets the same fate. When conditions become more favorable for germination and gibberellin concentration increases, DELLA itself is targeted for degradation by the UPS. This allows TOC159 to insert in the outer chloroplast envelope membrane and function in the protein import complex. Simultaneously, the photosynthetic pre-proteins are also released from UPS degradation, imported and assembled into the photosynthetic machinery. These findings provide molecular insight into early events of chloroplast biogenesis.

> SPSW researcher portfolio:
https://swissplantscienceweb.unibas.ch/en/kessler-felix

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TALK

The role of pathogens in driving host evolution and population dynamics in the wild

Anna-Liisa Laine

Department of Evolutionary Biology and Environmental Studies, University of Zurich

Given that pathogens are prevalent across all ecosystems, an individual's reproductive success and survival will depend on its ability to resist infection. Natural populations have been shown to support considerable diversity in resistance, and theory predicts that under pathogen-imposed selection variation in resistance is maintained by allocation costs with susceptible individuals having higher fitness in the absence of disease. Thus far the empirical evidence supporting costs of resistance as a mechanism that maintains resistance variation has remained mixed. Environmental variation across the landscape and variable rates of gene flow may play a key role in how variation in resistance is maintained, and hence on host demography. Here, my aim is to understand how host evolutionary potential and pathogen imposed selection vary across the landscape and what the consequences are for host demography. For this purpose, I've analyzed long term data on host population size and disease prevalence in the *Plantago lanceolata-Podosphaera plantaginis* interaction in the Åland Islands, SW Finland. The results show that the strength of pathogen imposed selection varies across the landscape, in a spatially structured manner, suggesting that environmental variation plays a key role in mediating host-pathogen interactions. The results highlight the importance of studying host-pathogen dynamics across multiple populations to truly understand what the consequences of infection are for the host.

ABCDEFGHIKL

TALK

The role of the endosperm in *Arabidopsis* early post-embryonic development

Julien De Giorgi, Woohyun Kim, Christelle Fuchs, Sylvain Loubery and **Luis Lopez-Molina**

Department of Plant Biology, University of Geneva

Seeds are capsules maintaining the plant embryo in a resistant state and promoting plant dispersal. To successfully produce a seedling, seeds are able to remain viable over time and block their germination under potentially fatal conditions for the seedling. The *arabidopsis* seed consists of two living entities, the embryo and the endosperm. In the mature seed the endosperm consists of a single cell layer surrounding the embryo. Seed germination is tightly controlled in response to abiotic environmental parameters such as light or temperature. Control of seed germination critically involves the endosperm, which releases the phytohormone abscisic acid in response to abiotic parameters unfavorable for seedling growth.

We will present evidence that the endosperm also participates in early post-embryonic development in absence of light (skotomorphogenesis) and presence of light (photomorphogenesis). This involves the release of diffusible compounds from the endosperm towards the embryo. This conclusion is based on endosperm dissection experiments and the use of a “seed coat bedding” assay (SCBA) where dissected embryos are cultured on a layer of dissected endosperms (Lee et al PNAS, 2010; 107(44): 19108-13). Endosperm dissection prevents normal early post-embryonic development. In the context of a SCBA, the endosperm restores normal development in a manner not necessitating direct contact between endosperm and embryo. The SCBA affords the use of combinations of different mutant endosperm and embryonic materials, thus allowing the in vitro genetic dissection of how the endosperm’s developmental activities influence early post-embryonic development.

> SPSW researcher portfolio:
https://swissplantscienceweb.unibas.ch/en/lopez-molina

TALK

Species delimitation in *Capurodendron* Aubrév. (Sapotaceae) using an integrative approach: patterns of diversification in an endemic genus of Madagascar

Yamama Naciri, Carlos Galan Boluda, Camille Christe, Laurent Gautier

Laboratoire de systématique végétale et biodiversité, Université de Genève & Conservatoire et Jardin botaniques de la Ville de Genève, Chambésy - Genève

Sound taxonomy is central to biodiversity assessments and downstream conservation strategies. However, the traditional approaches to species delimitation which has mainly relied on morphology and anatomy, is inefficient in some difficult groups. In order to achieve a more accurate delimitation of species, we combine species tree reconstruction using numerous molecular markers with morphological, ecological and biogeographical data on an endemic genus of Madagascar, *Capurodendron* Aubrév. (Sapotaceae).
Capurodendron presently includes 26 described primary forests species but more are suspected to exist. They are slow-growing trees, appreciated for their mechanical properties of their wood. Their logging and trade presently weaken and threaten species’ natural populations. It is therefore important to know exactly what a species is to efficiently protect the diversity within the genus.

Circa 800 nuclear genes were sequenced on 250 fresh and herbarium samples using NGS technologies and analysed under the Multi-Species Coalescent (MSC) framework. The resulting phylogenetic tree gives us an insight into the evolutionary history of the genus that shows a remarkable radiation in the dry and arid region of Madagascar. It is also used to delimit species on a genetic basis, the so-called MSC clusters, which consistency is then tested against other information such as morphology or ecology.

> SPSW researcher portfolio:
https://swissplantscienceweb.unibas.ch/en/naciri

TALK

Rapid breakdown of dioecy by experimental evolution

Guillaume G. Cossard, Jörn F. Gerchen, Xinji Li, Yves Cuenot, and **John R. Pannell**

Department of Ecology and Evolution, University of Lausanne

The evolution of dioecy was long thought to be an evolutionary dead end, but recent analysis points to frequent reversions from dioecy to hermaphroditism. Here, we use experimental evolution to demonstrate that such reversions can be extremely rapid. We deprived females of the wind-pollinated dioecious herb *Mercurialis annua* of their male mates, a situation that may occur naturally during periods of low population density, repeated colonization of disturbed habitat, or range expansion. Males and females of dioecious *M. annua* occasionally produce flowers of the opposite sex, potentially allowing sexual reproduction when mates are rare or absent; such 'leaky' sex expression is common in dioecious plants. In the absence of males in our experiment, leaky females increased rapidly in frequency and evolved both a 23-fold increase in average pollen production and significantly masculinized transcriptome. When evolved females were reintroduced into populations with males, their evolved male function was sufficiently competitive to partially suppress the production of sons, establishing conditions for the maintenance of androdioecy, a rare sexual system in which males co-exist with hermaphrodites.
Our study demonstrates the rapid dissolution of dioecy via masculinization of females in populations under severe mate limitation and strong competition for siring.

> SPSW researcher portfolio:
https://swissplantscienceweb.unibas.ch/en/pannell

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TALK

Impact of variation in nucleotides and transposable elements on linkage along chromosomes in natural populations of *Arabis alpina* (Brassicaceae)

Christian Parisod[1], Rimjhim R. Choudhury[1], Aude Rogivue[2], Felix Gugerli[2]

[1] Institute of Plant Sciences, University of Bern
[2] WSL Swiss Federal Research Institute, Birmensdorf

Advances in high-throughput sequencing have promoted the assessment of genome-wide single-nucleotide polymorphisms (SNPs) in natural populations. However, the major fraction of genomes represented by transposable elements (TEs) has been largely ignored. Here, the sequencing of 304 individual genomes from four nearby populations of *Arabis alpina* identified 291,396 SNPs and 20,548 polymorphic copies of long terminal repeat retrotransposons (polyTE; i.e. presence/absence at specific loci). Comparing their contributions to genome-wide variation and divergence, SNPs showed a high rate of population-specific variants, whereas most polyTEs segregated among populations.
SNPs appeared nearly-neutral with less than 5 % being identified as non-synonymous or affecting start/stop codons, while 43 % polyTEs were found next to genes enriched in functional categories related to environmental stresses.
This unprecedented dataset was further used to address how TEs and recombination interact at fine-scale along chromosomes and possibly affect the reshuffling of adaptive genetic variation. In particular, polyTEs appeared enriched in 18 recombinationally-inert regions up to 5.5Mb that were marked by locally increased linkage disequilibrium. Such blocks were enriched in genes related to ecologically relevant functions (responses to cold, salt stress or photoperiodism) and revealed strong evidence of selective sweeps. These results are consistent with the hypothesis that TEs are key modifiers of recombination landscapes and thus interact with selection in driving blocks of linked adaptive loci in natural populations.

> SPSW researcher portfolio:
https://swissplantscienceweb.unibas.ch/en/parisod

ABCDEFGHIJKLMNO **P**

TALK

Towards a holistic understanding of starch biosynthesis

Barbara Pfister[1], Martha Stadler[1], Adelaide Raguin[2], Oliver Ebenhöh[2], Samuel C. Zeeman[1]

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Starch, the major storage carbohydrate in plants, is the key nutritional component of our staple crops and a feedstock for industry. It is composed of glucose polymers that form massive semi-crystalline granules. The precise structure and composition of starch determine its functionality and thus applications. However, how structure and composition are controlled at the level of the biosynthetic machinery it is not well understood. We previously demonstrated that *Saccharomyces cerevisiae* can be engineered to produce starch-like glucans using *Arabidopsis* genes, thus serving as a model for starch biosynthesis. That study systematically investigated the contribution of individual biosynthetic enzymes, but did not address the potential importance of expression levels or enzyme ratios. Such ratios may have a strong influence on starch structure given that the starch-biosynthetic enzymes act simultaneously and in an interdependent fashion on the same substrate. Here we employ a refined version of the yeast system, implementing also controllable variation in enzyme expression. Using promoters and terminators of varying strengths, we created yeast strains with a broad range of ratios between single enzyme isoforms. We show that these yeast strains differ both in respect to the amounts and structures of the glucans produced, allowing us to dissect the roles of enzyme ratios vs. enzyme specificities. In collaboration with the Ebenhöh lab in Düsseldorf, we are now using these data to inform a mathematical model of starch biosynthesis. Ultimately, such a model will help generate a systems-wide understanding of the synthesis of complex glucans, providing a basis for the targeted biotechnological improvement of crops.

> SPSW researcher portfolio:
https://swissplantscienceweb.unibas.ch/en/zeeman

TALK

Micro- and macro-evolutionary trends in plant-herbivore-predator interaction along environmental gradients

Sergio Rasmann

University of Neuchâtel

Long standing theory predicts that plants associated with herbivores and predators should experience selection for increased plant defenses, such as the specific production of volatile organic compounds for attracting predators near the site of damage. Along elevation gradients a general pattern is that herbivores and predators are abundant at low elevation and progressively diminish at higher elevations. To determine whether plant adaptation along such a gradient shapes the strength of tritrophic interactions, we manipulated soil predatory nematodes, root herbivore pressure, and *Festuca rubra* plant genotypes in a reciprocal transplant experiment. Plant survival was significantly higher for low elevation plants, but only when in presence of predators. Using olfactometer bioassays, we showed correlated differential nematode attraction and plant ecotype-specific variation in volatile production. We next performed olfactometer bioassay with 18 species of *Festuca,* and found that volatile production is associated to phylogenetic history, while nematode attraction was mainly associated to the climatic niche of the species. This set of studies not only provide a first assessment of how ecological gradients modulate the strength of tritrophic interactions, but also demonstrate how habitat variation imposes selection on indirect plant defenses.

> SPSW researcher portfolio:
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TALK

Xylem differentiation and vacuolar loading: an intertwined road

Bojan Gujas, Anna Hunkeler, Emilia Hristova, Chloe Champeroux and **Antia Rodríguez-Villalon**

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In *Arabidopsis thaliana (Arabidopsis),* as in all higher plants, xylem vessels are essential in the transport of water and nutrients absorbed by the root to the above-ground organs. To become conductive elements, xylem cells undergo a specialized differentiation program which involves programmed cell death and autolysis. This process starts with the enlargement of the vacuolar compartment, whose tonoplast will eventually break down releasing hydrolytic enzymes responsible for organelle disintegration. Prior to cell clearance, a rigid secondary cell wall (SCW) is assembled in an annular/spiral pattern, a process that starts with the deposition of highly polymerized cellulose and is mainly driven by the activity of CELLULOSE SYNTHASES COMPLEX (CSC) at the plasma membrane (PM). The abundance of cellulose synthase subunits (CESA) at the PM is regulated by chlatrin-mediated endocytosis (CME), conferring plasticity to plant cells to remodel their cell wall upon environmental and developmental signals. While internalization of CESA subunits has been described upon abiotic stress, very little is known about their dynamic behaviour during developmental processes. Interestingly, evidences from our group demonstrated that vacuolar loading of the primary cell wall CESA6 subunit is required to boost CESA7 activity in xylem differentiating cells. Moreover, genetic interference with vesicle trafficking to the vacuole by depleting phosphatydilinositol 3-phosphate (PtdIns3P) levels results in defects in cellulose deposition specifically in xylem differentiating cells. In particular, overexpression of *PHOSPHATASE AND TENSIN HOMOLOG ON CHROMOSOME10 3 (PTEN3)* impairs not only vacuolar biogenesis but also CESA6 loading into the vacuole. Consistent with these findings, *PTEN3* overexpression leads to the appearance of undifferentiated cells in xylem strands. Together, these results suggest a vacuolar sensing mechanism by which plant cells coordinate vacuolar expansion with the cell growth restrictions imposed by SCW formation.

> SPSW researcher portfolio:
https://swissplantscienceweb.unibas.ch/en/rodriguez-villalon

TALK

A Golgi-localized glycosyltransferase mediates the response of plant cells to cellulose perturbations

Alexandra Menna, Gloria Sancho-Andrés,
Clara Sánchez Rodríguez

Institute of Molecular Plant Biology, D-BIOL,
ETH Zurich

The ability of plants to adapt to various stresses relies on rapid perception and subsequent response to external stimuli. Remodeling of the primary cell wall is essential for growth as well as adaptation to these external stresses. Cellulose, the main component of plant cell walls, is synthesized at the plasma membrane as glucan chains extruded into the apoplast, which assemble into paracrystalline microfibrils via interactions with other cell wall polysaccharides. This paracrystalline structure is important for tensile strength, cellular expansion, and response to invading pathogens. Recent works have demonstrated a role for apoplastic proteins in the maintenance of this cellulose paracrystalline structure, such as the chitinase-like protein CTL1/POM1. Regulation of perception and response to cellulose perturbations is a major driver towards balancing optimal plant development and stress response activation. To identify proteins involved in this equilibrium, we screened for *suppressors of ctl1-2 in adult stage (sca).* We isolated a mutant in a gene encoding for a Golgi-localized glycosyltransferase *(SCA18)* that reverts *ctl1-2* phenotypes back to wild-type (WT)-like. Mutations in *SCA18* attenuate growth inhibition and ectopic lignification in *ctl1-2* plants, but did not affect WT, resembling the phenotype of mutants affected in the cell-wall-integrity sensor THESEUS. To better understand the biochemical activity of SCA18, we are currently employing cell biology, glycoprofiling, glycoproteomics and spectroscopy approaches. Our data opens the possibility of a regulatory role of SCA18 in cell wall integrity maintenance pathways by activating cell-wall-integrity sensors, such as THESEUS.

> SPSW researcher portfolio:
https://swissplantscienceweb.unibas.ch/en/sanchez-rodriguez

Host specialization in fungal pathogens

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Plant pathogens are highly specialized to certain plant species and cultivars. Cultivar-strain specificity in plant pathosystems is mainly controlled by resistance genes on the host side and virulence factors on the pathogen side. In wheat some of the resistance proteins that recognize the necrotrophic pathogen *Zymoseptoria tritici* have been identified. In *Z.tritici,* however, the molecular determinants of host specialization remain largely unknown. We have recently identified new virulence factors involved in host specialization using a genetic mapping approach. These virulence factors in *Z.tritici* are highly polymorphic and tightly regulated. Their expression is strongly induced in cells attempting to penetrate the stomata. In addition, we have demonstrated that certain cultivars specifically recognize virulence factors and trigger an immune response that hinders the penetration of *Z.tritici* through the stomata. To better understand the function of virulence factors we are currently performing proteomic, cell biology and transcriptomic approaches. Our work unravels the molecular basis of host specialization and the components involved in the intricate communication system between plants and pathogens.

Plant root microbiome interactions: communication, traits and opportunities for smart farming

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Plants accommodate on and inside plant roots a specific and species-rich microbiota including a multitude of bacteria, fungi or oomycetes. These microbes collectively function as a microbiome and, similar to the microbial communities in human or animal guts, they impact nutrition and health of their host. Plants change the surrounding soil properties by root exudates and although the soil microbiota is known to play a key role in the resulting plant-soil feedbacks, the proximal mechanisms underlying this phenomenon remain unknown. We found that one component of maize root exudates – benzoxazinoids (BXs), being defensive metabolites produced by cereals such as wheat and maize – alter root-associated fungal and bacterial communities, decrease plant growth, increase jasmonate signaling and plant defenses, and suppress herbivore performance in the next plant generation. Complementation experiments demonstrate that the BXs, which accumulate in the soil during the conditioning phase, are both sufficient and necessary to trigger the observed phenotypic changes. Sterilization, fungal and bacterial profiling and complementation experiments reveal that BXs acts indirectly by altering the root-associated microbiota. Our results reveal a mechanism by which plants determine the composition of rhizosphere microbiota, plant performance and plant-herbivore interactions of the next generation.

> SPSW researcher portfolio:
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TALK

Integrating ancient DNA into plant genomics

Verena J. Schuenemann

Institute of Evolutionary Medicine, University of Zurich

In recent years, advances in sequencing technologies and simultaneous improvements in the ancient DNA field have revolutionized our understanding of the evolution of our own species, among others. By analyzing genomes of individuals who lived in distant past, we can now directly look at evolution in action. Concerning many plant species, only the first steps has been made. From the recovered ancient genomes two examples will be discussed here to showcase the potential and variety of ancient DNA studies: a historic plant pathogen and one of the oldest plant genomes sequenced so far.
The eukaryotic plant pathogen, *Phytophthora infestans* was reconstrued from the time of the Irish potato famine using herbarium samples. During the last 100 years, this plant pathogen evolved rapidly displaying different strategies of host adaptation such as an increase in ploidity and the loss of effector genes.
The ancient plant genome was recovered from directly dated 6,000-year-old barley grains excavated at Masada Fortress in the Judean Desert, Israel, and compared to contemporary wild and domesticated barley varieties. Our results point to continuity in contemporary landraces in Israel in past 6,000 years and support the suggested origin of domesticated barley in the Upper Jordan Valley.

TALK

Towards remote sensing of intraspecific variation

Meredith C. Schuman[1,2], Nora Adam[2], Silke Allmann[2,3], Rayko Halitschke[2], Ian T. Baldwin[2], Ewa Czyz[1], Kentaro Shimizu[4], Bernhard Schmid[1], Michael E. Schaepman[1]

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Genetic and phenotypic diversity within species is an important component of biodiversity because intraspecific diversity provides the raw material for evolution and adaptation. Recently, we showed that variation among plants in populations for genes controlling defense traits can have large effects on plant-insect interactions, and plant survivorship to reproduction.
Intraspecific variation has been difficult to capture on a large scale: destructive sampling and laborious tissue and data analyses are required to characterize genotypes and chemotypes.
Imaging spectroscopy (400-2400 nm) and other spectroscopic techniques can be high-throughput, non-destructive tools to detect variation in multiple important plant traits, and can be employed for remote sensing at large scales.
Recently, variation in spectroscopic images has been successfully used to assign plants to phylogenetic groups, and preliminary studies indicate that these images may even differentiate genotypes within species. Well-developed models assign specific spectral regions to protein, phenolic, and structural variation based on physical principles and observed correlations, and a few studies have associate spectral variation with concentrations of plant defense metabolites. These associations have rarely been tested using manipulations of the underlying traits. We will employ both manipulation and association studies in realistic environments to determine the contribution of genetic and chemical variation within plant species to spectroscopic data, and to develop spectroscopic approaches to measure genetic and chemical diversity non-destructively at different scales.

TALK

Advantages and disadvantages of polyploidy, revisited

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Ancient and recent polyploidization events are widespread in plants, and thus the advantages and disadvantages of polyploidization has long been discussed. However, genome-wide analysis of allopolyploid species has been difficult due to high sequence similarity of duplicated genes, or homeologs. We have developed bioinformatic workflow HomeoRoq and EAGLE-RC for RNA-seq and resequencing of polyploid species. To examine the pattern of selection at an early stage of allopolyploid speciation, we resequenced distribution-wide 25 individuals of the model allotetraploid *Arabidopsis kamchatica.* Negative selection was only slightly weaker than in diploid parental species, showing that homeologs are not totally redundant. We found significantly positive value of alpha, the proportion of adaptive substitutions, in contrast to most diploid plant species. Interestingly, the pairs of homeologs showed only weak correlation in diverse indices of the signature of selection, including the HEAVY METAL ATPASE4 (HMA4) homeologs responsible for zinc hyperaccumulation. This shows that pairs of homeologs evolves independently in the allopolyploid species and thus increased the opportunity of different evolutionary trajectories.

We also identified an ancient polyploidization occurred in the lineage of Dipterocarpaceae family, the dominant tree family of Southeast Asian tropical rain forests, by the whole genome assembly of *Shorea leprosula.* The estimated time of the polyploidization coincided with the mass extinction at the Cretaceous-Paleogene boundary around 65 million years ago. This support the hypothesis that polyploidization conferred tolerance to severe environments.

> SPSW researcher portfolio:
https://swissplantscienceweb.unibas.ch/en/shimizu

TALK

Insects may manipulate the release of plant volatiles to enhance the suitability of neighboring plants as host for their offspring

Ted Turlings

Institute of Biology, University of Neuchâtel

Herbivory by insects leads to the release of specific blends of volatiles. These herbivore-induced plant volatiles are known to serve as cues for other organisms that may, for instance, use them to locate the herbivores or to avoid infested plants. Inducible volatiles also serve as within and between plant signals, whereby the perception of the volatiles by neighboring plants usually primes the neighbors to prepare for an imminent attack, making them more resistant to insects.
I will present an example, however, of an insect triggering the release of a volatile blend that is more indicative of pathogen attack. The “wrong” signal primes pathogen defenses in neighboring plant, and suppresses the defense against insects. This apparent manipulation of a plant distress signal makes the neighbors more suitable for the offspring of the inducing insect. I have kept this abstract rather vague, because the work is not published yet.

> SPSW researcher portfolio:
https://swissplantscienceweb.unibas.ch/en/turlings

TALK

Cytoskeleton dynamics shape lateral root formation in *Arabidopsis*

Dorothee Stöckle[1], Amaya Vilches Barro[2], Martha Thellmann[1], Alexis Maizel[2] and **Joop EM Vermeer[1]**

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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. In able to emerge, a LR needs to deal with the mechanical constraints provided by the surrounding cells. It has been reported that the mechanical properties of the overlying cell layers, rather than cell division plane orientation, drive LR primordium morphogenesis. However, we still do not know the mechanism underlying the transition of LR founder cells into a dome-shaped stage I primordium and how the overlying tissues regulate primordium shape. Although we have learned a lot about the hormonal pathways involved, we still lack mechanistic insights into how plants can re-establish differential growth deep within a tissue.

We have previously shown that founder cells need to swell to support nuclear migration and asymmetric cell divisions. In addition, feedback from the overlying endodermis is essential for LR formation. Although it is widely accepted that the cytoskeleton is an important regulator of cell shape, there is still no detailed study scrutinizing the role of the cytoskeleton during LR formation and how this is intertwined with the hormonal pathway. By combining 4-dimensional live imaging, cell type specific perturbation of cytoskeleton dynamics, we propose a mechanistic framework from the transition from LR founder cell to a stage I primordium and growth through the endodermis.

> SPSW researcher portfolio:
https://swissplantscienceweb.unibas.ch/en/vermeer

TALK

FLAGELLIN SENSING2-ASSOCIATED KINASE1 regulates *Arabidopsis* abscisic acid-dependent stomatal immunity

Laurent Zimmerli

National Taiwan University, TW

Diseases caused by microbial pathogens significantly contribute to the overall loss in crop yield jeopardizing worldwide food security. To sense invaders, plants are equipped with surveillance machineries such as plasma membrane surface-localized proteins called pattern recognition receptors (PRRs), which detect microbe-associated molecular patterns. In order to better understand plant resistance to pathogens, my laboratory analyses the function of proteins that are involved in the *Arabidopsis thaliana* defense response and are part of PRR complexes. Notably, we study the role of Lectin Receptor Kinases, Leucine-Rich Repeat Receptor Kinases (LRR-RK) and Cysteine-Rich Receptor-Like Kinases in plant innate immunity. I will present data stressing the role of a Malectin-Like LRR-RK in stomatal immunity.

TALK

The kinase BIK1 orchestrates ion movements across the plasma membrane during plant immunity

Kathrin Thor[1], Thomas DeFalco[1,2], Julian Dindas[2], Jeoffrey George[1,2], Shushu Jiang[1], Lena Stransfeld[1,2], Frank Menke[1], **Cyril Zipfel[1,2]**

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An important layer of plant immunity is achieved through the perception of pathogen-associated molecular patterns (PAMPs) by cell-surface pattern recognition receptors (PRRs). Ion fluxes across the plasma membrane are some of the earliest signaling events induced upon PAMP perceptio. The identity and activation mechanisms of the underlying channel/transporter proteins are, however, mostly unknown. The cytoplasmic kinase BIK1 is an immediate substrate for many activated PRR complexes and regulates multiple cellular immune outputs, including ion fluxes. Here, we report the identification and characterization of several channels/transporters as BIK1 substrates. In particular, we identified a calcium-permeable channel that is required for PAMP-induced stomatal closure and anti-bacterial immunity. The role of this channel in calcium signaling during immunity will be constrated with that of additional potential calcium channels identified as BIK1 substrates in our study. In addition, the characterization of BIK1 substrates shed light on a potential dynamic regulation of phosphate homeostasis by immune signaling. All together, our work highlights the role of the central immune kinase BIK1 as a key regulator of ion fluxes during plant immunity, and provide further mechanistic details linking PRR activation at the plasma membrane to downstream immune cellulat outputs.

> SPSW researcher portfolio:
https://swissplantscienceweb.unibas.ch/en/zipfel

POSTER

A sulphur-containing volatile organic compound emitted by potato-associated *Pseudomonas* protects plants against late blight

Delphine Chinchilla[1], Charlotte Joller[1], Silvan Meyer[1], Daniela Zühlke[2], Floriane L'Haridon[1], Kathrina Riedel[2] and Laure Weisskopf[1]

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The production of volatile organic compounds (VOCs) by bacteria is now well recognized but their role in the interaction between plants and microbes remains largely unknown.
Recently our lab demonstrated that potato-associated *Pseudomonas* strains, promoting plant protection against pathogens, emitted VOCs of distinct chemical classes as complex blends. Interestingly, when assayed individually *in vitro* against the late blight agent *Phytophthora infestans,* different sulphur-containing VOCs (sVOCs) identified in the bacterial volatilomes show significant but divergent antimicrobial activities.
In a new study, we show that one of these sVOCs can protect efficiently potato and *Arabidopsis* against oomycete and fungal infections at doses not affecting plant growth. This protective effect is dose-dependent and can be curative to a certain extent. Thus, the anti-microbial activity of this sulphur VOC offers a new promising approach for plant protection, as an alternative to chemical treatment with fungicides.
These exciting results and the clear inhibitory effect of sVOCs on the oomycete prompted us to initiate a quantitative proteomic analysis on Phytophthora hyphae treated with the individual sulphur-VOCs to understand the biological processes affected. A differential regulation of proteins can be observed upon each VOC treatment, suggesting diverse modes of action: Two active sVOCs may affect the amino acid metabolism in two distinct manners, while a third one seems to impair mainly translation.
The question of the mode(s) of action of sulphur VOCs remains open: it clearly affects oomycete growth *in vitro* but it might also promote plant resistance by inducing plant defense responses. So we are also studying some defense responses, such as transcript regulation of defense genes and the production of reactive oxygen species in response to sulphur-VOCs to complete our analysis.

POSTER

Heterostyly in Connaraceae – a first phylogenomic analysis of an understudied tropical clade

Jurriaan M. de Vos

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Heterostyly is a widely studied model for the ecology, evolution, and genomic regulation of plant reproductive systems. According to textbook knowledge, heterostyly comes in two flavors: populations exist of two (distyly) or three (tristyly) morphs that differ in the spatial position of male and female sexual organs within flowers, combined with a sporophytic self- and intramorph incompatibility system. Contrary to this predominant view, early morphological studies suggested at least seven different types of heterostyly in the pantropical plant family Connaraceae (Oxalidales, ca. 200 spp.), including tristyly, distyly, several intermediate forms, and monomorphic species also occur. Thus, Connaraceae offers the potential to reconstruct the evolutionary pathways that lead to and from various heterostylous types, but a molecular-phylogenetic framework is lacking.

This poster presents the first molecular phylogeny for Connaraceae, including 45 species representing all accepted genera and major lineages within them. We sampled almost exclusively from herbarium specimens, and used a targeted enrichment approach for 353 putatively single copy genes that are conserved across angiosperms. The Illumina sequence data are analysed with a suit of traditional and coalescent-based approaches. Based on the results, we evaluate generic circumscription and present implications for the evolution of the heterostylous syndrome.

POSTER

Adaptation to plant communities across the genome of *Arabidopsis thaliana*

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Despite the importance of plant-plant interactions on plant community dynamics and crop yield, our understanding of the adaptive genetics underlying these interactions is still limited and deserves to be investigated in the context of complex and diffuse interactions occurring in plant assemblages. Studying the genetic architecture of adaptation while conserving an ecological realism is feasible through powerful ecological genomics approaches. Here, based on 145 natural populations of *Arabidopsis thaliana* characterized for plant communities, we conducted a Genome Environment Association analysis using more than 1.5 million SNPs to finely map adaptive genomic regions of *A. thaliana* associated with plant community descriptors. The candidate adaptive loci associated with species abundance were highly dependent on the identity of the neighboring species, suggesting a high degree of biotic specialization of *A. thaliana* to members of its plant interaction network. Moreover, the identification of adaptive loci associated with α-diversity and composition of plant communities supports the ability of *A. thaliana* to interact simultaneously with multiple plant neighbors, which in turn can help to understand the role of community-wide selection. This study provides keys information that will allow a better understanding of the co-evolutionary processes related to plant-plant interactions and highlights the importance to study the genomics of these interactions in natural habitats.

POSTER

Regulation and function of thylakoid protein phosphorylation in *Chlamydomonas*

Federica Cariti[1], Alexis Riché[1], Marie Chazaux[2], Martin Scholz[3], Linnka Lefebvre-Legendre[1], Paolo Longoni[1],[4], Michael Hippler[3], Xenie Johnson[2] and **Michel Goldschmidt-Clermont[1]**

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Phosphorylation of thylakoid proteins plays an important role in the regulation of light harvesting and of thylakoid membrane architecture. In *Arabidopsis,* two pairs of protein kinases (STN7 and STN8) and antagonistic protein phosphatases (PPH1/TAP38 and PBCP) control the phosphorylation of LHCII and of PSII. STN7 and PPH1/TAP38 control state transitions, which reflect the dynamic allocation of part of the LHCII antenna to PSII or PSI in response to changes in the redox state of the plastoquinone pool. More specifically, the phosphorylation of the LHCII isoform Lhcb2 is central to state transitions. On the other hand, STN8 and PBCP modulate the phosphorylation of the core subunits of PSII as well as other thylakoid proteins, and influence the architecture of thylakoid grana and PSII repair after photo-damage.

In the green alga *Chlamydomonas,* only the kinase STT7 (orthologous to STN7) has been characterized so far. We have analyzed mutants of *Chlamydomonas* defective for the phosphatases CrPPH1 and CrPBCP, the putative orthologues of the *Arabidopsis* thylakoid phosphatases. We found that both CrPPH1 and CrPBCP are involved in the control of state transitions, in contrast to the more specific roles of their orthologues in *Arabidopsis*.

To investigate the function of PSII phosphorylation, we have used *Chlamydomonas* chloroplast transformation to generate site-directed mutations in the major phosphorylation sites of the PsbC, PsbD and PsbH subunits of PSII. Our results indicate that some of these phosphorylation sites have redundant functions. A mutant defective for phosphorylation of both PsbH and PsbC shows delayed recovery from photoinhibition. Surprisingly, removal of a further phosphorylation site in a mutant lacking the sites in PsbD, PsbH and PsbC recovers like the wild type. These observations suggest that an intermediate level of overall phosphorylation may be suboptimal for efficient PSII repair.

POSTER

Crystal structures of two tandem malectin-like receptor kinases involved in plant reproduction

Julia Santiago

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A complex cell-to-cell communication between the male pollen tube and the female reproductive organs is required for plant fertilization. A family of Catharanthus roseus Receptor Kinase-1 (CrRLK1L) membrane receptors has been genetically implicated in this process. Here we present crystal structures of the CrRLK1Ls ANXUR1 and 2 at 1.48 and 1.1 Å resolution, respectively. Our structures reveal a novel arrangement of two malectin-like domains connected by a short β-hairpin linker and stabilized by calcium ions. The canonical carbohydrate interaction surfaces of related animal and bacterial carbohydrate binding modules are not conserved among plant CrRLKs. In line with this, we failed to detect binding of chemically diverse oligosaccharides to ANXUR1 and HERCULES1. Instead, CrRLKs have evolved a protein-protein interface between their malectin domains, which forms a deep cleft lined by highly conserved aromatic and polar residues. Analysis of the glycosylation pattern of different CrRLKs and their oligomeric states together suggests that this cleft could resemble a binding site for a ligand required for CrRLK1Ls receptor activation.

POSTER

A general role for *OCTOPUS-LIKE* genes in modulating root growth?

Simona Crivelli, M. Aguila Ruiz Sola, Mario Coiro, **Elisabeth Truernit**

Institute of Molecular Plant Biology, ETH Zurich

Plant root growth is strictly dependent on carbohydrate import via the phloem. For this reason, the observed early differentiation of protophloem cells in *Arabidopsis* root meristems is believed to be a prerequisite for efficient root development. We have identified the phloem specific *OCTOPUS (OPS)* gene as an important regulator of phloem differentiation in *Arabidopsis* roots. Our recent finding that *OCTOPUS-LIKE 2 (OPL2)* – a gene closely related to *OPS* – is also important for proper phloem differentiation corroborates these results. However, although phloem transport and root meristem growth in the *ops opl2* double mutant are more severely impaired than in the *ops* single mutant, protophloem differentiation in the root tip of the double mutant seems to be slightly restored. These observations highlight the complex interdependency between sink organ growth and protophloem differentiation and require further investigation. Moreover, since *OPL2* is expressed throughout the root meristem, we cannot exclude a more direct effect of OPL2 on root growth, which would be unmasked only in the ops mutant background. Another evidence pointing towards a more general contribution of *OPL* genes to root development comes from our studies of *OCTOPUS-LIKE 1 (OPL1),* the second gene displaying high sequence similarity with *OPS.* The triple mutant *ops opl1 opl2* is even more affected in growth than any double mutant combination. However, in contrast to *OPS* and *OPL2, OPL1* is not expressed in the phloem at any developmental stage. Rather, OPL1 seems to be active in the xylem, the tissue adjacent to the phloem.

POSTER

Involvement of a potential interactor for glutamate receptor in wound induced defense response

Qian Wu, Stéphanie Stolz, and Edward E. Farmer*

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To respond to herbivores and mechanical wounding, plants use the defense activating hormone jasmonate acid (JA) to deal with these stresses both at the site of damage and systemically, therefore protecting undamaged distal tissues against further attack. Recently, two *glutamate receptor-like (GLR)* genes *(GLR3.3* and *3.6)* in *Arabidopsis thaliana* were reported to function in long distance wound signalling by transmitting electrical signals leaf-to-leaf that stimulate *de novo* JA synthesis and defense responses in distal tissues. But our understanding of how GLRs are regulated and their downstream signalling components is still limited. Through yeast two-hybrid screening, we found one candidate, which potentially interacts with the C-tail of GLR3.3. Preliminary results showed the candidate mutant is involved in both wound and herbivore induced defense responses. And upon wounding, slightly but significantly more jasmonates are accumulated in the mutant than in wild type plants. Moreover, the candidate mutant partially compromised *glr3.3* functions in terms of wound induced defense gene expression, which indicates they are likely to act in the same genetic pathway. Further study will focus on elucidating the molecular basis for their interaction and understanding the detailed mechanism of GLR-mediated long distance defense responses.

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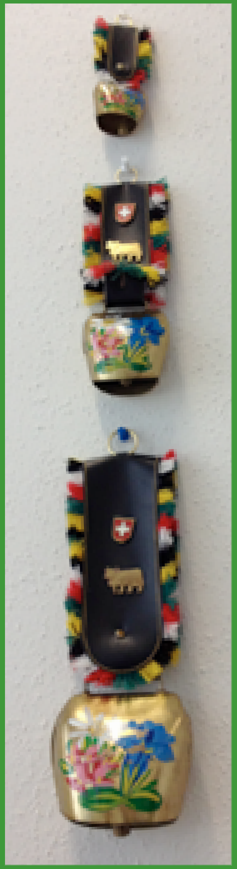

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