SwissPLANT2018

Symposium of the Plant Science Research Community in Switzerland

31 January – 2 February 2018
Meiringen, Switzerland

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SwissPLANT 2018

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31 January – 2 February 2018
Meiringen, Switzerland

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Venue

Parkhotel du Sauvage, Meiringen

Scientific Program Committee

Matthias Erb, Markus Fischer, Cris Kuhlemeier, Doris Rentsch, Tobias Züst
University of Bern, Switzerland

Conference Organization

Swiss Plant Science Web
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SwissPlant 2018 – Welcome by the president

The Swiss Plant Science Web (SPSW) held its first scientific conference "SwissPlant" in 2011 in the Hotel du Sauvage in Meiringen, a sequel of sorts of the "Swiss Plant Molecular and Cell Biology Conferences" that started in 1992 in Les Diablerets. This yearly conference of group leaders is well established and popular in our community. It highlights the current advances in plant science research in Switzerland. By presenting results from molecular biology to ecology, it offers an ample view and better understanding of the complexity and diversity of plant life.

By choosing an attractive place for our conferences, we wish to foster informal discussions among peers. This year, we are back in the refurbished Hotel du Sauvage in Meiringen.

I especially welcome all new members of our SPSW network and hope that they feel at ease in our community. With their new ideas, they will help to 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 Bern. I thank Matthias Erb, Markus Fischer, Cris Kuhlemeier, Doris Rentsch, and Tobias Züst 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 smooth and easy.

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, 31 January 2018

15:30	Swiss Plant Science Web strategic meeting for SPSW members
17:00	Welcome drink
17:25	Welcome by Thomas Boller, SPSW president
17:30	Opening remarks by the organizing committee
17:40	Bernhard Schmid | U Zurich | page 26 Plants: individuality and diversity (keynote)
18:30	Dinner
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20:00	Pauline Jullien | U Bern | page 18 Cell-specific functional characterization of *Arabidopsis* ARGONAUTE 3
20:20	Roman Ulm | U Geneva | page 29 UV-B photoreceptor signalling and responses
20:40	Jurriaan de Vos | U Basel | page 11 The whole-plant context of floral adaptation
21:00	Jules Deforges | U Lausanne | page 10 Identification of translation regulator antisense RNAs in *Arabidopsis*
21:20	Get-together at the hotel bar

Thursday, 1 February 2018

7:00 Breakfast begins

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News from the volatile warfare between potato-associated *Pseudomonas* and the late blight causing agent *Phytophthora infestans*

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Promiscuity in the Calvin-Benson cycle

09:00 Marie Barberon | U Lausanne | page 8
Secretion-dependent deposition of suberin lamellae

09:20 Philippe Reymond | U Lausanne | page 23
Low number of fixed somatic mutations in a long-lived oak tree

9:40 Coffee break

Session III, chair: Pauline Jullien

10:10 Christian Hardtke | U Lausanne | page 16
A molecular rheostat adjusts auxin flux to promote root protophloem differentiation

10:30 Stefan Grob | U Zurich | page 14
Transgene silencing in 3D – how a chromosomal knot can inactivate foreign DNA elements

10:50 Kentaro Shimizu | U Zurich | page 27
Cost and benefit of UVR8 UV-B receptor in naturally fluctuating environments

11:10 Chi Tam Nguyen | U Lausanne | page 20
GLRs control calcium fluxes in wounded tissues

11:30 Clara Sánchez Rodríguez | ETH Zurich | page 24
A Golgi-localized glycosyltransferase mediates the response of plant cells to cellulose perturbations

11:50 Leisure time (lunch on your own, skiing, hiking, snowshoeing …)

16:30 Poster session (with apéro) | pages 34–38

18:30 Dinner

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Transposable element insertions facilitate adaptation of a fungal wheat pathogen

20:20 Christiane Nawrath | U Lausanne | page 19
Identification and characterization of root cap cuticles in *Arabidopsis*

20:40 Xavier Perret | U Geneva | page 21
Synthetic plasmids to make recipient bacteria nodulate many legume hosts

21:00 Eric Allan | U Bern | page 7
Interactions between global change, biodiversity loss and ecosystem functioning

Friday, 2 February 2018

7:00	Breakfast begins
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8:20	Cyril Zipfel | The Sainsbury Laboratory | page 33 FERONIA and the regulation of receptor kinase-mediated signaling
8:40	Didier Reinhard | U Fribourg | page 22 Selection by the host for efficient bacterial nitrogen fixation during root nodule symbiosis of *Medicago truncatula*
9:00	Michael Hothorn | U Geneva | page 17 Mechanistic insights into the activation and regulation of plant membrane receptor kinases
9:20	Salim Bourras | U Zurich | page 9 Shifting paradigms in disease resistance: from flor's gene-for-gene model to effector-R interactomes
9:40	Coffee break
	Session VI, chair: Markus Fischer
10:10	Thomas Wicker | U Zurich | page 31 It's all about repeats – lessons from the very large genomes of wheat and barley
10:30	Ted Turlings | U Neuchâtel | page 28 Exploiting the chemical ecology of tritrophic interactions for crop protection
10:50	Pierre Goloubinoff | U Lausanne | page 13 A genetic screen to identify *Arabidopsis thaliana* genes involved in the heat sensing and heat-shock signaling
11:10	Mathieu Hanemian | U Bern | page 15 Amplification of reproductive isolation through hybrid necrosis in sympatric *Petunia* species
11:30	Markus Fischer | U Bern | page 12 Direct and biodiversity-mediated effects of land use on ecosystem processes in grasslands and forests: insights from 10 years of research in the Biodiversity Exploratories
11:50	Closing remarks

TALK

Interactions between global change, biodiversity loss and ecosystem functioning

Eric Allan

Institute of Plant Sciences, University of Bern

Human driven global change reduces biodiversity and many experiments have shown that such a loss of biodiversity can impair ecosystem functioning. However, global change drivers, such as nitrogen enrichment, cause many other alterations to ecosystems and the importance of biodiversity loss relative to these is not well known. To test this we have set up a new grassland field experiment to manipulate plant diversity, plant functional composition (presence of fast vs. slow growing species), nitrogen levels and foliar pathogen abundance. First results show that biodiversity is a major driver of biomass production, even in comparison with direct nitrogen fertilization effects or with effects of functional composition. Addition of nitrogen also alters the diversity-functioning relationship, by reducing complementarity and leading to more rapidly saturating relationships. Pathogens are most abundant in low diversity, fertilized plant communities and removal of pathogens reduces complementarity effects between plant species. These results show that biodiversity loss is a major driver of functioning and that biodiversity should not be considered in isolation but rather as part of suite of changes occurring in response to global change.

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A

TALK

Secretion-dependent deposition of suberin lamellae

Marie Barberon[1], Damien De Bellis[1,2], Lothar Kalmbach[1], Peter Marhavy[1], Jean Daraspe[2], Niko Geldner[1]

[1] Department of Plant Molecular Biology, DBMV, UNIL-Sorge, University of Lausanne, Lausanne, Switzerland
[2] EMF, UNIL-Sorge, University of Lausanne

Suberin is a hydrophobic polymer deposited in the extracellular matrix of mature endodermal cells, forming a diffusion barrier for water and nutrients. Suberin is a polyester built from the polymerization of hydrophobic monomers composed mostly of long-chain fatty acids and glycerol. Suberin precursors are produced at the reticulum endoplasmic and are polymerized in suberin lamellae in the cell wall. However, the process involved in the transport of hydrophobic suberin monomers in the extracellular matrix is poorly understood. By combining ultrastructure and fluorescent microscopy we observed the accumulation of secretory vesicles specifically in suberizing cells. Demonstrating a role of vesicular secretion in suberin deposition, interference with exocytosis/secretion impaired suberin deposition in the cell wall. Our results provide functional evidence for a secretion–dependent suberin deposition and paved the way for a better understanding of the mechanism controlling polyesters formation and regulation.

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TALK

Shifting paradigms in disease resistance: from flor's gene-for-gene model to effector-R interactomes

Salim Bourras

Department of Plant and Microbial Biology
University of Zürich

One of the biggest challenges of agriculture in the 21st century will be the transition from chemical pesticides as a mean to control pests and diseases. One possible way to meet this challenge is to gain deeper understanding of the basic mechanisms controlling disease resistance in crops, in particular those allowing pathogens to adapt, persist, and re-deploy in the agroecosystem. Cereal powdery mildews are agronomically important fungal diseases caused by only one species, *Blumeria graminis,* which can be divided into several subspecies, corresponding to highly specialized pathogens infecting only one crop. All cereal mildews are obligate biotrophs, meaning that they can only grow and reproduce on living host tissue. Resistance to cereal powdery mildews is mainly based on the deployment of major resistance (R) genes. R gene mediated resistance to the vast majority of fungal pathogens is commonly controlled by Flor's gene-for-gene model. One of the most prominent exceptions is *Blumeria graminis* f.sp. *tritici*, the wheat powdery mildew pathogen. Here, we present recent advances in understanding the genetic and molecular basis of R gene-mediated resistance of wheat to powdery mildew. In particular, we demonstrate a unique system involving several effectors from the pathogen and several R protein alleles from the host, and in one case an additional layer of control based on pathogen encoded siRNAs will be presented. Our work demonstrate that R gene mediated resistance in wheat is based on a complex interactome with several nodes and layers that can be high-jacked by the pathogen to suppress R protein based immunity.

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TALK

Identification of translation regulator antisense RNAs in *Arabidopsis*

Jules Deforges, Rodrigo Siqueira Reis, Yves Poirier

Department of Plant Molecular Biology, University of Lausanne

The development of high-throughput genomic technologies has revealed that a large fraction of the genomes of eukaryotes is associated with the expression of noncoding RNAs. One class of noncoding RNA, the cis-natural antisense transcripts *(cis*-NATs), are particularly interesting as they are at least partially complementary to the protein-coding mRNAs. Although most studies described *cis*-NATs involved in the regulation of transcription, a few reports have shown recently that *cis*-NATs can also regulate translation of the cognate sense coding genes, in plants and mammals. In order to identify novel examples of translation regulator cis-NATs in *Arabidopsis thaliana,* we designed a high-throughput experiment based on polysome profiling and RNA-sequencing. Expression of cis-NATs and translation efficiency of the cognate coding mRNAs were measured in roots and shoots in response to various conditions, including phosphate deficiency and treatment with phytohormones. We identified several promising candidates, and already validated a few of them experimentally, by translation assays in *Arabidopsis* protoplasts. These candidate translation regulator cis-NATs are currently being further characterized in order to investigate the underlying molecular mechanism of regulation. Meanwhile, *Arabidopsis* transgenic lines over-expressing in trans some of our best cisNAT candidates were created, and phenotypically characterized. These results should provide crucial insights about the biological relevance and the mode of action of this emerging class of non-coding RNAs.

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TALK

The whole-plant context of floral adaptation

Jurriaan M. de Vos[1], Lawrence D. Harder[2], Erika J. Edwards[3]

[1] Department of Environmental Sciences – Botany, University of Basel
[2] Department of Biological Sciences, University of Calgary, Canada
[3] Department of Ecology & Evolutionary Biology, Yale University, USA

Inflorescences have reproductive functions beyond those of individual flowers. While many aspects of floral diversity among angiosperm species are well-known to represent diversity in reproductive function, functional aspects of inflorescence diversity are much poorer understood. In particular, functional links between inflorescence structure and environmental conditions are expected but poorly understood. Here, I emphasize the extent to which reproductive adaptation to extreme environments (such as alpine areas and deserts) happens not just at the level of individual flowers, but also within inflorescences and across the whole plant. Using ecologcal and phylogenetic approaches on a group of perennial rosette herbs *(Lewisia,* Montiaceae), I test the hypothesis that the relation between flower number and per-flower investment, rather than floral structure per se, evolves along a seasonality gradient. I find that (1) environments with short periods for growth and development (such as high elevation deserts) contain species that complete their flowering season quickly, and that (2) that duration is largely mediated through correlated evolution of flower number, flower size, and investment in inflorescence branching scaffold, rather than floral longevity. Thus, extremely seasonal environments should select for small inflorescences that bear comparatively large flowers, due to relations between inflorescence architecture and flowering phenology. These results thus help explain the paradox that seasonally extremely constraint environments such as deserts and alpine areas may often contain large-flowered plant species.

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TALK

Direct and biodiversity-mediated effects of land use on ecosystem processes in grasslands and forests: insights from 10 years of research in the Biodiversity Exploratories

Markus Fischer and the Biodiversity Exploratories Consortium

Institute of Plant Sciences, University of Bern, and many further institutions

While land use effects on biodiversity and ecosystem processes, as well as the role of biodiversity in mediating land use – ecosystem process relations, are of very high ecological and applied relevance, our knowledge is limited due to a lack of long-term multi-site, multi-diversity and multi-process studies. The Biodiversity Exploratories, started in 2006 and involving hundreds of researchers in 45 subprojects, which all address the same guiding questions in a common study design, contribute to filling this gap for temperate grasslands and forests of various land use intensities (www.biodiversity-exploratories.de). In grasslands, more intense land use reduces biodiversity of most taxa. Most of the accompanying changes in grassland ecosystem processes appear negative from an anthropogenic point of view, and for many processes the effect of grassland use on ecosystem processes is mediated by biodiversity loss or change in community composition across many taxa. Various components of forest management affect forest structure, biodiversity and ecosystem processes, and many of these ecosystem-process changes are mediated by changes in forest structure or biodiversity. Important conclusions are that land use - ecosystem process relations are strongly mediated by biodiversity loss and changes in community composition; that relations between various facets of land use, biodiversity and ecosystem processes are constrained by various trade-offs; that these relations appear less straightforward for forests than grasslands; and that maintaining high levels of diversity and ecosystem functioning in the landscape requires areas under various types and intensities of land use.

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TALK

A genetic screen to identify *Arabidopsis thaliana* genes involved in the heat sensing and heat-shock signaling

Pierre Goloubinoff, Anthony Guihur, Baptiste Bougine

Department of Plant Molecular Biology, University of Lausanne

Global warming is a major challenge of the 21st century, causing severe stresses to wildlife, agriculture and human populations. Land plants have evolved various mechanisms to cope with multiple abiotic stresses, diurnal heat-shocks in particular. As sessile organisms, plants need to sense rising temperatures soon in the morning and readily accumulate heat-shock proteins (HSPs), instating various cellular mechanisms to preserve membrane integrity and maintain protein homeostasis during an upcoming noxious heat stress, occurring typically at midday.
Aiming to identify specific genes involved in the heat-sensing and heat-signaling pathway, and that lead to the expression of HSPs, and the onset of plant acquired thermotolerance, we performed a genetic screen in *Arabidopsis.* The screen was based on a transgenic *Arabidopsis* mother line that conditionally expressed from a heat-inducible promoter (pshsp17.6B), a nano-luciferase fused to the D-amino-acid-oxidase 1 (dao1) enzyme. In the presence of D-valine, the Dao1 produces toxic chemicals that can kill the plant. Whereas grown on D-valine without iterative heat shocks, or grown without D-valine with heat-shocks this line did not die, it died when grown on D-Valine under heat-shock.
Using this reporter line, we selected from 4900 EMS *Arabidopsis* mutants, ~20 different mutants that did not die when grown on D-valine under heat-shocks. These mutants were confirmed by western blot analysis, not to accumulate Hsp17.6B under heat-shock, contrary to the mother plant that did accumulate Hsp17.6B under heat-shock.
Moreover, we also isolated EMS mutants that abnormally expressed nano-luciferase in seedling grown without D-Valine and without heat-shock. We thus isolated ~half a dozen mutants that were defective at repressing the plant heat-shock response at low, non-inducing temperatures.
By forward genetics, we now seek to identity the loci controlling the initial heat sensing and controlling the heat-shock signaling pathway, leading to plant acquired thermotolerance. We also seek to identity the loci controlling the repression of the plant heat-shock response at low non-inducing temperatures.

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TALK

Transgene silencing in 3D – how a chromosomal knot can inactivate foreign DNA elements

Stefan Grob, Ueli Grossniklaus

Institute of Plant and Microbial Biology, University of Zurich

Cells require elaborate mechanisms to efficiently pack chromosomes in the nucleus, while still allowing access to the genetic information. In addition to packaging, three-dimensional (3D) chromosome architecture is tightly linked to epigenetic processes and transcriptional activity. Despite the rapid progress in the field, well-established cases of functional relationships between transcription and 3D chromatin architecture remain rare. We previously identified a 3D chromatin structure in *Arabidopsis* termed the *KNOT,* in which ten genomic regions *(KEEs)* physically contact each other. *KEEs* are preferred transposon landing sites and exhibit heterochromatic features.
Here we show that *KEEs* are also involved in the silencing of transgenes. Transgenes integrated in the genome can fold towards the *KNOT,* coinciding with their transcriptional silencing. Thus, transgene integration can lead to significant perturbation of 3D chromosome architecture. Interestingly, genomic regions adjacent to the insertion sites are not subjected to silencing, despite their dislocation within the nucleus. This novel silencing mechanism, termed *KNOT*-mediated Transgene Silencing (KMTS) may act independently of previously described silencing mechanisms, as we cannot observe any significant contribution of small RNAs and DNA methylation. KMTS is heritable across generation and shows trans-silencing effects, as the introduction of *KNOT*-silenced transgenes can lead to the silencing of previously active transgenes. In summary, we describe a potent and novel silencing mechanism involving 3D folding of chromosomes.

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TALK

Amplification of reproductive isolation through hybrid necrosis in sympatric *Petunia* species

Mathieu Hanemian, Cris Kuhlemeier

Institute of Plant Sciences, University of Bern

By impeding genetic exchange between populations, reproductive isolating barriers are at the root of the origin of new species. In sympatry, plant species can be almost totally isolated from each other solely through high pollinator preference towards one species. This is due to particular combinations of floral traits such as scent, color and morphology (termed pollination syndrome) that are adapted to attract specific animals. Using 2 distinct *Petunia* species, co-occuring in some region of Brasil, we set out to unravel the genetic basis of floral diversity through quantitative genetic approaches. *Petunia exserta* has a hummingbird pollination syndrome with red, UV-reflecting, nonscented petals and exserted reproductive organs, whereas the hawkmoth-pollinated *P. axillaris* has white, UV-absorbing, volatile-producing petals and nonexserted reproductive organs. Surprisingly, most of the QTLs identified are tightly linked in one big chromosomal region where recombination is inhibited, allowing a well-fit combination of floral traits (Hermann et al., 2013). We recently found out that this region is also triggering a necrosis when it comes from P. axillaris while the genetic background is from P. exserta. Since these 2 species are sympatric and can hybridize naturally, a necrosis locus could have been selected in the same chromosomal region to avoid genetic combination leading to maladapted flowers. With time, this would further promote pollinator isolation between these 2 species. Ongoing experiment to characterize and identify the genes underlying hybrid necrosis will be presented and further hypothesis about the potential role of necrosis in *Petunia* speciation discussed.

> SPSW researcher portfolio:
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TALK

A molecular rheostat adjusts auxin flux to promote root protophloem differentiation

P. Marhava[1], A.E.L. Bassukas[2], M. Zourelidou[2], M. Kolb[2,3], B. Moret[1], A. Fastner[3], W.X. Schulze[4], P. Cattaneo[1], U. Z. Hammes[2,3], C. Schwechheimer[2], **C.S. Hardtke[1]**

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Auxin impinges upon plant development through its distinct concentration-dependent effects on cell proliferation and differentiation-elongation. Auxin concentration differences occur as a consequence of polar auxin transport by polarly localized PIN-FORMED (PIN) proteins. Yet, how intricate patterns of auxin activity are established in detail at cellular resolution, and how they relate to cellular decision making still remains unclear. In the *Arabidopsis* root tip, polar auxin transport creates a local auxin accumulation that is required for stem cell niche maintenance. Proximally, stem cell daughters divide repeatedly before they differentiate. This developmental gradient is accompanied by a gradual decrease in auxin as cells divide, followed by a gradual increase as they differentiate. However, the timing of differentiation is not uniform across cell files. For instance, developing protophloem sieve elements (PPSEs), which are essential for root meristem maintenance, differentiate while neighboring cell files still divide. We found that PPSE differentiation involves local steepening of the post-meristematic auxin gradient. BREVIS RADIX (BRX) and the AGC family PROTEIN KINASE ASSOCIATED WITH BRX (PAX) are plasma membrane-associated, polar proteins that co-localize with PINs at the rootward end of developing PPSEs. Both, brx and pax loss-of-function mutants display impaired PPSE differentiation. Similar to other AGC kinases, PAX activates PIN-mediated auxin transport, but BRX strongly dampens this stimulation of auxin efflux. While BRX plasma membrane localization depends on PAX, auxin negatively regulates BRX plasma membrane association and promotes PAX activity. Our data support a model where BRX and PAX are antagonistic elements of a molecular rheostat that modulates auxin flux through developing PPSEs, thereby timing their differentiation. differentiation.

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TALK

Mechanistic insights into the activation and regulation of plant membrane receptor kinases

Michael Hothorn

Department of Botany and Plant Biology, University of Geneva

Plants have evolved unique membrane receptor kinases which control different aspects of growth and development and which form the first layer of the plant immune system. We have previously described a novel receptor activation mechanism for plant receptor kinases with leucine-rich repeat ectodomains, which relies on the interaction with a shape-complementary co-receptor kinase of the SERK family. How one SERK protein can mediate activation of different receptor kinases is poorly understood at the mechanistic level. I will present structural, quantitative biochemical and genetic engineering experiments that illustrate that two interaction surfaces in the SERK LRR domain allow for interaction with different receptors, and with very different ligands. Protein chimera between different receptor kinases reveal that the SERK activation mechanism is fully conserved among small molecule and peptide hormone pathways and that the kinase domain of the receptor encodes for the cytoplasmic signaling specificity. Genetic and structural analysis of a SERK gain-of-function allele reveals that the co-receptors are subject to negative regulation by a family of small receptor kinases. Together, our findings suggest that plant membrane signaling is highly organized already at the level of the cell surface, with positive and negative regulators competing for access to the co-receptor thereby generating sharp signal transitions.

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TALK

Cell-specific functional characterization of *Arabidopsis* ARGONAUTE 3

Pauline E. Jullien

Institute of Plant Sciences, University of Bern

During sexual reproduction, the fusion of highly differentiated cells, the gametes, has to give rise to a totipotent embryo. Consequently, fertilization entails a complex coordination of gene expression. The regulation of gene expression by DNA methylation has been shown to be crucial during gametogenesis and embryogenesis. However, little is known about how DNA methylation is maintained or modified during reproduction. During the past few years, it has been proposed that small RNA molecules might move from surrounding tissues to the reproductive tissue to maintain proper DNA methylation and transposon silencing in the embryonic lineage of *Arabidopsis.* Small RNAs are known to move systemically via the phloem. Interestingly, Argonaute3 (AGO3) is expressed specifically at phloem termination of flowers, stamens, ovules and seeds. Down-regulation of AGO3 affects gene expression in siliques and its expression is strongly induced upon proteasome inhibition. We demonstrated that AGO3 encodes a functional AGO able to bind sRNAs of 24nt in length with a 5' nucleotide bias for adenosine. Surprisingly 24nt sRNA starting with an adenosine are known to be loaded in AGO4. We demonstrated that AGO3 fractionates with Ribosomic monosomes and polysomes. Our results suggest that AGO3 acts to regulate gene expression by a novel RNA silencing pathway involving 24nt sRNA-directed PTGS.

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TALK

Identification and characterization of root cap cuticles in *Arabidopsis*

Alice Berhin[1], Damien De Bellis2, Rochus Franke[3], Moritz Nowack[4], Bruno M. Humbel[2] and **Christiane Nawrath[1]**

[1] University of Lausanne, Department of Plant Molecular Biology, Lausanne

[2] University of Lausanne, Electron Microscopy Facility, Lausanne

[3] Institute of Cellular and Molecular Botany, University of Bonn, Germany

[4] Center for Plant Systems Biology, VIB-University of Gent, Belgium

A cuticle is formed as specialized outer cell wall layer of epidermal cells of aerial plant organs. It plays crucial roles in organ development and protects against abiotic and biotic stresses. Genes encoding key steps of the biosynthetic pathway of the cuticular polyester cutin have been characterized in *Arabidopsis.* Intriguingly, several genes that are involved in cutin formation are not only expressed in epidermal cells of the shoot, but also at the root cap of the primary root or at the emerging lateral root, e.g. *DCR, ABCG11, BDG.* Transmission electron microscopy revealed that there is an electron-dense layer on the surface of the outer cell wall of root cap cells (columella and lateral root cap) of the primary root and emerging lateral root. Evidence will be presented that these structures contain aliphatic polyesters and were therefore named **r**oot **c**ap **c**uticles (RCCs). The ultrastructure and properties of the RCCs have been characterized in transgenic plants expressing a plant cutinase at the root cap as well as in mutants affected in the expression of genes involved cutin synthesis. Characterization of the polyester composition of 2 day-old roots revealed that the RCC of the primary root contains a cutin rich in C18:2 dicarboxylic acid as well as several mid-chain hydroxylated fatty acids. The incorporation of specific unsaturated cutin monomers in the RCC of the primary root depends on GPAT2, a member of the glycerol-3-phosphate acyltransferase family for which no function had been assigned up to now. The developmental origins as well as the biological functions of RCCs will be discussed.

> SPSW researcher portfolio:
https://swissplantscienceweb.ch/nc/research/home/portfolio/nawrath

TALK

GLRs control calcium fluxes in wounded tissues

Chi Tam Nguyen, Andrzej Kurenda, Stéphanie Stolz, Aurore Chételat, Edward E. Farmer

Department of Plant Molecular Biology, University of Lausanne

In *Arabidopsis,* clade 3 Glutamate Receptor-Like Proteins (GLRs) play important roles in propagating long-distance electrical signals generated in wounded leaves. GLR3.1, GLR3.3 and GLR3.6 appear to be essential for the propagation of leaf-to-leaf wound signaling. We identifed GLR expression domains within the leaf. The results show that *GLR3.1* is expressed mainly in xylem contact cells whereas *GLR3.3* is expressed in phloem and *GLR3.6* is expressed in xylem contact cells. Recent results from the lab point to possible roles of calcium signalling in the wound response. Moreover, it has been shown that several GLRs are calcium-permeable channels. We therefore adressed the question: Do GLRs affect the Ca^{2+} signature in tissues distal to wounds? To address this, we employed the calcium biosensor GCaMP3 as a tool to monitor the Ca^{2+} changes in different *glr* mutants. Calcium imaging coupled with membrane potential recording shows that Ca^{2+} changes in the cytosol are affected in the *glr* mutants. Interestingly, distal cytosolic Ca^{2+} concentration changes are abolished in different *glr* double mutant backgrounds accordingly with the suppression of membrane potential changes in leaves distal to the wound.

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TALK

Synthetic plasmids to make recipient bacteria nodulate many legume hosts

Jovelyn Unay, Romain Fossou, **Xavier Perret**

Department of Botany and Plant Biology, University of Geneva

To reduce atmospheric nitrogen for the benefit of legume hosts, rhizobia must first colonize root nodules and form persistent intracellular colonies of bacteroids. Sets of molecular cues exchanged by rhizobia and plants coordinate formation of mature nodules, infection of root tissues by rhizobia and differentiation of intracellular rhizobia into proficient bacteroids. At the onset of the symbiosis, plants exude cocktails of flavonoids to which rhizobia respond by secreting mixtures of nodulation factors (NFs) that trigger nodule ontogenesis. Additional rhizobial signals, such as surface polysaccharides and effector proteins translocated by type three or type four secretion systems (T3SS/T4SS), modulate host immunity and define symbiotic specificity. Unlike many rhizobia, *Sinorhizobium* (Ensifer) *fredii* strain NGR234 has the remarkable ability to trigger nodule formation on roots of more than 120 legume genera and fix nitrogen in associations with more than 150 legumes. Yet, which of the >80 different NFs, five known T3SS-dependent effectors (NopJ, NopL, NopM, NopP and NopT), and/or rhamnose-rich lipopolysaccharides (rhamnan) made by NGR234 contribute most to symbiotic promiscuity was not known. To address this question, we used a synthetic biology approach to construct broad host-range plasmids carrying different sets of NGR234 symbiotic genes. Synthetic plasmids were then mobilized into bacteria incapable of nodulating hosts of NGR234, and capacity of these transconjugants to induce mature-like or pseudo-nodules on legume roots was examined. Our results towards a minimal synthetic symbiotic replicon capable of turning soil bacteria into nitrogen-fixing plant symbionts will be presented.

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TALK

Selection by the host for efficient bacterial nitrogen fixation during root nodule symbiosis of *Medicago truncatula*

Israel Beyene, Laurent Falquet, Daniel Wegmann, **Didier Reinhardt**

Department of Biology, University of Fribourg

Biological nitrogen fixation accounts for nearly 50% of the fixed nitrogen that is introduced in the global nitrogen cycles. A large contribution comes from root nodule symbiosis (RNS) of the Fabaceae with bacteria known as rhizobia. Since RNS is facultative for both partners, it is inherently unstable, and in many cases, the mutualistic bacteria turn into parasitic cheaters that enjoy carbon supply from the plant without delivering fixed nitrogen. Natural populations of rhizobia that are compatible with a given host plant can exhibit a wide range of N-fixation potential, including cheaters that are completely unable to fix nitrogen. Theoretically, plants can avoid to become exploited by either selecting good partners (pre-infection meachanisms) or by sanctioning of bad mutualists (post-infection mechanisms), but potential mechanisms remain unclear. A special situation arises in nodulation, due to the fact that one or a few bacterial founder cells establish a final rhizobial population in the range of 10^6–10^9 cells, thus inevitably giving rise to many spontaneous mutants in genes required for N-fixation. Since such non-fixing clones have no metabolic burden from the energy-intensive N-fixation process, they have more resources for growth and proliferation and therefore could potentially outcompete the N-fixing population. We have used a publicly available dataset to test the hypothesis that plants can selectively promote nodule colonization by good symbionts. Using the complete transcriptome of nodules of *Medicago truncatula* and its symbiont *Sinorhizobium meliloti* we have assessed the level of polymorphisms over the entire bacterial genome, encompassing the chromosome, symbiotic plasmid A (pSymA) and pSymB. We find that a large gene cluster on pSymA shows significantly reduced levels of polymorphisms. This region encompasses the majority of nitrogen fixation (nif- and fix-genes), indicating that they may be under strong purifying selection during nodulation.

> SPSW researcher portfolio: https://swissplantscienceweb.ch/nc/research/home/portfolio/reinhardt

TALK

Low number of fixed somatic mutations in a long-lived oak tree

Philippe Reymond

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Because plants do not possess a defined germline, deleterious somatic mutations can be passed to gametes, and a large number of cell divisions separating zygote from gamete formation may lead to many mutations in long-lived plants. We sequenced the genome of two terminal branches of a 234-year-old oak tree and found several fixed somatic single-nucleotide variants (SNVs) whose sequential appearance in the tree could be traced along nested sectors of younger branches. Surprisingly, based on known fixed mutation rates in annual plants, the number of fixed mutations identified in oak is significantly lower. Our data suggest that stem cells of shoot meristems in trees are robustly protected from the accumulation of mutations.

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TALK

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

Alexandra Menna, Gloria Sancho-Andrés, **Clara Sánchez-Rodríguez**

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Plant adaptation to stress relies on their ability to quickly perceive and respond to environmental changes. This is possible by precisely controlled remodeling of the primary cell wall. Cellulose, the main component of plant cell walls, is synthesized at the plasma membrane as glucan chains extruded into the apoplast, where they interact with other polyssacharides generating a paracrystalline microfibrillar structure. This structure is important for tensile strength and cellular expansion, and probably for response to inaving microbes. The cellulose paracrystalline structure is partially regulated by apoplastic proteins, such as the chitinase-like protein CTL1/POM1. Mutations in *CTL1* result in cellulose-deficient plants characterized by a dwarfed phenotype in all developmental stages and altered response to various stresses. Sensing and reacting to cellulose perturbations should have a key role in balancing optimal development with stress-induced responses. To identify proteins involved in this equilibrium, we screened for ***s**uppressors of **c**tl1-2 in **a**dult stage (sca).* We isolated a mutant in a gene encoding for a Golgi-localized glycosyltransferase *(SCA18)* that almost completely reverts *ctl1-2* phenotypes back to wild-type (WT)-like. Mutations in *SCA18* attenuated growth inhibition and ectopic lignification in *ctl1-2* plants, but did not affect WT, resembling the phenotype of *THESEUS1* mutants. 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.

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TALK

Transposable element insertions facilitate adaptation of a fungal wheat pathogen

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Genomic plasticity facilitates adaptation to changing environments. Plant colonization by fungal pathogens involves surmounting of stress conditions, such as UV exposure, fungicide treatment and host immune responses. In many pathogens genes coding for virulence factors and stress-related genes are localized in highly polymorphic regions of the genome, rich in transposable elements. However, the contribution to adaptation of these regions and the role of the transposable elements remains largely unexplored. We showed that transposable elements largely contribute to gene expression regulation of genes essential for adaptation to stress conditions in the wheat pathogen *Zymoseptoria tritici.* Remarkably, insertions of transposable elements downregulated the expression of genes involved in melanin biosynthesis in different isolates, leading to high polymorphism in this trait. Furthermore, a cluster of genes involved in virulence, that was localized in a highly plastic region of the genome harboring presence/absence polymorphism of TEs, was silenced *in vitro* and specifically expressed during host colonization. Thus, TEs largely contribute to adaptation to the environment by finetuning gene expression regulation. Based on these findings we can now elucidate how TEs contribute to adaptation and virulence factor regulation.

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https://swissplantscienceweb.ch/nc/research/home/portfolio/mcdonald

TALK

Plants: individuality and diversity

Bernhard Schmid

Department of Evolutionary Biology and Environmental Studies, University of Zurich

There are several reasons why it is interesting to study plants. They are fundamentally different from higher animals and humans. They are also our most important food resource, making plant research responsible for far more human lives than biomedical research. The two aspects of plants that I found most fascinating during my personal career were the organismic integration of different levels of “individuals” into larger structures that still showed coordinated phenotypic expression (individuality) and the causes and consequences of variation between these entities (diversity). I will review these two topics from an autobiographic perspective, presenting some trends that I have observed and followed over the past four decades. My journey started from plant sociology and led me to systematics, population and evolutionary ecology and finally back to community ecology and evolution. Plant biologists can now benefit from the combination of ecological and molecular approaches to get at a deeper understanding of fundamental aspects of plant life and to embrace variation not merely as noise but rather as a provider of essential ecosystem services, including plant production.

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https://swissplantscienceweb.ch/nc/research/home/portfolio/schmid

TALK

Cost and benefit of UVR8 UV-B receptor in naturally fluctuating environments

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Plants protect themselves against deleterious ultraviolet-B (UV-B) radiation. UVR8 is the single gene of *Arabidosis thaliana* encoding the UV-B-specific photoreceptor for which previous work has attributed a major role in UV-B acclimation and stress tolerance. However, no obvious deleterious phenotype of its mutants has been detected in natural environments *(in natura).* We thus performed common garden experiments to address this gap in our understanding on how photoreceptors contribute to UV-B tolerance in the field and its interrelationship with visible light photoreceptors. Consistent with previous studies, we did not find significant differences in fitness between wildtypes and two independent *uvr8* loss-of-function mutants in diverse natural conditions such as different altitudes, seasons and developmental stages for 3 years. In contrast, in the laboratory with below-ambient UV-B light, *uvr8* mutants produced significantly higher number of seeds compared to wildtypes. This indicates that there is fitness cost of the UV responses mediated by UVR8, which may be balanced out by the benefit *in natura.* Importantly, the double mutant of *UVR8* and *CRYPTOCHROME 1 (CRY1)* sbowed severe reduction in fitness when grown in the field. UV-exclusion experiments using filters in the field verified that UV-B is responsible for the strong detrimental effect of sunlight on *uvr8 cry1,* which is associated with drastically reduced levels of the *CHALCONE SYNTHASE (CHS)* gene expression, CHS protein and anthocyanin accumulation. Our *in natura* experiments demonstrate the importance of the UVR8 and CRY1 photoreceptors to cope with UV-B intrinsic to sunlight in the field.

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https://swissplantscienceweb.ch/nc/research/home/portfolio/shimizu

TALK

Exploiting the chemical ecology of tritrophic interactions for crop protection

Ted Turlings

Laboratory of Fundamental and Applied Research in Chemical Ecology, Institute of Biology, University of Neuchâtel, Switzerland

Plants have the keen ability to respond to attacks by herbivores or pathogens attack with the production of various defense chemicals. A typical response to herbivory is the production and release of volatile organic compounds. These volatiles may serve a number of functions, such as direct toxic and repellent effects on herbivores, indirect defense through the attraction of natural enemies of the herbivore, and the volatiles can serve as signals that warn undamaged plant parts of incoming attack. It is widely recognized that plant-produced volatiles have great potential for application in agriculture. The use of companion or sentinel plants that are highly responsive or that release specific volatiles show great promise and some successes have already been booked, in particular in the context of the so-called "push-pull" strategy. Another intriguing prospect is the development of sensors that can capture the information contained in the volatile signals. For now, this may seem farfetched, but sensor technology is advancing rapidly. I will discuss the various ways in which herbivore- and pathogen-induced plant volatiles may be exploited for crop protection, with special emphasis on efforts to fully understand the specificity of inducible volatile blends.

> SPSW researcher portfolio:
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TALK

UV-B photoreceptor signalling and responses

Adriana Arongaus, Song Chen, **Roman Ulm**

Department of Botany and Plant Biology, University of Geneva, Switzerland

Plants are able to perceive ultraviolet-B radiation (UV-B) using the UV-B photoreceptor UV RESISTANCE LOCUS 8 (UVR8) which activates a molecular signalling pathway leading to UV-B acclimation. The evolutionarily conserved UVR8 UV-B photoreceptor exists as a homodimer that monomerises upon UV-B absorption via specific intrinsic tryptophans. The UVR8 monomer interacts with CONSTITUTIVELY PHOTOMORPHOGENIC 1 (COP1), an E3 ubiquitin ligase, initiating a molecular signalling pathway that leads to gene expression changes. This signalling output leads to UVR8-dependent responses including UV-B-induced photomorphogenesis and the accumulation of UV-B-absorbing metabolites that function as "sunscreens". I will present our latest understanding of how UVR8 regulates UV-B acclimation and developmental decisions.

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https://swissplantscienceweb.ch/nc/research/home/portfolio/ulm

TALK

News from the volatile warfare between potato-associated *Pseudomonas* and the late blight causing agent *Phytophthora infestans*

Mout De Vrieze[1], Aurélie Gfeller[1,2], Delphine Chinchilla[3], Aurélien Bailly[1], Floriane L'Haridon[3], **Laure Weisskopf[1,2,3]**

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During the last decade, the importance of bacterial volatiles in cross-kingdom interactions has become evident. In addition to promoting plant growth and root development, bacterial volatiles have been repeatedly shown to inhibit the growth of phytopathogenic fungi, although the molecules responsible for this effect are still largely unknown, with the notable exception of hydrogen cyanide. Our recent work has shown that oomycete pathogens such as *Phytophthora infestans,* causing late blight in potato, are particularly sensitive to the volatiles of potato-associated *Pseudomonas* strains, when compared to other potato disease-causing agents such as *Rhizoctonia solani* or *Helminthosporium solani.* In a screen aimed at identifying the chemical composition of the volatile blends from those efficient anti-oomycete *Pseudomonas,* Sulphur-based compounds were identified as potent inhibitors of all life stages of the pathogen, including mycelial growth, sporangia production and germination, as well as zoospore motility. Some of these Sulphur-containing volatiles were able to prevent disease establishment on infected plant material. One important and so-far unresolved question concerns the ability of bacteria to emit those bioactive volatiles when living in natural conditions, e.g. on leaf surfaces. We are currently investigating this question using sterile potato plantlets inoculated with bacterial strains of known volatile blend emission. First results indicate that typical bacterial smells such as the long-chained alkene 1-Undecene previously shown to inhibit growth and sporulation of *P. infestans* can be detected on inoculated plants. This highlights the so-far underexplored potential of bacterial volatile compounds for sustainable crop protection.

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https://swissplantscienceweb.ch/nc/research/home/portfolio/weisskopf

TALK

It's all about repeats – lessons from the very large genomes of wheat and barley

Thomas Wicker, Manuel Poretti, Coraline Praz, Anupriya Kaur Thind, Simon Krattinger, Simone Oberhänsli

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In large genomes, transposable elements (TEs) make the majority of genomic DNA, but it is still unclear how they contribute to evolution. Recent improvements in sequencing and assembly algorithms made it possible that the very large genomes of important crops such wheat and barely can be assembled at a chromosome scale. In these large genomes, genes make only about 2% of the total DNA. We analyze the 98% outside of "gene space" which is comprised mostly of repetitive DNA. In wheat and barley, the repetitive fraction comprises at least 350 different TE families. Over 50% of the genome is made of only 15 high-copy TE families, while all other families are present in relatively low copy numbers. Interestingly, the wheat and barley genomes are highly compartmentalized with different types of TEs occupying different chromosomal "niches". Furthermore, gene space represents its own distinct genomic compartment that is enriched in small non-autonomous DNA transposons which seem to specifically target genes. In the hexaploid wheat genome, different TE compositions of the three sub-genomes document the individual evolution of the diploid genome donors. Our data show that TEs are major determinants of chromosome structure and key contributors to the evolution of gene space.

> SPSW researcher portfolio:
https://swissplantscienceweb.ch/nc/research/home/portfolio/wicker

TALK

Promiscuity in the Calvin-Benson cycle

Martina Zanella, Michaela Fischer-Stettler,
Samuel C. Zeeman

Institute of Molecular Plant Biology, ETH Zurich

Metabolism is often presented as a precise set of reactions. However, an increasing number of observations show that metabolic processes as less stringent than previously thought. Enzymatic side reactions can lead to the accumulation of exotic compounds, generally absent in the classical representation of the plant metabolome. We observed that, in *Arabidopsis thaliana,* Fructose-1,6-bisphosphatase (cFBPaseI) and Sedoheptulose-1,7-bisphosphatase (SBPase) – enzymes from the regenerative phase of the Calvin-Benson cycle - demonstrate substrate promiscuity. This became apparent through studies of the knock-out mutants fbp and sbp, which display impaired growth, yet are viable. Our results show that each enzyme is able to do the reaction of the other. However, at the same time their catalytic promiscuity when acting on their non-canonical substrate leads to the accumulation of the previously unreported metabolites, which we believe to be fructose-1-phosphate (Fru1P) and sedoheptulose-1-phosphate (Sed1P).

These metabolites accumulate in the *fbp* and *sbp* mutants, respectively, but close examination of the wild type suggest that Fru1P and Sed1P are normally present at low levels. Furtherore, $^{13}CO_2$ labelling suggests that these compounds are actively metabolised, both in the wild type and in the mutants. We suggest that one or more as-yet unidentified phosphatases acts to convert Fru1P to fructose and Sed1P to sedoheptulose, salvaging the metabolites. We suspect there is a deeper complexity in many core metabolic processes that remains to be uncovered.

> SPSW researcher portfolio:
https://swissplantscienceweb.ch/nc/research/home/portfolio/zeeman

TALK

FERONIA and the regulation of receptor kinase-mediated signaling

Cyril Zipfel[1,2]

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Plants genomes encode hundreds of cell surface-localized receptor kinases (RKs) that control almost all aspects of plant life, ranging from reproduction, growth to responses to the external environment. Using RKs that function as immune receptors by perceiving microbial elicitors, we are studying the molecular basis of plant immunity, but also more generally how plant RKs work at the mechanistic level. Using the leucine-rich repeat RKs FLS2 and EFR (which perceive bacterial flagellin and EF-Tu, respectively) as model systems, we are investigating how plant RKs function as part of multimeric protein complexes at the plasma membrane – often in complex with other RKs, which act as regulatory proteins. Our recent work uncovered the importance of these regulatory RKs and RK-associated proteins in controlling the activity, but also the assembly of these heteromeric receptor complexes. These observations also raise the inherent question of how these dynamic receptor complexes get formed and organized at the plasma membrane. Notably, we have recently uncovered an important role of the malectin-like receptor kinase FERONIA (FER) as a regulatory RKs controlling immunity. Building on this recent published work, I will present our recent unpublished work that sheds light on the molecular basis of FER function, and on the more general role that FER plays in the regulation of multiple signaling pathways beyond immunity and reproduction.

POSTER

Transcriptomic and metabolic analyses of 35S:S523DNR tobacco plants

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Overexpressing a deregulated form of nitrate reductase (NR) under the control of a constitutive promoter in tobacco plants results in a redistribution of the nitrogen pool. A strong reduction of the free leaf nitrate and a concomitant increase of nitrogen accumulation into amino acids can be observed in these plants. Despite the significant changes observed in the distribution of nitrogen, 35S:S523DNR tobacco plants exhibited similar phenotypes to the control plants suggesting some adaptation of the whole plant cellular processes. To characterize this adaptation, transcriptomic and metabolomic analyses were performed on young and mature plants grown under different fertilization regimes.

POSTER

Exploring the action mechanisms of anti-microbial volatile organic compounds emitted by potato-associated *Pseudomonas*

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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 potatoassociated *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,* some VOCs show significant antimicrobial activities: the sulfur-containing volatiles (sVOCs), including dimethyl disulfide, can inhibit mycelium growth and spore production to various extents. To understand how sVOCs inhibit *Phytophthora* development, we have performed a quantitative proteomic analysis on hyphae treated with five individual sVOCs diverging in their anti-oomycete activity: a differential regulation of proteins is observed upon each VOC treatment, suggesting distinct modes of action. A more comprehensive analysis of those data is ongoing to unravel the molecular mechanisms controlling *Phytophthora* growth.
In addition to their activity on pathogens, VOCs might promote plant resistance as potato leaf discs treated with sVOCs restrained late blight disease. To understand their effects on plant, we are studying defense responses, such as transcript regulation of defense genes and the production of reactive oxygen species in response to sVOCs.

POSTER

Chlorophyll breakdown: complexity of chlorophyll catabolite modification

Mareike Hauenstein, **Stefan Hörtensteiner**

Department of Plant and Microbial Biology, University of Zürich

POSTER

Role of phloem-specific plasma membrane proton pumps in wound signaling

Archana Kumari, Aurore Chételat and Edward E. Farmer

Department of Plant Molecular Biology, University of Lausanne

Wounded leaves generate electrical signals that initiate the synthesis of jasmonate, a potent regulator of wound-induced defense responses (Mousavi et al., 2013). Plasma membrane proton pumps (AHAs) are electrogenic pumps, that generate electrical potential differences across the plasma membrane. Since electrical signals consist of transient plasma membrane depolarization, it has been hypothesized that proton pumps play important role in electrical signal transmission. Indirect electrophysiological and pharmacological evidence suggests transient inhibition of proton pumps during electrical signaling. However, genetic evidence for this phenomenon is still lacking.
Molecular studies have shown that the C-terminal, regulatory domain of proton pumps is a target for regulation in response to diverse environmental conditions that activate/inhibit proton pumping (Falhof et al., 2016).
In this study, a phloem specific proton pump (AHA3) was modulated by deletion of auto-inhibitory C-terminal domain and used as tool to investigate the electrical signal and jasmonate pathway activity in specific cell types. Our data indicates that cell-type-specific modulation of AHA3 can play an important role in wound signaling and defense responses.

POSTER

Utilization of di- and tripeptide in *Arabidopsis thaliana*

Doris Rentsch

Institute of Plant Sciences, University of Bern

POSTER

Suppressors of LRX1 potentially function in the RALF signalling pathway

Shibu Gupta and **Christoph Ringli**

Institute of Plant and Microbial Biology, University of Zurich

POSTER

Sugar transport to guard cells is essential for stomatal opening and plant growth

Arianna Nigro[1], Sabrina Flütsch[1], Franco Conci[1], Jiří Fajkus[2], Matthias Thalmann[1], Martin Trtílek[2], Klára Panzarová[2] and **Diana Santelia[1]**

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Microscopic adjustable pores on the leaf surface of plants, called stomata, control the fine-tuned trade-off between photosynthetic carbon dioxide (CO_2) uptake and water loss. Although sugars have been implicated in the regulation of stomatal movements, the cellular mechanisms of sugar accumulation in the surrounding guard cells have remained unexplored. Here we use an innovative interdisciplinary approach that integrates high-throughput non-invasive plant phenotyping with molecular physiology to study the function of sugars in the regulation of stomatal dynamics in the model plant *Arabidopsis thaliana*. We show that the synergistic action of the monosaccharide/proton symporters STP1 and STP4 in guard cell plasma membrane is necessary for stomatal opening and CO_2 uptake driving photosynthesis and biomass production. Furthermore, we reveal that the uptake of apoplastic sugars into guard cells is necessary to provide the main substrates for guard cell starch accumulation. Our results demonstrate that at the onset of light, guard cells rely predominantly on mesophyll-derived sucrose imported into guard cells in the form of monosaccharides as source of sugars to open stomata. This study highlights that a tight interplay between mesophyll and guard cell carbohydrate metabolism is essential to sustain stomatal opening and plant growth.and plant growth.

POSTER

Promoting productivity of an orphan crop tef through tackling key constraints

Zerihun Tadele and Tef Team

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POSTER

UniProtKB reference plant proteomes: a guarantee of quality

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The Universal Protein Resource knowledgebase (UniProtKB) provides the scientific community with a comprehensive and richly curated resource of protein sequences and functional information. The knowledgebase is composed of the expert curated UniProtKB/Swiss-Prot section and its automatically annotated complement, UniProtKB/TrEMBL. With the current massive genome sequencing efforts and the resulting explosion of publicly available sequence data, it has become crucial to reorganize and curate this data in order to avoid redundancy, facilitate searches, and to provide high quality reference sequence sets for plant species of interest. To this end UniProtKB has introduced the concept of the "reference proteome" (where a proteome is defined as the entire set of proteins thought to be expressed by an organism). We have selected among plant proteomes (manually and algorithmically) a set of 90 "reference proteomes" (http://www.uniprot.org/proteomes/?query=viridiplantae), including *Arabidopsis thaliana* cv. Columbia, which constitutes a representative cross-section of the plant taxonomic diversity that can be found in UniProtKB. UniProt reference proteomes are curated in active collaboration with other resources like Araport and Gramene, a process which includes comparative analysis of multiple reference proteomes, and are also complemented by information imported from other resources such as EnsemblPlants, in order to ensure the highest quality and coverage of protein sequence data for our user community. As an example, the UniProt *A. thaliana* reference proteome has been revised to take into account the complete genome reannotation proposed in the Araport11 release, and currently contains around 39 200 proteins (UniProt release 2017_12). This complete protein set can be downloaded from the UniProt Web site http://www.uniprot.org/proteomes/UP000006548.

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