SWISSPLANT2016



Symposium of the Plant Science Research Community in Switzerland

swissplantscienceweb.ch - 25th edition

25–27 January 2016 Les Diablerets (VD)



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Swiss Committee for Molecular Biology







SWISSPLANT 2016

Symposium of the Swiss Plant Science Web 25–27 January 2016 Les Diablerets, Switzerland

Venue

Eurotel Victoria, Les Diablerets http://www.eurotel-victoria.ch/diablerets/

Scientific Committee

Prof. Dr. Félix Kessler Prof. Dr. Jean-Marc Neuhaus Prof. Dr. Ted Turlings

Conference Organization

Swiss Plant Science Web Sylvia Martinez, SPSW coordinator sylvia.martinez@unibas.ch

www.spsw.ch swissplantscienceweb.ch





Table of content

- 1 Organization
- 3 Welcome by the president
- 4 Symposium program
- 9 Talks (abstracts in chronological order)
- 41 Posters (abstracts in alphabetical order)
- 50 List of participants
- 52 Impressum/Imprint



Welcome

The Swiss Plant Science Web (SPSW) held its first scientific conference «SwissPlant» in 2011. These yearly conferences are now well established and highly popular in our community, and they have become a showcase of the current advances of plant science research in Switzerland. They bring together research from molecular biology to ecology, and thereby allow a broader view and better understanding of the complexity and diversity of plant life. By choosing an attractive place for our conferences, we hope to foster informal discussions among peers, this year in Les Diablerets, a somewhat remote but very nice holiday resort in the region of Aigle (Canton of Vaud). We will stay in the Eurotel Victoria, known to many of you from previous meetings.

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 continuation of the Swiss Plant Science Web. «SwissPlant 2016» is the ideal place to start discussions on new collaborations!

This year's scientific conference committee is from the University of Neuchâtel. I thank Felix Kessler, Jean-Marc Neuhaus and Ted Turlings for setting up an exciting program. I am also very grateful to Sylvia Martínez, our SPSW coordinator, who took a big effort to organize all practical things and to make your stay smooth and easy.

PS: Please note that in the program of Wednesday morning, there are some surprises in store, so please stay in the conference up to the last talk!

Enjoy the science and leisure in Les Diablerets!

Thomas Boller University of Basel, SPSW president

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

Program Monday, 25 January 2016

17:00	Apéro				
17:30	Opening remarks by Thomas Boller, SPSW chair				
17:35	Opening remarks by the organisers				
	Session I: Cell Biology and Metabolism I				
17:40	Michel Goldschmidt-Clermont, U Geneva: Light acclimation of photosynthesis				
18:00	Katja Baerenfaller, ETH Zurich: Gene expression regulation in Arabidopsis leaves				
18:20	Diana Santelia, U Zurich: Mechanistic insights into the adaptive plasticity of plant starch metabolism				
18:40	Dinner				
	Session II: Cell Biology and Metabolism II				
20:20	Laurent Mène-Saffrané, U Fribourg: Understanding the genetic basis of vitamin E accumulation in plants				
20:40	Emily Demarsy, U Neuchâtel: Towards a 4D model of thylakoid biogenesis				
21:00	Jean-Marc Neuhaus, U Neuchâtel: RMR function in moss: reluctant vacuolar receptors				
21:20	Sebastian Streb, ETH Zurich: Establishing a universal method to predict protein complexes and generate protein interaction networks				



Program Tuesday, 26 January 2016

07:00	Breakfast				
	Session III: Epigenetics				
08:00	Célia Baroux, U Zurich: Uncovering the role of H1 dynamics in cell fate transitions				
08:20	Sylvain Bischof, UCLA: A one precursor one siRNA model for Pol IV-dependent siRNA biogenesis				
08:40	Pierre Goloubinoff, U Lausanne: A screen to identify genes involved in the heat- shock response in mosses				
09:00	Session IV: Ecology I Matthias Erb, U Bern: A below ground herbivore shapes root defensive chemistry in nature				
09:20	Stefan Hörtensteiner, U Zurich: The bialaphos resistance (BAR) protein interferes with amino acid metabolism in transgenic plants				
09:40	Coffee break				
10:10	Session IV: Ecology II Ted Turlings, U Neuchâtel: Exploiting tritrophic interactions in the rhizosphere for crop protection				
10:30	Didier Reinhardt, U Fribourg: The role of lipids in arbuscular mycorrhiza: signals or food for the fungus?				
10:50	Marcel van der Heijden, agroscope: Linking soil biodiversity, mycorrhizal fungal diversity and ecosystem multifunctionality				
11:10	Xavier Perret, U Geneva: Porphyrins as unusual markers for altered nodule homeostasis during symbiotic nitrogen fixation				
11:30	Sergio Rasmann, U Neuchâtel: Ecological and evolutionary drivers of plant defense variation against herbivores				
11:50	Leisure time (lunch on your own, skiing, swimming, hiking)				

17:00	Poster session (with apéro)		
18:30	Dinner		
20:20	Session V: Development Christian Hardtke, U Lausanne: Molecular switches in protophloem sieve element differentiation		
20:40	Clara Sánchez-Rodríguez, ETH Zurich: Plant cells in action: Cell wall remodelling and signalling via endocytosis		
21:00	Vinicius Costa Galvao, U Lausanne: Control of developmental transitions by PIF proteins in reponse to shade in <i>Arabidopsis thaliana</i>		
21:20	Luis Lopez-Molina, U Geneva: An <i>Arabidopsis</i> mature seed cuticle is essential for seed viability, dormancy and hormonal germination control		
21:40	Marie Barberon, U Lausanne: The endodermis as a checkpoint for nutrients		



Program Wednesday, 27 January 2016

07:00	Breakfast				
08:20	Session VI: Evolutionary Genetics Kentaro Shimizu, U Zurich: REDUCED POLLEN NUMBER1 isolated by genome- wide association mapping showed recent selection on pollen number in Arabidopsis thaliana				
08:40	Yamama Naciri, U Geneva: Combining modelling and genetic approaches in conservation: Application to the genus Capurodendron Aubrév. (Sapotaceae) in Madagascar				
09:00	Samuel Wuest, U Zurich: Discrete genetic elements underlie diversity effects in conspecific plant communities				
09:20	Nikolai Ivanov, Philip Morris International: <i>Nicotiana</i> genomic resources and their applications				
09:40	Coffee break				
10:10	Session VII: Plant defense and Signaling Pathways Lorenzo Borghi, U Zurich: Strigolactones, at the crossroad between plant growth and nutrition				
10:30	Simon Krattinger, U Zurich: A core gene set linked to the durable disease resistance gene Lr34				
10:50	Philippe Reymond, U Lausanne: <i>Arabidopsis</i> MYC transcription factors are the target of hormonal SA/JA crosstalk in response to <i>Pieris brassicae</i> eggs				
11:10	Georg Jürg Felix, U Tübingen: New receptors for old ligands				
11:30	Closing remarks				

TALK

1	M Goldschmidt-Clermont
2	Katja Bärenfaller
3	Diana Santelia
4	Laurent Mène-Saffrané
5	Emilie Démarsy
6	Jean-Marc Neuhaus
7	Sebastian Streb
8	Célia Baroux
9	Sylvain Bischof
10	Pierre Goloubinoff
11	Matthias Erb
12	Stefan Hörtensteiner
13	Ted Turlings
14	Didier Reinhardt
15	Marcel van der Heijden
16	Xavier Perret
17	Sergio Rasmann
18	Christian Hardtke
19	Clara Sánchez-Rodríguez
20	Vinicius Costa Galvao
21	Luis Lopez-Molina
22	Marie Barberon
23	Kentaro Shimizu
24	Yamama Naciri
25	Samuel Wuest
26	Nikolai Ivanov
27	Lorenzo Borghi
28	Simon Krattinger
29	Philippe Reymond
30	Georg Felix

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M Goldschmidt-C

Light acclimation of photosynthesis

Paolo Longoni, Geoffrey Fucile, Guillaume Allorent, Alexis Riché, Federica Cariti, Damien Douchi and Michel Goldschmidt-Clermont

Department of Botany and Plant Biology, University of Geneva

The photosynthetic electron transfer chain acclimates to rapid changes in the spectral quality and intensity of light. Differences in the absorption spectra of PSI and PSII can lead to unequal excitation of the two photosystems and an imbalance in the redox poise of the electron transfer chain. At low light intensities this is compensated by a mechanism called state transition which regulates the dynamic allocation of part of the LHCII antenna to PSI or PSII. Phosphorylation of LHCII by the protein kinase Stt7 in Chlamydomonas, or its orthologue STN7 in higher plants, plays a central role in state transitions. The protein kinase STN8, a paralog of STN7, is involved in the phosphorylation of several subunits of PSII as well as other thylakoid proteins, in the architecture of the thylakoid membrane system and in the repair cycle of PSII. Two protein phosphatases, PPH1/TAP38 and PBCP, counteract the activity of STN7 and STN8.

State transitions involve the STN7-dependent assembly of a PSI-LHCII supercomplex containing PSI, LHCI and an LHCII trimer. Two isoforms of the LHCII trimer subunits, Lhcb1 and Lhcb2, can be phosphorylated near their N-terminus. Both isoforms share high sequence similarity, but play distinct roles in light acclimation and the formation of photosystem supercomplexes [1,2]. Our quantitative measurements of the extent of phosphorylation show that in the PSI-LHCII supercomplex, Lhcb2 is completely phosphorylated while Lhcb1 is not detectably phosphorylated. In contrast, both are phosphorylated to different extents in other supercomplexes of the thylakoid membrane. Thus phosphorylation of Lhcb2 plays a central role in state transitions.

References

- [1] Leoni C et al. (2013) Plant J 76, 236–246
- [2] Pietrzykowska M et al. (2014) Plant Cell 26, 3646–3660

> SPSW researcher portfolio

https://swissplantscienceweb.ch/nc/research/home/portfolio/goldschmidt-clermont



Katja Bärenfaller

Gene expression regulation in Arabidopsis leaves



Katja Bärenfaller

Institute of Agricultural Sciences, ETH Zurich

For a proper understanding of the governing principles that drive complex biological processes, it is important to know the individual molecular components inside cells and their interdependencies. For a better understanding of how gene expression is regulated we therefore study the processes from transcriptional regulation to protein degradation and perform integrative analyses of protein and transcript levels in *Arabidopsis* leaves.

Comparing the molecular profiles of leaf growth in normal conditions and under continuous water deficit revealed a good correlation between transcript and protein levels and an adaptation response that is different from the drought stress response. In contrast, we found that a large number of transcripts show strong stage and condition dependent diurnal fluctuations that are not matched by protein level fluctuations. To identify diurnal chromatin modifications that accompany diurnal changes in transcript expression we sequenced chromatin immunoprecipitations (ChIPs) with antibodies against the histone H3 modifications K4me3, K9me2, K9ac, S10p, K27ac and S28p in fully expanded leaves of Arabidopsis thaliang in two different experimental conditions. We found a differential K9ac, K27ac and S28p chromatin modification pattern between the end of the day and the end of the night, which correlates with changes in diurnal transcript levels. Genes carrying this modification pattern contain over-represented promoter elements and the encoded proteins are significantly enriched for transcription factors and overrepresented in starch catabolic process and circadian rhythm. The data suggest a mechanism for diurnal transcript level regulation in which transcription factors guide chromatin modification complexes and in which the reduced binding of repressive transcription factors allows the placement of activating K9ac, K27ac and S28p chromatin modifications. The presence of the activating chromatin modification pattern only at times when the expression of the corresponding genes is required can explain why some genes are differentially inducible during the diurnal cycle.

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

Mechanistic insights into the adaptive plasticity of plant starch metabolism

Diana Santelia

Department of Plant and Microbial Biology, University of Zurich

Starch is the most abundant form in which plants store carbohydrate. Starch is intimately integrated with plant biology. Rearrangements of starch metabolism occur in response to changes in day length, light intensity, water deficit or extreme temperatures in a cell typespecific manner, such that carbon supply is ultimately optimized to sustain continued growth under changing environmental conditions. This adaptive plasticity of starch metabolism is a key plant survival strategy.

We made a new fundamental discovery on how the ability of the plant to adjust starch turnover to the need of the individual cells depends upon sub-functionalization amongst the chloroplastic members of the *Arabidopsis* β -amylase (BAM) gene family. BAM is the main starch-degrading enzyme. We showed that BAM1 and BAM3 are active under different conditions and in a cell-type specific manner. We identified important upstream components affecting BAM activity, demonstrating that an intricate network of differential transcriptional and post-translational regulation underpins BAM isoform sub-functionalization. Given that BAM are highly conserved in plants, our work will encourage further investigations on the influence of starch adaptive plasticity on plant survival in the environment in plants with commercial value.



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

Understanding the genetic basis of vitamin E accumulation in plants

Laurent Mène-Saffrané

Laurent Mène-Saffrané, Sébastien Pellaud

Department of Biology, University of Fribourg

Vitamin E encompasses a group of prenyl lipids that belong to the chemical class of tocochromanols. These organic compounds are synthesised exclusively by photosynthetic organisms such as plants, algae and some cyanobacteria. The vitamin E biosynthetic pathway, originally deduced from classic biochemical experiments using radiolabelled precursors, has been recently completed with the identification of vitamin E biosynthetic genes. Vitamin E naturally accumulates in plant tissues such as leaves, roots, petals, fruits and seeds. In addition, its accumulation is stimulated in response to many stresses. In both cases, the genetic factors such as transcription factors and signaling molecules that regulate its accumulation are not yet identified.

Inspired by techniques used in high-throuput drug screenings and animal behavior screenings, we designed a fast screening pipeline for quantitative metabolites such as vitamin E. This new procedure identified five tocochromanol complementation groups that shed light on mechanisms regulating vitamin E accumulation in *Arabidopsis*. The communication will first present the innovations implemented in the screening procedure that drastically accelerate mutant identification. It will then focus on the mapping and characterization of a new *Arabidopsis* tocochromanol mutant.



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Emilie Demarsy

Rosa Pipitone1, Gaëtan Glauser2, Simona Eicke3, Sam Zeeman3, Ioannis Xenarios4, Felix Kessler1, **Emilie Demarsy**1

1 Laboratoire de Physiologie Végétale, Université de Neuchâtel 2 Neuchâtel Platform for Analytical Chemistry, Faculty of Sciences, Université de Neuchâtel

3 Department of Biology, Institute of Agricultural Sciences, ETH Zurich 4 Vital-IT Systems Biology Division; SIB Swiss Institute of Bioinformatics; University of Lausanne

The photochemical reaction of photosynthesis takes place in the chloroplast thylakoid membranes. This membrane bilayer is organized in stacks (grana) interconnected by unstacked stroma lamellae and is constituted largely of galactolipids: mono- and digalactosyl diacyl glycerol (MGDG and DGDG), sulfoquinosyl diacylglycerol (SQDG), and contain neutral lipids such as prenylquinones (plasto- and phylloquinone, tocopherols) and carotenoids (beta-carotene, lutein and xanthophylls), and chlorophylls in association with large protein complexes (Photosystem I and II (PSI and PSII), and cytb6/f).

In plants, chloroplasts develop majorly from the undifferentiated form proplastids present in meristematic tissues or from the etioplasts specific of dark grown seedlings. Intricate genetic and metabolic processes are required to build up the photosynthetic machinery and the thylakoid network during chloroplast biogenesis but this process is not fully described. To fill this gap we are investigating the chloroplast biogenesis process in *Arabidopsis* seedlings. Quantitative data are generated using 3D electron microscopy to reveal the ultrastructural changes and lipidomics to determine the dynamics of lipid composition.

Our goal is to construct a set of 4D-models that link lipid composition to thylakoid architecture and therefore gain a comprehensive understanding of thylakoid biogenesis at the systems level.



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RMR function in moss: reluctant vacuolar receptors

Jean-Marc Neuhaus, Noémie Fahr, Carla Coppola, Sophie Marc-Martin and Didier Schaefer

Institut de Biologie, University of Neuchatel

In angiosperms vacuolar proteins are sorted by two different to sometimes distinct vacuoles. One system relies on Vacuolar Sorting Receptors (VSR) and works in a similar way as the sorting systems for the yeast vacuole or the animal lysosomes. The other system relies apparently on a different type of receptors, the Receptor-Membrane-RingH2 proteins (RMR). The RMRs are related to animal PA-TM-RingH2 proteins, which also reside in the endomembrane system but are not sorting receptors. Several of them are E3 ubiquitin ligases, tagging transmembrane proteins for lysosomal degradation. They could have been coopted by plants for vacuolar sorting by a ubiquitindependent mechanism.

In order to study their function we knocked out all five RMR genes in Physcomitrella patens. The moss secretory pathway behaved differently than expected:

A fluorescent protein reporter carrying various known C-terminal sorting determinants (Ct-VSD) expressed in moss was not always targeted to the vacuole. This could be due to a different sequence specificity of the moss RMRs. When expressed in the 5KO mutant line, the reporters showed the same intracellular distribution as in wild type. Only one reporter (and a second one partially) was affected by the absence of the RMR receptors.

Some localization patterns also differed between young and older cells and gametophores, suggesting a flexible use of the vacuolar system in the different cell types.



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

Jean-Marc Neuhaus

Alexander Graf1, Sebastian Streb2

1 Max Planck Institute of Molecular Plant Physiology Golm, Germany 2 Institute of Agricultural Sciences, ETHZ, Switzerland

The era of whole genome sequencing has yielded unparalleled amounts of detailed genetic information. However, what genetic information cannot tell us is how these proteins interact and work together in the cell. Many biological processes e.g. DNA replication, protein synthesis/degradation, primary and secondary metabolism require stable multimeric protein complexes. Unfortunately, our knowledge about their assembly is incomplete and a pastiche collection from several different species, often based on predictions. Until today, all attempts to define protein interactome maps required high investment of human resources and money.

Here, we describe a cost and time effective workflow to separate native protein complexes and predict their composition. We use four different separation techniques coupled with a proteomics approach to elucidate co-behavior of proteins. As all methods have distinct separation properties, the combination of their predictive power results in a multidimensional separation of complexes. Our setup has advantages over currently used approaches with improved resolution and strong reduced false positive predictions rates. We are able to define potential association in complexes for more than 4000 proteins in *Arabidopsis*. Surprisingly, most proteins assemble in multimeric long term complexes and the *in vivo* status of a protein in a monomeric form is rather exceptional. We build a database for soluble protein complexes in *Arabidopsis* enabling user friendly access about protein interaction and molecular weight of the complexes.

Our methodology can be applied to any biological sample for which the genome is known. With affordable cost, the composition and changes (e.g. under different conditions) of protein complexes can be studied now.

TALK



Sebastian Streb

Uncovering the role of H1 dynamics in cell fate transitions

Wenjing She, Kinga Rutowicz, Jasmin Schubert, Célia Baroux

Department of Plant and Microbial Biology, University of Zurich, Zurich-Basel Plant Science Center

The plant reproductive lineage initiates late during development, and occurs within a specialized niche in dedicated floral tissues. We have shown large-scale chromatin modifications and regorganization at the somatic-to-reproductive cell fate transition in *Arabidopsis*. Those dramatically alters the global transcriptional and epigenetic landscape in meiotic precursor cells of both the male and female lineages underpinning a common chromatin reprogramming scenario. In both sexes, H1 eviction precedes all further chromatin modifications and remodelling suggesting a driving force behind this dynamic. Interestingly, H1 dynamics also underlies reprogramming during plant cell transdifferentiation. I will present our current model and efforts to elucidate the mechanisms and role of H1 dynamics in plant cell fate transition.

She W, Grimanelli D, Rutowicz K, Whitehead MW, Puzio M, Kotlinski M, et al. (2013) Chromatin reprogramming during the somatic-toreproductive cell fate transition in plants. Development, 140(19): 4008-4019.

She W & Baroux C (2015) Chromatin dynamics in pollen mother cells underpin a common scenario at the somatic-to-reproductive fate transition of both the male and female lineages in *Arabidopsis*. Front Plant Sci 6: 294.

TALK

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Célia Baroux

Jixian Zhai1, **Sylvain Bischof1**, Haifeng Wang2,1, Suhua Feng1, Tzuu-fen Lee3, Chong Teng3, Xinyuan Chen4, Soo Young Park5, Linshan Liu5, Javier Gallego-Bartolome1,6, Wanlu Liu1, Ian R Henderson1,8, Blake C Meyers3, Israel Ausin2, and Steven E Jacobsen1,7

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5 Department of Chemistry and Biochemistry, University of California at Los Angeles, Los Angeles, CA, USA

6 Plant Biology Laboratory and Howard Hughes Medical Institute, The Salk Institute for Biological Studies, La Jolla, CA, USA

7 Howard Hughes Medical Institute, University of California at Los Angeles, Los Angeles, CA, USA

8 Present address: Department of Plant Sciences, University of Cambridge, UK

RNA-directed DNA methylation in *Arabidopsis thaliana* is driven by the plant- specific RNA Polymerase IV (Pol IV). It has been assumed that a Pol IV transcript can give rise to multiple 24-nt small interfering RNAs (siRNAs) that target DNA methylation. Here, we demonstrate that Pol IV-dependent RNAs (P4RNAs) from wild-type *Arabidopsis* are surprisingly short in length (30 to 40 nt) and mirror 24-nt siRNAs in distribution, abundance, strand bias, and 5'-adenine preference. P4RNAs exhibit transcription start sites similar to Pol II products and are featured with 5'- monophosphates and 3'-misincorporated nucleotides. The 3'-misincorporation preferentially occurs at methylated cytosines on the template DNA strand, suggesting a cotranscriptional feedback to siRNA biogenesis by DNA methylation to reinforce silencing locally. These results highlight an unusual mechanism of Pol IV transcription and suggest a "one-precursor, one-siRNA" model for the biogenesis of 24-nt siRNAs in *Arabidopsis*.

Sylvain Bischof



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A screen to identify genes involved in the heat-shock response in mosses

Pierre Goloubinoff1 and Andrija Finka1,2

1 Department Plant Molecular Biology, University of Lausanne 2 Faculty of Biology, University of Zadar, Croatia

Pierre Goloubinoff

Understanding how land plants sense and respond to temperature increments is of paramount importance in the context of global warming. Land plants have evolved a sophisticated sensing and signaling pathway to translate mild increments in the ambient temperature into a specific gene expression program, termed the heat shock response (HSR). The HSR leads to a transient adjustment of plant metabolism and cellular functions to prevent and avert heat-damages caused by noxious temperatures. We have recently identified specific Ca2⁺transducing cyclic nucleotide gated channels in the plasma membrane as being the primary heat-sensors of land plants. Yet, a central question remains: how may a common non-specific ion, such as Ca2⁺, transduce a specific HS signal from the CNGCs in plasma membrane to the heat-shock factors (HSFs) in the nucleus, resulting in the accumulation of hundreds of specific HSPs and in the setting of effective acquired thermotolerance?

We are using a genetic screen approach mediated by Piggybac transposon mutagenesis, to identify in the moss Physcomitrella patens the thermosensors and their downstream protein partners that mediate the heat-shock signal to the nucleus. Preliminary results show that our Piggybac transposon constructs can stably integrate into the moss genome and confer high sensitivity to mild daily warming treatments to 34°C.

We expect to gain knowledge on the molecular mechanisms by which land plants perceive temperature variations and translate them into acquired thermotolerance, to meet the challenge of global warming.

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Matthias Erb

A below ground herbivore shapes root defensive chemistry in nature

Matthias Erb1, Meret Huber2

1 Institute of Plant Sciences, University of Bern 2 Max Planck Institute for Chemical Ecology, Jena

Herbivorous insects have been hypothesized to be major drivers for the evolution of toxic plant metabolites. However, empirical evidence for this phenomenon is scarce, especially below ground. We studied the interaction between a major root herbivore in central European grasslands, the larvae of the cock chafer Melolontha melolontha and its native host plant, the common dandelion, *Taraxacum officinale*. Dandelion produces large quantities of secondary-metabolite rich latex in the roots [1], and we hypothesized that these metabolites may protect dandelion plants against cock chafer larvae. Through genetic manipulation, chemical complementation and large-scale common garden experiments, we show that the sesquiterpene lactone, taraxinic acid β -D-glucopyranosyl ester (TA-G) a major component of the latex of the common dandelion, deters *M. melolontha* and thereby directly decreases root damage and increases plant fitness [2]. By characterizing natural dandelion populations growing in the presence or absence of M. melolontha over the last 20 years, we demonstrate that variation in the abundance of the root herbivore determines heritable variation in TA-G concentrations in the latex. Our experiments reveal below ground herbivores as potential drivers of the evolution of plant secondary metabolites in nature.

[1] Huber M, Freese-Triebwasser D, Reichelt M, Heiling S, Paetz C, Chandran JN, Bartram S, Scheider B, Gershenzon J, Erb M (2015) Identification, quantification, spatiotemporal distribution and genetic variation of major latex secondary metabolites in the common dandelion (*Taraxacum officinale* agg.). Phytochemistry 115 (1): 89-98.

[2] Huber M, Epping J, Schulze-Gronover C, Fricke J, Aziz Z, Brillatz T, Swyers M, Köllner TG, Vogel H, Hammerbacher A, Triebwasser-Freese D, Robert CAM, Verhoeven K, Preite V, Gerhenzon J, Erb M (in press) A Latex Metabolite Benefits Plant Fitness under Root Herbivore Attack. PLOS Biology.

> SPSW researcher portfolio https://swissplantscienceweb.ch/nc/research/home/portfolio/erb Bastien Christ, Ramon Hochstrasser, Luzia Guyer, Sylvain Aubry and **Stefan** Hörtensteiner

Department of Plant and Microbial Biology, University of Zurich

Herbicide tolerance is a major commercial trait of genetically modified crops. Resistance to phosphinothricin, second most important in herbicide-tolerant crops and also widely used as selection marker for transgenic plants, is achieved by phosphinothricin acetyltransferase, encoded by the *BAR* or *PAT* genes, that inactivates the herbicide through N-acetylation.

We identified L-tryptophan and L-aminoadipic acid as previously unreported substrates of BAR. The respective products, N-acetyl-L-tryptophan and N-acetyl-L-aminoadipic acid, accumulated in senescent but not in green leaves of *BAR*-containing transgenic *Arabidopsis thaliana* plants from independent insertion mutant collections. This indicated that their formation was restricted to conditions when, likely because of senescence-linked high rates of protein degradation, respective substrates occur at significant concentrations. L-aminoadipic acid is an intermediate of L-lysine degradation in a pathway that involves the bifunctional enzyme lysine-ketoglutarate reductase/saccharopine dehydrogenase in *Arabidopsis*. A BAR-containing mutant deficient in this enzyme failed to accumulate N-acetyl-L-aminoadipic acid, but still senescencespecifically produced N-acetyl-L-tryptophan.

We expressed recombinant BAR to determine kinetic properties. Besides its well-known high affinity towards phosphinothricin, BAR was also able to acetylate both L-tryptophan and L-aminoadipic acid *in vitro*, *albeit* with much less efficiency.

Promiscuity of BAR seems to be restricted to the Brassicaceae, since senescent leaves or seeds of *BAR*-containing petunia, tobacco, wheat and barley lines do not accumulate N-acetyl-L-tryptophan or N-acetyl-L-aminoadipic acid, while they are found in *Brassica junceae* lines. We crystallized BAR together with phosphinothricin or L-aminoadipic acid, which enabled identification of residues that may affect substrate specificity and which will be targets for site-directed mutagenesis in the future.

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

Stefan Hörtensteiner



TALK

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Exploiting tritrophic interactions in the rhizosphere for crop protection

Ted Turlings

Laboratory of Fundamental and Applied Research in Chemical Ecology (FARCE), Institute of Biology, Université de Neuchâtel

Larvae of the beetle *Diabrotoca virgifera virgifera* (Western corn rootworm) cause tremendous damages to maize roots in the USA. Since its incidental introduction into the Balkan region in the 1990s it has rapidly spread and become a serious problem in Europe as well. Using advanced chemical analytical techniques and mutant maize plants we have found an explanation for the voraciousness of the rootworm. The larvae preferred to feed on crown roots of maize plants, despite the fact that they are full with toxic benzoxazinoids. Unlike other insects, WCR larvae are completely adapted to deal with these toxins and use them to identify these highly nutritious roots.

As a possible way to control WCR, we are studying entomopathogenic nematodes (EPN). EPN find their insect hosts by using a chemical signal that is emitted from maize after rootworm attack. This signal, the sesquiterpene E-(β)-caryophyllene, is no longer emitted by North-American maize varieties. By genetically transforming an American maize line we restored caryophyllene emission, resulting in reduced rootworm damage in the field.

Our research efforts now focus on the development of novel ways to apply EPN to crop fields. These efforts involve the encapsulation of EPN in alginate beads that can be "planted" during sowing. By adding specific plant-derived chemicals to the beads we can put the EPN in a state of quiescence, which significantly prolongs their shelflife. We also use root extracts to isolate and identify attractants and feeding stimulants that we wish to add in order to encourage pest insects to eat the beads. With these examples I hope to show that chemical ecologists can have an important role in developing novel strategies for crop protection.

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

The role of lipids in arbuscular mycorrhiza: signals or food for the fungus?

Didier Reinhardt1, Mélanie Rich2

Department of Biology, University of Fribourg

During the establishment of arbuscular mycorrhiza (AM), both partners, the plant and the AM fungus, undergo fundamental reprogramming of their gene expression patterns. Many of the AMinduced genes encode central elements in symbiotic functioning such as nutrient transporters, in particular phosphate transporters (PTs). Other AM-induced genes encode transcriptional regulators, signalling components or enzymes involved in symbiosis-related functions. We have recently cloned a transcription factor, REQUIRED FOR ARBUSCULAR MYCORRHIZA1 (RAM1) of Petunia hybrida, that is essential for the induction of many AM-related genes (Rich et al., 2015). Some of them encode close homologues of genes involved in cutin biosynthesis, in particular a glycerol-3-phosphate acyltransferase (GPAT) that produces monoacylglycerol (MAG), the lipidic precursor of cutin, and a pair of half-size ABC transporters that are responsible for secretion of the precursor into the apoplast. Based on its essential role in AM of *Medicago truncatula*, the GPAT homologue has been named RAM2. The two ABC transporters have also been found to be essential for AM symbiosis in *M. truncatula*, in particular for arbuscule morphogenesis, hence their name STUNTED ARBUSCULE (STR) and STR2.

RAM2, STR, and STR2 are expressed specifically in cells that harbor arbuscules, hence they may be involved in the release of a lipidic substance from the host to the AM fungus. This substance may function as a signal or as a growth substrate for the strictly biotrophic fungal symbiont. We are using combined genetic and biochemical tools to explore the identity of the putative lipids and their function in AM symbiosis.

MK Rich, M Schorderet, L Bapaume, L Falquet, P Morel, M Vandenbussche, D Reinhardt (2015) The Petunia GRAS transcription factor ATA/RAM1 regulates symbiotic gene expression and fungal morphogenesis in arbuscular mycorrhiza. Plant Phys 168:788-797.

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Linking soil biodiversity, mycorrhizal fungal diversity and ecosystem multifunctionality

Marcel van der Heijden

Plant Soil Interactions, Institute for Sustainability Sciences, Agroscope, Zurich and Department of Evolutionary Biology & Environmental Studies, University of Zurich

Biodiversity loss has become a global concern as evidence accumulates that it will negatively affect ecosystem services on which society depends. So far, most studies have focused on the ecological consequences of above-ground biodiversity loss; yet a large part of Earth's biodiversity is literally hidden below ground. Whether reductions of biodiversity in soil communities below ground have consequences for the overall performance of an ecosystem remains unresolved. In order to test this, we manipulated below ground diversity in microcosms with plant communities and in outdoor lysimeters. Our results demonstrate that the simplification of soil communities and a reduction of soil biodiversity reduces plant productivity and ecosystem functioning. Further experiments with specific groups of plant root symbionts (arbuscular mycorrhizal fungi and nitrogen fixing rhizobia bacteria) revealed that symbiont diversity and the presence of a widespread plant-fungal-bacterial symbiosis promotes plant growth, biodiversity and seedling establishment. Overall, our results highlight that changes in soil communities and the loss of soil biodiversity threaten ecosystem multifunctionality and sustainability.

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

TALK

Maged Saad1, Sophie Michalet2, Amela Muminovic2, Ivana Maksimović3, Marina Putnik-Delić3, Gérard Hopfgartner2, and Xavier Perret1

1 Department of Botany and Plant Biology, University of Geneva

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In nitrogen poor soils, legume plants associate with soil bacteria known as rhizobia and exchange reduced nitrogen against carbohydrates derived from photosynthesis. Symbiotic nitrogen fixation occurs inside specialized root organs called nodules, which provide the environment required to maximize activity of the rhizobial nitrogenase. In free-living diazotrophs such as Azotobacter vinelandii and Klebsiella pneumoniae, NifQ ensures synthesis of the iron-molybdenum cofactor (FeMo-Co) that is essential for nitrogenase activity. Hence, nifQ mutants of K. pneumoniae were unable to reduce nitrogen unless higher levels of Mo were provided. Yet, genome analyses showed that many rhizobia lack a *nifQ* gene, which suggested that NifQ was dispensable for assembly of nitrogenase inside nodules of many plants. Accordingly, a nifQ mutant (NGR_Δ*nifQ*) of the promiscuous *Sinorhizobium fredii* strain NGR234 was symbiotically as proficient as the wild type on most plants. On several hosts however, root nodules formed by NGR $\Delta nifQ$ were of an unusual dark red colour but continued to fix nitrogen. Mass spectral analyses carried out on extracts from nodules of Vigna unquiculata and V. radiata identified porphyrins as the plant compounds responsible for this unusual nodule coloration. Surprisingly, chemical analyses also revealed that symbiotically active nodules of V. radiata formed by NGR Δ nifQ contained ca. 20% less molybdenum than those infected by NGR234, whereas levels of other metals (e.g. Fe and Mg) were mostly unaffected. Thus, although homeostasis of nodules infected with NGR $\Delta nifQ$ appeared significantly altered, host plants did not compensate for absence of NifQ inside endosymbiotic bacteria by increased Mo levels inside nodules.

Xavier Perret



TALK

Ecological and evolutionary drivers of plant defense variation against herbivores

Sergio Rasmann

Institute of Biology, University of Neuchâtel

In most food webs, insect herbivores are one of the major conduits of energy flow between autotrophic plants and the higher trophic levels. Thus, it is not surprising that insect herbivory has led to the evolution of remarkably diverse and potent plant defenses. Natural selection imposed by insect herbivores appears to have resulted in the evolution of sandpapery leaves, digestion inhibitors, toxins as well as information chemicals that can be exploited by natural enemies to reduce herbivore fitness. Over the last half century, complementary theories and hypotheses have been developed to try to explain the extraordinary variation in plant defensive strategies, and, thanks to interdisciplinary interaction between ecologist, behaviorists, physiologist, and chemists, it has given rise to the body of work, collectively known as "plant defense theory". Nowadays, advances in community phylogenetic and metabolomic analysis are the key components for refining plant defense theories at a novel frontier. I will show examples of how regulation of plant defense strategies can be affected across the whole hierarchical organization of life, spanning from ecosystems to organisms and to genes. I will thus argue that only a holistic approach incorporating large-scale ecological gradients will enable us to fully grasp ecology and evolution of plant defenses against herbivores.





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Yeon Hee Kang, Ora Hazak, Alice Breda, Pietro Cattaneo, Christian S Hardtke

Department of Plant Molecular Biology, University of Lausanne

The evolution of the plant vascular system has had a crucial impact on the biosphere and earth history, because it enabled plants to effectively colonize land. Plant vasculature comprises two distinct transport systems, xylem and phloem. Xylem consists of connected vessels, which transport water and nutrients extracted from the soil to the rest of the plant body. Phloem is a more complex and versatile tissue, which distributes photosynthetic sugars, nutrients as well as developmental signals throughout the plant, typically from source to sink organs. Phloem sap conduits are formed by connected sieve elements, whose differentiation includes cell elongation, wall thickening and enucleation. Little is known about the moleculargenetic control of this vital differentiation process. The growth apices of plants, the meristems, connect to established vasculature via continuous production of early phloem, so-called protophloem.

An ideal system to investigate this process is the Arabidopsis root meristem, where protophloem strand formation can be followed along the spatio-temporal gradient of single cell files. Over the last vears, we have defined a molecular-genetic network that consists of two antagonistic modules and guides the formation of root protophloem sieve elements, starting from their stem cells. The positive regulators include polar plasma membrane-associated proteins that localize opposite to each other, while the negative regulators comprise receptor-like kinase signalling pathways that convey the response to autocrine peptide ligands. Because all positive and negative regulators identified so far are expressed from the beginning to the end of the differentiation process, developing protophloem cells must eventually escape their autocrine peptide signals to switch from proliferation to differentiation in a selforganizing spatio-temporal manner.

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

TALK



Clara Sánchez-Rodríguez, Kamil Sklodowski and Rudolf Schlechter

Department of Biology, ETH Zurich

The plant cell wall is a complex network of carbohydrate-based polymers that controls overall plant morphogenesis and protects the cell against biotic and abiotic stress factors. Among the cell wall components, cellulose is the main biomass contributor and is essential for several industries. One of the aims of our research is to understand the mechanisms underlying its synthesis and remodeling, especially those related with cellulose microfibril structure and its role in plant stress response.

We are also interested in the cell wall as the first coat by which the cell communicates with its neighbour cells and the environment. To fulfil this function, the cell wall needs to be a highly dynamic and responsive structure, able to sense and integrate external stimuli and to transmit them across the plasma membrane. A fine-tuned communication with the cytosol through endocytosis is especially important for fast and localized responses, for example in reaction to microbes. We aim to characterize the dynamic changes of the cell wall and the function of the endocytosis machinery at the cellular level in the microbe-plant interface.

Here we will present our last results regarding cellulose synthesis regulation and our preliminary data and future plans to characterize the dynamic response of the plant cells to eukaryotic pathogens.

TALK

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C Sánchez-Rodríguez

Vinicius Costa Galvão and Christian Fankhauser.

Center for Integrative Genomics, University of Lausanne

Environmental factors strongly impinges on plants growth and development. Among them, light constitutes an important signal regulating several events during plant development. For instance, the reduction of red:far-red light (R:FR) ratio available for plants growing in high density or under a dense canopy triggers several responses, collectively known as shade avoidance syndrome (SAS), such as promotion of stem and petiole elongation and leaf hyponasty. In addition to these growth responses, shade strongly affects plants life strategy by regulating developmental transitions, such germination, juvenile to adult transition and onset of flowering. However, in most cases the molecular mechanisms underlying these developmental transitions remain largely unknown.

Several evidences indicate that PIF proteins contitute a molecular link downstream of light perception by photoreceptor mediating SAS in seedlings, such as hypocotyl elongation and cotyledon expansion. To investigate whether PIFs are mediating vegetative development and reproductive transition we performed systematic mutant analysis in the model plant *Arabidopsis thaliana* both in plants growing under simulated shade (low R:FR) and using the constitutively shade avoiding *phyB* mutant. Our preliminary results suggest that PIF at least in part mediate these events in response to shade.

Vinicius Costa Galvão



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

TALK

An Arabidopsis mature seed cuticle is essential for seed viability, dormancy and hormonal germination control

Julien De Giorgi1, Urszula Piskurewicz1, Sylvain Loubery1, Anne Utz-Pugin1, Christophe Bailly2, Laurent Mène-Saffrané3 and Luis Lopez-Molina1

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3 Department of Plant Biology, University of Fribourg

The cuticle is among the earliest plant adaptations to terrestrial life. It consists of a waxy film coating the plant's aerial parts that regulates transpiration and gaseous diffusion with the outer environment. Cutin is a lipid polymer and main component of the cuticle. Seeds appeared much later during land plant evolution and consist of capsules enclosing a plant embryo in a guiescent and highly resistant state. The seed allows plant dispersal before seed germination and seedling establishment. Seeds are also able to control their germination in response to stressful environmental conditions, which involves the phytohormones abscisic acid (ABA) and gibberellic acid (GA). Transcriptomic and ChIP-seq studies in Arabidopsis led us to identify cutin biosynthesis genes as important regulatory targets of GA and ABA signaling pathways. We identified a thick cuticle located in the outer face of the Arabidopsis mature seed endosperm. This endosperm-associated cuticle contains cutin and cutin biosynthesis mutant seeds display a range of seed physiological and germination deficiencies including low seed viability and low dormancy, which is associated with high lipid oxidation stress accumulation. The endospermic cuticle is 10 times thicker than the leaf cuticle consistent with its role to shield the seed's live structures from environmental damage such as oxidative stress. Cutin biosynthesis mutant seeds are also unable to control their germination as a result of their inability to control cellular expansion. Thus, it appears that in the course of land plant evolution cuticular structures were co-opted to achieve key physiological seed properties.

TALK



Luis Lopez-Molina

TALK

The endodermis as a checkpoint for nutrients

Marie Barberon

Department of Plant Molecular Biology, University of Lausanne

In higher plants, roots acquire water and nutrients from the soil and transport them upwards to the aerial parts. This function is reflected by their histology: water and nutrients move radially through the concentric layers of epidermis, cortex, and endodermis before entering the central cylinder where they are loaded into the xylem for transport to the aerial parts. The endodermis is a single, epithelium-like cell layer, which surrounds the inner, conductive tissues of roots and forms a barrier that is considered crucial for the controlled uptake of nutrients into the vasculature. The barrier properties of the endodermis are mediated by Casparian Strips (CS) highly localized lignin-based modification of the primary cell wall, surrounding each endodermal cell and by a deposition of suberin lamellae in the secondary cell wall.

In the past decades, the endodermis has been largely studied at the histological and physiological level in various plant species. Our recent work in Arabidopsis identified specific mutants, markers and protocols that now provide an unprecedented opportunity to test the roles of the endodermis in nutrient uptake. Our research indicates that the generally accepted views of endodermal function have been overly simplistic. We could show that compromising the CS integrity does not lead to a massive allocation of nutrients to the aerial parts. Currently, we are investigating in much greater details the significance of the suberin lamellae, its development, function and plasticity. We found that suberization responds to a wide range of nutrient stresses, mediated by the stress hormones abscisic acid and ethylene. We revealed a striking ability of the root to not only regulate synthesis of suberin, but also to selectively degrade it in response to ethylene. Finally we demonstrated that changes in suberization constitute physiologically relevant, adaptive responses, pointing to a pivotal role of the endodermal membrane in nutrient homeostasis.



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REDUCED POLLEN NUMBER1 isolated by genomewide association mapping showed recent selection on pollen number in *Arabidopsis thaliana*

Takashi Tsuchimatsu1,2,3, Hiroyuki Kakui1, Misako Yamazaki1, Cindy Marona4, Dazhe Meng5, Hiroki Tsutsui6, Masahiro Kanaoka6, Afif Hedhli7, Ueli Grossniklaus7, Thomas Stadler8, Michael Lenhard4, Magnus Nordborg2 & Kentaro K Shimizu1

1 Department of Evolutionary Biology and Environmental Studies, University of Zurich

2 Gregor Mendel Institute, Vienna. 3 University of Tokyo. 4 University of Potsdam. 5 University of Southern California. 6 Nagoya University. 7 Department of Plant and Microbial Biology, UZH. 8 ETH Zurich

The number of male gametes (pollen/sperm) is a fundamental trait for the reproduction of plants and animals. The breeding system is a major selective force on the male gamete number both in animals (sperm number) and in plants (usually counted as pollen number per flower or as the pollen/ovule (P/O) ratio). In plants, the evolution of self-fertilization (selfing) has been considered a most frequent evolutionary transition, and the reduced number of pollen grains is one of the major hallmarks of selfing species (selfing syndrome). The reduction of pollen number could be advantageous because of trade-offs with other fitness components, such as pollen size and seed number. Classical studies of rice domestication suggested that a reduction of pollen number contributed to an increase in seed yield.

Despite extensive phenotypic and theoretical studies on male gamete numbers, very little is known about the genes responsible for the variation in pollen number. This is because mutant-based analysis was not efficient for studying these quantitative traits. We conducted a genome-wide association study (GWAS) using 144 accessions of *Arabidopsis thaliana*. We identified the *REDUCED POLLEN NUMBER 1 (RDP1)* gene, which explained about 20% of the phenotypic variance. The gene showed the molecular signature of selection, and age estimates suggested very recent selection (2200– 4600 years ago). Moreover, statistical analysis suggested that a considerable proportion of the top 68 GWAS candidates experienced recent selection. To our knowledge, this is the first reported genetic variation responsible for male gamete number.

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Kentaro Shimizu

Combining modelling and genetic approaches in conservation: application to the genus *Capurodendron* Aubrév. (Sapotaceae) in Madagascar

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Natural History Museum, London SW7 5BD, UK

Species identification and delimitation are central to the sound assessment of biodiversity and species richness for a given territory. However, the traditional view of species, which has mainly relied on morphology and anatomy, is more and more challenged by the use of molecular markers. In order to achieve a more accurate definition of areas with high conservation priorities, we combined species distribution modelling, species tree reconstruction using molecular markers and IUCN threat Categories on an endemic genus of Madagascar, *Capurodendron* Aubrév. (Sapotaceae).

Capurodendron includes 20 to 30 species which are mainly found in primary forests. They are hardwood slow-growing trees, appreciated for their mechanical qualities. Their logging and trade presently weaken and threaten species' natural populations. As for most Malagasy plants, the current available herbaria collections do not provide sufficient distributional data. A modelling based on known occurrences and environmental data was therefore conducted to produce potential species distribution maps, from which IUCN threat categories could thus be assigned to species.

To take into account the species' evolutionary history and the weight of each of them in the choice for priority areas, chloroplast and nuclear genes were sequenced and used to build a species tree under the Multi-Species Coalescent. The phylogenetic diversity contained in targeted areas was computed and helped defining priority areas.

This comprehensive approach is an attempt, when very few data is available, to find new ways to evaluate species threat levels and to define areas on which a conservation emphasis should be put, considering species' distribution and species' evolutionary history.



TALK



Discrete genetic elements underlie diversity effects in conspecific plant communities

Samuel E Wuest 1,2, Merten Ehmig3 and Bernhard Schmid1

1 Department of Evolutionary Biology and Environmental Studies, University of Zurich

2 Department of Plant and Microbial Biology, University of Zurich 3 Institute of Systematic Botany, University of Zurich

Recent research has frequently found a positive relationship between species diversity and ecosystem functioning, e.g. the productivity or stability of communities. Reports have further suggested that also within-species genetic diversity can promote ecosystem functioning (sometimes to a similar extent as species diversity), but little is know about the genetic principles underlying such diversity effects. A possible mechanism that can explain overyielding in more diverse communities is complementarity through niche partitioning amongst individuals in a community.

Here, we describe an approach to "screen" for positive interactions between genotype pairs of *Arabidopsis thaliana* and subsequently use a quantitive genetic approach to identify discrete genetic elements underlying positive community-levels properties. Preliminary results suggest that positive effects can be caused by allelic diversity at discrete loci. The identification and "mendelization" of such discrete genetic elements could provide a proof-of-concept for a new approach to breeding (i.e. diversity breeding), in which selection happens not for a given allele, but for alleleic diversity in a conspecific community. Cloning of the respective loci in future projects might provide insights into the mechansims that underlie niche differentiation in conspecific plant communities.

Samuel Wuest

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TALK

Nikolai V Ivanov

Philip Morris International R&D, Philip Morris Products S.A., Neuchâtel

Nicotiana tabacum (common tobacco) is a major crop species and a model organism, and as a Solanaceae shares significant similarities with tomato, potato, eggplant and pepper. The three most commonly used tobacco types are Flue-Cured (or Virginia), Burley and Oriental, which are traditionally grown and harvested under different agricultural practices in over 120 countries. Tobacco plant stands out as a complex allotetraploid with a large 4.5 Gb genome, a significant proportion of which represented by repeats. As a species, *N. tabacum* (2n=4x=48) evolved through the interspecific hybridization of the ancestors of two South American *Nicotiana* species about 200,000 years ago, *Nicotiana sylvestris* (2n=24, maternal donor) and *Nicotiana tomentosiformis* (2n=24, paternal donor).

Efforts to sequence a reference tobacco genome started almost 15 years ago with the Tobacco Genome Initiative, and several milestones have been reached and made available. A physical map of four bacterial artificial chromosome (BAC) libraries totaling 425,088 clones from Hicks Broadleaf was constructed using Keygene's Whole Genome Profiling (WGPTM) technology. Draft genomes for the diploid *Nicotiana* species *N. sylvestris* and *N. tomentosiformis* were completed, covering 72-83% of the 2.3-2.6 Gb genomes in 150-250 thousand scaffolds, and recently, draft genomes for three varieties of the tetraploid *Nicotiana* species *N. tabacum* were published, covering 81-84% of the 4.4-4.6 Gb tobacco genome in 150-250 thousand scaffolds. These genomes show both the low divergence of tobacco from its ancestor genomes and display microsynteny with other Solanaceae species.

We anticipate that these genomes will strengthen the use of *N. tabacum* as a versatile model organism for functional genomics and biotechnology applications.

TALK



Nikolai Ivanov

TALK



Strigolactones, at the crossroad between plant growth and nutrition

Lorenzo Borghi, Guo-Wei Liu, Joelle Sasse, Christian Gübeli and Enrico Martinoia

Department of Plant and Microbial Biology, University of Zurich

The phytohormone strigolactone (SL) is a carotenoid derivative, initially characterized as promoter of parasitic witchweed germination. Only recently SL was also reported as inducer of hyphal branching in arbuscular mycorrhizal fungi (AMF) of the Glomeromycota division and inhibitor of lateral bud outgrowth in plant shoots. Several additional functions were assigned to SLs as regulators of root and shoot architecture, cell identity, pathogen defense, aging and abiotic stress.

SLs are synthesized both in roots and shoots; nevertheless rootsynthetized SL still affects shoot development, indicating that a long-distance, shoot-ward transport of SL occurs. Our studies have recently provided some evidence how SLs are transported upwards from the root tip and outwards to the soil: we tracked the allocation of exogenous, radio-labelled GR24 (a synthetic SL) in plant tissues and its exudation from the root to the rhizosphere. The quantification of the radioactive molecule showed that the ABCG protein PLEIOTROPIC DRUG RESISTANCE 1 (PDR1) is the major shoot-ward SL transporter. SLs, in concert with phytohormones such as auxins and citokinins and sucrose signaling are emerging as the main players in regulation of lateral bud outgrowth: we report here our last results on this crosstalk.

SLs are not only root-to-shoot transported, but also exuded into soil, where they function as beacons to AMF. Specialized hypodermis cells, called hypodermal passage cells (HPCs), are SL exudation sites from plant roots as well entry point for AMF. HPCs have so far mainly been characterized at the structural level. In depth biochemical, molecular and genetic analyses are still missing. Our recent results show that SLs have a central role in establishing the number of HPCs. Furthermore, we have indications that either HPCs and/or SLs are important for the uptake of plant nutrients, mainly Mg2⁺ and K⁺.

Lorenzo Borghi

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

Simon Krattinger1, Joohyun Kang1, Harsh Chauhan1, Liselotte Selter1, Justine Sucher1, Marc W Schmid1, Mark D Robinson2, Enrico Martinoia1, Beat Keller1

1 Department of Plant and Microbial Biology, University of Zurich 2 Institute of Molecular Life Sciences, University of Zurich

Pathogenic fungi are a serious threat to agriculture. The wheat ABC transporter LR34 confers durable field resistance against multiple fungal diseases. The resistant Lr34 allele evolved after wheat domestication as a result of two spontaneous gain-of-function mutations in this ABC transporter gene. Hence, the resistant Lr34 version is only present in cultivated wheat but not in wild wheat progenitors. In addition, an Lr34-like disease resistance has so far not been reported in other globally important cereals like barley, rice or maize. Lr34 is functionally transferrable into rice where the gene conferred increased resistance against the fungal disease rice blast. Besides being an important food crop, rice is also a model plant for cereal genomics. We therefore used Lr34-expressing rice lines to elucidate the molecular function of Lr34. In a RNA sequencing experiment we identified a core set of Lr34-responsive genes that showed consistent differential expression in two Lr34-expressing rice lines. Interestingly, most of these genes are responsive to both biotic and abiotic stresses. Besides pathogen resistance, Lr34-containing rice plants also showed enhanced dehydration tolerance which was caused by reduced leaf water uptake, a process controlled by the phytohormone abscisic acid (ABA). This reduced water uptake could be phenocopied in wild-type plants by adding ABA and *Lr34*-rice plants showed ABA-hypersensitivity during early seedling establishment. We conclude that the Lr34 ABC transporter can have a positive effect on both abiotic and biotic stress tolerance and that the phytohormone ABA plays an important role in Lr34mediated resistance.

Simon Krattinger

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TALK

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Arabidopsis MYC transcription factors are the target of hormonal SA/JA crosstalk in response to *Pieris* brassicae eggs

André Schmiesing, Aurélia Emonet, Caroline Gouhier-Darimont and Philippe Reymond

Department of Plant Molecular Biology, University of Lausanne

In *Arabidopsis*, oviposition by insect eggs activates a patterntriggered immunity (PTI) response. Strikingly, SA accumulation after oviposition by *P. brassicae* has a negative effect on the expression of jasmonate (JA)-dependent genes and consequently enhances larval performance. We discovered that this egg-induced SA/JA crosstalk targets the MYC branch, but not the ERF branch, of the JA pathway. MYC2, MYC3 and MYC4 proteins were degraded in response to egg extract treatment and this effect was dependent on the accumulation of SA. In addition, we found that WRKY75 is a negative regulator of egg-induced SA/JA crosstalk. These results reveal a molecular mechanism by which insect eggs may favor the performance of their progeny and illustrate the complex interaction between defense signalling pathways.



29 Philippe Reymond

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

TALK

New receptors for old ligands



Lei Wang, Markus Albert, Ulla Fürst, Philippe Chatelain and Georg Felix

Zentrum für Molekularbiologie der Pflanzen, Eberhard-Karls-Universität Tübingen, Germany

Membrane bound receptors play fundamental roles for the regulation of cellular behaviour by external signals. Higher plants have >600, often >1000, genes encoding receptor like kinases (RLKs) and receptor like proteins (RLPs). With respect to this high number of potential receptors, the number of receptors with identified and specified ligands, although steadily increasing, still remains rather low. In turn, a number of biologically highly active substances, notably peptides, have been identified that remain orphan with respect to the identity of their corresponding receptors. Here, we set out to identify the receptors for two of these orphan ligands, the peptidic wound hormone systemin and csp22, a peptide representing the RNP-1 domain of bacterial cold shock protein. Interestingly, both peptides trigger the same type of defence-type of responses at nano- or even subnanomolar concentrations but only in some species of the Solanaceae family. Under the premise that responsiveness/non-responsiveness is likely due to the presence or absence of a functional receptor we made use of the natural variation in responsiveness between S. lycopersicum and S. pennellii to map genomic regions, to identify receptor candidates and to demonstrate functionality of the receptors by ligand binding assays and functionality assays after heterologous expression in Arabidopsis thaliana.

TALK

Georg Felix

POSTER



1 Emmanuel Boutet

Expert curation of plant proteins in UniProtKB / Swiss-Prot

Emmanuel Boutet1, Michel Shneider1, Damien Lieberherr1, Michael Tognolli1, Lydie Bougueleret1, Ioannis Xenarios1,2 and the Swiss-Prot group.

1 Swiss-Prot group, SIB Swiss Institute of Bioinformatics, CMU, Geneva 2 Vital-IT group, SIB Swiss Institute of Bioinformatics, University of Lausanne

The UniProt KnowledgeBase (UniProtKB) provides a unique, centralized and freely available resource for protein sequences and functional information. For plants, UniProtKB/Swiss-Prot expert annotation is focused on *Arabidopsis* and rice proteins with some functional characterization. Expert manual curation process includes both sequence verification, often leading to the correction of wrong gene model predictions, and integration of experimental evidence derived from literature and numerous resources, such as biochemical and genetic analyses, 3D-structures, mutagenesis experiments, information about protein interactions and post-translational modifications.

Our plant annotation program is actively collaborating with other resources. As an example, we provide Araport, the *Arabidopsis* portal, with all the gene model corrections that we introduced on the bases of our trans-species family annotation. We are also completing the knowledgebase by importing missing information from EnsemblPlants.

The UniProt consortium is also actively involved in GO annotation, and manual annotation has been added to more than 3'000 plant proteins. Experimental peptides from high-throughput proteomics experiments that uniquely match the product of a single gene are used to generate annotations describing post-translational modifications and protein processing events. UniProtKB serves as a central hub for biomolecular information with access to more than 150 other resources, including nucleotide sequence databases, 2D and 3D resources, InterPro or MODs.



Simon Goepfert

Reducing TSNAs in burley tobaccos through alteration of the N-assimilation pathway

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Burley tobaccos require a much higher level of N-fertilization than other tobacco types in order to achieve acceptable yields. As a consequence, Burley plants accumulate higher levels of free nitrate in their leaves than other tobacco types. In the literature high levels of nitrate have been correlated with high nitrosation of alkaloids leading to the formation of tobacco-specific nitrosamines (TSNA) which are reported for their carcinogenic activity.

In order to investigate the relationship between nitrate levels and nitrosation and to reduce TSNAs in tobacco leaf and smoke, a strategy was developped to deplete the pool of nitrate accumulated in Burley leaf by altering the N-assimilation pathway. Nitrate reductase (NR) is the first key controlled enzyme of the N-assimilation pathway reducing nitrate to nitrite. A deregulated form of S523DNR was overexpressed in Burley tobacco under the control of a constitutive promoter to increase nitrate accumulation into amino acids and thereby reducing the free nitrate pool accumulated in leaf, expecting thus a decrease in nitrosating agents responsible for TSNA formation. Günter Hoch

Do carbon reserve concentrations really indicate the carbon balance of a tree?

Günter Hoch, Anna Mösch, Andrea Schwendener

Department of Environmental Sciences – Botany, University of Basel

Tissue concentrations of non-structural carbohydrates (NSC) are often used to infer the C balance of trees, assuming that they are largely regulated by the net-balance between photosynthesis and all C sink activities ('passive' regulation). More recently, this simple model has been questioned by new findings suggesting the regulation of C reserve pools against the demand from other C sink activities in trees ('active' regulation). The formation of C reserves might thus be in competition with other C sinks, like growth, which would limit the applicability of NSC concentrations as proxies for a tree's C balance. Here, we present two experiments that investigated the controls of C reserve formation in broad-leaved tree saplings by inducing C-limitation via shading and complete darkening.

In response severe shading, C reserves in woody tissues reacted like 'passive' pools during the first half of the growing seasons, with strong declines of NSC concentrations, but increased again towards the end of the season (probably against prevailing C demand from other sinks), resulting in comparatively smaller, but still significant, differences of NSC concentrations among the shading treatments. This experiment showed the general usability of C reserves as indicators for C limitation, but the increased late-season C allocation to storage even under severe C shortage might limit the explanatory power of NSC to accurately quantify net C balances.

Within a second experiment, broad-leaved, deciduous tree saplings were exposed to continuous darkness, which they survived for about 12 weeks. In all investigated woody tissues, starch and surprisingly also low molecular weight sugar concentrations declined to almost zero within the first three weeks of the treatment. With this experiment we could demonstrate that virtually all C reserves are available under C starvation, and broad-leaved tree saplings survive more than a month without the presents of a significant C reserve pool.

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Transcription ON/OFF: Characterization of new components of gene silencing and heterochromatin confinement in *A. thaliana*

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Precise organization of the genome in the nucleus is essential for proper gene expression and cell integrity. DNA methylation and dimethylation of Histone 3 at Lysine 9 (H3K9me2) are epigenetic marks used by most eukaryotes to transcriptionally silence DNA repeats and transposons. Together with other epigenetic factors, these marks contribute to the silencing of heterochromatin and define its epigenetic signature. Conversely, the transcribed euchromatic regions show a depletion of these silencing marks and enrichment of H3K4 methylation and histone acetylation. In animals, the lamina, which is a filamentous meshwork of proteins, plays an important role in sequestering the heterochromatin at the nuclear periphery. Composed among other proteins of lamins, the lamina contacts the heterochromatin, contributing to its silencing. Plants are deprived of lamins but, a lamina-like structure is observed in the plant nuclei. and the Nuclear Matrix Component Proteins (NMCPs) could be the plant lamin analogs. I am currently investigating the role of the four Arabidopsis thaliana NMCP Crowded Nuclei (CRWN1-4) proteins in gene silencing using transcriptomic, biochemical and confocal microscopy approaches. In addition, I am developing an unbiased forward genetic screen to identify inhibitors of heterochromatin spreading. Although well studied in animals, only a few repressors of heterochromatin spreading are known in plants. Together, these different approaches will give more insights into the mechanisms involved in heterochromatin silencing, its subnuclear localization and the repression of its spreading in plants.



Doris Rentsch

Identifying regulators of di- and tripeptide utilization in *Arabidopsis thaliana*

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Nitrogen (N) is limiting plant growth and reproduction. N uptake from the soil, its assimilation and subsequent reallocation are therefore key processes driving primary productivity of plants. While inorganic N represents the largest pool of soluble N in many fertilized soils, organic N forms, including amino acids, peptides and proteins (soluble and bound to the soil matrix), often dominate non-fertilized soils. It is generally assumed that plants use predominantly inorganic N, but there is increasing evidence that plants also acquire organic N from the soil. It remains however unclear, how much the direct uptake of organic N contributes to plant N needs.

Transport of small peptides of two to three amino acids is suggested to be important for translocation of organic N within the plant, for plant nutrition and development. The plasma membrane-localized peptide transporter PTR1 of *Arabidopsis thaliana* mediates transport of diand tripeptides with low selectivity and high affinity (1). Consistent with AtPTR1 transport properties and the expression in roots, atptr1 T-DNA insertion lines displayed reduced growth compared to wild type plants on medium with dipeptides as sole N source, while overexpressing lines (35S::*AtPTR5*) produced more biomass (2).

Comparison of 38 Arabidopsis on dipeptides identified accessions with either poor or efficient growth. While Col0 produced little biomass, accession Est-0 and Tanz-1 were most efficient in utilizing dipeptides as N source. Advanced intercross-recombinant inbred lines (Est-1xCol-0) were used for QTL mapping (3). This identified two major QTLs on chromosome 3 and 4, respectively.

- 1 Hammes et al. (2010) J Biol Chem. 285:39710-7
- 2 Komarova et al. (2008) Plant Physiol. 148:856-69
- 3 Balasubramanian et al. (2009) PLoS One 4(2):e4318

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LRR-extensins potentially link the cell wall and plasma membrane

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LRR-extensins (LRXs) are extracellular proteins involved in cell growth and cell wall development. As shown for LRX1, the extensin domain of these proteins has an anchoring function in the cell wall by insolubilizing the protein via covalent linkages with cell wall components. The leucine-rich repeat (LRR) domain does interact with a so far unidentified binding partner. Mutations in *LRX* genes causes development of aberrant cell walls and changes in cell wall composition. Together, these data suggest that LRX proteins are involved in cell wall development by regulating an extracellular process.

Expression of extensin-less LRX proteins suggested that the LRR domain binds to the plasma membrane, indicating a possible membrane association of the binding partner of the LRR domain. Recent analyses of *Irx* mutants revealed that these show aberrant intracellular distribution of cations. This might be an indication for a role of LRX proteins in regulating ion homeostasis. We are currently investigating the biological relevance of these observations, by assessing the importance of the changed ion distribution for the establishment the growth defects of Irx mutants.





Joop Vermeer

Lateral root formation; A force awakens

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Intercellular communication is central for the development of an organism. It is mediated by biochemical gradients as well as physical forces that collectively regulate differentiation and development. To date, this fascinating interplay between forces and local cellular reorganization during plant development is poorly understood. Many plant developmental processes critically depend on accommodating responses from the surrounding cells.

Lateral root formation is a developmental process in which the integration of chemical signals and physical forces is evident. Lateral roots are initiated deep within the primary root from dividing pericycle cells, necessitating growth through overlying endodermal, cortical and epidermal cell layers. During its development, the lateral root heavily depends on accommodating responses of these overlaying cell layers.

We demonstrated that these responses include a dramatic volume loss and a controlled degradation of their Casparian strips. Moreover, by specifically manipulating SHY2-mediated auxin signaling in the endodermis, we were able to completely block cell proliferation in the pericycle. It appears that the pericycle perceives the nonaccommodating endodermis as an increased resistance to its expansion. The pericycle-endodermis interaction provides a unique opportunity to elucidate the molecular and cellular mechanisms underlying spatial accommodation in plant development. Currently, we are using different approaches to elucidate the mechanistic framework underlying spatial accommodation. The pericycleendodermis interaction model will provide fundamental new insights into many other developmental processes that heavily depend on spatial accommodation by surrounding tissue.



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