

SWISSPLANT 2015



28–30 January 2015
Leukerbad, Switzerland



SWISSPLANT 2015

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Swiss Committee for Molecular Biology



PHILIP MORRIS
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Symposium of the Swiss Plant Science Web 28–30 January 2015, Leukerbad, Switzerland

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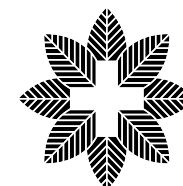
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Prof. Dr. Christian Hardtke
Prof. Dr. John Pannell
Prof. Dr. Philippe Reymond

Conference Organization

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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.

In addition, by choosing an attractive mountain resort for our conferences, we hope to foster informal discussions among peers, this year on the snow-covered slopes and trails or in the thermal spas of Leukerbad.

I especially welcome all new members of the 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 2015» is the ideal place to start discussions on new collaborations!

This year's scientific conference committee is from the University of Lausanne. I thank Christian Hardtke, Christian Fankhauser, John Panell and Philippe Reymond 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 here smooth and easy.

Enjoy the science and leisure in Leukerbad!

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 Wednesday, 28 January

17:00	Welcome Apéro
18:00	Welcome address
18:10-18:40	Opening talk, Olivier Voinnet, ETH Zurich: <i>Tba</i>
19:00	Dinner
20:30	Christoph Ringli, U Zurich: <i>Flavonols influence plant development via modulating auxin homeostasis</i>
20:50	Timothy Paape, U Zurich: <i>Zinc accumulation and transcriptional response in the allopolyploid Arabidopsis kamchatica</i>
21:10	Lorenzo Borghi, U Zurich: <i>Asymmetric localizations of the ABC transporter PaPDR1 trace paths of directional strigolactone transport</i>
21:30	Wilhelm Gruissem, ETH Zurich: <i>Function of the Arabidopsis Retinoblastoma-related protein in stem cell maintenance and differentiation</i>
21:50	Socializing at the hotel bar



Program Thursday, 29 January

08:30	Consuelo De Moraes, ETH Zurich: <i>Chemical signaling in interactions among plants, insects, and other organisms</i>
09:00	Michael Hothorn, U Geneva: <i>The twists and turns of plant membrane signaling</i>
09:20	Christian Parisod, U Neuchâtel: <i>Genome reorganization and introgression in hybrids between wild wheats uncovers the role of retrotransposons in reproductive isolation</i>
09:40	Antia Rodriguez Villalon, ETH Zurich: <i>Locally impaired protophloem differentiation systemically affects root branching</i>
10:00	Coffee break
10:30	Cris Kuhlemeier, U Bern: <i>How a plant survives pollinator failure</i>
11:00	Christiane Nawrath, U Lausanne: <i>Pathogen-resistance in cutin mutants: Rice is not Arabidopsis</i>
11:20	Matthias Erb, U Bern: <i>A functional continuum of plant secondary metabolites</i>
11:40	Didier Schaefer, U Neuchâtel: <i>Genetic Analysis of Gene Targeting in Physcomitrella patens</i>
12:00	Leisure, skiing etc.
17:00	Poster session with apéro
19:00	Dinner
20:30	Thomas Boller, U Basel, Farewell talk: <i>A botanical hike from the yeast vacuole to plant innate immunity and symbiosis</i>
21:15	Jean-Pierre Métraux, U Fribourg, Farewell talk: <i>Plants, microbes and life</i>
22:00	Socializing at the hotel bar

Program

Friday, 30 January

08:30	Bernhard Schmid, U Zurich: <i>Evolutionarily increased performance of plant species mixtures</i>
09:00	Debora Gasperini, U Lausanne: <i>Multilayered organization of jasmonate signaling in the regulation of root growth</i>
09:20	Philipp Schlüter, U Zurich: <i>Genic differences between Ophrys orchids with different pollinators</i>
09:40	Niko Geldner, U Lausanne: <i>The endodermis – a tale of two cell types</i>
10:00	Coffee break
10:30	Roman Ulm, U Geneva: <i>UV-B photoreceptor signalling in Arabidopsis</i>
11:00	Bruno Müller, U Zurich: <i>The role of Purine Permeases in controlling Cytokinin Signaling Domains</i>
11:20	Claudia Cosio, U Geneva: <i>Mechanisms of mercury accumulation in the aquatic plant Elodea nuttallii</i>
11:40	John Pannell, U Lausanne: <i>Mating-system evolution in metapopulations and range expansions</i>
12:00	Departure



TALK

1	Olivier Voinnet
2	Christoph Ringli
3	Timothy Paape
4	Lorenzo Borghi
5	Wilhelm Gruissem
6	Consuelo De Moraes
7	Michael Hothorn
8	Christian Parisod
9	Antia Rodriguez-Villalon
10	Cris Kuhlemeier
11	Christiane Nawrath
12	Matthias Erb
13	Didier Schaefer
14	Thomas Boller
15	Jean-Pierre Métraux
16	Bernhard Schmid
17	Debora Gasperini
18	Philipp Schlueter
19	Niko Geldner
20	Roman Ulm
21	Bruno Müller
22	Claudia Cosio
23	John Pannell

1 Olivier Voinnet

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Tba

Olivier Voinnet

ETH Zurich, Institute of Agricultural Sciences

> SPSW researcher portfolio
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Christoph Ringli



Flavonols influence plant development via modulating auxin homeostasis

Christoph Ringli, Benjamin Kuhn, Sanae Errafi, Rahel Bucher, Petre Dobrev, Markus Geisler, Laurent Bigler, Eva Zazimalova

Institute of Plant Biology, University of Zürich

Flavonols are a class of secondary metabolites known to influence cellular process both in plant and animal organisms. In Arabidopsis, flavonols are glycosylated mainly by glucose and rhamnose, resulting in a number of different flavonol glycosides. The mechanism by which flavonols influence plant development is only starting to be understood. It is also not yet clear, whether all flavonols or only specific ones are actively influencing cellular processes.

Previously, we had identified the rol1-2 mutant of Arabidopsis, which develops a strong growth defect that is induced by flavonols. Flavonol glycosylation is modified in rol1-2 seedlings, presumably resulting in the accumulation of more active flavonol glycosides. One of the effects induced by these flavonols is a reduction in the auxin transport activity and, hence, a change in auxin concentrations in the seedling (1, 2).

We have identified a number of EMS-induced suppressors of the flavonol-induced growth defect of rol1-2. One of these cause a defect in a flavonol-specific glycosyltransferase, resulting in the depletion of one type of flavonol glycosides. The absence of these flavonol glycosides changes auxin concentrations back to wild-type levels. However, this happens not via modulating auxin transport activity in the plant but rather by changing levels of the auxin precursor IAN, auxin derivatives, and auxin catabolites. This reveals a new mechanism by which flavonols influence auxin homeostasis and, hence, plant developmental processes.

1 Ringli et al., Plant Cell, 2008, 20: 1470-1481

2 Kuhn et al., Plant Physiol, 2011, 156: 585-595

> SPSW researcher portfolio
<https://swissplantsciencweb.ch/nc/research/home/portfolio/ringli>

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Zinc accumulation and transcriptional response in the allopolyploid *Arabidopsis kamchatica*

Tim Paape¹, Masaomi Hatakeyama¹, Jun Sese², Rie Shimizu-Inatsugi¹, Kentaro K. Shimizu¹

¹ Institute of Evolutionary Biology and Environmental Studies and Institute of Plant Biology, University of Zurich, Switzerland

² Computational Biology Research Center (CBRC), AIST, Tokyo, Japan

The allopolyploid species *A. kamchatica* is derived from the diploid progenitors *A. halleri* subsp. *gemma* and *A. lyrata* subsp. *petraea*, the former being a known heavy metal hyperaccumulating species. Compared with the diploid parental species, *A. kamchatica* leaf zinc levels were of the order expected for a high zinc accumulating species with significantly greater leaf accumulation than non-accumulating *A. lyrata*. Using de novo assembled reference genomes of both diploid parents and naturally collected *A. kamchatica* from Japan and Alaska we characterize gene regulation among 19,820 homeologous gene copies using RNAseq. We detected significant regulatory changes in 1009 homeologous gene copies in leaf and 3349 genes in root tissues in two allopolyploid genotypes. Expression patterns are consistent with several previously identified candidate genes in *A. halleri* involved in heavy metal tolerance and hyperaccumulation such as *A. kamchatica* orthologs of *HMA3*, *HMA4*, *MTP1*, *MTP3*, *ZIP9* and *ZIP10*, among others. In particular the hyperaccumulator ATPase gene *HMA4* shows 15–70 fold increased expression in *A. halleri* vs. *A. lyrata* derived copies in the allopolyploid. A large genomic region surrounding shows significantly different patterns of sequence diversity consistent with strong selective constraint and hitch-hiking on the *A. halleri* derived *HMA4* region, providing evidence that despite its hybridization with a non-tolerant *A. lyrata* like ancestor, the allopolyploid species maintains metal homeostasis mechanisms likely derived from the *A. halleri* common ancestor.

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Asymmetric localizations of the ABC transporter PaPDR1 trace paths of directional strigolactone transport

Lorenzo Borghi¹, Joëlle Sasse¹, Siby Simon², Christian Gübeli¹, Guo-Wei Liu¹, Xi Cheng³, Jiří Friml², Harro Bouwmeester³ and Enrico Martinoia¹

¹ Institute of Plant Biology, University of Zürich, Zürich, Switzerland

² Institute of Science and Technology Austria, Klosterneuburg, Austria

³ Wageningen UR, Wageningen University, NL

Strigolactones (SL), firstly discovered as germination stimulants for parasitic weeds, are carotenoid-derived phytohormones that play major roles in inhibiting lateral bud outgrowth and promoting plant-mycorrhizal symbiosis. Furthermore it was shown that strigolactones are involved in the regulation of lateral and adventitious root development, root cell division, secondary stem growth and leaf senescence. Recently, we discovered the strigolactone transporter *Petunia axillaris* PLEIOTROIC DRUG RESISTANCE 1 (PaPDR1), which is required for efficient mycorrhizal colonization and inhibition of lateral bud outgrowth. However, how strigolactones are transported through the plant remained unknown. Here we show that PaPDR1 exhibits a cell-type, specific asymmetric localization in different root tissues. In root tips, PaPDR1 is co-expressed with the strigolactone biosynthetic gene *DAD1* (*CCD8*) and it is localized at the apical membrane of root hypodermal cells, presumably mediating the shootward transport of strigolactone. Above the root tip, in the hypodermal passage cells (HPCs) that form gates for the entry of mycorrhizal fungi, PaPDR1 is present in the outer-lateral membrane, compatible with its postulated function as strigolactone exporter from root to soil. Transport studies using radiolabeled strigolactone support our localization studies, since a *papdr1* mutant displays impaired transport of strigolactones out of the root tip to the shoot as well as into the rhizosphere. In line with this, *DAD1* expression and PIN1/PIN2 levels change in plants deregulated for PDR1 expression, indicative of variations in endogenous strigolactone contents. In conclusion, our results suggest that the polar localizations of PaPDR1 mediate directional shootward strigolactone transport as well as localized exudation into the soil.

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Wilhelm Gruissem

Function of the *Arabidopsis* Retinoblastoma-related protein in stem cell maintenance and differentiation

Asuka Kuwabara, Johannes Fütterer, **Wilhelm Gruissem**

Department of Biology, ETH Zurich



The Retinoblastoma-related (RBR) protein is the plant homolog of the negative cell cycle regulator pRb. Recent findings have shown that in addition to its canonical function in cell cycle control, RBR is involved in stem cell maintenance and cell differentiation [1]. In *Arabidopsis*, RBR is encoded by a single gene and *RBR* loss-of-function mutants are gametophytically lethal. Conditional mutants using inducible RNAi-mediated down-regulation of the RBR protein (RBRi) have provided new insights into the function of RBR during plant development. Here we are focusing on the role of RBR in meristemoids, the pluripotent stem cells that give rise to epidermal and stomatal lineage cells. After rounds of amplification by asymmetric cell divisions, the meristemoid cell commits to differentiation into the guard mother cell (GMC). The final GMC division then forms the stomata with two guard cells. In the conditional RBRi mutant, the stomatal lineage is affected when RBR is reduced. Meristemoids cannot undergo asymmetric cell division and rapidly over-proliferate, indicating that their cell identity is compromised. Most of the over-proliferating meristemoids fail to undergo further differentiation, suggesting that RBR functions as a key switch to regulate meristemoid proliferation and differentiation into guard cells. Transcription profiling of sorted *TMMp::GFP*-marked meristemoids revealed the deregulation of key genes for cell cycle regulation and differentiation. Ectopic expression of a dominant-negative CDKB1;1 protein (CDKB1;1-DN) in RBRi plants can partially restore meristemoid function when RBR is down-regulated. Together, the results suggest that RBR regulates timing of the meristemoid cell cycle and connects it to asymmetric division and the stomatal cell lineage.

Supported by the Swiss National Science Foundation

1. Gutzat R, Borghi L and Gruissem W (2012) Emerging roles of RETINOBLASTOMA-RELATED proteins in plant development. Trends in Plant Sci 17: 139-148.

> SPSW researcher portfolio
<https://swissplantsciencweb.ch/nc/research/home/portfolio/gruissem>

Consuelo De Moraes

Chemical signaling in interactions among plants, insects, and other organisms

Consuelo De Moraes

Department of Environmental Systems Science, ETH Zürich



Olfactory cues mediate diverse interactions among plants and other organisms. Over the past two decades a key focus of chemical ecology has been on elucidating the role of constitutive and induced plant volatiles in conveying information to insect herbivores and their natural enemies. It is now well established that volatile blends can carry complex information about the identity and status of emitting plants, and that insects and other organisms perceive and respond to such cues in sophisticated and sometimes surprising ways.

A great deal of research has documented the role of volatiles in tri-trophic interactions and explored implications for the control of herbivorous pests in agricultural ecosystems, and recent work is extending these insights in a variety of exciting directions. These include increasing attention to population-level and evolutionary processes occurring in natural communities, to the role of volatile chemistry in mediating interactions in complex environments in which plants simultaneously interact with a diverse community of other organisms (including microbial symbionts and pathogens as well as insects), and on the perception of olfactory cues by plants themselves. In this talk, I will describe these developments and discuss recent work from our program in each of these areas.

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Michael Hothorn

The twists and turns of plant membrane signaling

Julia Santiago, Jacobo Martinez, Ulrich Hohmann, **Michael Hothorn**

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

Plants have evolved membrane-integral leucine-rich repeat (LRR) receptor kinases that can sense diverse extracellular ligands, ranging from small steroid molecules to peptides and intact proteins. These stimuli can trigger diverse responses, allowing plants to grow, to develop and to interact with their environment. I will present how plant LRR receptor kinases sense their ligands at the cell surface, transduce these signals across the membrane and finally trigger cytoplasmic signaling cascades. We have recently uncovered that LRR kinases rely on essential helper proteins to perform these complex tasks. I will discuss the roles of these co-receptor kinases in ligand sensing, signal transduction and in enabling signaling crosstalk at the plasma membrane.



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Christian Parisod



Genome reorganization and introgression in hybrids between wild wheats uncovers the role of retrotransposons in reproductive isolation

Natacha Senerchia¹, François Felber^{1,2}, **Christian Parisod**¹

¹ Laboratory of Evolutionary Botany, University of Neuchâtel
² Musée et Jardins botaniques cantonaux, Lausanne

Interspecific hybridization leads to new interactions among divergent genomes, revealing the nature of genetic incompatibilities having accumulated after the origin of species. Conflicts associated with misregulation of transposable elements in hybrids expectedly results in their activation and genome-wide changes that may be a key issue to species boundaries. Here, we first used experimental reciprocal F1 hybrids between three *Aegilops* species to assess restructuring and epigenetic repatterning in relation to the strength of reproductive isolation. Asymmetrical reorganization of long terminal repeat retrotransposons (LTR-RTs) predicted to cause conflicting interactions matched differential survival of F1 hybrids. In particular, non-random sequence losses and methylation appeared coherent with the necessary repression of incompatible TE loci in sustaining hybrid viability. We then used natural hybrid zones between *Aegilops geniculata* and *Aegilops triuncialis* to further tackle the consequences of such conflicts for maintaining species boundaries in face of recurrent gene flow. Coherent with insights from experimental populations, conflicting LTR-RTs presented asymmetrical introgression and specific reorganization among natural hybrids. Genomic conflicts involving LTR-RTs are thus highlighted as key incompatibilities supporting reproductive isolation and shaping species boundaries in the long term.

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Locally impaired protophloem differentiation systemically affects root branching

Antia Rodríguez Villalon¹, Bojan Gujas² and Christian S. Hardtke²

¹ ETH Zürich
² University of Lausanne

Antia Rodríguez Villalon

Protophloem is a specialized vascular tissue in growing plant organs, such as root meristems. In *Arabidopsis* mutants with impaired primary root protophloem differentiation, *brevis radix (brx)* and *octopus (ops)*, meristematic activity and consequently overall root growth are strongly reduced. Second site mutation in the protophloem-specific presumed phosphoinositide 5-phosphatase *COTYLEDON VASCULAR PATTERN 2 (CVP2)*, but not in its homolog *CVP2-LIKE 1 (CVL1)*, partially rescues *brx* defects. Consistent with this finding, *CVP2* hyperactivity in wild type background recreates a *brx* phenotype. Paradoxically however, while *cvp2* or *cvl1* single mutants display no apparent root defects, the root phenotype of *cvp2 cvl1* double mutants is similar to *brx* or *ops*, although as expected *cvp2 cvl1* seedlings contain more phosphatidylinositol-4,5-bisphosphate. Thus, tightly balanced phosphatidylinositol-4,5-bisphosphate levels appear essential for proper protophloem differentiation. Genetically, *OPS* acts downstream of phosphatidylinositol-4,5-bisphosphate levels, since *cvp2* mutation cannot rescue *ops* defects, whereas increased *OPS* dosage rescues *cvp2 cvl1* defects. Finally, all three mutants display higher density and accelerated emergence of lateral roots, which correlates with increased auxin activity in the root differentiation zone. This phenotype is also created by application of peptides that suppress protophloem differentiation, *CLAVATA3/EMBRYO SURROUNDING REGION 26 (CLE26)* and *CLE45*. Thus, local changes in the primary root protophloem systemically shape overall root system architecture.

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How a plant survives pollinator failure

Cris Kuhlemeier, Hester Sheehan, Michel Moser, Avichai Amrad, Holly Summers, Sarah Robinson, Agata Burian, Korinna Esfeld

Institute of Plant Sciences, University of Bern

Cris Kuhlemeier



The recruitment of animals to perform pollination services is a major innovation in angiosperm evolution. Animal-mediated pollination, however, is exquisitely vulnerable to fluctuations in pollinator availability, a problem that has become more urgent due to climate change. Plants can evolve to attract a new pollinator, or alternatively, reduce their reliance on pollinators. We use a combination of genetics, genomics, biophysics and behavioral ecology to study how plants adapt to the loss of a pollinator. The genus *Petunia* (Solanaceae) comprises species that are adapted to distinct pollinators, bees, nocturnal hawkmoths and hummingbirds. The genetic architecture of shifts in pollination syndromes is surprisingly simple. Even the modification of single genes can strongly affect pollinator preference and thereby cause reproductive isolation.

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Christiane Nawrath

Pathogen-resistance in cutin mutants: Rice is not *Arabidopsis*

Imène Garroum, Przemyslaw Bidzinski, Jean-Benoit Morel and
Christiane Nawrath

Department of Plant Molecular Biology, University of Lausanne

In the rice genome, a single gene shows a high homology to the *Arabidopsis* PEC1/ABCG32 gene encoding an ABCG transporter hypothesized to function in cutin precursor export. A conserved function of the rice OsABCG31 in cutin synthesis has been therefore postulated. Because of the extreme dwarf phenotype of the null *Osabcg31* mutant, RNAi lines have been generated to enable a detailed study of the mutant phenotypes. Rice RNAi lines had a decreased deposition of cutin and the polymer contained low amounts of oxygenated aliphatic monomers, two features also observed in the *Arabidopsis pec1* mutant. Reductions in cutin deposition correlated well with an increased permeability of the cuticle and characteristic ultrastructural changes in the leaf cuticle. Thus, OsABCG31 represents a true orthologue of the *Arabidopsis* PEC1/ABCG32.

Cutin mutants of *Arabidopsis*, including the *pec1/abcg32* mutant, have an unexpected resistance to the fungal pathogen *Botrytis cinerea*. The susceptibility of *osabcg31* mutants and RNAi lines to the agronomical important rice blast fungus *Magnaporthe grisea* has therefore been assessed. A strong resistance to *Magnaporthe* has been observed in inoculated *osabcg31* plants. Interestingly, the mechanism leading to pathogen resistance shows characteristic differences between the rice-*Magnaporthe* and *Arabidopsis-Botrytis* interaction. In *Arabidopsis*, defense gene expression is very low in cutin mutants before inoculation, but quickly induced by the medium potato dextrose broth used for *Botrytis* inoculation. In rice, defense genes are constitutively expressed in *OsABCG31* plants, which may explain the distinctive dwarf phenotype of *OcABCG31* plants and other cutin mutants in rice.

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Matthias Erb

A functional continuum of plant secondary metabolites

Matthias Erb

Institute of Plant Sciences, University of Bern

Plant secondary metabolites are abundant and structurally diverse. However, knowledge about their functional diversity is still limited, which constrains evolutionary frameworks that try to explain their prevalence in the plant kingdom. We manipulated secondary metabolite biosynthesis and processing in maize (*Zea mays*) and dandelion (*Taraxacum officinale*) and used the resulting genetic resources to understand their importance for plant-environment interactions. Through this approach, we uncovered a number of surprising features of the studied metabolites. Maize benzoxazinoids for instance do not only function as direct defenses, but also influence the expression of other defensive traits, with important consequences for aphid and leaf pathogen resistance. Furthermore, benzoxazinoids are exuded into the rhizosphere, where they are misused as foraging signposts by specialized root feeders. We are currently elucidating other functions of benzoxazinoids, including their capacity to shape the root microbiome and their impact on nutrient uptake and higher trophic levels, to explain why they are released in such significant amounts by the roots. In dandelion, we focus on sesquiterpene lactones, which are of central importance for plant resistance, but seem to influence the expression of other defensive traits as well. Overall, our research suggests that plant secondary metabolites act along a functional continuum, and that some of them may be in an evolutionary transition state between simple resistance factors and within-plant signals.



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Genetic analysis of gene targeting in *Physcomitrella patens*

Didier G. Schaefer

Lab of Mol. and Cell. Biology, Institute of Biology, University of Neuchâtel

The moss *Physcomitrella patens* ranks No1 for its competency for gene targeting (GT) among Eukaryotes, with frequencies around 90% and efficiencies above 1/1000 cells. To characterise this unique feature, we have analysed *Physcomitrella* deletion mutants in conserved core genes of the DNA DSB repair pathway.

At the phenotypic level, the absence of *PpMre11* or *PpRad50* generates a severe developmental phenotype, while loss of function of *PpRad51*, of *PpCtIP* and of the Rad51 paralogues leads to a detectable growth retardation phenotype without impacting morphogenesis. These data pinpoint to an important role of MRE11 and RAD50 in coordinating DNA repair with plant development. Deletion of all these genes except *PpNbs1* also led to increased sensitivity to UV-B, MMS and bleomycin. Furthermore, deletion of *PpRad51* and of the Rad51 paralogues increased the rate of spontaneous mutation in the genome, while no mutator phenotype could be detected in the absence of *PpMre11* or *PpRad50*.

GT was completely abolished in the absence of *PpRad51* and of the Rad51 paralogues and its efficiency was significantly reduced in *PpCtIP*, *PpRad54*, *PpMre11* or *PpRad50* deletion mutants. On the other hand, illegitimate integration frequencies were enhanced in the absence of *PpRad51*, *PpRad54* and of the Rad51 paralogues, but not significantly affected in *PpRad52*, *PpCtIP*, *PpMre11* or *PpRad50* deletion mutants. Globally these data are consistent with a direct involvement of the DNA DSB repair pathway in transgenesis in moss. Further analyses of these and new *Physcomitrella* DNA repair mutants will allow us to understand the molecular mechanisms that control this balance.



Didier Schaefer

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Farewell talk: A botanical hike from the yeast vacuole to plant innate immunity and symbiosis

Thomas Boller

Department of Environmental Sciences – Botany, University of Basel,
Zürich-Basel Plant Science Center

When I was a boy, my family undertook a hiking tour of several days every year, in Switzerland and the neighbouring countries. On our first tour, when I was ten, I remember carrying a microscope in my backpack to study the microflora of ponds and fountains on our way. Ever since, I have a passion for botanical hikes, and in this farewell talk, I would like to take you on such a hike through my career.

My interest in plant physiology was awakened by Professor Philippe Matile [1932-2011] at ETH Zürich, who started his lecture not with a blackboard full of body plans or dry chemical formulas (as other professors did), but with the biography of the medieval philosopher Nicholas of Cusa [1401-1464], the first advocate of experimental science. Thus, I started my PhD in his laboratory. During my PhD on yeast vacuoles (1974-1977), I made the acquaintance of Prof. Hans Kende [1937-2006] and joined him for a postdoc (1977-1978) in the MSU/DOE Plant Research Laboratory, to study the vacuoles of real plants. Serendipitously, I also discovered there the key enzyme of ethylene biosynthesis, ACC synthase. In 1979, I went as a postdoc to the Botanical Institute of Basel to study chitinases and glucanases as a plant defense against fungi. In due course, I became a professor of botany in Basel, and 1987-2001, I also served as a group leader at the Friedrich Miescher-Institute. At the FMI, my team discovered that plant cells are able to perceive bacterial flagellin – a phenomenon that has now become the paradigm for “plant innate immunity”. At the same time, at the Botanical Institute, together with Prof. Andres Wiemken, we studied microbes as friendly partners of plants, both in the nodule symbiosis of legumes and in the very widespread symbiosis of mycorrhiza. During the last ten years, I had much pleasure to organize field studies for biology students, together with my colleague Dr. Vreni Wiemken, to show them how plant physiology works in real life. Hopefully, I can continue to guide such botanical hikes – for young students, for interested lay people, or for my grandchildren – for many years to come.

Thomas Boller

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Farewell talk: Plants, microbes and life

Jean-Pierre Métraux

Department of Biology, University of Fribourg



Jean-Pierre Métraux

Over the past years, we have examined if cuticular components liberated by fungi penetrating through the leaf surface during an infection might be recognized by the plant and act as DAMPs. In agreement with this model, treatment of plants with synthetic cuticle breakdown products leads to enhanced resistance and associated defense responses. Also, *Arabidopsis thaliana* plants expressing a fungal gene encoding cutinase produce a more permeable cuticle and display immunity to *Botrytis cinerea* together with induced defenses. Similarly, ectopic treatment of *A. thaliana* with a fungal cutinase also results in enhanced resistance with attending defense responses. We have now isolated and are characterizing several *insensitive to cutinase (icu)* mutants that remain susceptible to *B. cinerea* after cutinase treatment. We are also studying a number of mutants with defects in cuticle biosynthesis that display enhanced cuticular permeability and strong resistance to *B. cinerea*. Possibly, perception of cuticular breakdown products and/or a faster perception of PAMPs/DAMPs through the permeable cuticle could explain the increased resistance. But we have also asked the question if modifications in the cuticle structure/composition might affect the composition of the microflora on the phylloplane that in turn might affect the resistance to pathogens. When the resistant cuticle mutant *bodyguard* is grown under sterile conditions, the resistance to *B. cinerea* is lost, indicating a role for microbes in the resistance. In comparison, the cuticle mutant *lacs2* remains resistant under the same conditions. These observations highlight the importance of “neutral” phylloplane microbes in plant resistance. They open a number of conceptual considerations on the problem of plant resistance to pathogens.

The second part of the talk will be dedicated to the delicate enterprise of autobiographical reflections with various highlights of my thirty five years of activity.

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Evolutionarily increased performance of plant species mixtures

Sofia van Moorsel, Debra Zuppinge-Dingley, Terhi Hahl and
Bernhard Schmid

Institute of Evolutionary Biology and Environmental Studies and URPP
Global Change and Biodiversity, Universität Zürich

The diversity of plant communities shapes the evolutionary trajectory of plants growing together over short time frames. We propagated plants from a long-term experiment in the grasslands of Jena, Germany, where plant diversity has been manipulated to investigate the consequences of biodiversity loss since 2002. Plants from high-diversity communities (mixtures) outperformed those from low-diversity communities (monocultures) when replanted in mixtures. Most strikingly, mixture plants differed more strongly between species in functional traits, leaf thickness, height, and reproductive output, than did monoculture plants. This phenomenon so far was only known as long-term evolutionary character displacement, allowing species to differentiate from each other over geological time scales.

The newly observed rapid evolution of character displacement over ecological time scales, leading to enhanced mixture performance, was a general feature of the investigated plant species and communities and not restricted to a few specific cases. Although the phenomenon may seem implausible as it has all the features expected under a process of “community evolution”, the fact that it exists should encourage novel approaches in plant breeding. Breeding plants for increased mixture yields could access a huge untapped potential. This applies to both, mixtures of different species in mixed cropping systems and to mixtures of different varieties within a single crop, as we have recently shown for mixtures of genetically modified wheat lines. Compared with the currently used monoculture strategies, cultivating high-diversity crops will not only provide higher yields but also do so with lower inputs of pesticides and fertilizers, thus increasing sustainability.



Bernhard Schmid

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Debora Gasperini

Multilayered organization of jasmonate signaling in the regulation of root growth

Debora Gasperini, Aurore Chételat and Edward E. Farmer

Department of Plant Molecular Biology, University of Lausanne

Insect attack or mechanical wounding triggers the synthesis of the hormone jasmonate (JA) to activate defense responses and inhibit leaf growth. We have found that a JA-dependent shoot-to-root growth-reducing signal also reaches belowground tissues and, similarly to exogenous JA applications, decreases root growth by reducing meristem cell number and cell elongation. However, mutants in *NINJA*, a co-repressor of JA responses, display constitutive JA signaling and shorter roots in the absence of JA due to a defect in cell elongation only. It is likely that other regulatory mechanisms are still present in the root meristem of *ninja* mutants to repress JA signaling and maintain normal meristem size. To investigate these mechanisms we characterized the spatial organization of JA signaling components and their contribution to the *ninja* mutant phenotype. We have also identified a gain-of-function allele of the master activator of JA responses *MYC2*, which exhibits ectopic JA signaling and reduced root growth through reduced meristem cell number and cell elongation. Thus, individual elements of the JA signaling pathway affect root growth in different manners. When mutants compromised in specific growth processes are combined, synergistic effects in root growth are observed. Our data reveal a primary function of JA in coordinating organ size after wounding and suggest the existence of several layers of negative regulation that, in a healthy plant, keep JA responses at bay to allow normal root development.

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Genic differences between *Ophrys* orchids with different pollinators

Khalid E.M. Sedeek, Philipp M. Schlüter

Institute of Systematic Botany, University of Zurich

Mediterranean orchids of the genus *Ophrys* are well known for cheating their pollinators, mimicking sexual signals of insects in their floral odours, to achieve highly specific pollination. We studied reproductive barriers between closely related *Ophrys* species, and the genomics of species divergence by employing a population genomic approach. Pollinator-mediated reproductive isolation, probably primarily mediated by floral odours, is the strongest barrier to gene flow. The genomes of *Ophrys* species revealed remarkably little differentiation; only a small proportion of loci are strongly and consistently differentiated between species, and among these are candidate genes for odour biosynthesis.

Philipp Schlüter

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The endodermis – a tale of two cell types

Niko Geldner

Department of Plant Molecular Biology, University of Lausanne

Classical anatomical literature on the endodermis defines three different stages of endodermal differentiation. The first being the formation of Casparian strips, the second the formation of suberin lamellae all around the endodermal surface (the third does not exist in *Arabidopsis*). However, some endodermal cells never form suberin lamellae. These cells were suggestively termed „passage cells“, hinting towards a possible function of those cells in continued uptake of nutrient within a mature and otherwise non-permissive endodermis. Passage cells were shown to be always occurring above xylem poles. I will report on the occurrence of passage cells in *Arabidopsis* and on our efforts to understand the mechanisms controlling their numbers and positioning. I will also present our efforts to describe their physiological relevance and the influence of environmental stresses on their formation.

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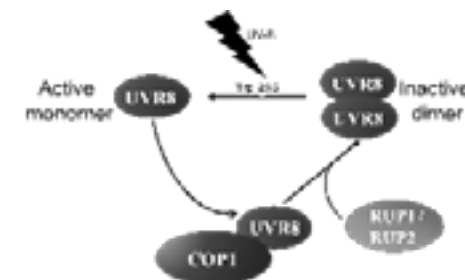


UV-B photoreceptor signalling in *Arabidopsis*

Ruohe Yin, Roman Ulm

Department of Botany and Plant Biology, University of Geneva

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. UVR8 exists as a homodimer that instantly monomerises upon UV-B absorption via specific intrinsic tryptophans which act as UV-B chromophores. 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”. Negative feedback regulation of the pathway is provided by the WD40-repeat proteins REPRESSOR OF UV-B PHOTOMORPHOGENESIS 1 (RUP1) and RUP2, which facilitate UVR8 redimerization, disrupting the UVR8-COP1 interaction.



I will present our latest understanding of the early events in UV-B signal transduction.

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The role of Purine Permeases in controlling Cytokinin Signaling Domains

Evelyne Zürcher, **Bruno Müller**

Institut of Plant Biology, University of Zürich

Visualisation of the Cytokinin signaling domains by a synthetic reporter reveals their precise localisation throughout the plant life cycle. Tight control of the signaling domains is important for normal development. Various mechanisms, such as localised ligand production and inactivation, or control of cellular competence to sense a stimulus, ensure no harmful ectopic signalling centres occur. Genetic evidence suggests a ligand transport system that operates at the tissue level as an additional level to control the localisation of signaling output. The expression patterns, genetic and cellular functions of members of the family of PURINE PERMEASES (PUP), transmembrane proteins that can transport Cytokinins, suggest that selected PUP genes define a prepattern for the cytokinin response in different developmental contexts.



Bruno Müller

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Mechanisms of mercury accumulation in the aquatic plant *Elodea nuttallii*

Claudia Cosio

Institute F.-A. Forel, Department of Earth and Environmental Science, University of Geneva



In aquatic ecosystems, anthropogenic contamination with Hg is a topic of great concern, and threatens all levels of the ecosystems. Biomagnification of Hg in food webs is notably a big concern in aquatic ecosystems. In shallow waters the highly toxic methyl-Hg (MeHg) is formed and aquatic plants are the predominant primary producers playing a key role in Hg uptake in food webs. However, mechanisms of Hg accumulation are still unclear with earlier data suggesting passive uptake, while few recent data suggest carrier mediated accumulation.

The present study aimed at investigating the mechanism of Hg accumulation in a representative aquatic plant, *Elodea nuttallii*. High Hg tolerance and accumulation were observed in *E. nuttallii*. Competition with Cu resulted in a significant 97.2±0.6% inhibition of Hg uptake while other metals (Fe, Mg, Mn, Ca, K and Zn) had no significant effects on accumulation. RNAseq and RT-qPCR analysis further revealed a correlation between the level of expression of *EnCOPT1* gene and Hg exposure. As COPT1 is known to transport Cu from the surrounding medium inside cells in different organisms, we further tested the function of COPT1 in Hg accumulation in yeast and *Arabidopsis thaliana*. Analyses of *EnCOPT1* gene in yeast confirmed its ability to uptake Cu and confer tolerance to Hg. Lines of *A. thaliana* deficient and overexpressing COPT1 showed a clear correlation between the expression of *COPT1* and accumulation of Hg. Results supports the hypothesis that Hg is accumulated through the Cu homeostasis network in plants, further suggesting that Hg accumulation is carrier mediated, and not passive in plants. Mechanistic understanding of bioaccumulation of Hg in primary producers will strongly contribute to environmental risk assessment of Hg and will help environmental managers to take appropriate decisions to limit Hg transfer in food webs.

Claudia Cosio

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Mating-system evolution in metapopulations and range expansions

John Pannell

Department of Ecology and Evolution, University of Lausanne

It is a common finding that plant populations are enriched for an ability to self-fertilize at the edge of species' geographic ranges, often also showing high rates of self-fertilization. I will review two hypothesis for this pattern and introduce a third: because range edges are often reached by range expansion, the accompanying depletion of genetic diversity causes a loss of inbreeding depression, and this loss directly favours the automatic selection of selfing. I will illustrate this idea with data from two plant species, one in which colonisation has favoured the evolution of hermaphroditism from dioecy, and the other in which there has been a loss of self-incompatibility. Computer simulations reveal that mating-system transitions at the edge of a species' range can permeate back into ancestral conditions only when rates of recombination are low. Interestingly, selfing species often present reduced numbers of chromosomes, which might contribute to conditions favouring such a spread of self-fertilization. I will offer an intuitive explanation for this apparent dependence of the expansion of selfing on rates of recombination in the genome..

John Pannell

- 1 Sylvain Aubry
- 2 Célia Baroux
- 3 Emilie Demarsy
- 4 Simon Goepfert
- 5 Victor Golyaev
- 6 Manfred Heinlein
- 7 Stefan Hörtensteiner
- 8 Felix Kessler
- 9 Enrico Martinoia
- 10 Reto Nyffeler
- 11 Didier Reinhardt
- 12 Sebastian Streb
- 13 Michael Tognolli
- 14 Elisabeth Truernit
- 15 Samuel Wuest

1 Sylvain Aubry

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Not as green as cabbage-looking: Complex interplay between chlorophyll breakdown and pathogen responses in Arabidopsis

Sylvain Aubry, Bastien Christ and Stefan Hörtensteiner

Department of Plant Biology, University of Zürich

Detoxification of chlorophyll during leaf senescence in higher plants is a complex and tightly regulated process. It aims at opening the chlorophyll porphyrin ring to produce non-photoreactive degradation products, which are transport to the vacuole. Interestingly, three key enzymes, i.e. PHEOPHYTINASE, STAY-GREEN and PHEOPHORBIDE a OXYGENASE (PAO), involved in this pathway are co-regulated at the transcriptional level. We performed deep-sequencing of transcriptomes from single mutants for these genes, which as a common feature do not degrade chlorophyll and thus retaining the green leaf colour. Interestingly, despite a conserved senescence-specific signature, all three mutants show modifications in expression of genes involved in jasmonic acid related responses. In particular *pao1* that accumulates pheophorbide a presents several features mimicking pathogen responses: overexpression of JAZ genes and accumulation of camalexin. Combining LC-MS/MS, pharmacological and genetic approaches, we show that a complex tetrapyrrole-based signalling pathway mimicks these pathogen responses and, more generally, how this pathway might be used for plastid-to-nucleus signalling in mature and senescing leaves.

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Célia Baroux

The nucleus is more than a genetic container: non-random spatial organization of a triploid genome – what can that mean?

Ales Pecinka¹, Jorg Fuchs², Gregor Kreth³, Armin Meister², Ingo Schubert², Ueli Grossniklaus⁴ and Célia Baroux⁴

¹ MPI Plant Breeding Research, Cologne, Germany

² IPK Gatersleben, Germany

³ Kirchhoff-Institute of Physics, Universität Heidelberg, Germany

⁴ Institute of Plant Biology, Zürich-Basel Plant Science Center, University of Zürich, Switzerland

Referred to as a “monstruous embryo” in the early days of its discovery, the endosperm still remains a developmental curiosity for botanists: 1) for its developmental origin: the endosperm is a product of double fertilization, 2) for its fate: the endosperm is a short-lived compatriot and nurse tissue of the embryo in the seed, and 3) for its genetic constitution: the endosperm is triploid with two maternal and one paternal genome complements. But also for its nuclear organization: we found that unlike somatic nuclei, endosperm nuclei harbor an atypical nuclear organization with a dosage-sensitive heterochromatin fraction and a preferential association of two parental complements. I will report on our nuclear organization studies using chromosome painting, fluorescent in situ hybridization, high-resolution imaging, 3D processing and computed random model simulations. Whether this peculiar, non-random genome configuration is functionally relevant for epigenetic regulations in the endosperm will be discussed.



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Emilie Demarsy

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Thylakoid biogenesis and influence of the light environment

Emilie Demarsy, Rosa Pipitone, Felix Kessler

Laboratoire de Physiologie végétale, University of Neuchâtel

By being sessile, plants have developed capacity to adapt to environmental changing conditions. Among factors that affect plant growth and metabolism, light is maybe the most important parameter. Not only it provides the plant with energy, but it also serves as a signal to inform about the time of the day, the season, or importantly about the presence of competitive neighbors. Last but not least, during early stage of plant development light triggers the differentiation of chloroplasts, the crucial step ensuring the switch from heterotrophic metabolism of seeds to autotrophic metabolism of photosynthetic seedlings.

One of the specificities of the chloroplasts compared to the non-photosynthetic etioplasts is the presence of a sophisticated network of membranes called thylakoids, which host the photosynthetic machinery composed of protein complexes and surrounded by specific lipids. Biogenesis of thylakoids network is fundamental for chloroplast biogenesis. The transition from etioplast to chloroplast thus relies on massive synthesis of lipids and proteins that are accompanied by important changes at the ultrastructural level. How the thylakoid membranes are assembled and how light environment regulates this process is not clear, however. To fill this gap, we plan to combine high throughput and state-of-the art techniques such as lipidomics (collaboration with Gaetan Glauser, UniNE) and 3D electron microscopy (collaboration with Zeeman Lab, Zurich), in order to obtain a comprehensive understanding of this process at the systems biology level.

Here I present a comparative lipidomic analysis suggesting that thylakoid biogenesis strongly depends on light intensity but weakly on light quality.

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Simon Goepfert

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The tobacco genome sequence

Nicolas Sierro, James N.D. Battey, Sonia Ouadi, Nicolas Bakaher, Lucien Bovet, Adrian Willig, **Simon Goepfert**, Manuel C. Peitsch & Nikolai V. Ivanov

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

Nicotiana tabacum (common tobacco) is a major crop species and a model organism, for which only very fragmented genomic sequences have been available until recently. 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 (>70%) of which represented by repeats. As a species, *N. tabacum* ($2n=4x=48$) evolved through the interspecific hybridization of the ancestors of *Nicotiana sylvestris* ($2n=24$, maternal donor) and *Nicotiana tomentosiformis* ($2n=24$, paternal donor) about 200,000 years ago. Considerable interest has centered on understanding the origin, organization and evolution of the *N. tabacum* genome. Here we report high-quality draft genomes for three main tobacco varieties. These genomes show both the low divergence of tobacco from its ancestor genomes and display microsynteny with other Solanaceae species. We identify over 90,000 gene models and determine the ancestral origin of tobacco mosaic virus and potyvirus disease resistance in tobacco. We anticipate that the draft genomes will strengthen the use of *N. tabacum* as a versatile model organism for functional genomics and biotechnology applications.

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Victor Golyaev



Interactions of rice tungro bacilliform pararetrovirus and its protein P4 with plant RNA silencing machinery

Victor Golyaev, Rajendran Rajeswaran, Jonathan Seguin, Anna Zvereva, Laurent Farinelli, and Mikhail M. Pooggin

Institute of Botany, University of Basel, and FASTER SA, Geneva

Small interfering RNA (siRNA)-directed gene silencing plays a major role in antiviral defense. Virus-derived siRNAs inhibit viral replication in infected cells and potentially move to neighboring cells, immunizing them from incoming virus. Viruses have evolved various ways to evade and suppress siRNA production or action. Here we show that 21-, 22- and 24-nucleotide (nt) viral siRNAs together constitute up to 19% of total small RNA population of *Oryza sativa* plants infected with *Rice tungro bacilliform virus* (RTBV) and cover both strands of the RTBV DNA genome. However, viral siRNA hotspots are restricted to a short non-coding region between transcription and reverse transcription start sites. This region generates double-stranded RNA (dsRNA) precursor of siRNAs and, in pregenomic RNA, forms a stable secondary structure likely inaccessible to siRNA-directed cleavage. In transient assays, RTBV protein P4 suppressed cell-to-cell spread of silencing but enhanced cell-autonomous silencing, which correlated with reduced 21-nt siRNA levels and increased 22-nt siRNA levels. Our findings imply that RTBV generates decoy dsRNA that restricts siRNA production to the structured non-coding region and thereby protects other regions of the viral genome from repressive action of siRNAs, while the viral protein P4 interferes with cell-to-cell spread of antiviral silencing.

This work has been funded through Swiss National Science Foundation grant 31003A_143882 to M.M.P. and Swiss Government Excellence Scholarship to V.G, and in part published in *Molecular Plant-Microbe Interactions* (Rajeswaran, Golyaev et al. 2014).

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Manfred Heinlein



Myosins VIII and XI play distinct roles in *Tobacco mosaic virus* infection

Khalid Amari^{1,2}, Martin Di Donato¹, Valerian V. Dolja³,
Manfred Heinlein^{1,2}

¹ Department of Environmental Sciences – Botany, University of Basel

² IBMP-CNRS, Strasbourg, France

³ Oregon State University, Corvallis, USA

Viruses are obligatory plant cell parasites that depend on host cellular factors for their replication as well as for their local and systemic movement to establish infection. Recent studies indicate that plant virus infection involves myosin motor proteins. However, the exact role of myosins in the specific infection steps have not been addressed. To gain insight into the role of myosins in plant virus replication and transport, we investigated the cell-to-cell and systemic spread of *Tobacco mosaic virus* (TMV) upon inhibition of specific myosin classes by expression of the respective dominant-negative *N. benthamiana* myosin tails. We found that overexpression of tails of three class VIII myosins and tails of two class XI myosins significantly inhibits the local and long-distance movement of the virus. To explain this effect, we further show that inactivation of myosins XI-2 and XI-K affects the structure and dynamic behavior of the ER leading to the accumulation of the viral movement protein (MP) in large aggregates and to a delay in the targeting of the MP to plasmodesmata (PD). The inactivation of myosin XI-2 but not that of myosin XI-K affects the accumulation pattern of the 126k replicase subunit and TMV replication. The inhibition of myosin VIII-1, 2 or B blocks the accumulation of MP at PD and instead causes the accumulation of the protein at the plasma membrane. These results indicate that the *N. benthamiana* myosins XI-2 and XI-K, but not XI-F, play direct or indirect roles in the replication and intracellular movement of TMV and that myosins VIII-1, VIII-2 and VIII-B are required for the intercellular movement through PD. Together, our results demonstrate that the different processes involved in the cell-to-cell spread of TMV infection require specific myosins.

Amari K, Di Dinato M, Dolja VV, Heinlein M (2014) Myosins VIII and XI play distinct roles in reproduction and transport of Tobacco mosaic virus. *PLoS Pathog.* 10: e1004448

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Differences in dephytylation during chlorophyll breakdown in tomato leaves and fruits

Luzia Guyer¹, Silvia Schelbert Hofstetter¹, Bastien Christ¹, Bruno Silvestre Lira², Magdalena Rossi² and **Stefan Hörtensteiner¹**

Stefan Hörtensteiner

¹ Institute of Plant Biology, University of Zurich, Zurich
² Departamento de Botânica, Instituto de Biociências, Universidade de São Paulo, Brazil

Chlorophyll breakdown through the so-called PAO/phyllobilin pathway occurs in different plant tissues such as leaves and fruits. One key step of breakdown is the hydrolysis of phytol, which releases the pigment from the thylakoid membrane. During leaf senescence in *Arabidopsis* PHEOPHYTINASE (PPH) was shown to be crucial for dephytylating pheophytin (i.e. Mg-free chlorophyll), while in lemon fruits, CHLORO-PHYLLASE (CLH) is the phytol hydrolytic enzyme during ethylene-induced color break.

In this study, we chose tomato (*Solanum lycopersicum*) as a model plant to compare dephytylation during leaf senescence and fruit ripening. We show that the PAO/phyllobilin pathway is active in tomato and we identified tomato PPH (*SIPPH*), which, like its *Arabidopsis* ortholog, was specifically active on pheophytin and localized to chloroplasts. *SIPPH* was transcriptionally up-regulated during leaf senescence and fruit ripening, indicating it to be active in both organs. We could confirm this assumption for leaves of *SIPPH*-silencing lines which exhibit a stay-green phenotype after ethylene-induced senescence. However, in contrast to leaves, fruits of *SIPPH*-silencing lines were able to break down chlorophyll comparable to wild type. Interestingly, pheophytin accumulated transiently, but was detected to be at wild-type level in ripe fruits. Nevertheless, *SIPPH* hydrolytic activity could be measured in isolated chromoplasts, thus proving the presence and involvement of *SIPPH* in chlorophyll breakdown during fruit ripening. However, other hydrolases must be present (in addition), which are able to compensate for the absence of *SIPPH* in the silencing lines. Based on transcript profiles of the four tomato *CLH* genes, we assume that *SICLHs* are not the core hydrolytic enzymes in tomato fruits, but that additional unknown hydrolases are involved. In conclusion, we show that *SIPPH* is the major dephytylating enzyme during tomato leaf senescence, but in fruits other enzymes are active.

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Plastoglobules: plastid lipid droplets remodel the photosynthetic membrane

Felix Kessler

Institut de biologie, Université de Neuchâtel

Felix Kessler

The photosynthetic machinery consists of protein complexes embedded in the thylakoid lipid bilayer. To maintain optimal activity, it must adapt to constantly changing light and temperature conditions. Therefore, (and amongst other responses) the thylakoid lipid composition is continuously remodeled. This particularly concerns the neutral prenyl lipids. Plastoglobules (PG), lipid droplets attached to the curved region of the thylakoid stromal lamellae, play a key role in remodeling processes. PG have a neutral lipid core that is surrounded by a polar lipid monolayer contiguous with the thylakoid outer leaflet. Thus, PG constitute a microdomain at the thylakoid membrane. Lipid exchange between PG and the thylakoids likely occurs at the contact sites. The PG polar lipid monolayer is studded with enzymes, including regulatory kinases, that participate in thylakoid lipid de novo synthesis, repair and turnover. Using state-of-the-art lipidomics we will demonstrate how prenyl lipid composition is remodeled under high light stress and regulated by the plastoglobule-localized ABC1-like kinases K1 and K3.



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Enrico Martinoia



AtALMT9, a vacuolar malate/chloride channel involved in guard cell movement and salt stress

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Water availability is critical for crop production. Drought and salinity have a great impact on water uptake. Stomata play a central role in regulating CO₂ uptake required for photosynthesis and water consumption in response to changing environmental conditions. The aperture of the stomatal pore is regulated by changes in the osmotic potentials of the guard cells that are mainly achieved by changes in ion transport across cellular membranes. Despite the importance of anion transport, until recently the molecular identity of these transporters remained elusive. In the past decade the CLC, SLAC and ALMT protein families have been found to be involved in the transport of anions, shedding light on the nature of anion fluxes across the plasma and vacuolar membrane. Here, I will present data on the vacuolar malate activated chloride channel AtALMT9. I will show that this channel plays an important role in guard cell opening as well as during salt stress.

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Reto Nyffeler



Swiss herbaria provide historical distribution data to document large-scale regional species loss

Reto Nyffeler, Carmen Hiltbrand

Herbarium of the University of Zurich, Institute of Systematic Botany

The leafless hawk's beard (*Crepis praemorsa* (L.) Tausch) is a perennial dandelion confined to natural and semi-natural, summer-dry edges, meadows and pastures and open forests. It is rare and reported as declining in several western European countries, presumably due to habitat loss as a result of landscape changes and cessation of traditional land use. In Switzerland it is listed as vulnerable in the Red List of Threatened Ferns and Flowering Plants from 2002. This species shows a restricted distribution in four distinct regions (i.e., Central and Eastern Jura and Eastern Swiss Plateau, Bernese Prealps, and Northern Grison with nearby Rhine Valley). The current distribution is documented on the basis of 129 records with accuracy greater than 250 m and collected since 1980 as stored in the database of InfoFlora (www.infoflora.ch). The massive regional loss is very evident from a comparison with the historical distribution data housed in the Swiss herbaria. Some 272 specimens from 16 public herbaria dating back until 1806 contain adequate geographical information to allow georeferencing the documents to individual localities within municipalities. A plot of the distributional record provides the following insight: (1) complete regional loss for the Western part of the Jura in the Canton of Neuchâtel and in the Northern part of the Plateau in the Cantons of Schaffhausen; severe declines in the cantons of Thurgau and Zürich, and also in the Rhine Valley of the Cantons of Graubünden and St. Gallen; (2) current positive observations without a historical record are found in rather remote areas in the Jura of the Cantons of Bern, Basel-Landschaft and Solothurn, in the Bernese Prealps, and in the Prättigau of the Canton of Graubünden. This latter observation may be the result of a biased collection effort that was in the past focused on better accessible areas.

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Gibberellic acid mediates negative regulation of arbuscular mycorrhiza by phosphate

Eva Nouri, Rohini Surve, **Didier Reinhardt**

Department of Biology, University of Fribourg

Didier Reinhardt

Arbuscular mycorrhiza (AM) is the most wide-spread symbiosis of plants. It comprises the majority of land plants including all cereals and many other crops. A dedicated pathway in the plant mediates recognition of the fungal partner by the plant, and leads to establishment of the symbiotic interface for nutrient exchange. The sites of nutrient exchange are the arbuscules of the fungus, which are surrounded by the periarbuscular membrane of the host, which carries transporters for phosphate and other mineral nutrients that are provided by the fungus. When plants are grown under rich nutrient conditions that enable them to realize their maximal growth potential, AM colonization is repressed, thus reducing the drain of carbon by the fungus, which under these conditions does not confer any benefit the plant. In particular phosphate is known to inhibit AM (Breuillin et al., 2010; Nouri et al., 2014), but the underlying mechanism is unknown. We have taken a combinatorial transcriptomic, genetic, and physiological approach to elucidate the hormonal basis of this phenomenon.

We show that gibberellic acid (GA) inhibits AM symbiosis. GA is induced under conditions of high phosphate, which are inhibitory to fungal colonization. Finally, we used GA-defective plants to show that GA is required for P-dependent inhibition of AM. This work documents a new hormonal mechanisms that mediates negative feedback regulation of mycorrhizal colonization at elevated phosphate levels.

Breuillin et al. (2010) Phosphate systemically inhibits development of arbuscular mycorrhiza in *Petunia hybrida* and represses genes involved in mycorrhizal functioning. *Plant J.* 64, 1002-1017.

Nouri et al. (2014) Phosphorus and nitrogen regulate arbuscular mycorrhiza in *Petunia hybrida*. *PLoS One* 9 (3), e90841.

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Sebastian Streb



Establishing a universal method to predict protein complexes and generate protein interaction networks

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

Here, we show that with three basic native separation methods coupled to a proteomics approach, we can predict the subunit composition based on co-behavior of the proteins. Currently, we are able to define potential association in protein complexes for more than 2000 proteins in *Arabidopsis thaliana* and *Saccharomyces cerevisiae*. Surprisingly, the majority of the proteins assemble in multimeric long term complexes and the *in vivo* status of a protein in a monomeric form is rather exceptional.

The next goal is to develop a standard methodology which can be applied to any organism for which the genome is known with affordable cost for “standard” laboratory to study protein complex composition and changes in their biological samples of interest.

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Michael Tognolli

Dealing with mass spectrometry large-scale experiment data in UniProtKB/Swiss-Prot

Michael Tognolli¹, Lydie Bougueleret¹, Ioannis Xenarios^{1,2,3} and the Swiss-Prot group.

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We have developed a flexible pipeline for the selection, integration and continuous update of mass spectrometry proteomics data that are of suitable quality for UniProtKB/Swiss-Prot.

To deal with the heterogeneity of confidence levels in published material, and in order to keep the level of false positive as low as possible in UniProtKB/Swiss-Prot annotations, we have defined explicit metadata requirements and associated rules confidence thresholds that are used to filter the identification results as published in scientific journals. The stringency of these rules can be increased as methodologies improve.

Currently, our pipeline is limited to 6 model proteomes including *Arabidopsis thaliana*. The system includes a resource of high quality experimental peptides that uniquely match a single UniProtKB protein sequence. These peptides are used for annotation of UniProtKB/Swiss-Prot, and currently generate more than 33K reliable annotations of post-translational modifications.



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Elisabeth Truernit



The role of a Brassicaceae specific homolog group in vascular development

Mario Coiro, Signe Schmidt Kjølner Hansen, Elisabeth Truernit

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Phloem, the tissue for long distance carbohydrate transport, represents one of the most important innovations in the history of land plant evolution. However, despite its importance, at present we know very little about the genetic determinants of phloem development.

OCTOPUS (OPS), a membrane associated protein of unknown function, represents one of the few known phloem development regulators. It is expressed early during phloem development and locates to the basal side of phloem cells. Mutations in *OPS* result in gaps of undifferentiated cells in the root phloem cell files, reduced root growth, and simpler cotyledon venation patterns.

To understand the evolution of OPS and its function in phloem development, a phylogenetic analysis was conducted. OPS-like proteins seem to be present in all seed plants. An ancestral duplication in the eudicots generated two different classes of OPS-like (OPL) genes. OPS represents one of the three Class I genes in *Arabidopsis*.

Currently we are investigating the potential role of the other Class I genes, *OPL1* and *OPL2*, in vascular development. Preliminary data from our analyses will be presented.

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Samuel Wuest



Family-planning in a monocarpic plant

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We study resource allocation strategies of maternal plants towards their offspring. As plants have a modular body plan, they often initiate reproductive organs sequentially. The maternal plant has to balance current and future expenditure on offspring to produce an optimal number of seeds. Maternal control over investment in offspring can happen through a series of developmental decisions, such as changes in branch or fruit numbers, seed size or abortion of seeds. The hierarchy between these developmental units is however not well understood. Furthermore, the production of offspring often induces a global proliferative arrest in maternal meristems and suppresses the initiation of new reproductive units. We are examining the developmental and genetic bases of resource allocation hierarchies and feedbacks in the monocarpic plant *Arabidopsis thaliana*. Ongoing work will be presented:

Firstly, by manipulating maternal nutrient levels during different ontogenetic stages, we are characterizing this hierarchy in traits important for reproductive allocation. We have found that plasticity varies between traits and genotypes, and that partial uncoupling between normally correlated traits is possible.

Secondly, we have performed a genetic screen for extended maternal growth under greenhouse conditions. We have identified a handful of mutants that show an increase in total seed mass, and are currently in the progress of characterizing these. It is expected, that an increase in “fitness” will result from alteration in a process that exhibits trade-offs with reproduction.

Thirdly, we are studying the feedback controls that offspring exerts over maternal growth, using genome-wide expression studies. Meristematic tissues do not undergo senescence, as previously postulated; rather, they seem to enter a state of dormancy that is associated with signatures of hormonal and stress-related expression responses.

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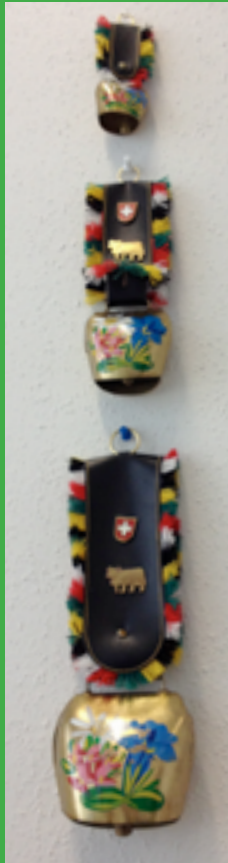
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