Swiss Plant Symposium 2022
13–15 June 2022
Meiringen, Switzerland

Venue
Parkhotel du Sauvage, Bahnhofstrasse 30, 3860 Meiringen BE, Switzerland

Scientific Program Committee
Roman Ulm, Marie Barberon, Emilie Demarsy, Teresa Fitzpatrick, Michael Hothorn, Luis Lopez-Molina, Yamama Naciri
University of Geneva

Conference Organization
Swiss Society of Plant Biology / Swiss Plant Science Web
Sylvia Martinez

swissplantscienceweb.ch

We gratefully acknowledge Syngenta’s financial support of the conference.
Welcome by the president

A lot of significant things have happened since the last SwissPLANT symposium held in 2020 in Ovronnaz. During the Strategic Meeting, participants agreed that the Swiss Plant Science Web enrolls in the process of waking up the dormant Swiss Society of Plant Physiology. The society should remain inclusive in the sense that it aims to represent plant science in its full breadth. The overall goal of this endeavor is to strengthen plant science research in Switzerland by giving it a voice and highlighting its importance.

Since Ovronnaz, we had to cancel the 2021 SwissPLANT conference and the one in January 2022. Nevertheless, a lot went on in the background to revive a long-lasting structure for plant science research in Switzerland. After several zoom meetings and General Assemblies, the newly formed society committee succeeded in forming a renewed society with historical continuity that incorporates new perspectives. Christian Fankhauser, Thomas Boller, Kerstin Bomblies and Cyril Zipfel together with Sylvia Martinez, prepared new bylaws, adapted the society’s goals to current scientific developments, and re-activated the society’s membership and alliance within the Swiss Academy of Sciences (SCNAT).

Our new name is Swiss Society of Plant Biology. And our Society is part of the SCNAT platform Biology. The Swiss Plant Science Web (SPSW) has merged with the Swiss Society of Plant Biology and will incorporate its vigor. The annual SwissPLANT symposium will remain a core activity of our network. We will also hold the General Assembly before we start the SwissPLANT symposium to “talk science” and discuss fruitful collaborations.

Fortunately, the Scientific Conference Committee from Geneva was not deterred by the pandemic and insisted on holding the meeting – this year in June. I cordially thank Roman Ulm, Emilie Demarsy, Michael Hothorn, Luis Lopez-Molina, Yamama Naciri for their perseverance. I am also very grateful to Sylvia Martinez, our executive secretary, who organizes the meeting to make your stay both, smooth and inspirational.

Hence, I welcome you in Meiringen to discuss current advances in plant science research “made in Switzerland”. As usual, we aim to present research on form, function, genetics, ecology, and evolution of plants. Moreover, we strive for an integrative approach to improve understanding of the complexity and diversity of the green world. We want to spread the word that plants are the fundamental components of the earth’s biosystem and are therefore at the center of the life sciences rather than at their margins.

Enjoy

Christian Fankhauser, president of the Swiss Society for Plant Biology

The Swiss Society of Plant Biology and its portal – the Swiss Plant Science Web – serve as an information and communications tool for academic plant sciences in Switzerland. The network enhances the visibility of plant biology and the achievements of plant science research for society. By joining forces, it advances research and education efforts in Switzerland.

Program

Monday, 13 June 2022

15:30 Swiss Society of Plant Biology, General Assembly 2022

17:00 Welcome apéro

17:30 Opening remarks by Christian Fankhauser, chair Swiss Society of Plant Biology

17:35 Opening remarks by Roman Ulm, chair Scientific Program Committee

Session I

17:40 Etienne Bucher | Agroscope
Using crop genome dynamics for stress adaptation and the challenges in breeding innovation in Europe

18:00 Martina Legris | U Lausanne
Phototropins perceive light direction in the leaf to regulate blade flattening

18:20 Wojciech Wietrzynski | U Basel
Architecture and maintenance of thylakoid membranes visualized by Cryo-electron Tomography

18:40 Dinner

Session II

20:20 Darina Koubínová | U Neuchâtel
Simple sequence repeat (SSR) mining in the chloroplast genomes of Ophioglossaceae ferns

20:40 Thomas Wicker | U Zurich
Molecular dynamics and evolutionary history of wheat centromeres

21:00 Markus Geisler | U Fribourg
A phospho-switch provided by LRR receptor-like kinase, ALK1/QSK1/KIN7, prioritizes ABCG36/PEN3/PDR8 transport toward defense

21:20 Christian Fankhauser | U Lausanne
A combination of plasma membrane sterol biosynthesis and autophagy is required for shade-induced hypocotyl elongation
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<td>08:20</td>
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<td>08:40</td>
<td>Klaus Schlaeppi</td>
<td>U Basel Exudate-microbiome interactions on Maize roots</td>
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<td>09:00</td>
<td>Joelle Sasse Schläpfer</td>
<td>U Zurich How dynamic is root exudation?</td>
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<td>09:20</td>
<td>Celia Baroux</td>
<td>U Zurich Citrullination – a novel epigenetic modification unlocking germline fate?</td>
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<td>Pauline Jullien</td>
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<td>Charles Pouchon</td>
<td>U Geneva &amp; CJBG Phylogenomic study of the whole Alpine flora: When bioinformatic development is needed!</td>
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<td>11:20</td>
<td>Luis Lopez-Molina</td>
<td>U Geneva The <em>Arabidopsis</em> endosperm is a temperature-sensing tissue that implements seed thermoinhibition through phyB and PIF3</td>
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<td>11:40</td>
<td>Stefanie Ranf</td>
<td>U Fribourg Mechanistic insights into plant-bacteria interactions</td>
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<td>Poster session, with apéro</td>
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<td>20:20</td>
<td>Cyril Zipfel</td>
<td>U Zurich Perception of a conserved family of plant signaling peptides by the receptor kinase HSL3</td>
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<td>20:40</td>
<td>Sara Simonini</td>
<td>U Zurich When it’s the right time to divide: conflicting parental influence guides cell cycle reactivation at fertilization</td>
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<td>Stefan Grob</td>
<td>U Zurich Paramutation in <em>Arabidopsis</em> is linked to 3D genome folding</td>
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<td>21:20</td>
<td>Diana Santelia</td>
<td>ETH Zurich <em>Arabidopsis</em> guard cell chloroplasts import cytosolic ATP for starch turnover and stomatal opening</td>
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Germline separation from the soma is key to sexual reproduction in multicellular organisms. This process occurs at drastically different times during development in animals and plants. While the germline is set aside during embryogenesis in animals, plant precursors differentiate de novo during the adult phase, in floral organs. Despite these very distinct developmental strategies, we found a remarkable conservation of large-scale chromatin reprogramming in plant spore mother cells (SMC) (She et al., Development 140, 2013) and animal primordial germ cells (PGC) (Hajkova et al., Nature 452, 2008). One striking similarity is the eviction of somatic linker histones that precedes a breadth of changes in chromatin structure and composition in SMC. In a quest for potential post-translational modifications regulating H1 eviction, we found evidence for a citrullination-ubiquitination module to operate specifically in the SMC. Furthermore, pre-meiotic eviction of H1 seems to serve post-meiotic fate and to control gametophytic competence. This suggests an essential role for H1 citrulination in SMC to unlock germline fate.
**Volatile-mediated interaction between plant-associated beneficial microorganisms and phytopathogenic fungi**

**Sébastien Bruisson**, Abhishek Anand, Nicolas David Rappo, Floriane L’Haridon, Laure Weisskopf

Department of Biology, University of Fribourg

Many beneficial microorganisms contribute to plant resistance towards biotic and abiotic stresses. Recently, there has been growing evidence that plants are protected from diseases by their microbiome and the volatile organic compounds (VOCs) they emit could have a major role in this process. Emission of VOCs is an important means of communication among microorganisms. These volatiles have various effects, they contribute to the stabilization of microbial communities, they can attract or repel different species, promote growth or display antimicrobial properties. Recently, several pieces of evidence have shown that the volatilome emitted by a microorganism depends on the volatiles of its surrounding. Thus, the volatilome of two different microbes grown together is different from the sum of the two individuals grown separately. These differences may include inhibition and promotion of various compounds, and more interestingly, the production of new compounds. However, the set up used so far to highlight these kinds of interactions did not allow to determine which compounds are responsible for the modifications and who is the emitter of the new compounds. To solve this problem, we have developed a solution enabling us to trap the whole volatilome of an organism and to use it to expose another one unilaterally. It is thus possible to study the volatile-mediated interactions more precisely by identifying more easily the compounds responsible for the changes in the volatilome and the emitter of any newly produced compound.

**Using crop genome dynamics for stress adaptation and the challenges in breeding innovation in Europe**

Haoran Peng1, Maria Estefania Lopez2, David Roquis1, Mahnaz Katouzi1, Victoria Widrig2, Javier Sanchez Martin2 and Etienne Bucher1

1 Crop Genome Dynamics Group, Agroscope
2 Department of Plant and Microbial Biology, University of Zurich

Accelerating climate change and ongoing wars have reminded us of the importance of wheat to feed the global population. It has further highlighted the central role that crop breeding must take to contribute to fight these challenges. And yet, even though the emergency could not be clearer, innovations in crop breeding are blocked at all levels in Europe. In this presentation I will show how we have developed a novel crop breeding method that is based on endogenous transposable element mobilization and the induction of random epimutations. I will present how this novel method can for instance produce high resistance to powdery mildew in wheat. We then take advantage of these results to identify new bioactive compounds against important crop pathogens. This project will also help us to have a better understanding of processes occurring in plant-associated microbial communities that could help us to find new solutions to protect crops against diseases. New strategies could be introduced using volatile compounds able to activate plant defenses or able to trigger the release of antimicrobial compounds by the native microbiome.
Genomic local adaptation of a generalist plant species to pollinator communities, soil, and climate

Frachon Léa, Arigo Luca, Rusman Quint, Poveda Lucy, Qi Weihong, Scopece Giovanni, Schiestl Florian P.

Department of Systematic and Evolutionary Botany, University of Zurich

The combined effect of changes in pollinator communities, and the direct impact of soil and climate variation on plant-pollinator interactions can strongly affect the reproductive success of flowering plants. However, knowledge of the adaptive potential of plants to complex ecological networks and the underlying genetic mechanisms is still limited. Based on a pool-sequencing approach of 21 natural populations of *Brassica incana* in Southern Italy, we combined a genome-environmental association (GEA) analysis with a genome scan for signature of selection to discover genetic variants associated with pollinator communities, edaphic and climatic variation. We demonstrated that *B. incana* is locally adapted to both single pollinator species and the overall pollinator interactions. Interestingly, we observed a significant number of genetic variants shared between the soil texture (fine silt) and the visits of bumblebees and hoverflies, while few genetic variants involved in both pollinator and climate variation were identified. Our results highlight the adaptive potential of generalist species to complex biotic interactions, and the importance of considering multiple environmental factors to describe their adaptive landscape.

A combination of plasma membrane sterol biosynthesis and autophagy is required for shade-induced hypocotyl elongation

Yetkin Çaka Ince1, Anne Sophie Fiorucci1, Martine Trevisan1, Vinicius Costa Galvão1, Johanna Krahmer2, Leonore Wigger2, Sylvain Pradervand2, Laetitia Fouillen3, Pierre Van Delft3, Sebastien Mongrand1, Héctor Gallart-Ayala3, Julijana Ivanisevic1 and Christian Fankhauser1*

1 Center for Integrative Genomics, Faculty of Biology and Medicine, University of Lausanne
2 Genomic Technologies Facility, Faculty of Biology and Medicine, University of Lausanne
3 Laboratoire de Biogénèse Membranaire, UMR 5200, Univ. Bordeaux, CNRS, 33140 Villenave d’Ornon, France.
4 Metabolomics Platform, Faculty of Biology and Medicine, University of Lausanne

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Plant growth ultimately depends on fixed carbon, thus the available light for photosynthesis. Due to canopy light absorption properties, vegetative shade combines low blue (LB) light and a low red to far-red ratio (LRFR). In shade-avoiding plants, these two conditions independently trigger growth adaptations to enhance light access. However, how these conditions, differing in photosynthetically-available light, similarly promote hypocotyl growth remains unknown. Using RNA sequencing we show that these two features of shade trigger different transcriptional reprogramming. LB induces starvation responses, suggesting a switch to a catabolic state. Accordingly, LB promotes autophagy. In contrast, LRFR promotes anabolism including biosynthesis of plasma-membrane sterols downstream of PHYTOCHROME-INTERACTING FACTORS (PIFs) acting in hypocotyls. Genetic analyses show that in vegetative shade the combination of sterol biosynthesis and autophagy is essential for hypocotyl growth promotion. We propose that vegetative shade enhances hypocotyl growth by combining autophagy-mediated recycling and promotion of specific lipid biosynthetic processes.
A phosho-switch provided by LRR receptor-like kinase, ALK1/QSK1/KIN7, prioritizes ABCG36/PEN3/PDR8 transport toward defense

Based on its proposed substrate preferences, the ABC transporter, ABCG36/PDR8/PEN3, from the model plant Arabidopsis stands at the cross-road between growth and defence. Recently, ABCG36 was shown to export a few indolic compounds, including the auxin precursor, indole-3-butyric acid (IBA), and to be implicated in the export of the major phytoalexin of Arabidopsis, camalexin, although clear-cut proof of camalexin transport activity is still lacking.

Here we provide strong evidence that ABCG36 catalyses the direct, ATP-dependent export of camalexin over the plasma membrane, however, most likely in functional interplay with non-camalexin transporting ABCG isoforms.

We identify the leucin-rich repeat receptor-like kinase, Auxin-induced LRR Kinase1 (ALK1/KIN7/QSK1), as a functional kinase to physically interact with and phosphorylate ABCG36.

ABCG36 phosphorylation by ALK1 represses unilaterally IBA but not camalexin export leading to a prioritization of ABCG transport toward defense. As a consequence, phosho-dead mutants of ABCG36, like alk1 and abcg36 alleles, are hypersensitive toward infection with the root pathogen, F. oxysporum, caused by elevated fungal progression.

Our findings indicate a novel, direct regulatory circuit between a receptor kinase and an ABC transporter determining transporter substrate specificity. It appears that growth and defense balance decisions in plants are performed on the transporter level by means of a reversible phosho-switch.

Paramutation in Arabidopsis is linked to 3D genome folding

Paramutation is one of the earliest described and most prominent epigenetic phenomena. It is best described as an “infectious” epigenetic state, whereby a transcriptional state can be transferred from one locus to another. The transmission of epigenetic states leads to the violation of Mendelian segregation of phenotypic traits. Hence, it has fascinated geneticists for decades.

Despite being widespread in various eukaryotes, the underlying mechanisms of paramutation remain poorly understood.

In an ongoing project, we investigate paramutagenic effects in silenced transgenic Arabidopsis lines, for which we have previously shown that their transcriptional state (silenced vs. active) is strongly associated to a specific 3D genome folding signature.

Our latest results indicate that the yet unknown paramutation-inducing-agent is likely non-chromosomal and possibly cell-to-cell mobile. Therefore, classic hallmarks of epigenetics, such as DNA methylation and histone modification may not be directly involved.

We currently focus our efforts to uncover this agent to better understand the mechanistic basis of paramutation initiation and maintenance in Arabidopsis.
Delving into the mechanisms of root xylem plasticity

Ora Hazak, Salves Cornelis, Samy Carbonnel, and Sara Vimercati
Department of Biology, University of Fribourg

In plants, xylem tissues transport water, minerals, and signaling molecules to maintain efficient long-distance communication and water supply. During embryogenesis, the precursors of xylem are formed and they divide and differentiate immediately with the seed germination to make the functional water-conducting tissue. Remarkably, growing root continuously monitors the soil environment, and developing root xylem tissues are influenced by stress conditions. We still do not have a clear picture of the molecular mechanisms underlying root xylem plasticity and many key regulators are still missing. In our work, we study how receptor-peptide-dependent pathways regulate xylem formation in normal and stress conditions. First, we focused on the group of small peptides called CLE peptides and their receptors BARELY ANY MERISTEM (BAM). We could identify CLE peptide genes, that are specifically expressed in xylem and we found that they facilitate lignification. To understand better the mechanism of BAM-CLE-mediated cell lignification, we performed proteomics studies. We found several candidates interacting with BAM1 in presence of a xylem-specific CLE peptide. Our data imply, that BAM1-CLE module may directly affect the lignin biosynthesis machinery, and this plays a central role not only in development but also in adaptation to high salinity.

MET2a and MET2b DNA methyltransferases are required for trans-generational methylome stability

Louis Tirot1, Diane M.V. Bonnet1, Marco Catoni2, Pauline E. Jullien*1
1 Institute of Plant Sciences, University of Bern, Bern
2 University of Birmingham, Birmingham, UK
* Corresponding author: Pauline E. Jullien, pauline.jullien@ips.unibe.ch

In plants, DNA methylation patterns are relatively stable though generation. However, several changes of DNA methylation occur during sexual reproduction. Such process is thought to be necessary to ensure genomic stability by maintaining the proper silencing of transposable elements (TEs). MET1 is the main DNA methyltransferase that ensure TEs silencing in the model plant Arabidopsis thaliana. Indeed, in a met1 mutant, TEs reactivation cause a pleiotropy of phenotypes due to the presence of new insertion. In wild Arabidopsis accession, it was hypothesized that a homologue of MET1, MET2a might play a role in TEs silencing. In this paper, we study in detail the function of MET2a as well as its closely related homologue MET2b. We showed that MET2a and MET2b proteins are detectable in mature central cell where they are addressed to the cell nuclei. MET2a and MET2b are likely functional DNA methyltransferases as they could partially complement the met1 mutation. MET2a and MET2b are regulating the ovule transcriptome prior to fertilisation. Interestingly, the plant methylome is not globally affected by mutations affecting met2a and/or met2b. Their effect on the methylome is revealed when introduced in a met1 background where we could identify several DMRs which were surprisingly mostly hypermethylated DMRs.

Finally, we show that met2a;met2b lead to an increased transgenerational silencing of the FWA locus or transgene. Overall, our work suggests that MET2a and MET2b are involved in a non-cell autonomous regulation of the embryo DNA methylation.
Atypical kinases ABC1K1 and ABC1K3 maintain plastoquinone homeostasis in the chloroplast electron transport chain

Felix Kessler
Laboratory of plant physiology, University of Neuchâtel

Photosynthesis depends on an electron transport chain (ETC) embedded in the thylakoid membrane. Apart from photosynthetic protein complexes and membrane lipids, thylakoid membranes contain prenyl quinones (plastoquinone, phyloquinone, tocopherols). These function as lipid anti-oxidants and electron carriers in the ETC. They can be consumed by reaction with omnipresent reactive oxygen species and must be replenished and recycled constantly. This is where plastoglobules (PG; lipid droplets attached to the thylakoids) come into play. They harbor a large proportion of the prenyl quinones that function in thylakoids. This together with some of the associated metabolic enzymes and a handful of other proteins, including atypical kinases and fibrillins. It stands to reason that prenyl quinones are trafficked between PG and thylakoids but the evidence is little. Here, it will be shown that two atypical kinases ABC1K1 and -K3 located in PG contribute, in opposing fashion, to the maintenance of constant plastoquinone concentration in the ETC. In a “push-pull” model, ABC1K1 allocates fresh plastoquinone from PG to thylakoids whereas ABC1K3 retains it in PG. The process has been termed “plastoquinone homeostasis”.

Unraveling the genetic control of disease resistance in outbreeding forage crop species

Roland Kölliker, Lea A. Frey, Florian Goettelmann, Bruno Studer
Molecular Plant Breeding, Institute for Agricultural Sciences, ETH Zurich

Forage grasses and legumes are important components of permanent and temporary grasslands, contributing to sustainable ruminant livestock production. Forage crops are challenged by a range of fungal and bacterial pathogens and disease resistance is one of the main breeding targets. Forage crop cultivars are usually bred as populations consisting of many different genotypes which makes fixation and introgression of resistance traits demanding. We thus aim at developing genomics-based tools to facilitate resistance breeding.

In Italian ryegrass (Lolium multiflorum), QTL mapping in a bi-parental mapping population consisting of 306 F1 progeny identified a major QTL for resistance to bacterial wilt (caused by Xanthomonas translucens pv. graminis). Furthermore, pooled-sequencing in a large bi-parental F2 population identified one genomic location significantly associated with anthracnose resistance and consisting of three genes orthologous to putative resistance genes in Medicago truncatula. The QTL and candidate genes identified provide a valuable resource for developing genomics-assisted strategies for resistance breeding in forage crops.
Final text: 

**Phototropins perceive light direction in the leaf to regulate blade flattening**

*Martina Legris, Christian Fankhauser*

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

Leaves are the main photosynthetic organ in plants, and their anatomy optimizes light absorption and gas exchange. One conserved feature of leaves is their thin flat blade. To grow flat leaves, plants rely on a genetically controlled developmental pattern, but also integrate environmental signals. In particular, light perceived by the blue light receptors phototropins is required for leaf flattening, with the null *phot1phot2* mutant showing curled leaves in *Arabidopsis*. In hypocotyls and stems phototropins perceive light direction, but whether this was conserved in leaves was unknown. To address this, we performed a detailed spatiotemporal characterization of phototropin function in *Arabidopsis* leaves. We found that, similar to their role in hypocotyls, phototropins perceive light direction, and control the spatial pattern of auxin signaling to ultimately regulate cell expansion. However, phototropin signaling components in the leaf partially differ from hypocotyls. Moreover, the light response on the upper and lower sides of the leaf blade suggests a partially distinct phototropin signaling network on each side. Overall, our results show that directional blue light perception by phototropins is a key aspect of leaf development, and that studying phototropin signaling in leaves is a promising field to uncover new mechanisms underlying their action.
The *Arabidopsis* endosperm is a temperature-sensing tissue that implements seed thermoinhibition through phyB and PIF3

Urszula Piskurewicz¹, Maria Sentandreu¹, Gaëtan Glauser² and Luis Lopez-Molina¹³

¹ Department of Botany and Plant Biology, University of Geneva
² Neuchâtel Platform of Analytical Chemistry, Université de Neuchâtel
³ Institute of Genetics and Genomics in Geneva (iGE3), University of Geneva

Seed thermoinhibition, the repression of germination under high temperatures, prevents seedling establishment under potentially fatal conditions. Thermoinhibition is relevant for ecology, phenology and agriculture, particularly in a warming globe. The temperature sensing mechanisms and signaling pathways sustaining thermoinhibition are unknown. We found that thermoinhibition in *Arabidopsis thaliana* is not autonomously controlled by the embryo but is rather implemented by the endosperm surrounding the embryo. High temperature is sensed through endospermic phyB by accelerating its reversion from the active signaling Pfr form into the inactive Pr form, as described in seedlings. This leads to stabilization of endospermic PIF3, which represses the expression of the endospermic ABA catabolic gene *CYP707A1* and promotes endospermic ABA synthesis and release towards the embryo to block its growth. Furthermore, endospermic ABA represses embryonic PIF3 accumulation that would otherwise promote embryonic growth. Hence, under high temperatures PIF3 exerts opposite growth responses in the endosperm and embryo.

The *Sapotaceae* of Madagascar: molecular genetics for conservation

Yamama Naciri, Carlos Galan Boluda, Aina Randriarisoa, Camille Christe, Charles Pouchon, Laurent Gautier

Laboratoire de Systématique végétale et Biodiversité, Université de Genève & Conservatoire et Jardin botaniques, 1292 Chambéry

On Madagascar, the family *Sapotaceae* currently encompasses 11 genera and around 95 described species. They are hardwood, slow-growing trees, mainly found in primary lowland evergreen humid forests but have radiated to all biomes including the dryest environments. Their life traits and reproductive strategy are perfectly adapted to the long turnover of untouched forest, and they rapidly disappear in anthropized landscapes. As they are appreciated for their mechanical qualities, their illegal logging in protected areas further weakens and threatens species’ natural populations. This is why we undertook a revision of the family to accurately circumscribe and name species, while defining their threat categories in order to protect them efficiently.

We used sequence capture and NGS technologies to generate more than 500 nuclear genes on a large number of herbarium and fresh specimens to address issues at the genus, species and population levels. Phylogenetic reconstructions were obtained under the Multi-Species-Coalescent framework and population genetics approaches were applied when the sampling was large enough. In all genera presently analysed the number of recovered species is 50-100 % higher than initially forseen. Several species complexes were identified for which population genomics helped disentangling the species and processes involved. A new generic circumscription had to be proposed that shed light on flower evolution and resulted in the genus *Faucherea* to be subsumed in *Labourdonnaisia*. This work will serve as a basis for a field book for in situ identification and in herbaria. It will be designed to reach also a non-specialist audience including local people involved in conservation incentives and reforestation programs.
Phylogenomic study of the whole Alpine flora: When bioinformatic development is needed!

Charles Pouchon1,3, Nikolaus E. Zimmermann2, Sébastien Lavergne3
1 Laboratoire de Systématique végétale et Biodiversité, Université de Genève & Conservatoire et Jardin botaniques, 1292 Chambésy
2 Swiss Federal Research Institute WSL, 8903 Birnensdorf
3 Laboratoire d’Ecologie Alpine, CNRS, Université Grenoble-Alpes, Grenoble, France

Understanding the assembly rules of alpine plant communities and the historical and contemporary processes that shape biodiversity is of paramount importance to preserving biodiversity in the face of global and climate changes. The OriginAlps project (LECA and WSL) aims to understand the past macroevolutionary dynamics of the whole Alpine Flora and to analyse the co-variation and scale dependence of taxonomic, phylogenetic and functional diversity on community structures that have resulted from evolutionary processes. To do this, 4,500 species were collected and sequenced at very low coverage for assembling chloroplast genomes (cpDNA), which are overrepresented in cells, in order to infer phylogenetic relationships at a biome-wide scale. However, numerous bioinformatic challenges remain to accurately obtain such data in organisms with complex genomic structures as for mitochondrial genomes in plants or for cpDNA in some plant families, where traditional plastome assembler failed. In such context, I developed ORTHOSKIM, a user-friendly pipeline, to perform in silico capture of targeted sequences without assembling whole organelle genomes through global genomic assemblies and mapping onto reference databases. This pipeline allowed us to capture cpDNA genes for 1278 additional libraries to the 3223 ones previously assembled, representing 1167 new species, 436 new genera and 28 new families, critical to accurately infer evolutionary relationships of the whole Alpine Flora. Importantly, this pipeline also allows the capture of any nuclear data, as ones targeted at the CJBG from hybrid capture libraries, and works well on genomic and transcriptomic data obtained from both well-preserved and degraded DNA, which will be of interest for the broad plant scientist community.

Mechanistic insights into plant-bacteria interactions

Stefanie Ranf
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My lab studies the dynamic interplay between plant hosts and bacteria at the molecular, cellular and physiological level. A major aspect of this work is a mechanistic understanding of how plant receptors sense and control microbial colonisation. Pattern-recognition receptors at the cell-surface sense so-called microbe-associated molecular patterns and activate broad-spectrum pattern-triggered immunity. We identified the receptor kinase LORE (LIPOOLIGOSACCHARIDE-SPECIFIC REDUCED ELICITATION) in Arabidopsis thaliana as PRR that senses 3-hydroxy fatty acid metabolites of medium chain-length, such as 3-hydroxydecanoic acid (3-HDA), released by Gram-negative bacteria (1,2). LORE alias SD1-29 belongs to the class of S-domain-1 (SD1) receptor kinases. How S-domain receptor kinases are activated and trigger downstream signalling is largely unknown. To unravel the mechanism of 3-HFA sensing by LORE and activation of downstream PTI signalling is largely unknown. To unravel the mechanism of 3-HFA sensing by LORE and activation of downstream PTI signalling at the molecular level, we apply a combination of biochemistry, genetics, computational modelling, and natural diversity screening. Complementarily, we investigate remodelling of the cell envelope as a bacterial virulence strategy to promote plant colonisation. I will present an overview of our current and planned work.

How dynamic is root exudation?

Sarah Brecht, Alexandra Siffert, Joelle Sasse Schläpfer

Institute for Plant and Microbial Biology, University of Zurich

Plants produce a vast variety of metabolites, ranging from simple sugars and amino acids to complex secondary metabolites with many functions, among them defense and signaling. A mixture of such plant-derived compounds, or root exudates, is found in the rhizosphere, the part of soil adjacent to roots majorly shaped by plants. Root exudates serve as nutrients and signaling compounds to the microbial community present and are thus a means to shape how plants interact with the belowground microbiome.

Little is known about the dynamics of root exudation, about diurnal signatures, adjustment of exudation to presence of different beneficial or pathogenic microbes, to environmental factors such as different soils. Also, it is mostly unclear to what degree plants regulate exudation, and if transporter proteins are major players in exudation.

We investigate the effects of experimental and biological factors on exudation, establishing a framework to study exudation in multiple plant species.
EXHIBITION

Exudate-microbiome interactions on Maize roots

Lisa Thoenen1,3, Marco Kreuzer2, Pierre Matteo1, Tobias Zuest1, Marco Hetc1, Rémy Bruggmann2, Matthias Erb1, Klaus Schlaeppi1

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Plants secrete a complex array of compounds from their roots to the surrounding soil and thereby interact with the surrounding root microbes. Plant root exudates can have many functions including to act as semiochemical for the recruitment of specific microbes, to serve as carbon substrates for microbial growth, or to structure the composition of the microbiome. Mechanistically however, relatively little is known how root microbes deal and cope with specialized plant exudates. Here we investigated toxicity, tolerance, and metabolism of plant-derived benzoxazinoids, a group of bioactive and antimicrobial secondary metabolites of grasses including crops such as maize. We have built a culture collection of maize root bacteria to study their growth and metabolic capabilities towards benzoxazinoids.

Using synthetic community experiments we discovered that the maize root microbiota divided labor and cooperated in the degradation and metabolism of benzoxazinoids. We further found a high functional specialization in metabolizing the typical secondary metabolites of their native host. Our work points to microbial adaptation to host-specific exudates, which could explain the composition host-specific microbiomes.

Machine learning of image and transcriptome data of Arabidopsis and wheat polyploid plants in natura

Kentaro K. Shimizu1,2, Toshiaki Tamashige1, Jianqiang Sun3, Reiko Akiyama1, Takao Goto4, Moeko Okada1,2, Misako Yamazaki1, Yasuhiro Sato1, Rie-Shimizu-Inatsugi1, Yoko Kamiya2, Tomohiro Ban2, Ken Kuroki1, Shuhei Nasuda2, Jiro Sugisaka3, Hiroshi Kudoh1, Atsushi J. Nagano4, Thomas Wicker2, Beat Keller2, Tanaka Kenta2, Junichi Akita9, Aya Tonouchi4, Yuki Shimahara4, Natsumaro Kutsuna4, Jun Sese10

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Plants in naturally fluctuating environments, or in natura, are subjected to complex conditions. We grew Arabidopsis and wheat polyploid plants for three seasons in natural fields in Switzerland and Japan. We collected RNA tissues every week and obtained 10,378 RNA-seq data. We developed automatic imaging system, obtained >10 millions of plant images, and extracted phenome information using deep learning.

Two analyses using machine learning will be discussed. First, we developed a cost-efficient automatic imaging system to analyze images using deep learning. Estimated amounts of anthocyanin of Arabidopsis species were verified experimentally. We estimated the daily amount of anthocyanin for five months in three seasons. Interestingly, the synthetic allopolyplloid A. kamchatica derived from A. hal-leri and A. lyrata recapitulated the pattern of natural accessions of A. kamchatica. This suggests that A. kamchatica inherits the environmental regulation of anthocyanin from the two parental species. Second, we analyzed the time-course transcriptome data of wheat using LASSO regression, a standard machine learning tool for variable selection. Regulatory mutations usable for fine-tuning of heading time were identified by modeling and were experimentally verified. Selected climatic variables are used to predict the heading time in response to warming.
When it’s the right time to divide: conflicting parental influence guides cell cycle reactivation at fertilization

Sara Simonini, Ueli Grossniklaus
Institute of Plant and Microbial Biology, University of Zurich

During the process of fertilization of sexually reproducing organisms, maternal and paternal gametes, egg and sperm respectively, fuses together to give rise to the zygote. Differently from animal, in flowering plants the so-called double fertilization involves a second female gamete, the central cell, from which originates the endosperm, a triploid and ephemeral tissue that nurtures and sustains the growth of the embryo. The fusion of the paternal and maternal gametes generates a series of dramatic events, including the re-activation of the cell cycle that is, somehow, strongly inhibited before fertilization to avoid premature division. Genetic evidences show that both parents exert a tight control over cell cycle progression: the mother represses cell division in the seeds, whereas the father provokes the opposite. The lack of this control then has dramatic and conflicting effects as the development of seed-like structure from unfertilized ovules, or suicidal cell divisions as result of unbalanced DNA content after fertilization. The molecular mechanisms underlying these processes are yet to be fully understood. I will present some of our recent data about the characterization of such mechanisms, showing how maternal factors keep female gametes quiescent, and how paternally-derived signals trigger cell cycle progression specifically at fertilization. Lastly, I will introduce how the knowledge acquired by the identification of such mechanisms lays the foundation for a new research direction that I will lead at the University of Zurich.

Loss of redundancy in a conserved developmental pathway during tomato domestication

Marion Brechet1, Anna Glaus1, Ludivine Lebeigle1, Giti Ghazi Soltani1, José Jiménez-Gómez2 and Sebastian Soyk1*
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Gene redundancy contributes to robustness of genetic systems but likely dampens the potential of beneficial mutations during crop domestication and breeding. In tomato, mutations in a conserved basic leucine zipper transcription factor gene are exploited for optimization of shoot architecture by delaying the transition to flowering. Here, we discovered that late flowering is suppressed in the wild tomato ancestor by a second-site mutation in a closely related gene, which leads to the loss of a conserved DNA-binding residue. We show that this cryptic variant arose during early tomato domestication and reduces transcription factor activity, thereby sensitizing domesticated genotypes for architectural modification. By applying genome editing in wild and domesticated tomato, we generate allelic series to facilitate fine-tuning of flowering and shoot architecture. Our findings highlight how standing genetic variation affects trait variation during domestication and breeding, and emphasize the need for a better understanding of genetic interactions for predictable crop improvement.
Phosphatidylcholines from *Pieris brassicae* eggs activate an immune response in *Arabidopsis*

Elia Stahl and Philippe Reymond

Department of Plant Molecular Biology, University of Lausanne

Recognition of conserved microbial molecules by plasma membrane localized receptors activates immune responses in plants, a process termed pattern-triggered immunity (PTI). Similarly, insect eggs trigger plant defenses that impede egg development or attract predators. By bioactivity-guided fractionation of eggs of the butterfly *Pieris brassicae*, followed by NMR spectroscopy and mass spectrometry of active fractions, we recently identified phosphatidylcholines (PCs) as immunogenic patterns from insect eggs. PCs induce salicylic acid accumulation, defense gene expression and cell death in *Arabidopsis*. We show here, that PCs additionally induce the phosphorylation of the immune regulatory mitogen-activated protein kinases (MAPK) 3 and 6, a rapid cytosolic Ca\(^{2+}\) influx, the accumulation of H\(_2\)O\(_2\), and trigger root growth inhibition, all of which constitute a hallmark of PTI. Strikingly, PC-treatment increases *Arabidopsis* resistance against microbial pathogens such as *Pseudomonas syringae* and *Botrytis cinerea*. Induction of plant immune signaling in response to PCs is dependent on functional Brassica-specific L-type lectin receptor kinase LecRK-I.8, which we previously reported to be an early component of insect egg perception in *Arabidopsis*.

Molecular dynamics and evolutionary history of wheat centromeres

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Even though multiple high-quality chromosome-scale genome assemblies of wheat, barley and rye recently became available, centromeres were still assembled in moderate to poor quality. This has prevented detailed and conclusive analysis of how *Triticaceae* centromeres evolve. Here, we analyzed two new genome assemblies of the diploid wheat *Triticum monococcum* (accessions TA10622 and TA299) in which centromeric regions were assembled practically without sequence gaps. We found that the wheat centromeres lack typical tandem satellite repeats and are instead comprised almost exclusively of two families of LTR retrotransposons: *RLG_Cereba* which comprises ~60% of the centromeric region and *LRG_Quinta* which contributes ~30%. The sizes of the currently active centromeres were determined to be 5-8 Mb through data on CENH3 histone modifications. Interestingly, our data indicate that the centromere on chromosome 1Am has moved by several Mb approximately 500,000 years ago. Additionally, the centromere of chromosome 4Am of *T. monococcum* accessions TA299 underwent multiple large inversions as recently as 10,000 to 40,000 years ago, which were then followed by a centromere shift of several Mb.

From our data, we modeled the molecular mechanisms that drive centromere evolution in *Triticaceae*: we propose that *RLG_Cereba* retrotransposons specifically target CENH3 modifications in active centromeres with the help of a chromodomain (contained in the integrase protein). *RLG_Cereba* also cross-mobilizes the non-autonomous *LRG_Quinta* family and inserts its new copies to the active centromeres. This results in a continuous flow of new retrotransposon copies into the active centromeres, while “older” sequences are “pushed” into pericentromeric regions. Our data suggest that *LRG_Quinta* retrotransposons contain signal sequences which, in turn, attract CENH3 modifications that re-new the epigenetic centromere signal. We also propose that chromosomal rearrangements and stochastic and unevenly distributed *RLG_Cereba* and *LRG_Quinta* insertions can trigger occasional shifts in the location of active centromeres.
Starch, the most abundant carbohydrate reserve in plants, occurs as insoluble, semi-crystalline granules, a property conferred by the major, branched glucan component amylopectin. Phase transition from a soluble to insoluble form depends on amylopectin architecture, with a compatible distribution glucan chain length, and branchpoint frequency/distribution enabling the assembly of semi-crystalline lamellae. My lab recently discovered that two starch-bound proteins, LIKE EARLY STARVATION 1 (LESV) and EARLY STARVATION 1 (ESV1), both of which possess an unusual, conserved carbohydrate-binding surfaces, appear to promote phase transition of amylopectin-like glucans. This was shown firstly in engineered yeast cells expressing the Arabidopsis starch biosynthetic machinery, where the expression of the LESV and ESV1 promotes the accumulation of glucans in an insoluble form. Second, overexpression of the proteins in Arabidopsis mutants compromised in amylopectin biosynthesis (such that they accumulate phytoglycogen – a soluble glucan with a suboptimal branching pattern – rather than amylopectin), promotes the phase transition of their soluble glucans into an insoluble form. In contrast, the mutation of LESV or ESV1 in this Arabidopsis background exacerbated the phytoglycogen-accumulating phenotype.

We propose a model wherein LESV serves a nucleating role, with its carbohydrate-binding surface helping to align glucans and promote their phase transition into semi-crystalline lamellae, which are then stabilized by ESV1. Since both proteins are widely conserved, we suggest that protein-facilitated glucan crystallization and stabilization may be a general feature of starch biosynthesis, including our key starch crops.

Thylakoid membranes of cyanobacteria and chloroplast scaffold an assortment of large protein complexes that work together to harness light energy. Thylakoids constantly adapt to diverse environmental conditions and stress. However, it has been a longstanding challenge to visualize how the thylakoid network organizes at molecular level to assert its morphology and finely tune the photosynthetic reactions. We use Cryo-electron Tomography (Cryo-ET) combined with novel methods to detect and map the native molecular landscapes of thylakoid membranes in cyanobacteria, green algae and vascular plants. Our tomograms show detailed membrane organization and its interactions with photosynthetic complexes embedded within it. We are able to provide insights into molecular forces that drive thylakoid stacking and reveal the distribution of photosynthetic complexes in appressed and non-appressed membrane domains. We extend this new approach into dissecting photosynthetic regulation at the scale of single protein complexes as well as mechanisms of thylakoid formation and maintenance during severe environmental changes.
Perception of a conserved family of plant signaling peptides by the receptor kinase HSL3

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Plant genomes encode hundreds of secreted peptides; however, relatively few have been characterized. We report here an uncharacterized, stress-induced family of plant signaling peptides, which we call CTNIPs. Based on the role of the common co-receptor BRASSINOSTEROID INSENSITIVE 1-ASSOCIATED KINASE 1 (BAK1) in CTNIP-induced responses, we identified the orphan receptor kinase HAESA-LIKE 3 (HSL3) as the CTNIP receptor via a proteomics approach. CTNIP binding, ligand-triggered complex formation with BAK1, and induced downstream responses all involve HSL3. Notably, the HSL3-CTNIP signaling module is evolutionarily ancient, predating the divergence of extant angiosperms. The identification of this signaling module will help establish its physiological role and provides a resource to understand further receptor-ligand co-evolution.

Patterns of variation in a novel defence reveal evolutionary drivers of chemical diversification

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Institute of Systematic and Evolutionary Botany, University of Zurich

Phytochemical diversity can result from coevolutionary cycles, as specialization in herbivores imposes diversifying selection on plant chemical defences. Plants in the speciose genus *Erysimum* (Brassicaceae) produce evolutionarily novel cardenolides as defences on top of ancestral glucosinolates, allowing plants to escape a diverse community of specialist glucosinolate-adapted herbivores. This gain-of-function thus provides a unique opportunity to identify the selective drivers of phytochemical diversification. The annual plant *Erysimum cheiranthoides* is widely distributed across Eurasia, and sampling of natural genotypes from the full range of its distribution reveals substantial qualitative as well as quantitative among-genotype variation in the novel cardenolide defences. In contrast, glucosinolates variation is exclusively quantitative and independent of variation in cardenolides, suggesting different selective pressures acting on the two types of defence. Both defences also vary substantially within-plant, with evidence for species-specific responses in the feeding behaviour of different *Erysimum*-associated herbivores. By linking variation in the ancestral and novel defences of this species to performance of its current and past herbivore community, we can thus conclude that ancestral glucosinolate defences are most likely maintained by selection from generalist herbivores, whereas novel cardenolide defences have enabled the plant to specifically target more specialized, glucosinolate-resistant herbivores. Even in this unique plant system with a functionally entirely novel defence, the diversity of selective pressures imposed on the plant by its herbivores thus prevents an ancestral defence to become obsolete. Therefore, the substantial phytochemical diversity found within virtually all plants is likely similarly favoured and maintained by selection from the plant’s natural enemies.
**Molecular architecture of thylakoid biogenesis**

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Photosynthesis is a finely tuned process carried out by a series of protein complexes embedded in specialized thylakoid membranes. Although the individual complexes involved in photosynthesis have been studied in great detail, much less is known about the processes that establish the supramolecular organization of the thylakoids needed for efficient light harvesting and energy conversion. Due to the fundamental and practical importance of understanding photosynthesis, we aim to investigate how membrane remodeling proteins (including Curt1 and Vipp1) help shape the thylakoids by characterizing their effects on thylakoid biogenesis inside native cells. We will study the cyanobacterium Synechocystis and a mutant of the green alga Chlamydomonas reinhardtii, both of which can be induced to ‘regreen’, thus synchronously producing thylakoids from a thylakoid-depleted state. By combining focused ion beam (FIB) milling with cryo-electron tomography, we will obtain thin sections of intact frozen cells appropriate for transmission electron microscopy (TEM). Then, we will use a series of tilted TEM images to generate a 3D tomographic view of the cellular interior. In these tomograms, the different complexes can be identified and mapped throughout the thylakoid membranes. By collecting tomograms at different stages of regreening in Curt1 and Vipp1 mutants, we will visualize how these two proteins help shape the thylakoids, revealing a new perspective on how the thylakoid membrane ultrastructure is formed.

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**HSP70 and HSP40 are the central hub of the HSP-chaperone network**

Anthony Guihur1 and Pierre Goloubinoff1

1 Department of plant molecular biology, University of Lausanne

Plants are sessile organisms that are exposed to persistently changing stresses. Climate change is increasingly affecting the quality of life of organisms on the planet. More frequent extreme and lengthy heat waves compromise crop yields. This urges for a better understanding of the molecular mechanisms by which plant cells can feel the heat and establish effective molecular defenses such as chaperones. HSP70s are ubiquitous molecular chaperones that use ATP to transiently unfold and thereby solubilize protein aggregates, as well as perform structural changes in particular native protein oligomers, thereby regulating stress-related and the activity of native proteins carrying physiological functions. HSP70’s involved in the regulation of biotic and abiotic stress responses, and act in a large variety. HSP70s function at all stages of the life of proteins, from synthesis to degradation and are thus crucial for maintaining of cellular protein homeostasis. To perform its protein-remodeling action on various misfolded and (alter)natively folded protein complexes, HSP70 depends on J-domain proteins (JDPs, HSP40), act as specific obligate “HSP70-targetase” co-chaperone that upload misfolded or alternatively folded protein substrates onto the HSP70 machineries. Whereas JDPs type A and B seem to act more in the unfolding of stress-induced protein aggregates, the JDPs type C are involved in recruiting HSP70 to switch native proteins between inactive and active structures.
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