SwissPLANT 2022

Symposium Plant Science Research in Switzerland

swissplantscienceweb.ch
30th edition

13 – 15 June 2022
Meiringen, Switzerland

24 – 26 January 2022
Les Diablerets, Switzerland

Photo: Tanguy Bilus
Photo ©VisualPs.ch

SwissPLANT 2022

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

Table of content

We gratefully acknowledge Syngenta's financial support of the conference.

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 Martínez

swissplantscienceweb.ch

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 Martínez, 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

Tuesday, 14 June 2022

07:00 Breakfast

Session III

08:20 Ora Hazak | U Fribourg
Delving into the mechanisms of root xylem plasticity

08:40 Klaus Schlaeppi | U Basel
Exudate-microbiome interactions on Maize roots

09:00 Joelle Sasse Schläpfer | U Zurich
How dynamic is root exudation?

09:20 Celia Baroux | U Zurich
Citrullination – a novel epigenetic modification unlocking germline fate?

09:40 Coffee Break

Session IV

10:20 Sébastien Bruisson | U Fribourg
Volatile-mediated interaction between plant-associated beneficial microorganisms and phytopathogenic fungi

10:40 Pauline Jullien | U Bern
MET2a and MET2b DNA methyltransferases are required for trans-generational methylome stability

11:00 Charles Pouchon | U Geneva & CJBG
Phylogenomic study of the whole Alpine flora: When bioinformatic development is needed!

11:20 Luis Lopez-Molina | U Geneva
The *Arabidopsis* endosperm is a temperature-sensing tissue that implements seed thermoinhibition through phyB and PIF3

11:40 Stefanie Ranf | U Fribourg
Mechanistic insights into plant-bacteria interactions

12:00 Leisure time (Lunch on your own, hiking, Sherlock Holmes Museum, sightseeing…)

18:00 Poster session, with apéro

18:40 Dinner

Session V

20:20 Cyril Zipfel | U Zurich
Perception of a conserved family of plant signaling peptides by the receptor kinase HSL3

20:40 Sara Simonini | U Zurich
When it's the right time to divide: conflicting parental influence guides cell cycle reactivation at fertilization

21:00 Stefan Grob | U Zurich
Paramutation in *Arabidopsis* is linked to 3D genome folding

21:20 Diana Santelia | ETH Zurich
Arabidopsis guard cell chloroplasts import cytosolic ATP for starch turnover and stomatal opening

Wednesday, 15 June 2022

07:00 Breakfast

Session VI

08:20 Elia Stahl | U Lausanne
Phosphatidylcholines from Pieris brassicae eggs activate an immune response in *Arabidopsis*

08:40 Léa Frachon | U Zurich
Genomic local adaptation of a generalist plant species to pollinator communities, soil, and climate

09:00 Tobias Züst | U Zurich
Patterns of variation in a novel defence reveal evolutionary drivers of chemical diversification

09:20 Felix Kessler | U Neuchâtel
Atypical kinases ABC1K1 and ABC1K3 maintain plastoquinone homeostasis in the chloroplast electron transport chain

09:40 Coffee Break

Session VII

10:20 Kentaro Shimizu | U Zurich
Machine learning of image and transcriptome data of *Arabidopsis* and wheat polyploid plants in natura

10:40 Yamama Naciri | U Geneva & CJBG
The Sapotaceae of Madagascar: molecular genetics for conservation

11:00 Roland Kölliker | ETH Zurich
Unraveling the genetic control of disease resistance in outbreeding forage crop species

11:20 Samuel Zeeman | ETH Zurich
Proteins that induce glucan phase transition in starch biosynthesis

11:40 Sebastian Soyk | U Lausanne
Loss of redundancy in a conserved developmental pathway during tomato domestication

12:00 Closing remarks

Citrullination – a novel epigenetic modification unlocking germline fate?

Yanru Li, Danli Fei, Jasmin Schubert, **Célia Baroux**

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

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.

TALK

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. We are currently using this new procedure to study volatile-mediated interactions between several associations of beneficial and pathogenic plant-associated microorganisms. Several compounds possibly involved in the communication are under investigation. With this work, we expect to unravel a poorly understood dimension of interspecific communication in microbes and 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.

TALK

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

Haoran Peng[1], Maria Estefania Lopez[1], David Roquis[1], Mahnaz Katouzi[1], Victoria Widrig[2], Javier Sanchez Martin[2] and **Etienne Bucher[1]**

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

Accelerating climate change and ongoing wars have remined 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 novel disease resistance genes and learn more about their (epigenetic) regulation. For that, we use whole genome and epigenome sequencing approaches.
Finally, I will briefly outline what happens if one dares to invent a novel crop breeding method in Switzerland and Europe.

TALK

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

Yetkin Çaka Ince[1], Anne Sophie Fiorucci[1], Martine Trevisan[1], Vinicius Costa Galvão[1], Johanna Krahmer[1], Leonore Wigger[2], Sylvain Pradervand[2], Laeticia Fouillen[3], Pierre Van Delft[3], Sebastien Mongrand[3], Hector Gallart-Ayala[4], Julijana Ivanisevic[4] and **Christian Fankhauser**[1,*]

[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 Biogenèse Membranaire, UMR 5200, Univ. Bordeaux, CNRS, 33140 Villenave d'Ornon, France.
[4] Metabolomics Platform, Faculty of Biology and Medicine, University of Lausanne
[*] Materials & correspondence to: christian.fankhauser@unil.ch

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.

TALK

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 adaptative 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 associ-ated 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.

TALK

A phospho-switch provided by LRR receptor-like kinase, ALK1/QSK1/KIN7, prioritizes ABCG36/PEN3/PDR8 transport toward defense

Bibek Aryal[1], Jian Xia[1], Zehan Hu[1], Klaus Harter[2], Clara Sánchez-Rodríguez[3], Michał Jasiński[4], Sabine Rosahl[5] and **Markus Geisler**[1]

[1] University of Fribourg, Department of Biology
[2] Zentrum für Molekularbiologie der Pflanzen, Pflanzenphysiologie, Universität Tübingen DE
[3] Department of Biology, ETH Zurich
[4] Department of Plant Molecular Physiology, Institute of Bioorganic Chemistry, Polish Academy of Sciences, Poznań, Poland
[5] Biochemistry of Plant Interactions, Leibniz Institute of Plant Biochemistry, Halle (Saale), Germany

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, phospho-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 phospho-switch.

TALK

Paramutation in *Arabidopsis* is linked to 3D genome folding

Diana Zörner, Edouard Tourdot, Elizabeth Kracik-Dyer, Victor Mac and **Stefan Grob**

Institute of Plant and Microbial Biology, University of Zurich

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.
Using genetic and transcriptomic means, we found that the observed paramutation does not ubiquitously occur in an individual plant but rather affects certain sectors. This allowed us to trace back paramutation initiation to plant meristems. Next-generation seedlings stemming from flowers of branches that derived from paramutagenic meristems exhibit the paramutation-related phenotype. The paramutation is subsequently further epigenetically inherited across several generations. 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.*

TALK

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.

TALK

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

Louis Tirot[1], Diane M.V. Bonnet[1], Marco Catoni[2], **Pauline E. Jullien[1]***

[1] Institute of Plant Sciences, University of Bern, Bern
[2] University of Birmingam, Birmingam, 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* assession, 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.

TALK

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, phylloquinone, 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”.

TALK

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, using a pooled-sequencing approach with 7484 F2 individuals, we were able to narrow down the QTL region and to identify several candidate genes potentially involved in resistance.
To investigate sources of resistance to southern anthracnose (caused by *Colletotrichum trifolii),* we performed genome-wide association studies (GWAS) in a diverse, worldwide collection of 397 red clover *(Trifolium pratense)* accessions using a pooled genotyping-by-sequencing approach with 200 plants per accession. The level of resistance to *C. trifolii* varied considerably between accessions and GWAS identified several QTL explaining up to 16.8 % of the variation. 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.

TALK

Simple sequence repeat (SSR) mining in the chloroplast genomes of Ophioglossaceae ferns

Darina Koubínová[1], Li-Yaung Kuo[2] and Jason R. Grant[1]

[1] Institut of Biology, University of Neuchâtel
[2] Institute of Molecular & Cellular Biology, National Tsing Hua University, Hsinchu City, Taiwan

The Ophioglossaceae is a worldwide distributed family of ancient ferns consisting of about 112 species. They are characterized by extremely large genomes and one of the highest numbers of chromosomes described among all extant eukaryote multicellular organisms. Microsatellites, or simple sequence repeats (SSRs) are one to six nucleotide repeats that are commonly used as molecular markers, e.g., in assessing genetic diversity. They are usually highly abundant in the genome and highly polymorphic. With the advances in whole genome sequencing, the focus moved also to mapping the SSRs present in the whole genomes (nSSRs), plastomes (cpSSRs) or mitogenomes (mtSSRs), in order to understand their distribution and potential function. In this study, fourteen chloroplast genome sequences of eleven Ophioglossaceae species were examined in order to identify chloroplast simple sequence repeats (cpSSRs). In the whole dataset, 374 SSRs were detected. Each of the sequences contained 20-40 SSRs, with the density of 0.14-0.29 SSRs/kb. The mononucleotids were the most abundant repeats; the highest number of repeats was (C)73. The highest number of SSRs and density were detected in *Sceptridium ternatum/japonicum,* whereas the lowest number of SSRs and density were found in *Helminthostachys zeylanica.* Out of the total number of SSRs (n = 374), 318 were found in the long single copy region (LSC), 24 in the short single copy region (SSC) and 32 in the inverted repeat regions (16 in each). 117 of the SSRs were present in 27 distinct gene coding regions, the remaining 257 were in non-coding regions. The observed SSRs were further classified according their presence at the same region (with same flanking sequences) in one or several species to unique (present in only one species), polymorphic (present in different number of repeats in more than one species) and shared (present in same for in more than one species). Finally, the distribution of the shared and polymorphic SSRs was compared to the phylogenetic relationships of the respective species. SSRs were shared both among closely related and distant species.

TALK

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 in the blade, 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.

TALK

The *Arabidopsis* endosperm is a temperature-sensing tissue that implements seed thermoinhibition through phyB and PIF3

Urszula Piskurewicz[1], Maria Sentandreu[1], Gaëtan Glauser[2] and **Luis Lopez-Molina[1,3]**

[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.

TALK

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 Chambésy

On Madagascar, the family Sapotaceae currently encompases 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 genbomics 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.

TALK

Phylogenomic study of the whole Alpine flora: When bioinformatic development is needed!

Charles Pouchon[1,3], Niklaus E. Zimmermann[2], Sébastien Lavergne[3]

[1] Laboratoire de Systématique végétale et Biodiversité, Université de Genève & Conservatoire et Jardin botaniques, 1292 Chambésy

[2] Swiss Federal Research Institute WSL, 8903 Birmensdorf

[3] Laboratoire d'Écologie 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.

TALK

Mechanistic insights into plant-bacteria interactions

Stefanie Ranf

University of Fribourg, Department of Biology, Fribourg & Technical University of Munich, Department of Plant Sciences, Phytopathology, Freising-Weihenstephan, Germany

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 at the molecular level, we apply a combination of biochemistry, genetics, computational modelling, and natural diversity screening. Complimentarily, 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.

(1) Ranf S, et al. (2015) A lectin S-domain receptor kinase mediates lipopolysaccharide sensing in *Arabidopsis thaliana.* Nature Immunology 16:426-433.
(2) Kutschera A, et al. (2019) Bacterial medium-chain 3-hydroxy fatty acid metabolites trigger immunity in *Arabidopsis* plants. Science 364, 178-181.

TALK

Arabidopsis guard cell chloroplasts import cytosolic ATP for starch turnover and stomatal opening

Shey-Li Lim[1,*], Sabrina Flütsch[2,*], Jinhong Liu[1], Luca Distefano[2], Boon Leong Lim[1], **Diana Santelia[2]**

[1]School of Biological Sciences, University of Hong Kong, Hong Kong, China

[2]Institute of Integrative Biology, ETH Zurich

Stomatal opening requires the provision of energy in the form of ATP for proton pumping across the guard cell (GC) plasma membrane and for associated metabolic rearrangements. The source of ATP for GCs is a matter of ongoing debate that is mainly fuelled by controversies around the ability of GC chloroplasts (GCCs) to perform photosynthesis. By imaging compartment-specific fluorescent ATP and NADPH sensor proteins in *Arabidopsis*, we show that GC photosynthesis is limited and mitochondria are the main source of ATP. Unlike mesophyll cell (MC) chloroplasts, which are impermeable to cytosolic ATP, GCCs import cytosolic ATP through NUCLEOTIDE TRANSPORTER (NTT) proteins. GCs from ntt mutants exhibit impaired abilities for starch biosynthesis and stomatal opening. Our work shows that GCs obtain ATP and carbohydrates via different routes from MCs, likely to compensate for the lower chlorophyll contents and limited photosynthesis of GCCs.

TALK

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.

TALK

Exudate-microbiome interactions on Maize roots

Lisa Thoenen[1,3], Marco Kreuzer[2], Pierre Matteo[1], Tobias Zuest[4], Mirco Hecht[1], Rémy Bruggmann[2], Matthias Erb[1], **Klaus Schlaeppi[3]**

[1] Institute of Plant Sciences, University of Bern
[2] Interfaculty Bioinformatics Unit, University of Bern
[3] Department of Environmental Sciences, University of Basel
[4] Department of Systematic and Evolutionary Botany, University of Zurich

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 metabolization 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 metabolization 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.

TALK

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

Kentaro K. Shimizu[1,2], Toshiaki Tamashige[2], Jianqiang Sun3, Reiko Akiyama[1], Takao Goto[4], Moeko Okada[1,2], Misako Yamazaki[1], Yasuhiro Sato[1], Rie-Shimizu-Inatsugi[1], Yoko Kamiya[2], Tomohiro Ban[2], Ken Kuroki[5], Shuhei Nasuda[5], Jiro Sugisaka[5], Hiroshi Kudoh[5], Atsushi J. Nagano[6], Thomas Wicker[7], Beat Keller[7], Tanaka Kenta[8], Junichi Akita[9], Aya Tonouchi[4], Yuki Shimahara[4], Natsumaro Kutsuna[4], Jun Sese[10]

[1] Dept Evol Biol Env Studies, University of Zurich
[2] Kihara Institute for Biological Research, YCU
[3] NARO
[4] LPixel Inc.
[5] Kyoto Univ.
[6] Ryukoku Univ., Keio Univ.
[7] Dept Plant Microb Biol, University of Zurich
[8] Tsukuba Univ.
[9] Kanazawa Univ.
[10] Humanome Lab Inc.

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 allopolyploid *A. kamchatica* derived from *A. halleri* 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.

TALK

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 reins 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.

TALK

Loss of redundancy in a conserved developmental pathway during tomato domestication

Marion Brechet[1], Anna Glaus[1], Ludivine Lebeigle[1], Giti Ghazi Soltani[1], José Jiménez-Gómez[2] and **Sebastian Soyk[1*]**

[1] Center for Integrative Genomics, University of Lausanne

[2] Institut Jean-Pierre Bourgin, INRAE, AgroParisTech, Université Paris-Saclay, Versailles, France

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.

TALK

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_2O_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.*

Recent in vitro analytical approaches try to uncover a potential interaction of LecRK-I.8 with PCs and PC-derivatives. In summary our results indicate, that *Arabidopsis* recognize extracellular PCs from insect eggs to detect early signs of herbivore attack in a LecRK-I.8-dependent manner.

TALK

Molecular dynamics and evolutionary history of wheat centromeres

Matthias Heuberger[1], Simon Krattinger[2], Beat Keller[1], **Thomas Wicker[1]**

[1] Institute of Plant and Microbial Biology, University of Zurich

[2] King Abdullah University of Science and Technology, Public university in Thuwal, Saudi Arabia

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 *Triticeae* 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 Triticeae: we propose that *RLG_Cereba* retrotransposons specifically target CHEN3 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.

TALK

Architecture and maintenance of thylakoid membranes visualized by Cryo-electron Tomography

Wojciech Wietrzynski, Benjamin D. Engel

Biozentrum, University of Basel
Helmholtz Pioneer Campus, Helmholtz Zentrum München, Neuherberg, Germany

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.

TALK

Proteins that induce glucan phase transition in starch biosynthesis

Samuel C. Zeeman

Institute of Molecular Plant Biology, ETH Zurich

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 in 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 com-promised 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.

TALK

Perception of a conserved family of plant signaling peptides by the receptor kinase HSL3

Jack Rhodes[1], Andra-Octavia Roman[3], Marta Bjornson[2], Benjamin Brandt[2,5], Paul Derbyshire[1], Michele Wyler[4], Marc Schmid[4], Frank L.H. Menke[1], Julia Santiago[3] and **Cyril Zipfel[1,2]**

[1] The Sainsbury Laboratory, University of East Anglia, Norwich Research Park, NR4 7UH, Norwich, UK.

[2] Institute of Plant and Microbial Biology, Zurich-Basel Plant Science Center, University of Zurich

[3] The Plant Signaling Mechanisms Laboratory, Department of Plant Molecular Biology, University of Lausanne

[4] MWSchmid GmbH, 8750 Glarus

[5] Present address: Biozentrum der Ludwig-Maximilians-Universität München, Department Biologie I – Botanik, 82152 Planegg-Martinsried, Germany.

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.

TALK

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

Tobias Züst

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.

POSTER

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

Anthony Guihur[1] and Pierre Goloubinoff[1]

[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.

The functional specificities of JDPs and their interactions with HSP70s, is key to a wide range of stress-related and physiological cellular functions. Using transcriptomics and proteomics, we describe here a unique family of *Arabidopsis thaliana* JDPs, named the Anthonines, the are specific to higher plants. We have accumulated experimental evidence that Anthonines recruit HSP70 to reload specific heat-depolarized calcium channels in the plasma membrane, using energy from ATP hydrolysis.

POSTER

Molecular architecture of thylakoid biogenesis

A. Perez-Boerema[1]**,** L. Bučinská[2], W. Wietrzynski[1], B. Engel[1]

[1] Biozentrum, University of Basel, Basel
[2] Centre Algatech, Institute of Microbiology of the Czech Academy of Sciences, Trebon, Czech Republic

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.

List of participants

First Name	*Last Name*	*Affiliation*	*E-mail*
Celia	Baroux	U Zurich	cbaroux@botinst.uzh.ch
Sylvain	Bischof	U Zurich	sylvain.bischof@uzh.ch
Thomas	Boller	U Basel	thomas.boller@unibas.ch
Sébastien	Bruisson	U Fribourg	sebastien.bruisson@gmail.com
Etienne	Bucher	Agroscope	etienne.bucher@agroscope.admin.ch
Emilie	Demarsy	U Geneva	emilie.demarsy@unige.ch
Christian	Fankhauser	U Lausanne	christian.fankhauser@unil.ch
Léa	Frachon	U Zurich	lea.frachon@systbot.uzh.ch
Markus	Geisler	U Fribourg	markus.geisler@unifr.ch
Pierre	Goloubinoff	U Lausanne	pierre.goloubinoff@unil.ch
Stefan	Grob	U Zurich	sgrob@botinst.uzh.ch
Anthony	Guihur	U Lausanne	anthony.guihur@gmail.com
Ora	Hazak	U Fribourg	ora.hazak@unifr.ch
Matthias	Heuberger	U Zurich	matthias.heuberger@botinst.uzh.ch
Michael	Hothorn	U Geneva	michael.hothorn@unige.ch
Pauline	Jullien	U Bern	pauline.jullien@ips.unibe.ch
Beat	Keller	U Zurich	bkeller@botinst.uzh.ch
Felix	Kessler	U Neuchâtel	felix.kessler@unine.ch
Roland	Kölliker	ETH Zurich	roland.koelliker@usys.ethz.ch
Darina	Koubínová	U Neuchâtel	darina.koubinova@gmail.com
Martina	Legris	U Lausanne	martina.legris@unil.ch

First Name	*Last Name*	*Affiliation*	*E-mail*
Luis	Lopez-Molina	U Geneva	luis.lopezmolina@unige.ch
Sylvia	Martinez	U Basel	sylvia.martinez@unibas.ch
Yamama	Naciri	U Geneva & CJBG	yamama.naciri@ville-ge.ch
Annemarie	Perez Boerema	U Basel	annemarie.perezboerema@unibas.ch
Charles	Pouchon	U Geneva & CJBG	charles.pouchon@ville-ge.ch
Stefanie	Ranf	U Fribourg	stefanie.ranf-zipproth@unifr.ch
Christoph	Ringli	U Zurich	chringli@botinst.uzh.ch
Diana	Santelia	ETH Zurich	dsantelia@ethz.ch
Joelle	Sasse Schläpfer	U Zurich	jschlaepfer@botinst.uzh.ch
Klaus	Schlaeppi	U Basel	klaus.schlaeppi@unibas.ch
Kentaro	Shimizu	U Zurich	kentaro.shimizu@uzh.ch
Sara	Simonini	U Zurich	sara.simonini@botinst.uzh.ch
Sebastain	Soyk	U Lausanne	sebastian.soyk@unil.ch
Elia	Stahl	U Lausanne	elia.stahl@unil.ch
Roman	Ulm	U Geneva	roman.ulm@unige.ch
Thomas	Wicker	U Zurich	wicker@botinst.uzh.ch
Wojciech	Wietrzynski	U Basel	wojciech.wietrzynski@unibas.ch
Samuel	Zeeman	ETH Zurich	szeeman@ethz.ch
Cyril	Zipfel	U Zurich	cyril.zipfel@botinst.uzh.ch
Tobias	Züst	U Zurich	tobias.zuest@systbot.uzh.ch

Impressum / Imprint

Editor: Sylvia Martínez, University of Basel
Graphics & Layout: estherschreier.ch
Cover picture: Visualps.ch
Print: BSB Medien, Basel, Switzerland
Print run: 40 copies
Paper: Navigator FCS 80g/m^2 (pages); Image Impact FSC 160g/m^2 (cover)

SwissPLANT 2022

Plant Science Research in Switzerland

Symposium

13–15 June 2022
Meiringen, Switzerland

swissplantscienceweb.ch