Plants and People

IMPRS for Molecular Plant Science
INTERNATIONAL MAX PLANCK RESEARCH SCHOOL

Abstract Book

6th Plants & People Conference

Exploring Plan(t)s

#PnP23
#PlantsAndPeople

Welcome to Plants and People 2023!

We are excited to gather once again and learn more about plant science! We are very happy to be back after the pandemic, motivated to open a new chapter of "Plants and People", offering an opportunity to expand our knowledge and our social network.

The theme of this new edition of Plants and People is "Exploring Plan(t)s". You will get the chance to meet a broad range of high-profile international researchers covering various topics in plant biology, as well as speakers who left academia presenting their own experiences in choosing their career path. Our two conference days include five sessions of talks and two poster sessions. We will conclude with a podium discussion, awards for the best posters, and a barbecue!

We hope you will find our conference programme most interesting and inspiring, and we wish you a very pleasant "Plants and People"!

The P&P 2023 organizing committee

Diego, Esra, Fabienne, Jinghan, Jonathan, Josephin, Koki, Mustafa, Thekla and Varsha
Take a look at the last page of this abstract book to meet the organizing committee!

Thank you!

We would like to acknowledge all the people who made "Plants and People" 2023 possible, in particular our sponsors: Agrisera, New England BioLabs, GenScript, Potsdam Science Park, metasysX and Targenomix.

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Exploring Plan[t]s

Conference Programme

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11:10 – 11:40	Nicoletta Liguori (ICFO, Spain) Photosynthetic proteins in action! How do photosynthetic organisms switch photoprotection on?
11:40 – 12:00	Viviana Correa Galvis (Infarm, Germany) Control Environment Agriculture: How plant scientists can contribute to overcome the challenges humanity faces when it comes to food production
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14:00 – 14:30	Heidi Webber (ZALF, Germany) Climate risk and the sustainable intensification of cropping systems
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15:00 – 15:20	Shreya Agrawal (Neoplants, France) From an obscure lab in India to the forefront of science & innovation
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16:45 – 17:30	**Podium discussion**
17:30 – 17:40	**Closing remarks & poster award**
From 18:00	**BBQ**

Conference Venue

Max Planck Institute of Molecular Plant Physiology

Plants and People Conferences are hosted by the Max Planck Institute of Molecular Plant Physiology, and take place on the Max Planck Campus in Potsdam-Golm.

Our institute was established in 1994, with founding director Prof. Dr. Lothar Willmitzer and his Department "Molecular Physiology" (1994-2022) focusing investigations on plant central metabolic pathways and analysis of plant gene function. In the years that followed, two further Departments were established: "Metabolic Networks" led by Prof. Dr. Mark Stitt from 2001 to 2021, and "Organelle Biology, Biotechnology and Molecular Ecophysiology" headed by Prof. Dr. Ralph Bock since 2004.

Almost 30 years after its formation, our institute comprises around 300 staff – graduate students, post docs, technicians and support staff, independent and associated group leaders – originating from all corners of the earth. Our current Directors are Prof. Dr. Ralph Bock, Prof. Dr. Claudia Köhler, heading the Department "Plant Reproductive Biology and Epigenetics" (since 2021), and Prof. Dr. Caroline Gutjahr, heading the Department "Root Biology and Symbiosis" (since 2022). Our research focusses on fundamental processes of how plants grow, reproduce and interact with the abiotic and biotic environment, and how they perceive and integrate exogenous and endogenous signals to ensure their health, survival, biomass acquisition and seed formation. We use an interdisciplinary approach combining molecular biology, genetics, genomics, epigenomics, metabolomics, biochemistry, biophysics and microscopy with bioinformatics and modelling.

For more details about the Max Planck Institute of Molecular Plant Physiology, our people and our science, please go to the institute website: https://www.mpimp-golm.mpg.de/

Information for Talks and Poster Sessions

Talk location

All talks will take place in the lecture hall of the central building at the Max Planck Campus.

Poster locations

Location 1: Central building 1st floor, Seminar room
Location 2: Central building ground floor, outside the Lecture Hall

Please mount your poster according to your poster number before the poster session on Wednesday, and be present at your poster during the respective session for your poster number.

Posters presentations: odd numbers on Wednesday, even numbers on Thursday.

Speaker

Biographies & Abstracts

Session 1

Markus Schmid (SLU, Sweden)

Biography

The field of plant sciences has captured Markus Schmid´s interest ever since he pursued biology at the TU München, where he also earned his PhD. Following a 2-year postdoc at the Salk Institute for Biological Studies in La Jolla, California, he relocated to the MPI for Developmental Biology (now MPI for Biology) in Tübingen, where he continued as a postdoc before advancing to the role of project leader. In 2015, he was appointed as a full professor at the Umeå Plant Science Centre, Umeå University, and was a visiting PI at the Beijing Forestry University from 2018-2021. In 2023, he joined the Department for Plant Biology at the Swedish University of Agricultural Sciences (SLU) in Uppsala, Sweden. Throughout the years, Markus Schmid has developed a particular fascination for how environmental signals shape plant growth and development. For example, his team contributed to the identification of the FLOWERING LOCUS T (FT) protein as an evolutionary conserved "florigen" that promotes flowering in response to daylength. Their research also demonstrated the indispensable role of carbohydrate signaling in flowering and unveiled the regulation of *FT* through temperature-dependent alternative splicing of the floral repressor *FLOWERING LOCUS M*. These discoveries kindled his interest in alternative RNA splicing and its significance in plant responses to temperature, leading to the identification of a mutant in the core spliceosome subunit PORCUPINE, which renders plants particularly susceptible to cool ambient temperatures. Such strong temperature-specific phenotypes are uncommon in plants, and they are currently investigating this initial discovery further within the framework of his ongoing Wallenberg Scholar project. Throughout his career, he has been interested in and has been an early adopter of cutting-edge genomics methodologies. Most recently, his team developed Sequencing of Protein-Protein Interactions (SoPPIs; unpublished), an innovative approach for parallelized analysis of protein-protein interactions. | Homepage: https://www.upsc.se/researchers/5841-schmid-markus-regulation-of-plant-growth-development-by-the-environment.html

Abstract

How to Tame a PORCUPINE: A short tale of temperature, splicing, and plant development

An environmental factor that strongly influences physiology and development of organisms is ambient temperature. This is particularly true for plants, which as sessile organisms cannot evade unfavorable environmental conditions. To overcome this limitation, plants have evolved complex temperature perception and signaling mechanisms, which enable them to adjust to their environment, resulting in a stunning phenotypic plasticity. How this acclimation to suboptimal conditions is accomplished at the molecular level is only partially understood. However, alternative splicing of pre-mRNA has been suggested to contribute to this process[1,2].

For example, we have recently we have identified a loss-of-function mutant in the gene encoding SmE1, one of the subunits of the heptameric Sm ring at the core of the U1, U2, U4, and U5 snRNPs[2,3]. Interestingly, the *sme1* mutant (aka *porcupine*, *pcp*) looks like wildtype at a permissive temperature of 23°C but shows severe developmental defects at 16°C. Such temperature-sensitive mutants were thought to be rare in plants, but we have since then found that temperature-sensitive phenotypes are rather frequent among genes encoding components of the core spliceosome, indicating that alternative RNA splicing might indeed play a crucial role in plant temperature acclimation. I will discuss our latest findings regarding the function of (alternative) pre-mRNA splicing in plant temperature acclimation.

1 Capovilla, G. *et al.* Role of alternative pre-mRNA splicing in temperature signaling. *Current Opinion Plant Biology*, **2015**, 27, 97-103. https://doi.org/10.1016/j.pbi.2015.06.016

2 Dikaya, V. *et al.* Insights into the role of alternative splicing in plant temperature response. *J. Exp. Botany*, **2021**, 72, 7384-7403. https://doi.org/10.1093/jxb/erab234

3 Capovilla, G. *et al.* PORCUPINE regulates development in response to temperature through alternative splicing. *Nature Plants,* **2018,** 4, 534–539. https://doi.org/10.1038/s41477-018-0176-z

Nicoletta Liguori (ICFO, Spain)

Biography

Nicoletta Liguori is a physicist with experimental and computational experience in biomolecular physics, especially in photosynthesis. She graduated cum laude in physics at Università degli Studi Roma Tre (IT), after an MSc thesis in molecular dynamics (MD) simulations of biomolecules at UC Berkeley (US) in T. Head-Gordon's group. For her Ph.D., she joined the group of Biophysics of Photosynthesis headed by R. Croce at the VU Amsterdam (NL). During her Ph.D., she combined ultrafast spectroscopy with MD simulations to investigate how the light-harvesting complexes of plants and algae activate photoprotection.
In 2018 she obtained a competitive VENI grant from the Dutch Research Council (NWO), that allowed her to to establish her independent research line in the LaserLab of the VU Amsterdam. The focus of her project was to develop novel experimental and computational approaches to study the response of photoactive (bio)molecules to pH changes. In 2022, N.L. was appointed professor and group leader at ICFO, within the elite CELLEX NEST fellow program and was later awarded a La Caixa Junior Leader fellowship in support of her research. Her group develops novel experimental and computational tools to study the functional response of photoactive systems to changes in structure, light and environment.

Homepage : https://www.icfo.eu/research-group/32/photon-harvesting/home/437/

Abstract

Photosynthetic proteins in action! How do photosynthetic organisms switch photoprotection on?

Plants, algae and cyanobacteria provide natural examples of how solar energy can be converted into chemical energy in the presence of oxygen, while avoiding photooxidation. Nowadays, it has been established that these organisms avoid photooxidation by activating a rapidly inducible and reversible photoprotective mechanism at the level of their light-harvesting complexes. However, it is still unknown how this photoprotective mechanism is activated.

In this lecture the audience will be introduced to the current knowledge on: i) how light-harvesting is regulated in a biodiversity of oxygenic photosynthetic organisms, and ii) which experimental tools are being developed by this group to determine at the molecular level how and how fast photosynthetic organisms switch photoprotection on.

Understanding how and how quickly photosynthetic organisms can activate/deactivate photoprotection will provide answers to a longstanding open question in the field of biophysics and physical chemistry and help elucidating what are the intermediate steps and bottlenecks in this regulatory mechanism.

Viviana Correa Galvis (Infarm, Germany)

Biography

Viviana Correa Galvis is a passionate plant biologist who after more than 10 years as a photosynthesis researcher as a PhD student at Heinrich-Heine-Universität Düsseldorf and as a Postdoc at the Max-Planck Institute for Molecular Plant Physiology moved to lead a research team at Infarm, one of the pioneers of vertical farming in Europe.

Homepage : https://www.infarm.com/

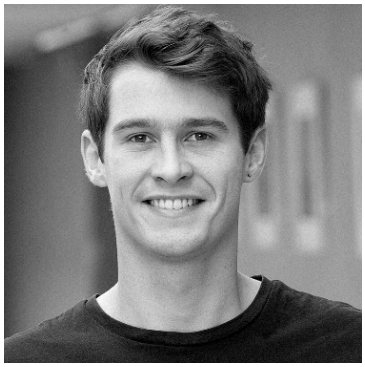
Abstract

Control Environment Agriculture: How plant scientists can contribute to overcome the challenges humanity faces when it comes to food production.

In the last five years the emergence of control environments for food production has increased notably. Terms such as indoor farming or vertical farming have started to shape the way we produce food in various parts of the world. However, in order to become a viable alternative for food production there is a need to introduce innovative developments that require the interdisciplinary work of engineers, plant researchers in various areas and software developers.
I would like to introduce you to the various interesting research areas in which plant biologists can contribute to one of the most exciting developments in the food industry since the green revolution.

Charlie Cotton (Cambrium, Germany)

Biography



Charlie Cotton is the Chief Scientific Officer and one of the co-founders of Cambrium GmbH. Cambrium is a Berlin-based next-generation materials company utilising the molecular superpowers of proteins to rethink the way we make everything. Prior to working at Cambrium, Charlie completed a four-year postdoc at the MPIMP under Dr. Arren Bar-Even working on the C1 bioeconomy. Earlier research focused on the structural biology of carbon fixation and the potential of synthetic biology for sustainable research. He is currently most interested in the commercialisation of technologies to enable a more sustainable future, at scale.

Homepage: https://www.cambrium.bio/

Abstract

Founding a start-up in Germany

I left the MPI in April 2020, and was a co-founder of Cambrium by August 2020. In this talk I will give a description of this experience, given in the context of other options for founding companies in Europe and talk about the benefits and downsides of the options available to you. Europe is filled with fantastic scientists, let's encourage each other to take risks and create!

Session 2

Alexander Jones (University of Cambridge, UK)

Biography

Alexander Jones graduated from UC Davis and got his PhD at UC Berkeley, where he focused on the role of the immune hormone salicylic acid (SA) in both root development and in crosstalk between host plants and a bacterial pathogen that synthesizes SA. After his PhD, he continued his research as a Postdoc with Wolf Frommer (Department of Plant Biology, Carnegie Institution for Science). There he developed a platform for accelerated engineering of FRET biosensors. Using this platform, he screened over 1,500 biosensor designs and succeeded in generating both an Abscisic Acid Concentration and Uptake Sensor (ABACUS) and Gibberellin Perception Sensor (GPS). A key early finding was determining, for the first time, cell-type and timing of specific ABA dynamics and GA distribution patterns in actively growing Arabidopsis roots. Also during my postdoc, I led the completion and analysis of a large-scale membrane protein interactome project (Associomics.org) which greatly added to the current knowledge of individual protein-protein interactions and also the characteristics of interactome networks generally (Associomics.org).
His research group at the Sainsbury Laboratory, Cambridge University investigates how plant hormones serve as signal integrators and master regulators of physiology and development. In multicellular organisms, these functions are crucial for the coordination of the activities of individual cells – each having an independently tuneable hormone level and hormone response – into an ensemble behaviour appropriate for the organism as a whole. Our recent advent of ABACUS and GPS biosensors permits analysis of ABA and GA levels with cellular resolution and we are now observing hormone patterns that were previously unknown. We also continue to develop new technologies for high-resolution sensing and perturbation of plant hormones in vivo.

Abstract

Bringing into focus the cellular dynamics of plant hormones using fluorescent biosensors

How do multicellular organisms solve the challenge of coordinating signals across cells, tissues and organs to respond to environmental stresses? A big part of the answer lies in hormones. In animals, these are often produced in special glands and target specific organs, but in plants they are produced by a much wider range of cells and can target many cell types. With such distributed 'decision making', how do specific and appropriate responses to these mobile small molecules arise? Our view is that internal signals and external cues encode information in cellular hormone dynamics, and then spatiotemporally specific hormone signalling processes this information to activate appropriate downstream responses. In order to visualize these crucial cellular hormone dynamics, we develop high-resolution fluorescent biosensors. Gibberellin Perception Sensors (GPS1, GPS2) are FRET based biosensors that we use to unravel how cellular GA dynamics are determined as well as which aspects of these cellular GA dynamics are functionally relevant for root growth, apical hook development, and root symbioses. We also recently developed FRET biosensors for other important plant hormones. For example, next-generation Abscisic Acid Concentration and Uptake Sensor 2s (ABACUS2s) provide unprecedented resolution in our understanding of cellular ABA dynamics and allowed us to detect inter-organ growth coordination in response to humidity fluctuations. Additional hormone sensors still in development as well as a novel optogenetic gene expression switch for plants will also be discussed.

Georg Hochberg (MPI-TM, Germany)

Biography

Georg Hochberg studied biology and was then trained as a biochemist during his PhD (both at Oxford). He then moved to Chicago to learn evolutionary biochemistry with Joe Thornton. Since then, he has had an interest in the evolution of protein complexes that spans both general mechanisms of evolutionary change and the evolution of historically important protein complexes. Since 2019, he leads the Evolutionary Biochemistry group in Marburg, where a substantial part of his group's work is now focusing on the evolution of photosynthesis related proteins.

Homepage: https://www.mpi-marburg.mpg.de/hochberg

Abstract

Evolution of the Rubiscosome

Rubisco is the central CO2 fixing enzyme of the Cavin cycle and responsible for the vast majority of all CO2 fixation on our planet today. In plants, Rubisco undergoes an elaborate set of steps involving the sequential action of at least 4 different dedicated assembly chaperones to assemble into its enzymatically active form. This complexity evolved from much simpler Rubisco ancestors that functioned without any of these additional factors. In this talk I will summarize my lab's work on retracing the evolution of Rubisco's complex present-day assembly requirements. Using ancestral sequence reconstruction and the resurrection of billion-year-old Rubiscos, we are learning how this crucial enzyme gradually elaborated its structure and assembly mechanism. Some of these elaborations had history-changing effects on Rubisco's catalytic properties, whereas others appear to be evolutionary accidents that simply became impossible to lose. This work is beginning to illuminate key events in Rubisco's history leading up to and following the evolution of oxygenic photosynthesis, one of the most consequential events in the history of life on earth. It also raises the possibility of learning from evolution to re-simplify and improve the assemblies of agriculturally important Rubiscos.

Nadine Töpfer (University of Cologne, Germany)

Biography

Nadine Töpfer is a professor for Metabolic Reconstruction and Flux Modelling at the University of Cologne and the Center of Excellence on Plant Sciences. Prior to this, she was an independent research group leader at IPK Gatersleben from 2019 to 2022 and a postdoc at the Weizmann Institute of Science in Israel and the University of Oxford. Nadine Töpfer obtained her PhD from the Max-Planck Institute of Molecular Plant Physiology and the University of Potsdam in 2014. Her research aims to gain a better understanding of the behaviour of plant metabolic systems and their interactions. Her research group uses computational approaches that are centred around the analysis of large-scale metabolic networks and works closely with experimental labs. Key topics of her work are the development of flux-balance methods to study tissue- and organ interactions, the curation and computational integration of specialised metabolism and the study of plant-environment interactions. The gained knowledge shall guide metabolic engineering strategies for improved crop plant productivity and quality.

Homepage: https://ag-toepfer.botanik.uni-koeln.de/

Abstract

“Metabolic flux modelling as a useful tool for predicting crop improvement strategies”

Large-scale metabolic modelling has emerged as an important field of research for quantifying metabolic fluxes in plant systems. It has become a platform for multi-scale data-integration and analysis, has helped elucidate constraints and capacities in metabolic systems, and has generated hypotheses for further experimental testing. In this presentation, I will give a brief overview of the history of large-scale metabolic modelling of plant systems. I will present my group’s research line and highlight some of our recent studies which generated novel insights and suggested targets for metabolic engineering attempts to improve water-use efficiency and crop performance in changing climate conditions.

Sylwia Kierszniowska (metaSysX, Germany)

Biography

Sylwia received a master's degree in biochemistry in 2005 at the University of Wroclaw. Her work concentrated on studies of interactions of cytoskeletal proteins with the plasma membrane in red blood cells. In 2006, she started her PhD at MPIMP in Golm in the Signaling Proteomics group of prof Waltraud Schulze and obtained her PhD in biochemistry in 2010. Following years, she was a postdoc in groups, which employed mass spectrometry-based methods to study plant proteomics, metabolomics, and protein-metabolite interactions (Waltraud Schulze, Alexander Graf and Lothar Willmitzer). In 2015, she moved to metaSysX (metabolomics and systems biology company) as a scientist and data analyst. In 2019, she was offered the position as the head of analytical platform. From 2023 she hold the position of CEO in metaSysX.

Abstract

Chasing success. How to quantify 100 000 metabolites?

The total number of expected metabolites in humans is 100 000. This number is also communicated for different plant species. Current mass spectrometry-based technologies enable detection of around 5 000-10 000 compounds of which around 10-30% can be identified using different methods. The main achievement of successful metabolomic analysis is to profile as many metabolites as possible and link them with the treatments and environmental conditions. Offering competitive products is one but not the only challenge that the small life sciences company faces. I am going to discuss some of them.

Session 3

Jonathan Gershenzon (MPI-CE, Germany)

Biography

Jonathan Gershenzon has long been fascinated by the world of plant natural products, including their astounding chemical diversity, their biosynthesis and their roles in ecological interactions. He received his PhD at the University of Texas for research on the terpene natural products of sunflowers and went on to serve as a post-doctoral researcher and group leader at Washington State University studying terpene biosynthesis. He joined the Max Planck Institute for Chemical Ecology in Jena, Germany in 1997 and is currently director of the Department of Biochemistry and Professor at Friedrich-Schiller University. He has continued investigating the biosynthesis of specialized plant metabolites, especially terpenes and glucosinolates, using the isolated genes to manipulate pathways and study the roles of the end products in defense against herbivores and pathogens. He also explores the evolutionary recruitment of genes into specialized metabolic pathways. At the Plants and People Conference 2023, he will discuss the glucosinolates of Brassicaceae plants and how what we have learned about their ecological interactions can be exploited in protecting crops such as cabbages and oilseed rape from agricultural pests.

Abstract

Cabbage Plants and Cabbage Pests: Coopting 100 Million Years of Coevolution for Sustainable Crop Protection Today

People have a long history with plants of the Brassicaceae (the cabbage family) as vegetables, condiments and oilseed crops. The tastes and smells of these plants arise from metabolites known as glucosinolates, sulfur-rich natural products that serve as activated defenses against herbivores. We have been investigating the roles of glucosinolates in defense of Brassicaceae plants and the responses of insect herbivores. This information can be exploited to minimize insect damage on Brassicaceae crops.

Certain insects, such as the diamondback moth and cabbage white butterfly, feed on Brassicaceae without apparent negative effects, and are known to metabolize glucosinolates in various ways. However, it is not easy to prove that these reactions actually serve in detoxification. By employing isotopic tracers and silencing herbivore genes, we demonstrated that desulfation of glucosinolates by diamondback moth larvae is an effective detoxification mechanism that improves herbivore fitness when feeding on plants with glucosinolates. Blocking this metabolism with RNA interference may provide very specific controls against pests that make existing glucosinolate defenses more effective.

Once herbivores have developed the ability to detoxify glucosinolates, plants have been selected for their own adaptations to counter herbivores. Among these, we have demonstrated that the deployment of mixtures of glucosinolates instead of single compounds may protect plants against herbivores resistant to individual glucosinolates. In addition, attraction of herbivore enemies that prey on or parasitize insect herbivores can be an effective strategy to cope with herbivores that circumvent glucosinolates. These plant adaptations can be mirrored in an agricultural context by selective breeding and application of behaviorally-active chemicals. In this way, information about the traits that arose during the long coevolutionary history between Brassicaceae and their insect herbivores gives us many leads for new approaches to crop protection.

Iva Mozgová (Biology Centre CAS, Czech Republic)

Biography

Iva Mozgová is a group leader at the Biology Centre, Czech Academy of Sciences (CAS) in České Budějovice (Budweis) in Czechia, where she came in 2019. In 2011, she obtained her PhD form Central European Institute of Technology - Masaryk University (CEITEC MU) in Brno, CZ. After that she spent five years at the Swedish University of Agricultural Sciences (SLU) in Uppsala (Sweden) as a postdoc in the lab of Prof. Lars Hennig, and almost three years as an independent researcher at the Institute of Microbiology CAS, Centre Algatech, in Třeboň (CZ). During her stay in Uppsala, she became intrigued by the function of Polycomb repressive complexes during the seed-to-seedling transition, not only in terms of the developmental changes that take place, but also the metabolic reprogramming that happens during this transition. Since then, the research focus of her independent group has been the control of primary metabolism by PRC2 in the developmental but also operational context. In addition to *Arabidopsis thaliana*, her lab has adopted model species including the moss *Physcomitrium patens* and several species of chlorophyte algae to address the evolution and conservation of the PRC2 function in the green lineage. Thanks to generous start-up funding form the Czech Academy of Science and several MSCA fellowships, her lab is now completing the first set of work that she is happy to share.

Homepage : https://mozgovalab.umbr.cas.cz/

Abstract

Seed-to-seedling transition: the hardship of greening without Polycomb

The establishment of a photoautotrophic seedling involves complex developmental and metabolic reprogramming, mediated by chromatin remodelling and orchestrated changes in gene expression. Similar to other major developmental transitions in plants, the seed-to-seedling transition requires the activity of Polycomb Repressive Complexes (PRCs) - evolutionarily conserved chromatin-modifying protein complexes that establish facultative heterochromatin at repressed genes. PRCs have been long known to repress the embryo maturation programme during the seed-to-transition[1,2]. Recently, however, a more complex picture is emerging[3] implementing Polycomb repression in developmental as well as metabolic reprogramming during the developmental transition.
Our work focuses on understanding the functions of the H3K27me3 histone methyltransferase PRC2 in orchestrating the seed-to-seedling transition, with an emphasis on primary metabolism and greening. We have recently observed a role for PRC2 in seedling establishment that is independent of embryo maturation programme suppression, but ensures stable repression of metabolic pathways associated with seed germination and early seedling emergence. Using transcriptome and H3K27me3 distribution profiles of source and sink tissues at different developmental time points, we identified genes involved in primary metabolism, chloroplast development and operational control that are subject to PRC2-dependent transcriptional repression. These and other recent findings extend our understanding of PRC2 function beyond its well-studied effects on developmental gene regulatory networks and raise important questions about the interplay between metabolic and developmental cell identities.

1. Chen, D., Molitor, A., Liu, C. & Shen, W.-H. The Arabidopsis PRC1-like ring-finger proteins are necessary for repression of embryonic traits during vegetative growth. *Cell Res.* **20**, 1332–44 (2010).
2. Bouyer, D. *et al.* Polycomb repressive complex 2 controls the embryo-to-seedling phase transition. *PLoS Genet* **7**, e1002014 (2011).
3. Ye, R. *et al.* Glucose-driven TOR–FIE–PRC2 signalling controls plant development. *Nature* **609**, 986–993 (2022).

Raphael Trösch (Nature Plants, Germany)

Biography

Raphael spent almost 15 years investigating chloroplasts before joining Nature Plants in 2022. After undergraduate studies at ETH Zurich (Switzerland), he obtained a PhD from the University of Leicester (UK) where he investigated mutants that suppress defects associated with chloroplast protein import. After that, he worked for several years as a post-doc at the TU Kaiserslautern and the Max Planck Institute of Molecular Plant Physiology, studying translational regulation of chloroplast gene expression in algae and flowering plants, respectively. Although his main expertise is chloroplast biology, his interest is and always was to understand plant life as a whole. Or else, as much of it as is possible.

Homepage: https://www.nature.com/nplants/editors

Abstract

The work life of a plant science editor

With plenty more PhD students and post-docs than available academic positions, it is important to envisage alternative careers. The difficulty lies in the challenge to estimate for which type of career one's skills are particularly suitable. In this talk I will focus on the skills that are required to apply for and get a job as science editor, and on the skills that are required to be successful as an editor after getting the job.

Session 4

Martina Ried (IPB, Germany)

Biography

Martina Ried is an independent research group leader at the Leibniz Institute of Plant Biochemistry in Halle (Saale) since 2020. She obtained her doctoral degree at the University of Munich in the group of Prof. Parniske as fast-track student supported by the Graduate School Life Science Munich, where she analysed the interplay and signalling role of different plant receptor kinases implicated in the interaction with symbiotic and pathogenic microbes. After that, Martina joined the lab of Prof. Hothorn at the University of Geneva as an EMBO long-term fellow and dissected how inositol pyrophosphates and their SPX receptors regulate plant phosphate homeostasis. Martina is eager to understand the fascinating relationship between plants and microbes in the context of symbioses and disease. Her main focus is on the interplay of plant roots and beneficial microbes in light of general nutrient homeostasis. Her goal is to use basic research to contribute to a future-oriented environmentally compatible agriculture. | Homepage: https://www.ipb-halle.de/forschung/molekulare-signalverarbeitung/forschungsgruppen/symbiose-signaling/

Abstract

Early signalling events in symbiosis

The world population is growing constantly and hence also the demand for food, fibre and energy, which are produced by crop plants. Plant growth and yield are maximized by the extensive application of chemical fertilizers with severe implications for human, animal and environmental health. However, there is an alternative that could help to reduce the extensive use of synthetic fertilizers. In the course of evolution, plants have developed powerful strategies to evade nutrient deficiencies, such as Arbuscular mycorrhiza (AM) with phosphate-acquiring fungi and root nodule symbioses with diazotrophic bacteria. Intriguingly, both plant root symbioses rely on a shared genetic toolkit consequently named common symbiosis genes[1-3]. Lysin motif receptor kinases perceive microbe-derived factors at the plasma membrane and activate downstream signalling involving the common symbiosis gene products[4-8]. The malectin-like domain leucine-rich repeat receptor kinase SYMRK constitutes the entry point of common symbiosis signalling, which results in the activation of rhythmic calcium oscillations in and around the nuclear envelop. Subsequently, Calcium and Calmodulin dependent kinase CCaMK and its phosphorylation target and transcriptional activator CYCLOPS decode the symbiotic calcium signatures and induce the expression of symbiosis-related genes[9-11]. However, the signalling events that take place between the plasma membrane and the nucleus remain largely obscure. We are eager to understand this fascinating mutual interplay between plant roots and beneficial microbes in the context of general nutrient homeostasis. We seek to illuminate the early signalling events that initiate coordinated and reciprocal cellular reprogramming and finally result in the development of a fully functional and compatible symbiosis. Our ultimate goal is to use basic research to contribute to a future-oriented environmentally compatible agriculture.

1. Kistner, C. *et al.* Seven *Lotus japonicus* Genes Required for Transcriptional Reprogramming of the Root during Fungal and Bacterial Symbiosis, Plant Cell. (2005).
2. Gutjahr, C. *et al.* Arbuscular Mycorrhiza-Specific Signaling in Rice Transcends the Common Symbiosis Signaling Pathway, Plant Cell. (2008).
3. Delaux, P.M. *et al.* Evolution of the plant-microbe symbiotic "toolkit," Trends Plant Sci. (2013).
4. Radutoiu, S. *et al.* Plant recognition of symbiotic bacteria requires two LysM receptor-like kinases. Nature. (2003).
5. Madsen, E.B. *et al.* A receptor kinase gene of the LysM type is involved in legume perception of rhizobial signals. Nature. (2003).
6. Maillet, F. *et al.* Fungal lipochitooligosaccharide symbiotic signals in arbuscular mycorrhiza. Nature. (2011).
7. Broghammer, A. *et al.* Legume receptors perceive the rhizobial lipochitin oligosaccharide signal molecules by direct binding. Proc. Natl. Acad. Sci. (2012).
8. Genre, A. *et al.* Short-chain chitin oligomers from arbuscular mycorrhizal fungi trigger nuclear Ca^{2+} spiking in *Medicago truncatula* roots and their production is enhanced by strigolactone. New Phytol. (2013).
9. Lévy, J. *et al.* A Putative Ca^{2+} and Calmodulin-Dependent Protein Kinase Required for Bacterial and Fungal Symbioses. Science. (2004).
10. Yano, K. *et al.* CYCLOPS, a mediator of symbiotic intracellular accommodation. Proc. Natl. Acad. Sci. (2008).
11. Singh, S. *et al.* A DNA-binding transcriptional activator, orchestrates symbiotic root nodule development. Cell Host Microbe. (2014).

Desalegn W. Etalo (WUR, Netherlands)

Biography

Desalegn Etalo's work revolves around unraveling the complex language of chemicals that facilitate communication and interactions among different organisms. By deciphering these chemical signals, he aims to gain deeper insights into the mechanisms that drive the relationships between plants, microbes, and their environment. He and his team combine tools and concepts from various fields, including molecular plant-microbe interactions, chemical biology, and microbial ecology. His group's ultimate objective is to develop innovative and sustainable approaches that counteract the declining state of agroecosystems, promoting their long-term health and productivity to contribute to global food security.

Homepage:
https://www.wur.nl/en/research-results/chair-groups/plant-sciences/laboratory-of-phytopathology/research/translational-phytopathology.htm

Abstract

The Chemical Dance between Plants and Microbes

The plant microbiome is a complex network of microbes, including bacteria and fungi, closely associated with plants. These microscopic organisms play a significant role in shaping their host plants' chemistry and physiological processes, resulting in both positive and negative effects. My research studies plant chemistry, particularly the chemical signatures associated with beneficial and detrimental partnerships. My presentation delves into the profound impact of microbes on the chemistry of host plants, emphasizing the role of chemicals in bridging the plant-microbiome interface. This understanding opens up exciting opportunities in agriculture, such as harnessing beneficial microbes for sustainable crop production and protection and enhancing agricultural product quality.

Hua Jiang (IPK, Germany)

Biography

Hua Jiang's academic career has mainly focused on plant reproduction, starting from his master's degree, Ph.D., postdoctoral positions, and now as a principal investigator (PI). He obtained his Ph.D. from Fudan University, China. Following that, he conducted his first postdoctoral work in Prof. Sheila McCormick's group at UC Berkeley and the second postdoctoral research in Prof. Claudia Kohler's group at SLU, Sweden. Since 2018, he has been leading his own research group at IPK, Gatersleben. His current research revolves around the genetic and epigenetic regulation of germline development in plants. Specifically, he aims to understand how chromatin status is regulated in germline cells and how chromosomes are equally divided in germline development. Additionally, considering that male germline development is highly susceptible to heat waves, which pose a growing threat to agriculture, his lab also aims to explore the genetic and epigenetic basis of thermotolerant male germline development in plants. This research will contribute to the development of climate-resilient crops for future agriculture.

Homepage: https://www.ipk-gatersleben.de/en/research/independent-research-groups/applied-chromosome-biology

Abstract

H3K9 Demethylation Facilitates Arabidopsis Male Germline Development

H3K9me2 is a histone modification that is usually associated with transcriptional silencing. H3K9me2 mainly deposits at transposable elements or repetitive sequences but is exclusive to the area of protein-coding genes. It is known that the removal of H3K9me2 plays versatile roles in plants, such as stomatal development or plant pathogen response, yet its function in plant reproduction is unclear. Moreover, while the enzymes responsible for removing H3K9me2 are predictable, the mechanism by which H3K9 demethylases find their targets at chromatin is far from clear, as well as the downstream components of H3K9 demethylase-mediated transcriptional regulation. Here, our aim is to understand the function of H3K9 demethylation in male germline development in Arabidopsis and explore the upstream and downstream components of this pathway. First, I will discuss the role of H3K9 demethylation in homologous chromosome recombination during male meiosis, a process crucial for genetic diversity and male fertility. In addition to the canonical function in H3K9 demethylation, we have found that H3K9 demethylases are also capable of recruiting cohesin cofactors, known as PDS5s, to chromatin to regulate gene expression independently of H3K9 demethylation. This suggests a novel element in H3K9 demethylase-dependent transcriptional regulation. Furthermore, I will discuss the function of H3K9 demethylation in pollen development, demonstrating the mechanism by which H3K9 demethylases are recruited to their targets, as well as the downstream components involved in H3K9 demethylation during this process. Therefore, our work explores two functional modules of H3K9 demethylase-mediated transcriptional regulation in two stages of male germline development.

Amrit Nanda (Plant ETP, Belgium)

Biography

Amrit Nanda is originally from Copenhagen, Denmark, and obtained a PhD in Plant Molecular Biology and Physiology from the Australian National University. Subsequently, she pursued her academic research in Japan, the Philippines and Sweden, specialising on plant development in response to abiotic stress. During her time in Sweden, she also took part and organised several science outreach activities, including the Fascination of Plants Day, and took on the role of Coordinator of the Linnean Centre for Plant Science in Uppsala. With a desire to promote science-based policymaking and a more innovation-friendly policy environment in Europe, she joined Plant ETP as the Executive Manager in February 2020.

Homepage : https://www.plantetp.eu/

Abstract

The EU Green Deal – From aspirational vision to implementation
The challenges and opportunities of the plant sector

The EU Green Deal aims to make Europe a world leader in sustainability. It kick-starts a change process that will require a thirty-year period of learning and improving. At the same time, maintaining food supply and business continuity throughout the transition will be crucial, to avoid socio-economic trade-offs and offshoring Europe's carbon footprint.
Plants for the Future ETP (Plant ETP) is a European multi-stakeholder platform working at the intersection of research, policy and the implementation of both. Through its activities, Plant ETP supports the transition to more sustainable agri-food systems by providing realistic views from the perspective of the different value chain players, developing a vision of the future and identifying bottlenecks and research and innovation needs, promoting science-based policymaking, as well as raising awareness of the importance of plant sciences and plant breeding.

Session 5

Achim Walter (ETH Zurich, Germany)

Biography

Achim Walter has been professor of 'Crop Science' at ETH since 2010, had been study director of Agricultural Sciences between 2011 and 2017 and is currently head of the Institute of Agricultural Sciences. He is member of scientific advisory boards of several national and international agricultural research institutions, such as the 'Forschungsinstitut für Biologischer Landbau' (FiBL, Switzerland), the IPK Gatersleben (crop breeding, Germany), Phenorob (cluster of excellence, Germany) and the Agroscope-Rat (Switzerland). He received a diploma in Physics in 1995 and in Biology in 1997 and spent parts of his Postdoctoral career at Biosphere 2 Center in the US and at Forschungszentrum Jülich, Germany. He has more than 20 years of experience in developing imaging-based solutions for plant growth analysis and in developing indoor as well as outdoor plant phenotyping facilities. Current research foci of his group are phenotyping for wheat and legume breeding as well as the use of imaging technologies and artificial intelligence to improve the sustainability of agriculture.

Abstract

AI for Future Crops

Plants form the basis of our nutrition. The way how we cultivate plants as crops needs to change due to well-known global challenges such as climate change, loss of biodiversity and overuse of pesticides. Digitalisation and artificial intelligence play an important role in the current transformation of our agricultural systems. Yet, a more sustainable production of food requires more than an update in technology. It requires differentiated solutions that take into account the social, economical and ecological boundary conditions of the food system. In this talk, I'd like to point out, how technology can contribute to a 'green revolution of our time' that will result in a food system that is plant based, low on waste and rich in variety.

Heidi Webber (ZALF, Germany)

Biography

Heidi Webber is a system agronomist with a focus on climate risk management in the context of smallholder farming systems. Her research uses a combination of on-farm experimentation, process-based crop model improvement and model-based climate change impact assessments at field, farm and regional scales. Her model development expertise is in the consideration of multiple abiotic stressors on crop growth, particularly the interaction of temperature and drought stress controlling canopy temperature. Her research also explores the integration of bio-physical and bio-economic modelling approaches to assess climate risk to cropping systems. Heidi co-leads the Agricultural Landscape Systems' Research Area at the Leibniz Centre for Agricultural Landscape Research (ZALF) and holds the Professorship of Integrated Crop System Analysis and Modelling at the Brandenburg University of Technology in Germany.

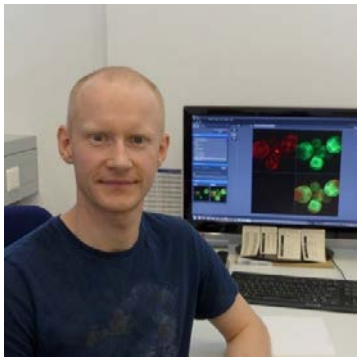
Abstract

Climate risk and the sustainable intensification of cropping systems

Drought, heat or excessive rainfall events can cause considerable production risk for cropping systems. This is projected to increase under climate change, challenging food security and incomes in some world regions and generally serving as a barrier to making longer term investments in more sustainable cropping practices. A number of modelling and assessments approaches support understanding climatic risk and its management are available. In this talk, existing approaches and exemplary applications will explore: (1) process based crop models to better understanding mechanisms and adaptive traits for different drought and stressor scenarios; (2) combined process based and data driven approaches to identify important stressor combinations; (3) integrated bio-economic simulation and optimization models to assess economic feasibility of risk management strategies; (4) driving data in risk assessments, e.g., large weather ensembles; and (5) probabilistic approaches to support more robust tradeoff assessments will be highlighted. Finally, research gaps around consideration of multiple stressors, new modelling approaches, farmer decision and the relevance of model simulations to support decision making will be discussed.

Cezary Smaczniak (Humboldt University, Germany)

Biography



Cezary Smaczniak is a research scientist and a faculty member at the Institute for Biology, Humboldt-Universität zu Berlin. He obtained his PhD degree from the Wageningen University (The Netherlands) in 2013, studying MADS-domain transcription factor (TF) protein complexes to understand the mechanisms that govern flower organ specification. He continued his postdoctoral studies in Wageningen until 2015 when he received the Humboldt Research Fellowship for postdoctoral researchers from the Alexander von Humboldt Foundation that allowed him to study regulatory roles of post-translational modifications of MADS-domain TFs at the Potsdam University (Germany). Since 2019, he is a project leader at the Institute for Biology, Humboldt-Universität zu Berlin (Germany) studying molecular function of transcriptional co-regulatory machineries in plants. His current research focus is to understand how plant co-regulators act together with TFs to regulate the expression of the downstream genes.

Abstract

Dynamic regulome modulation by transcriptional cofactor LEUNIG_HOMOLOG in Arabidopsis flower development

Flower development is a complex biological process that is controlled by a dynamic gene regulatory network. Within this network, MADS-box transcription factors (TFs) play a significant role in coordinating gene expression. They are the master regulators of many developmental processes, particularly flower development. Despite being a well-conserved protein family, each member has specific functions that are critical for flower organ specification. The mechanism by which MADS-domain TFs achieve their functional specificity is still unknown. Previously, we identified MADS-domain protein complexes and their complex partners by in vivo immunoprecipitation. Our results indicate that MADS-domain proteins interact not only with each other but also with non-MADS transcriptional regulators, which may assist in the target gene regulation. Therefore, depending on the complex composition, MADS-domain TFs may acquire different function at different developmental stages, leading to specific transcriptional responses and pattern formation during flower development. Some of the known and identified by us complex partners of MADS-domain proteins are transcriptional co-regulators SEUSS (SEU) and LEUNIG_HOMOLOG (LUH).
Here, we focused on characterizing the regulatory activities of LUH during different stages of flower development, specifically in conjunction with MADS-domain TFs APETALA1 (AP1) and SEPALLATA3 (SEP3). Through immunoprecipitation assays followed by mass spectrometry (IP-MS), we discovered that LUH interacts with a multitude of factors, with MADS-domain TFs playing a major role in these interactions. Co-immunoprecipitation assays revealed that the N-terminal part of LUH alone is sufficient for its interaction with AP1 and SEP3. Additionally, chromatin immunoprecipitation followed by sequencing (ChIP-seq) experiments indicated that LUH is involved in multiple flower developmental programs and shares a substantial number of common binding sites (BSs) with various MADS-domain TFs, particularly AP1.
These studies contribute to our understanding of how MADS-domain TFs govern the specification of floral organ identities. The integration of our findings suggests that the regulation of flower developmental processes by MADS-domain TFs may involve collaborative action with transcriptional co-factors. These findings open up promising avenues for further research on this subject.

Shreya Agrawal (Neoplants, France)

Biography

Shreya Agrawal carried out her bachelor's and master's in the field of Biotechnology. She worked on enhancing abiotic stress tolerance in tomato plants as her master's thesis project at Indian Institute of Technology, Guwahati, India followed by research on elucidating the role of autophagy in lipid accumulation during nitrogen starvation in model alga Chlamydomonas reinhardtii as a junior research scholar at Tata Institute of Fundamental Research, Mumbai, India. She carried out her Ph.D. research as a part of the International Max Planck Research Schools (IMPRS), 2014 program at the Max Planck Institute of Molecular Plant Physiology, Potsdam, Germany. Her Ph.D. work involved production of high-value metabolites in plants and assessing the chloroplast glutamyl-tRNA's role in translation and tetrapyrrole biosynthesis. She carried out her Post-doctoral research at University of Copenhagen, Denmark. Currently, she is working as a Molecular Biology Scientist at Neoplants, Paris, France on developing the first plant bio-engineered to purify the air in homes.

Abstract

From an Obscure Lab in India to the Forefront of Science & Innovation

Coming from a country with a career focus on Information Technology (IT) and Computer Engineering, my talk will highlight examples from my life that shaped my career choice to be in science. I will share what triggered and motivated me to become a plant scientist, the struggles that had to be overcome, both as a woman and as a researcher, along with the soft skills that helped reach the forefront of science and innovation.

I will talk about my scientific journey as a Ph.D. candidate at Max Planck Institute that truly shaped my scientific career and my adventure as a Post-doc in a field very different from plant sciences. My desire to put my work directly in the hands of the people led me to Neoplants. Neoplants, a French innovative start-up, working on developing the first bioengineered plant that is capable of purifying indoor air. Just like Golden rice where nature and synthetic biology were put together to prevent blindness in developing countries at no extra cost for the population, we aim to harness the power of nature to have a positive impact on our environment. I would like to share my experience working in this dynamic environment and the challenges we are working on to make a difference in everyone's life through synthetic biology.

Podium Discussion

Plants and People 2023 includes a Podium Discussion with a panel consisting of academic researchers and professionals involved in plant research and its outreach. In line with this year's conference theme 'Exploring Plan(t)s', the aim of the podium discussion is to provide a platform to discuss topics ranging from the impact of AI on the future course of plant research to job opportunities that await the young researchers.

Our panelists are :

Amrit Nanda

See page 21 for her biography.

Marion Clavel

Marion did her PhD at the University of Perpignan in France, working on double stranded RNA binding proteins and their effect on RNA dependent DNA methylation. She then did a postdoc in the lab of Pascal Genschik at IBMP Strasbourg, France, working on viral hijacking of an E3 ligase by a viral suppressor of RNA silencing to degrade the AGO1 protein. She did a second postdoc at the GMI Vienna, Austria, with Yasin Dadgas, working on a novel selective autophagy pathway that controls virus-associated cellular damage. Since August 2023, she has her independent group at the Max Planck Institute of Molecular Plant Physiology working on virus interaction with the autophagy pathways and how viruses orchestrate manipulation of the host endomembranes for their replication.

Mark Stitt

Mark grew up in the UK (West Midlands), BA & PhD in Cambridge, Postdoc in Munich and Göttingen, Professor in Bayreuth (W2) and Heidelberg (W3), Director at the MPI-MP Golm 2000-2021. He is often moonlighted in the Bay Area, California.

Raphael Trösch

See page 17 for his biography.

Sebastian Klie

Sebastian was a member of the IMPRS at the MPI-MP from 2008 and obtained a PhD in Bioinformatics with the focus of network analysis and multi-omics data integration in 2011. After a postdoc, he decided in 2013 to seize the opportunity to translate systems biology approaches into industry application with a committed team in the newly founded spin-off Targenomix GmbH, jointly with Bayer.

The podium discussion will be moderated by :

Maria Grazia Annunziata

Grazia has a background in plant biology. After her PhD graduation she left Italy for a PostDoc at the MPI-MP, where she worked on plant carbon metabolism for about ten years. Aside from research, she was selected to be part of the first *Plant Physiology* Assistant Features Editors group in 2018. In summer 2022, after a short PostDoc experience at the University of Potsdam, she moved into science management and joined the Standortmanagement Golm GmbH (StaGo), the company behind the Potsdam Science Park management and development. At StaGo she is responsible for building bridges between scientists and companies of the Potsdam Science Park.

Poster Abstracts

Overview: Poster Numbers and Presenters

POSTER NO.	PRESENTER	POSITION
1	Badia, Clara	PhD researcher
2	Bianchi, Anita	Intern
3	Brinkmann, Charlotte	PhD researcher
4	Chen, Siye	PhD researcher
5	Dangol, Anuma	PhD researcher
6	Dayou, Olivier	PhD researcher
7	Demarchi, Mariana	PhD researcher
8	Demircan, Nil	PhD researcher
9	Ebert, Alina	PhD researcher
10	Fusco, Giovanna Marta	PhD researcher
11	Gandhi, Akanksha	PhD researcher
12	Hao, Let Kho	PhD researcher
13	Hernandez, Luelmo Sofia	PhD researcher
14	Hitaj, Heni	PhD researcher
15	Howe, Vicky	Postdoc
16	Jeevankumar Reddy Singiri	PhD researcher
17	Kumari, Karishma	PhD researcher
18	Kerckhofs, Elise	PhD researcher
19	Kithinji, Hildah	PhD researcher
20	Köhl, Karin	PI
21	Kulaar, Dilsher	PhD researcher
22	Leman, Julia	PhD researcher
23	Lima, Rita	PhD researcher
24	Luo, Qiuci	PhD researcher
25	Ma, Yingrui	PhD researcher
26	Ma, Ziming	PhD researcher
27	Montulet, Orianne	PhD researcher
28	Mülders, Jens	Student
29	N. Kinoshita Satoru	Postdoc
30	Nakazato, Issei	Student
31	Nötzold, Svenja Ivonne	PhD researcher
32	Pankaj, Rishabh	PhD researcher
33	Pratibha Pratibha	PhD researcher
34	Priyanka Govindegowda	Student
35	Pulickal, Rency Tomy	PhD researcher
36	Rashkov, Georgi	Postdoc
37	Reddy, Priya	PhD researcher
38	Rönspies, Michelle	Postdoc
39	Salaün, Camille	Postdoc
40	Saß, Annika	PhD researcher
41	Schütte, Dominic	PhD researcher
42	Shagun Shagun	PhD researcher
43	Stanic, Matija	PhD researcher
44	Stefanov, Martin	Postdoc
45	Strohmeier, Joanna	PhD researcher
46	Takatsuka, Ayumu	Student
47	Tiozon, Rhowell JR	PhD researcher
48	Vilarrasa Blasi, Josep	Postdoc
49	Wie, Hua	PhD researcher
50	Wenig, Ziling	Student
51	Wittemeier, Luisa	PhD researcher
52	Yirmibesoglu, Side Selin Su	Student
53	You, Lili	PhD researcher
54	Zhao, Lina	PhD researcher
55	Zhou, Chang	Student

1. Complete plastid genome of *Hatiora salicornioides* (Haw.) Britton & Rose (Cactaceae) and structural analysis

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Cactaceae includes keystone species inhabiting arid and semiarid biomes. Morphological, anatomical, physiological and genetic evolutionary features have likely favored their adaptation to these environments. Beyond their conspicuous presence in the diversity hotspots, cacti are also present in all Brazilian biomes. We sequenced and analyzed the structural features of the plastid genome of *Hatiora salicornioides* (Haw.) Britton & Rose, occurring in Caatinga, Cerrado and Atlantic Forest biomes of Brazil under epiphytic and rupicolous habits. The sequencing was performed in Illumina MiSeq platform. *De novo* assembly was performed in CLC Genomics Workbench software. Single sequence repeats (SSRs) were identified by MISA webserver. We identified a typical quadripartite circular molecule of 121.958 bp containing a large single copy (LSC) of 80.747 bp and a small single copy (SSC) of 23.185 bp interspersed by two palindromic repeats of 9,013 bp each. A total of unique 104 genes was identified, being 72 protein-coding genes, 4 rRNA, and 28 are tRNA. A GC content of 36.1% was identified. Two tRNA and 5 *ndh* gene were lost in comparison to typical angiosperms, but the general structure and size-reduction already observed in the tribe was maintained. Of the 43 SSRs identified, 25 were located in intergenic spaces, 10 in coding sequences and 8 in intron regions; 36 of them were mono-, 1 di-, 2 tripolymers, and 4 compounds. Unveiling the SSRs of a species enables population genetics studies to understand the species' spatial distribution.

2. Autophagy unmasked: Cytosolic enzymes mediate selective autophagy during RNA virus infection

Anita Bianchi[1], Roan Groh[1], Roksolana Kobylinska[1], Ethan Stewart[2], Jakub Jez[2], Lorenzo Picchianti[1], Juan Carlos De La Concepcion[1], Marion Clavel[1,3] and Yasin Dagdas[1]

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Autophagy is a conserved intracellular degradation pathway that sequesters damaged or toxic cargoes and directs its degradation to the cell's lytic compartment. Selective autophagy is achieved through specific interaction of selective autophagy receptors (SARs) with ATG8 proteins via ATG8-interaction motifs (AIMs) present in SARs. Selective autophagy is also implicated in the response to viral infection in many organisms, including plants. However, very few SARs acting during infection have been identified so far. Using an AP-MS screen in ss(+)RNA viruses-Arabidopsis interactions, we identify two metabolic enzyme families that bind with ATG8 in an AIM-dependent manner and undergo virus-dependent autophagic degradation. We propose that these enzymes possess a "moonlighting" function, as they transition to a monomeric state upon virus infection, acting as scaffolds to trigger cell death. Additionally, we hypothesise that selective autophagy plays a crucial role in sustaining the survival of infected cells by preventing the excessive buildup of pro-cell death factors. To investigate further, we assess the cellular health monitoring capabilities of one of these enzymes by expressing a putative cell-death-inducing monomeric mutant and its AIM-mutated version, which cannot bind to ATG8, in *Nicotiana benthamiana* and *Arabidopsis thaliana*.

3. XopM, a FFAT motif containing protein from *Xanthomonas*, suppresses PTI responses at the plant plasma membrane

Charlotte Brinkmann, Jennifer Bortlik, Margot Raffeiner, Frederik Börnke

Leibniz-Institute of Vegetable and Ornamental Crops (IGZ), Großbeeren, Germany. Institute for Biochemistry and Biology, University of Potsdam, Germany
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Many Gram-negative pathogenic bacteria use type-III effector proteins (T3Es) as essential virulence factors to suppress host immunity and to cause disease. However, in many cases the molecular function of T3Es remains unknown. The plant pathogen *Xanthomonas campestris pv. vesicatoria* (*Xcv*) is the causal agent of bacterial spot disease on tomato and pepper plants and is known to translocate around 30 T3Es into its host cell. XopM is an *Xcv* effector protein with unknown function that has no similarity to any other known protein. We found that XopM interacts with a vesicle-associated membrane protein (VAMP)-associated protein (VAP) in an isoform specific manner. The endoplasmic reticulum (ER) integral membrane protein VAP is a common component of membrane contact sites involved in both tethering and lipid transfer by binding directly to proteins containing a FFAT [two phenylalanines (FF) in an acidic tract (AT)] motif. Sequence analyses revealed that XopM displays two FFAT motifs that cooperatively mediated the interaction of XopM with VAP. When expressed in plants, XopM supports growth of a non-pathogenic bacterial strain and dampens the production of reactive oxygen species, indicating its ability to suppress plant immunity. Further analyses revealed that the interaction with VAP and the ability to suppress PTI are structurally and functionally separable. We discuss a working model in which XopM uses FFAT-motifs to target the host cell PM to interfere with early PTI responses.

4. A dynamic tissue-specific transcriptome atlas of the Arabidopsis flower

Siye Chen, Manuel Neumann, Xiaocai Xu, Julia Schumacher, Kerstin Kaufmann

Plant Cell and Molecular Biology, Institute of Biology, Humboldt-Universität zu Berlin, Germany
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Flower morphogenesis is characterized by the organ-specific modulation of common genetic pathways giving rise to different cell and tissue types. Tissue-specific and single-cell transcriptomics can help to elucidate the developmental trajectories of cellular differentiation. An important bottleneck in single-cell omics analysis is the limited information on gene expression patterns in floral tissue types. Here, we generated a set of tissue-specific reporter lines in the developing flower based on available and novel reporter gene constructs. We used selected reporter gene constructs to generate dynamic transcriptome atlases of the epidermis, adaxial cells, abaxial cells, stem cells, diving cells, and xylem tissues in the developing flower. This study will serve as an important resource for future studies on flower cell development and differentiation, as well as the single-cell omics analysis.

5. How does Setaria respond to combined biotic and abiotic stresses?

Anuma Dangol and Vered Tzin

French Associates Institute for Agriculture and Biotechnology of Drylands, Jacob Blaustein Institutes for Desert Research, Ben-Gurion University of the Negev, Sede Boqer Campus, Israel.
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In plants, serotonin, an indole-derived molecule, is involved in flowering, senescence, and development, and it is modified in response to biotic and abiotic stresses. We recently reported that *Setaria viridis* (green foxtail), a resilient crop with high yield in dry and marginal land, synthesizes serotonin in response to aphid feeding. However, the overall effects of salinity, an abiotic stress, on Setaria plants and the relation to serotonin biosynthesis have not been studied yet. Here, we elucidate the impacts of the combination of abiotic and biotic stress on *S. viridis*. Setaria seedlings were exposed to sodium chloride as an abiotic stress and bird-cherry oat aphids (*Rhophalosiphum padi*) as a biotic stress. Measuring the metabolic profile of these plants indicated that the combination of salt and aphid stresses resulted in significantly higher amounts of serotonin compared to the single stresses and untreated control plants. High-throughput transcriptomic analysis suggested that genes involved in serotonin biosynthesis were significantly up-regulated. An aphid bioassay indicated that salt-stressed plants were more susceptible to aphids than the control. Our results reveal the combined effects of abiotic and biotic stresses on *S. viridis*, with salinity dominating the response. These findings could help facilitate the development of crops with greater stress tolerance.

6. A multidimensional study of *Rhamphicarpa fistulosa* parasitism in diverse host-parasite pathosystem

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Parasitic weeds are one of the most destructive biotic threats that cause substantial agricultural yield losses. *Rhamphicarpa fistulosa* (Orobanchaceae) is a facultative root parasite initially reported to affect monocots, mainly rice, in Sub-Saharan Africa, causing up to 100 % yield losses. Host resources are translocated to the parasite through a haustorium, a physical and physiological bridge between both organisms. The biology and the underlying genetic mechanism(s) of *Rhamphicarpa* parasitism remain unknown. To decipher its biology and understand the mechanism of host infections, we sequenced the parasite's complete genome and obtained comparative transcriptomic data of *Rhamphicarpa* growing on rice, pearl millet, cowpea, tomato, and itself. In doing so, we pinpointed the essential parasitic genes of *Rhamphicarpa* expressed host-specifically and differentially during host and self-parasitization. We complemented our omics-based genetic analysis of parasite-host pairs with histopathological studies. The results of these revealed that *Rhamphicarpa* successfully invades the various hosts' vascular systems by establishing a xylem-xylem connection, signifying full compatibility with both monocot and dicot crops. Regardless of the host species, our data also suggest that xylem cell initiation in *Rhamphicarpa* begins at the pericycle of the stele and progresses outwards. Beyond that, we found through chlorophyll fluorescence measurement using an imaging PAM system that *Rhamphicarpa*'s photosynthetic activity is reduced when growing on rice and tomato but not when parasitizing pearl millet and cowpea. These data indicate that rice and tomato are the parasite's preferred hosts from which it can live without own photoassimilates. Together, the results of this study provide novel insights into the biology of *Rhamphicarpa* and its molecular host-parasite interplay. In the long run, this work may contribute a critical knowledge base to develop sustainable and durable management strategies.

7. Unravelling the contribution of mesophyll and bundle sheath chloroplasts to increased tolerance in maize by Flavodoxin technology

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Maize is the crop with largest global production, and its products are important as food and energy supply, being a major source of economic development. However, it is extremely susceptible to stress, which ultimately limits the corn yield. This specie was domesticated in the tropical regions of southern Mexico and has been spread to habitats with dramatically different environmental conditions, in many cases, adverse to its development. Given its economic relevance, improving stress tolerance in maize could represent a major achievement in agricultural terms. Application of the Fld technology to a C4 specie is, however, a still uncharted territory. Photosynthesis in C4 plants is shared between two different cells: mesophyll (M) and bundle sheath (BS). M cells are responsible for the primary carbon assimilation, as long as BS cells perform the classic photosynthesis through the Benson-Calvin cycle. Moreover, while M chloroplasts perform C3-type linear electron transport, those present in BS cells display only cyclic electron flow. In order to elucidate the contribution of each cell type to the stress tolerance and to determine if Fld can productively interact with cyclic and/or linear electron transport as it does in C3 chloroplasts, we generated transgenic maize plants expressing Fld specifically in the chloroplasts of M (pfld-Ms, for Zea mays M plastidic Fld) or BS cells (pfld-BS, for Zea mays BS plastidic Fld).

We had already confirmed the presence of Fld in M and BS chloroplasts in pfld-Ms and pfld-BS genotypes, respectively, confirming tissue-specific location. Besides, application of oxidative conditions by paraquat, which act as an alternative electron acceptor from photosystem I generating superoxide, showed lower electrolyte leakage for pfld-Ms in comparison to control and pfld-BS genotypes. Furthermore, pfld-Ms plants subjected to extreme drought in soil also exhibited a tolerant phenotype, because of their higher photosynthetic activity obtained from chlorophyll fluorescence measurements, together with an evident lower loss of turgor.

To sum up, our results indicate that presence of Fld in M chloroplasts provide an advantage facing adverse situations. We expect to determine if the lack of Fld effect when expressed in BS chloroplasts is due to a null interaction with the cyclic electron transport, and in general to thoroughly establish the features of the conferred tolerance.

8. Determination of Halotropismic Response of Different *Arabidopsis thaliana* Ecotypes (Col-0, Wt-5, Uod-7, Wei-0, and Paw-3) and Extreme Halophyte *Eutrema parvulum* in Different Salts and Effect of Potassium

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As a sessile organism, during the stresses like salinity, plants must direct their growth towards or avoid a stimulus. Halotropism, which is one the tropism response of plants to move their roots toward low salt concentrations or to move away from high salt concentrations. In this study, we experimented the halotropism assay of different *Arabidopsis thaliana* ecotypes (Col-0, Uod-7, Wt-5, Wei-0, Paw-3) and extreme halophyte *Eutrema parvulum* under increasing different salt concentrations to observe root growth and orientations for 5 days. Also, we determined the effect of potassium in root orientation during the halotropism assay. Our results indicate that all *Arabidopsis thaliana* ecotypes and *Eutrema parvulum* performed different halotropismic responses to different salt concentrations. In all *Arabidopsis thaliana* ecotypes, a significant increase in the halotropismic response occurred especially under 200mM and 300mM NaCl while extreme halophyte *Eutrema parvulum* showed less orientation than all *Arabidopsis thaliana* ecotypes even in 300mM NaCl. In contrast to NaCl, halotropismic response could not be detected in increasing KCl concentrations. On the last day of the experiment all *A. thaliana* ecotypes and *E. parvulum* roots grew towards KCl-containing medium. This reveals that plant roots avoid the low water potential caused by ions and the specificity of the halotropismic orientation to Na ions. In TEA-containing halotropism assay we observed that the halotropism response of Col-0, Wei-0 and Paw-3 ecotypes was increased. Conversely to TEA, low K concentration weakened the halotropismic response in some ecotypes such as Col-0 and Wei-0, in contrast, it increased in Wt-5.

9. Synthetic allopolyploidisation of *Nicotiana tabacum* causes transgressive accumulation of nicotianoside metabolites: Understanding rapid metabolic evolution

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Allopolyploidy is the merging of genomes from two different species yielding an organism having multiple sets of chromosomes. *Nicotiana* is a genus in which natural allopolyploidy is widespread. It was possible to create synthetic tobacco allopolyploids out of *N. tabacum* and *N. glauca* using horizontal genome transfer. However, the metabolomes of this new synthetic species have not been characterised yet. Here, we analyse the polar secondary metabolome of the first generation of these synthetic allopolyploids using liquid chromatography coupled to mass spectrometry. We observed positive transgression in which metabolite levels exceed those in both of the progenitor species. The most pronounced positive transgression of a secondary metabolite was seen for a nicotianoside with the molecular mass of 1154.54 U. Nicotianosides are glycosylated diterpene metabolites present in *Nicotiana* species and provide defence function against insects. To understand the observed nicotianoside accumulations we cloned candidate glycosyltransferases, which we selected from phylogenetic and metabolite-transcript correlation analyses, into *Agrobacterium tumefaciens*. We plan to transiently overexpress these enzymes in tobacco leaves, analyse the resulting nicotianoside profiles and reveal the responsible enzymes for the observed positive transgression phenomenon. Our study shows that synthetic allopolyploids can produce new chemotypes that combine favourable traits of different tobacco species.

10. Microbial biostimulants: an environmentally sustainable approach to boost the quality and safety of food crops

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Plant biostimulants (PBs) are defined as products that stimulate plant nutritional processes, with the aim of improving nutrient use efficiency (NUE), tolerance to abiotic stress, crop quality traits or availability of limited nutrients in the soil and rhizosphere. In particular, the use of microbial PBs, such as plant growth promoting bacteria (PGPB), arbuscular mycorrhizal fungi (AMF) or fungi of the genus *Thichoderma*, represents a promising eco-friendly approach to increase the yield and quality of food crops. In our study, we perform a PRISMA-compliant (Preferred Reporting Items for Systematic Review and Meta-Analysis) meta-analysis to identify, select and evaluate all relevant literature studies from 2010 to 2022 dealing with the application of microbial PBs, as allowed by Regulation (EU) 2019/1009. We also performed in-depth morphological and metabolic profile analysis of different tomato varieties treated with PBs of different microbial composition. Three tomato varieties were chosen for the work. In particular, we studied two ecotypes of the Pomodoro del Piennolo del Vesuvio (PPV), which enjoy immense popularity in Campania region, and which are cultivated according to a strict 'production specification' that makes it a DOP (Denominazione di Origine Protetta) product. The second variety was the mini plum tomato Pixel and finally, the industrial tomato Heinz cultivar 1534. Treatment with microbial PBs had positive effects on the different tomato varieties. In fact, treatment with *Trichoderma harzianum* (T22) increased the content of beneficial minerals, such as Ca, P, Zn and Mn, Ca, Zn and Mg. PBs also resulted in an increase in amino acids content. In particular, in PPV increased the content of aspartate, an amino acid essential for improving the taste and quality of tomato fruits. T22 increased the glutamate content in Pixel, but on the Heinz tomato it did not have the same effect. Probably, as this experiment was conducted in the open field and the environmental stress conditions resulted in the synthesis of several protective metabolites, such as tyrosine, GABA, alanine and MEA. The lycopene content also increased in all tomato plants and regardless of the biostimulant used. These PBs, which determined positive effects on primary and secondary metabolites and tolerance to abiotic stresses, contribute to the creation of sustainable cultivation systems and the development of biofunctional foodstuffs, thus promoting the agricultural progress of the future.

11. Effect of a novel *Trichoderma* strain on the physiological response of *Arabidopsis thaliana* under salt stress

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Salt stress is one of the major environmental factors that limits crop productivity. To mount an effective response to cope with salt stress, plants rely on the salt overly sensitive (SOS) pathway. This includes SOS1, SOS2 and SOS3 proteins that are crucial for the maintenance of ion homeostasis and the *sos1* mutants are hypersensitive to salt stress. Symbiotic association of plants with beneficial microbes can increase the tolerance of plants to various abiotic stresses. One such versatile endophytic plant symbiont is *Trichoderma spp*. that can protect plants against salt stress. However, the molecular mechanism by which it mitigates the damage caused by salt stress remains elusive. In this study, we examined the effect of a novel *Trichoderma* strain on the growth of *glabara1* (*gl1*) and *salt overly sensitive* (*sos1*) mutants in *Arabidopsis thaliana* under salt stress. Our results demonstrate that several plant growth parameters such as fresh weight, quantum efficiency of photosystem II and chlorophyll content were improved in *Trichoderma* inoculated *sos1* plants under salt stress. Moreover, higher transcript levels of genes involved in ROS scavenging were observed in *sos1* shoots colonized by *Trichoderma.* Also, *Trichoderma* enhanced the levels of osmolytes such as proline as a protective adaptation to salt stress. We found that the levels of phytohormones such as SA, ABA, JA was elevated under salt stress but were not influenced by fungal inoculation. Taken together, our results will unveil the beneficial role of *Trichoderma* spp. in improving the antioxidant and osmo-protective status of plants under salt stress.

12. The role of wheat benzoxazinoids in adjustment to biotic and abiotic stresses

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Plants produce specialized metabolites for survival under hazardous environmental conditions and/or to minimize damage caused by insect herbivory. Benzoxazinoids (BXDs) are specialized metabolites that are produced by important cereal crops, such as wheat, maize, and rye. These metabolites are mostly known for plant defense against herbivores. It was recently discovered that BXDs also accumulate under different abiotic stresses such as drought, high salinity, and cold conditions. However, the function of these molecules in drought tolerance remains largely unknown, and whether they play a dual role in combined drought tolerance and herbivore resistance. Here we show the potential roles of BXDs in response of bread wheat (*Triticum aestivum*) seedlings to combined drought and *Rhopalosiphum padi* aphid stresses. Under drought conditions, BXD levels were increased in the leaves and negatively affected aphid fecundity and feeding behavior. However, the levels of BXDs were lower in the phloem sap of wheat seedlings by both combined and individual treatments. Interestingly, the expression level of *callose-related* genes and MYB *transcription factor* genes involved in callose biosynthesis were upregulated in leaves of wheat seedlings under drought conditions. It suggested that callose is deposited between cell wells which might interfere with aphid feeding. Moreover, the MYBs might play a regulatory role in wheat response to combined stresses. A deeper understanding of BXDs' function in wheat response to biotic and abiotic stresses could lead to better breeding strategies for stress tolerance in wheat.

13. SUMOylation may be a novel mechanism of RAM1 regulation

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More than 80% of land plants establish symbiotic interactions with arbuscular mycorrhiza fungi (AMF) (1). During these interactions, AMF provide water and mineral nutrients, mainly phosphate (P_i), to the host plant and increase its resilience against (a)biotic stresses (1). In the last decade, intense research efforts have been made to untangle the plant molecular mechanisms involved in the establishment of this symbiosis. REQUIRED FOR ARBUSCULAR MYCORRHIZATION 1 (RAM1) has been identified as one of the central players (2). RAM1 is a GRAS transcription factor (3), which plays an essential role in development of arbuscules, the fungal structures at which nutrient exchange between the plant and the fungus takes place. However, RAM1 regulation and its molecular function are not yet fully understood. To better understand its function, we set out to identify and characterize interaction partners of RAM1. Furthermore, we found four *in silico* predicted SUMOylation sites in the sequence of *Lotus japonicus* RAM1. SUMOylation is a widespread post-translational modification in eukaryotes which involves attaching a member of the SUMO (small ubiquitin-like modifier) protein family to the target protein (4). SUMOylation has been reported to alter protein subcellular localization (5), stability (6), or interaction partners (7). We are now investigating RAM1 SUMOylation and its role in fine-tuning RAM1 functionality and dynamics and, thereby, AM symbiosis.

[1] Luginbuehl LH and Oldroyd GED (2017) Curr Biol. 27(17):R952-R963.

[2] Gobbato E, Wang E, Higgins G, Bano SA, Henry C, Schultze M, Oldroyd GE. (2013) Plant Signal Behav. 8(10):e26049.

[3] Rich MK, Courty PE, Roux C, Reinhardt D. (2017) BMC Genomics. 18(1):589.

[4] Wilkinson KA, Henley JM. (2010) Biochem J. 428(2):133-45.

[5] Sakin V, Richter SM, Hsiao HH, Urlaub H, Melchior F. (2015) J Biol Chem. 290(39):23589-602.

[6] Kim SI, Park BS, Kim DY, Yeu SY, Song SI, Song JT, Seo HS. (2015) Biochem J. 469(2):299-314.

[7] Orosa-Puente B, Leftley N, von Wangenheim D, Banda J, Srivastava AK, Hill K, Truskina J, Bhosale R, Morris E, Srivastava M, Kümpers B, Goh T, Fukaki H, Vermeer JEM, Vernoux T, Dinneny JR, French AP, Bishopp A, Sadanandom A, Bennett MJ. (2018) Science. 362(6421):1407-1410.

14. Insights into the Dynamics and Regulatory Mechanisms of Thylakoid Ascorbate Peroxidase (tAPX) in the Thylakoid Membrane of Arabidopsis thaliana

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Thylakoid ascorbate peroxidase (tAPX) serves a plethora of pivotal roles against photooxidative stress, in scavenging of chloroplast reactive oxygen species, in signaling, stress acclimation as well as immunity control in plants (Maruta et al., 2010; Maruta et al., 2012; Baier et al., 1999; Yabuta et al., 2002). Moreover, it does so with a higher efficiency when compared to its counterpart stromal ascorbate peroxidase.

We investigate the distribution and characteristics of tAPX by analyzing its abundance and diurnal turnover. Additionally, we compare protein abundances in solubilized thylakoid membranes. Lines that have different expression patterns of tAPX (van Buer et al., 2019) are utilized and cross-compared using gel electrophoresis and Western blotting techniques. Furthermore, the composition of the thylakoid supra-complex is explored in depth using blue native gel electrophoresis, allowing for a comprehensive overview of tAPX and distribution.

Recently, we demonstrated the impact of tAPX micro-environment for supracomplex regulation and its role in photoprotection and signaling (Seiml-Buchinger et al., 2022). For refined analysis, we will employ low doses of cleavable cross-linkers to covalently bind neighboring surface proteins to tAPX. This approach will provide insights into the *in vivo* protein environment of tAPX. Furthermore, potential interaction partners will be identified using mass spectrometry.

By integrating these experimental approaches and methods, we aim to enhance our understanding of the dynamics of thylakoid membrane composition and the regulatory role of tAPX in gene expression. The findings from this study will contribute to unraveling the intricate mechanisms underlying the function and regulation of tAPX, providing valuable insights into the processes occurring within the thylakoid membrane and their impact on plant physiology.

Baier M, Dietz KJ (1999). Protective function of chloroplast 2-Cysteine peroxiredoxin in photosynthesis. Evidence from transgenic arabidopsis1. Plant Physiology, 119, 1407–1414.
Maruta T, Tanouchi A, Tamoi M, Yabuta Y, Yoshimura K, Ishikawa T, Shigeoka S (2010). Arabidopsis chloroplastic ascorbate peroxidase isoenzymes play a dual role in photoprotection and gene regulation under photooxidative stress. *Plant and Cell Physiology*, *51*, 190–200.
Maruta T, Noshi M, Tanouchi A, Tamoi M, Yabuta Y, Yoshimura K, Ishikawa T, Shigeoka S (2012). H2O2-triggered retrograde signaling from chloroplasts to nucleus plays specific role in response to stress. *The Journal of Biological Chemistry*, *287*, 11717–11729.
Seiml-Buchinger V, Reifschneider E, Bittner A, Baier M (2022). Ascorbate peroxidase postcold regulation of chloroplast NADPH dehydrogenase activity controls cold memory. *Plant Physiology*, *190*, 1997–2016.
van Buer J, Prescher A, Baier M (2019). Cold-priming of chloroplast ROS signaling is developmentally regulated and is locally controlled at the thylakoid membrane. *Scientific Reports*, *9*, 3022.
Yabuta Y, Motoki T, Yoshimura K, Takeda T, Ishikawa T, Shigeoka S (2002). Thylakoid membrane-bound ascorbate peroxidase is a limiting factor of antioxidative systems under photo-oxidative stress. *The Plant Journal*, *32*, 915–925.

15. What is ACR4 doing at plasmodesmata?

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ACR4 is a receptor-like kinase known for its roles in seed coat and leaf epidermal development, root meristem maintenance and lateral root initiation. In addition to being PM-localised, ACR4 is enriched at plasmodesmata. Furthermore, in maize endosperm, CR4 preferentially localises to plasmodesmata between aleuronal cells, leading to the hypothesis that ACR4 regulates symplastic movement of molecules via plasmodesmata to establish tissue patterning.

Although several ACR4 interaction partners have been identified, including CLV1 and the CIK family of co-receptors, as well as downstream phosphorylation targets such as PP2A-3 and WOX5, the nature of ACR4 signalling complexes and any further downstream targets remain to be elucidated. Likewise, despite possessing a putative ligand binding pocket, no ligand has been shown to bind directly to ACR4. Furthermore, whether ACR4 actually regulates plasmodesmata function, or if plasmodesmata are rather acting as microdomains to facilitate intercellular signal transduction via ACR4 and its associated signalling complexes, remains to be seen.

We aim to identify ACR4's interaction partners and downstream targets using proximity labelling, Y2H screens and co-immunoprecipitation. In addition, we will use immunogold labelling and electron microscopy to pinpoint the localisation of ACR4 within plasmodesmata. In characterising ACR4's interactome and precise localisation, we hope to gain functional insights into ACR4's role at the plasmodesmata.

16. Unveiling the effects of full moonlight on plant cellular metabolism and growth

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Animals are known to sense and respond to solar radiation reflected by the moon, but the effects of moonlight on plants, often observed in lunar agriculture, have been doubted and often regarded as a myth. Consequently, lunar farming practices are not well scientifically supported, and the influence of the moon, on plant biology has hardly been investigated. We studied variation in nuclear organization, protein and metabolite profiles in tobacco and Arabidopsis plants following exposure to full moonlight (FML). Results showed that exposure to FML resulted in a significant increase in nuclear size accompanied by changes in protein and metabolite profiles. A notable increase was found in proteins and metabolites associated with stress response, including photoreceptors, heat shock proteins as well as amino acids (e.g., proline, serine), sugars (e.g., raffinose, trehalose) and the phytohormone salicylic acid. Furthermore, exposure of mustard (Brassica juncea) seedlings to FML enhanced growth. Thus, our data showed that despite the low light intensity emitted by the moon, it is an important environmental factor perceived by plants as a 'stress' signal leading to alteration in cellular activities and consequently in plant growth and development.

Singiri, J. R., Priyanka, G., Trishla, V. S., Adler-Agmon, Z., & Grafi, G. (2023). Moonlight Is Perceived as a Signal Promoting Genome Reorganization, Changes in Protein and Metabolite Profiles and Plant Growth. Plants, 12(5), 1121.

17. Identification and Functional Characterization of an AM - induced Lipid Transfer Proteins in *Lotus japonicus*

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Arbuscular Mycorrhiza (AM) is a symbiotic association between land plants and Glomeromycotina fungi that emerged around 400 million years ago. In this symbiotic association, the fungus provides mineral nutrient to the plant, mainly phosphate, while the plant provides up to 20% of its photosynthetically fixed carbon in the form of hexoses and lipids. Lipids are provided from the plant to the fungus through a lipid biosynthesis pathway that specifically occurs in arbuscule-containing cells. However, the mechanism of the lipid transport across the hydrophilic peri-arbuscular space is not known. We hypothesise that lipid transfer proteins (LTPs) might be involved in this transfer. Lipid transfer proteins are small, soluble, and cysteine-rich proteins that bind to lipids. LTPs are in general, synthesized with the N-signal peptide that mediates apoplastic localization. Moreover, LTPs have a conserved 8-cysteine motif and form a hydrophobic cavity that confers their ability to bind lipids. Based on transcriptome data and qPCR-gene expression data, we found 4 *LTP* genes in *Lotus japonicus*, which are strongly induced in roots colonized by arbuscular mycorrhiza fungi. One of them was localized in the apoplast surrounding arbuscules supporting our hypothesis that they act in the peri-arbuscular space, possibly by facilitating the transfer of lipids towards fungus.

18. Heat stress memory in the unicellular red alga *Cyanidioschyzon merolae*

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An exposition to a sub-lethal heat dose can prime plants to survive normally lethal doses of heat in the future, a process termed heat stress (HS) memory. The molecular mechanisms of HS memory are not fully investigated yet. However, in times of global warming it is more important than ever to understand how this major food source can adapt to rising temperatures. We use the unicellular red alga *Cyanidioschyzon merolae* as a simplified model organism to identify key regulators and molecular pathways underpinning the establishment and maintenance of HS memory in photosynthetic eukaryotes. *C. merolae* has a small genome, consisting of approximately 5,300 genes with many genes present in single copies. Moreover, it has a short reproduction time of less than 24 hrs, which compared to crops, enables a very fast conduction of experiments. *C. merolae* optimally grows at 42 °C. We revealed that it can be primed to survive up to 2.5 hrs at 60 °C, while unprimed algae already die after less than 1 hr. Moreover, primed algae exhibit higher Photosystem II fitness than unprimed algae when being exposed to the triggering HS. A screening revealed that loss of the splicing factor homologue SERINE/ARGININE-RICH SPLICING FACTOR HOMOLOGUE 2 (SRSF2) or of the temperature-sensitive kinase CDC2-LIKE KINASE 1 (CLK1) negatively affects the alga's ability to establish HS memory. This indicates a relation between alternative splicing and HS memory in this organism, which interestingly contains only 39 introns in total and whose spliceosome's function has not yet been characterized.

19. 2D and 3D visualization of herbaceous plant-plant contact zones using High Resolution X-ray Computed Tomography (HRXCT)

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High resolution X-ray computed tomography (HRXCT) enables sectioning-free 2D imaging of biological structures and reconstruction of 3D objects. Although its application is common in many areas of biomedicine and despite its flexibility regarding resolution levels, the technology remains underutilized in the plant sciences. Here, we established HRXCT for the study of parasitic plant-plant interactions by presenting a sectioning-free protocol to access soft-tissue host-parasite contact zones at cell level resolution. We tested various sample preparation methods and contrast stains for their efficiency to improve the resolution of haustorium-host samples at the cellular level. In doing so, we achieved the visualization of the cellular organization of haustorium structures, especially of the vascular system for fresh and contrast-stained samples. Fresh stained and dehydrated haustorium sample preparation enabled the highest spatial resolution with a fine-cellular discrimination of haustorium vs. host cells. Application of cell-level resolved HRXCT to the pathosystems *Alectra*-cowpea, *Phelipanche*-tomato, *Striga*-sorghum, *Phtheirospermum*-tomato, and *Rhamphicarpa*-tomato highlighted a lifestyle-specific organization and uncovers an yet undescribed internal displacement of host tissue at parasite-host contact zones. Following image-based training, our HRXCT approach can invoke AI-based cell recognition for automated parasite cell-host cell differentiation. Superseding extensive microsectioning for 3D imaging, the newly established HRXCT protocol for 2D- and 3D- visualization of plant-plant contact zones and the first insights gained from it, is promising and useful for mid-throughput, comparative studies of parasitic plant-host interactions.

20. From controlled environment to field: confounding factors in container trials

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Global climate change models predict an increase of extreme weather events, among them drought and heat. Maintenance of agricultural yield requires breeding of resilient crops. The bottleneck in drought tolerance breeding is phenotyping in managed field environments. Fundamental research on drought tolerance uses container-based test systems in controlled environments as a proxy. However, breeders debate the portability of results from these systems to performance under field conditions. Thus, we analyzed the effects of climate conditions, container size, starting material, and substrate on yield and drought tolerance assessment of potato genotypes in pot trials compared to field trials. The tolerance ranking in the field was obtained from seven multisite-multiyear trials. The tolerance ranking in controlled environments was highly reproducible, but weakly correlated with field performance. Changing to variable climate conditions, increasing container size and substituting cuttings by seed tubers did not improve the correlation. Substituting horticultural substrate by sandy soil resulted in yield and tuber size distributions similar to those under field conditions. However, as the effect of the treatment × genotype × substrate interaction on yield was low, drought tolerance indices that depend on relative yields can be assessed on horticultural substrate too. Realistic estimates of tuber yield and tuber size distribution, however, require the use of soil-based substrates

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21. Role of DNA methylation in seed development and gametogenesis

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Apomixis is a fertilisation-independent process which can lead to clonal offspring, genetically identical to the maternal parent. It has high agronomical importance since it would allow maintaining hybrid vigour and other favourable traits, and would enable seed production even when pollen/pollinators are limited (Figueiredo and Köhler, 2018). Engineering of apomixis into sexual species has seen some major advances recently (Vernet et al., 2022), but engineering of an autonomous endosperm, one of the key steps involved, is yet to be achieved. The manipulation of auxin levels or removal of the epigenetic repressor Polycomb Repressive Complex 2 (PRC2) can initiate endosperm development even without fertilisation, but these endosperms do not proliferate as much as sexual endosperms, and they fail to cellularise, eventually leading to non-viable seeds (Figueiredo et al., 2016, 2015; Roszak and Köhler, 2011). Vinkenoog et al. showed that loss of DNA methylation in a PRC2 mutant background can overcome this and lead to a highly proliferative and cellularised endosperm (Vinkenoog et al., 2000). Resorting to mutants impaired in DNA methylation and to chemical inhibitors of this epigenetic mark, we wish to investigate this further and assess the degree up to which DNA methylation can affect autonomous endosperm development. We will then try to uncover the loci that may be the key players in this process, and check if their *in planta* manipulation can be used to produce functional autonomous endosperms.

Figueiredo DD, Batista RA, Roszak PJ, Hennig L, Köhler C. 2016. Auxin production in the endosperm drives seed coat development in Arabidopsis. *eLife* **5**:e20542. doi:10.7554/eLife.20542

Figueiredo DD, Batista RA, Roszak PJ, Köhler C. 2015. Auxin production couples endosperm development to fertilization. *Nat Plants* **1**:15184. doi:10.1038/nplants.2015.184

Figueiredo DD, Köhler C. 2018. Auxin: a molecular trigger of seed development. *Genes & Development* **32**:479–490. doi:10.1101/gad.312546.118

Roszak P, Köhler C. 2011. Polycomb group proteins are required to couple seed coat initiation to fertilization. *Proc Natl Acad Sci U S A* **108**:20826–20831. doi:10.1073/pnas.1117111108

Vernet A, Meynard D, Lian Q, Mieulet D, Gibert O, Bissah M, Rivallan R, Autran D, Leblanc O, Meunier AC, Frouin J, Taillebois J, Shankle K, Khanday I, Mercier R, Sundaresan V, Guiderdoni E. 2022. High-frequency synthetic apomixis in hybrid rice. *Nat Commun* **13**:7963. doi:10.1038/s41467-022-35679-3

Vinkenoog R, Spielman M, Adams S, Fischer RL, Dickinson HG, Scott RJ. 2000. Hypomethylation promotes autonomous endosperm development and rescues postfertilization lethality in fie mutants. *Plant Cell* **12**:2271–2282. doi:10.1105/tpc.12.11.2271

22. Parasitic success of the pathogenic plant *Phelipanche ramosa* (Orobanchaceae) is reduced in some re-infected versus naïve tomato cultivars

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Plants are exposed to infection and predation by organisms from most kingdoms of life, including their own. Layers of molecular defence mechanisms have evolved to limit damage and disease from microbial and insect pathogens, and plants can also defend themselves against attack by members of their own kingdom. Those so-called parasitic plants attach to and take up nutrients from a host plant. It is not yet known whether parasites belonging to the plant kingdom can elicit a systemic defence response in their hosts, to which they have much more in common molecularly than viruses and fungi. To gain insight as to whether previous infection reduces the susceptibility of a host, we used multiple rounds of infection of the same host plants with the holoparasitic plant Phelipanche ramosa ("broomrape", Orobanchaceae). We tested seven cultivars of tomato, and found that the 'Moneymaker' cultivar was re-infested at a lower rate than its naïve counterpart and supported fewer parasites than other cultivars. Throughout the experiment, we collected host-parasite interface tissue and subjected it to RNA sequencing. These data revealed tomato cultivar-specific transcriptional profiles in the parasite. Furthermore, we detected the upregulation of lignin biosynthesis genes in 'Moneymaker' tomato plants when those were pre-infected with the holoparasitic plant. Together, our data suggest that some tomato cultivars may be naturally able to build up defences against parasitic plant infection.

23. Seed coat-derived brassinosteroids non-cell autonomously regulate endosperm development

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The seed is formed by the embryo, endosperm and seed coat, which communicate to ensure synchronized development. Auxin was shown to play a crucial role in the communication between the endosperm and the seed coat. Upon fertilization, auxin is produced in the central cell triggering its replication and consequently, leading to endosperm development. The endosperm-derived auxin is transported to the integuments, where it promotes the expression of genes necessary for seed coat development, thereby promoting seed coat formation. Interestingly, this does not seem to be a single way communication, since genetic evidence from our group and others indicates that the seed coat also influences endosperm development: the endosperm proliferation rate is dependent on seed coat expansion and fate acquisition. Therefore, other signalling mechanisms between the seed coat and the endosperm promote and sustain its growth.

Here, we show that brassinoteroids (BR) participate in endosperm development, as mutants impaired in BR biosynthesis and signaling show reduced endosperm proliferation rates. Our data reveals that BR intermediates likely move between distinct domains of the seed coat to originate brassinolide, which then non-cell autonomously regulates endosperm development. We propose that this regulation is driven by modifications of the mechanical properties of the seed coat cell walls, which culminates in the modulation of auxin responses in the endosperm. Furthermore, the effect of BR on endosperm size is independent of the timing of endosperm cellularization, challenging previous models. We thus propose that seed coat expansion, as driven by BR activity, is a non-cell autonomous driver of endosperm proliferation.

24. Exploring plastid-nucleus interactions in the genus Nicotiana through horizontal transfer of plastids

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Plastid capture refers to the acquisition of plastids from one plant species by another through asexual means. Recent research has demonstrated that this phenomenon can occur through horizontal genome transfer during grafting. However, due to complex interactions between the nuclear and organellar genomes after long-term coevolution, captured plastids may not be always compatible with the recipient nuclear genome, resulting in phenotypic abnormalities such as bleaching, variegation, or lethality. The mechanisms underlying these incompatibilities are poorly understood. In this study, we aim to transfer the plastid genome of Nicotiana tabacum into different Nicotiana species through grafting. We are interested in investigating the compatibility of the captured plastids with the nuclear genomes of the recipient plants. To date, we have generated and characterized 12 Nicotiana species whose plastids were replaced with plastids from Nicotiana tabacum by grafting and horizontal genome transfer. These plastid capture events will be comprehensively characterized to study the resulting phenotypic and physiological changes during growth under different environmental conditions.

25. Regulating the Organelle Band through Actin Dynamics in Male Meiosis of *Arabidopsis*

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Meiosis is a unique cell division process for sexual reproduction in plants and animals. In the meiotic cell cycle, a single round of DNA replication is followed by two rounds of chromosome division, called meiosis I and meiosis II. Both rounds of the meiotic cell cycle contain prophase, metaphase, anaphase, and telophase. The chromosomes segregate at metaphase and form two cells after a new cell wall is built during telophase. In dicotyledons, instead of a real cell wall, a band structure consisting of vesicles derived from different organelles is formed after the first chromosome division. The reason why dicotyledons form such a structure is unclear. However, the disruption of this structure in meiosis II can result in nuclear restitution and the production of unreduced gametes. The mutation that leads to the disorder of the organelle band is named *jason* (*jas*). In this study, a suppressor of *jas*, called *pel*, was obtained through forward genetic screening. Analysis of the phenotype of *jas pel* suggests that *pel* might perform its function through actin dynamics.

26. Molecular mechanism of PHO2 regulating arbuscular mycorrhiza development

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Arbuscular mycorrhizal fungi (AMF) can establish a symbiotic relationship with most terrestrial plants. They transfer nutrients to the plant in exchange for carbohydrates and lipids. Plants majorly benefit from symbiotic transfer of the poorly accessible phosphate, which is very important for plant growth and development. There are two main ways for plants to obtain nutrients: Plant roots can directly absorb nutrients from the soil, which is called the direct nutrient absorption pathway. In most natural situations plants obtain nutrients from the external environment through arbuscular mycorrhizal fungi, which is called the indirect (or mycorrhizal) nutrient uptake pathway. However, AM formation is inhibited at high phosphate status, and this is regulated by the PHR-SPX phosphate response system. However, the involvement of other components of the phosphate signalling pathway in AM symbiosis remains unclear. Here we show that the E2-ubiquitin conjugating enzyme PHOSPHATE 2 (PHO2), which attenuates phosphate uptake responses at high plant phosphate status by mediating the degradation of crucial phosphate transporters, participates in regulating AM development. We identified two *PHO2* genes in the *Lotus japonicus* genome, called respectively *PHO2A* and *PHO2B*. Root colonization of *pho2* mutants is increased under low (20µM) as well as high phosphate (500µM) fertilization, when compared to wild type. Interestingly, the colonization of single *pho2* mutants does not differ from *pho2a,b* double mutants, suggesting that both PHO2a and B are equally important in the regulation of AM. In addition, root colonization of *pho2* mutants depends on the nitrate status of the plant. It is decreased with respect to the wild-type at low nitrate (0.75mM) and increased with respect to the wild type at high nitrate (7.5mM) fertilization. We are currently investigating the molecular role of PHO2 in modulating root colonization by AMF and its role in mediating the cross-talk between the plant phosphate and nitrogen status.

27. A complex complex - new components of the CESA complex

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The plant cell wall plays a crucial role in plant development and serves as a defense mechanism against both biotic and abiotic stresses. Cellulose microfibrils are the primary load-bearing components of cell walls, and their synthesis is guided by microtubule-associated cellulose synthase (CESA) complexes (CSC). While some CSC members, like CSI1 or the CC proteins, have been identified, the full characterization of the complex is still incomplete. Additionally, the regulation of cellulose synthesis under different environmental stresses remains unclear.

In our study, we have discovered two new protein components within the CSC, which belong to a larger protein family. Through live-cell imaging, we observed that these proteins colocalize and comigrate with the CSC at the plasma membrane. When exposed to oryzalin treatment, which destabilizes microtubules, these proteins relocalized to the remaining microtubules, indicating a tight interaction. Notably, double mutants lacking these two proteins displayed increased sensitivity to cellulose synthesis inhibitors. Furthermore, the quadruple mutant, which lacked both CC1 and CC2 proteins, was unable to grow on salt media, suggesting that these proteins play a vital role in growth under salt conditions.

Our findings highlight the incomplete characterization of the CSC and suggest that other members of the protein family may also contribute to cellulose synthesis. This research sheds new light on the intricate regulation of cellulose synthesis, particularly under abiotic conditions. Understanding these processes better could have significant implications for plant growth and response to environmental challenges.

28. Differential effects of geminiviral proteins on the plant cell cycle

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Viruses have a limited genome, so they heavily rely on the host molecular machinery to fulfill different functions, including the replication of their genome (1). Geminiviruses are circular ssDNA viruses, which infect crops worldwide. Their genome is amplified in the nucleus of the host cells by the plant's DNA replication machinery. As geminiviruses infect fully differentiated cells, the expression of this machinery must be re-activated by the virus (2). The geminiviral Rep protein is sufficient to mediate viral replication, but recently it was shown that other factors aid in the induction of a permissive cell environment, including C2 from beet curly top virus (BCTV) (3). In this project we are aiming to investigate how different viral proteins, selected for their ability to promote viral replication, manipulate the cell cycle. All the tested proteins were able to upregulate cell cycle-related genes. By using flow cytometry, we showed that C2 from BCTV can also induce replication of the plant genome. This indicates that C2 is sufficient to restore the DNA replication competence in the transfected cells, which would facilitate the recruitment of the host machinery by Rep. Rep from BCTV seems to be able to use its activation of the cell cycle to only enable replication of the viral genome without causing replication of the host genome. Taken together, our results shed light on the diversity of molecular mechanisms deployed by geminiviruses to enable their DNA replication.

(1) Hanley-Bowdoin L., Bejarano E., Robertson D. and Mansoor S. (2013) – *Nat Rev Microbiol*;
(2) Wu M, Bejanaro E, Castillo A. and Lozano-Duran R. (2022) – *Geminivirus: Detection, Diagnosis and Management*;
(3) Caracuel Z., Lozano-Duran R., Huguet S., Arroyo-Mateos M., Rodríguez-Negrete E. and Bejarano E. (2012) - *New Phytol.*

29. “Sattheit” of plant photosynthesis: Investigation on the full-sugar-driven repression of photosynthesis

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Photosynthesis produces carbohydrates by assimilating atmospheric carbon dioxides upon illumination. Carbohydrates from photosynthesis, called photosynthates, are pivotal energy sources for many organisms on earth, including plants. However, excess accumulation of photosynthates induce the suppression of the expression of various photosynthetic nuclear-encoded genes, which is referred to “full-sugar-driven repression of photosynthesis”. By the genetic screening on Arabidopsis seedling development under high amount of sugar feeding, diverse research groups have revealed the key molecules that regulate the full-sugar-driven repression during the seedling stage (Pego et al. 2000). However, the molecular mechanism of full-sugar-driven repression remains to be elucidated in photosynthetically active leaves.

Here, we sought to identify the key molecules of full-sugar-driven repression in leaves, by a suppressor screening with full-sugar plants, which has a point mutation on *SUC2, suc2-7* (Okumura et al. 2016). The leaves of full-sugar plants highly accumulate the photosynthates due to the low sugar loading of the phloem and show a dwarf growth. Using the growth phenotype as the first indicator, ca. 18000 EMS-mutagenized Arabidopsis seeds were screened, and 20 mutants (Revertant of Full-Sugar, RFS) were isolated. Many of RFSs showed the recovery of growth phenotype as well as the recovery of repression of photosynthetic genes. In this poster, we will present the screening strategy and report on the characterisation of some RFS mutants.

30. Targeted C-to-T base editing in the organellar genome of *Arabidopsis thaliana*

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Modifying plastid and mitochondrial genomes (organellar genomes), which encode photosynthesis- and respiration-related genes, respectively, may enhance crop productivity. Therefore, developing tools to modify these genomes is important for crop breeding and basic science. Targeted gene insertion into plastid genomes (plastid transformation) that is the representative method for modifying plastid genomes is applicable to only a limited number of species than nuclear transformation. Mitochondrial genomes of terrestrial plants can be stably modified by mitochondria-targeted programable nuclease (mitoTALEN). Although mitoTALEN could disrupt mitochondrial genes, it also caused structural changes in mitochondrial genomes. Here we report a method for editing a target cytosine to thymine in organellar genomes of plantlets of *Arabidopsis thaliana*, using plastid- or mitochondria-targeted base editors (ptpTALECD, ptpTALECD_v2, and mitoTALECD). These base editors substituted targeted C:G pairs to T:A pairs in all copies of the polyploid organellar genomes in some T_1 plants. T_2 progenies stably inherited the introduced substitutions, independently of the inheritance of the nuclear-introduced base editor gene. Overall, off-target base substitutions by ptpTALECD and mitoTALECD were low in number and frequency, and mitoTALECD did not cause the structural change of mitochondrial genomes as mitoTALEN did[1, 2]. Although ptpTALECD_v2 more efficiently substituted targeted C:G pairs, it more frequently introduced undesired substitution than ptpTALECD[3]. Our method can introduce amino acid substitutions, create premature stop codons, and change the secondary structure of RNA. In addition, the ptpTALECD method can be applied to more species than plastid transformation. Thus, these base editors would accelerate basic research for organellar genomes of plants as well as contribute to crop breeding using organellar genomes.

1, Nakazato *et al*., *Nature Plants*, 7, 906-913 (2021); 2, Nakazato *et al*., *PNAS*, 119 (20), e2121177119 (2022);
3, Nakazato *et al*., *The Plant Journal*, published online (2023), https://doi.org/10.1111/tpj.16311

31. Carbon concentrating mechanism-related protein induction and plastid rearrangement during submersion in hornworts

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Plastids play an important role in plants' responses to changing environments. In hornworts, chloroplasts can contain a RuBisCO-enriched protein matrix (pyrenoid), which enables them to perform biophysical carbon concentration at the single-cell level (CCM) – a unique feature among land plants. Based on homology to green algal CCM genes and an in-silico predicted plastid proteome, we identified a set of CCM candidate genes in Anthoceros agrestis. In doing so, we also assessed hornwort-specific plastid processes by label-free proteomic analysis under H2O submersion in the pyrenoid-forming A. agrestis and the pyrenoid-free A. fusiformis. Under submersion, both species expressed CCM-like homologs, despite otherwise predominant idiosyncratic protein expression profiles. Furthermore, exposure of submersed plants to additional H2O2 could induce or diminish the expression of CCM-like homologs in a species-specific manner within a 48 hour timeframe. Ultrastructural analysis of plastids revealed an increase in pyrenoid-like structures and rearrangement within the first 24 hours of submersion in A. agrestis. In contrast, A. fusiformis showed no de novo birth of such pyrenoid-like structures, but an increased formation of putative plastid lipid droplets. Together, our data indicate that Anthoceros species exhibit different acclimation to submersion including the induction of pyrenoid-like structures.

32. Epigenetic reprogramming of the seed coat: a role for Brassinosteroids?

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Angiosperm seed development begins with a double fertilization process, which involves the fusion of a maternal egg cell and of a central cell with two paternal sperm cells. This results in the formation of the diploid embryo and the triploid endosperm, which are subsequently surrounded by the seed coat, which is generated solely from the maternal integuments. Epigenetic regulators known as Polycomb Group (PcG) proteins actively limit seed coat development in *Arabidopsis thaliana* before fertilization. These proteins leave a repressive histone mark known as H3K27me3, which must be eliminated after fertilization in order for the seed coat to develop. In this project, we investigated the mechanism of H3K27me3 removal from the integuments after fertilization, which allows for seed coat development. We hypothesized that this removal would be aided by histone demethylases from the JMJ family and could be regulated by Brassinosteroids (BRs). The expression patterns of the JMJ protein REF6 as well as BR biosynthesis and signaling genes, which are exclusively expressed in the integuments and seed coat, corroborated this idea. Furthermore, mutations in both these processes cause developmental defects such as decreased ovule viability and delayed seed coat growth. Our findings imply that BR signaling is crucial in recruiting JMJ-type histone demethylases to target loci involved in seed coat development for H3K27me3 removal. Furthermore, we uncovered an additional pathway via which BRs regulate seed coat formation that is unrelated to their influence on H3K27me3 marks. This discovery highlights the various activities of BRs in seed formation, which go beyond their well-known participation in plant growth and development.

33. Volatile components as novel biomarker for non-destructive early assessment of scab-disease tolerance in apple genotypes

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Apple scab (caused by the fungus *Venturia inaequalis*) is one of the most destructive diseases of apple, world-wide. Plant-pathogen interactions produce an array of volatile components (VCs). VC profile of scab-resistant and susceptible apple genotypes is expected to differ substantially. Further, scab-infection would change the VC profile substantially and dynamically over healthy plants. This work aimed at discovering novel VC biomarkers for the non-destructive prediction of scab tolerance level of different Apple genotypes. The study analyzed ten different apple cultivars for their VC emission profile using solid-phase microextraction (SPME) GC-MS analyses and multivariate statistical analyses. Results showed that scab-resistant cultivars (cv. “Florina”, “Firdous”, “Liberty”) emitted more sesquiterpenes than susceptible cultivars and contained unique volatile biomarkers such as 2-hexenoic acid and benzoic acid-methyl ester. Notably, 2-Hexenoic acid also exhibited strong in vitro antifungal activity against *Venturia inaequalis*, a common apple pathogen, and could serve as a promising alternative to traditional fungicides. The detection of 2-Hexenoic acid was robustly applicable for precise screening of scab-resistance in apple breeding lines. These novel scab-related volatile biomarkers are promising candidates for non-destructive chemo-typing of apple genotypes.

34. Full moonlight (FML) induces stress response and enhances post germination growth of *Brassica juncea* (mustard)

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Beyond the myth, many creatures on earth sense solar radiation reflected by the moon. Moonlight and the lunar cycle can affect behavior of vertebrate and invertebrate species including reproduction, communication, foraging and predation. Rhythmic exposure to moonlight is believed to affect the life cycle of plants, from seed germination to fruit maturation and dispersal. In traditional lunar farming 'above ground crops' are commonly planted between the new moon and the full moon while 'below ground crops' between the full moon and the next new moon; though these lunar farming practices have no solid scientific support. Here we addressed the effect of full moonlight (FML) on post germination growth of *Brassica juncea* (an above ground crop). Accordingly, 10-day-old seedlings were exposed to FML for three consecutive nights (5h each night, starting a day before FML) and their growth parameters were recorded after 1 and 2 weeks and compared to dark-exposed plants. The results showed that seedling performance (shoot and root dry and fresh weights) after 1 week or 2 weeks was significantly improved under FML compared to dark. Metabolic analysis showed that exposure of seedlings to 5h FML resulted in increase in stress metabolites including salicylic acid, a plant hormone implicated in defence against a variety of biotic and abiotic stresses and in amino acids (valine, proline, serine). It appears that FML serves as a signal that induces stress response, which in turn enhances post-germination growth under normal, unstressed conditions.

35. Phytohormonal regulation of cellular endosperm development in tomato

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The endosperm is a nourishing tissue present in angiosperm seeds, whose emergence contributed to angiosperms becoming the dominant land plants. Based on its cellularization pattern there are three types of endosperm development: nuclear, cellular, and helobial. Cellular and nuclear development being the most common patterns. Studies on the model organism *Arabidopsis thaliana*, which has a nuclear-type endosperm, showed that the plant hormones auxin and Brassinosteroids (BRs) have a significant role in endosperm formation. However, a detailed insight regarding cellular endosperm development, including its genetic regulation and the role of different phytohormones, is yet to be undertaken. To investigate this, we used tomato *(Solanum lycopersicum)* as a model organism. Exogenous hormone applications showed that manipulation of auxin is sufficient to stimulate fertilization-independent seed development through the proliferation of the endothelium layer in tomato seeds. However, BR applications show repressive effects on tomato seed development. To better explore this, we knocked-out SlBZR1, a master transcription factor (TF) involved in BR signalling pathway, and which is paternally expressed in tomato endosperms. The *slbzr1* CRISPR-Cas9 mutant showed defects in endosperm cellularisation and expansion. Thus, I propose that auxin has a positive effect on seed expansion in tomato and the TF SlBZR1 has an important role in the development of cellular endosperm.

36. Impact of nitric oxide on photosynthesis in maize and sorghum

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The effects of foliar application of different concentrations of the sodium nitroprusside (SNP, as a donor of nitric oxide) on sorghum (*Sorghum bicolor* L. Albanus) and maize (*Zea mays* L. Kerala) were investigated. Chlorophyll fluorescence (PAM and JIP test), P700 photo-oxidation, pigment analysis, determination of the membrane integrity and antioxidant markers were used for characterization of the impact of NO under physiological conditions. Data revealed that SNP influences the pigment content, the amount of the open photosystem II (PSII) centers and their efficiency, the electron transport flux from Q_A to Q_B (ETo/RC), the electron flux reducing photosystem I (PSI) end acceptors (REo/RC), the number of active reaction centers per PSII antenna chlorophylls, the performance index (PI_{total}) and rate of the photosynthesis (R_{FD}). In addition, results showed an influence on the photochemistry of both subpopulations of PSI. The analysis of the P_{700} photooxidation revealed an influence on the photochemistry of both subpopulations of PSI. The effects of NO under physiological conditions were concentration-dependent and variety-specific. The results of this study provide new information about the role of this signaling molecule in photosynthetic performance.

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37. Plant's distress talk through the signalling molecule Azelaic acid

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Plant – microbial interaction is a complex web of interactions. Plants in their natural environment face drought, salinity, temperature, and other biotic stresses. After local perception of stress, the information is spread within the plant body to activate appropriate responses in systemic tissues or organs. Azelaic acid (AzA), a C9 oxylipin ("HOOC $(CH_2)_7$ COOH"), plays a prominent role in this scenario. The oxylipin AzA is synthesized in the plastid outer membrane and triggers immunity through an AZI1/EARLI1/MPK3/6-dependent pathway; but the traverse of AzA in the plant system remains a mystery. Upon fungal or bacterial elicitor application to roots, AzA accumulates in the leaves and triggers the expression of the gene of its receptor AZI, a lipid transfer protein. I investigate how the Azi1 gene expression can be stimulated in the systemic tissue and intend to decipher its traverse pathway, while also examining its specificity compared to its related genes.

38. Massive crossover suppression by CRISPR-Cas-mediated plant chromosome engineering

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Several studies have demonstrated that not only genes but also entire chromosomes can be engineered using clustered regularly interspaced short palindromic repeats (CRISPR)/CRISPR-associated protein 9 (Cas9)[1-5]. A major objective of applying chromosome restructuring in plant breeding is the manipulation of genetic exchange[6]. Recently, we were able to show that meiotic recombination can be suppressed in nearly the entire chromosome using chromosome restructuring[7]. We were able to induce a heritable inversion of a >17 Mb-long chromosome fragment that contained the centromere and covered most of chromosome 2 of the *Arabidopsis* ecotype Col-0. Only the 2 and 0.5 Mb-long telomeric ends remained in their original orientation. In single-nucleotide polymorphism marker analysis of the offspring of crosses with the ecotype Ler-1, we detected a massive reduction of crossovers within the inverted chromosome region, coupled with a shift of crossovers to the telomeric ends. The few genetic exchanges detected within the inversion all originated from double crossovers. This not only indicates that heritable genetic exchange can occur by interstitial chromosome pairing, but also that it is restricted to the production of viable progeny.

1. Schmidt, C. et al. Changing local recombination patterns in Arabidopsis by CRISPR/Cas mediated chromosome engineering. Nat. Commun. 11, 4418 (2020).
2. Beying, N., Schmidt, C., Pacher, M., Houben, A. & Puchta, H. CRISPR– Cas9-mediated induction of heritable chromosomal translocations in Arabidopsis. Nat. Plants 6, 638–645 (2020).
3. Lu, Y. et al. A donor-DNA-free CRISPR/Cas-based approach to gene knock-up in rice. Nat. Plants 7, 1445–1452 (2021).
4. Schwartz, C. et al. CRISPR–Cas9-mediated 75.5-Mb inversion in maize. Nat. Plants 6, 1427–1431 (2020).
5. Filler Hayut, S., Melamed Bessudo, C. & Levy, A. A. Targeted recombination between homologous chromosomes for precise breeding in tomato. Nat. Commun. 8, 15605 (2017).
6. Rönspies, M., Dorn, A., Schindele, P. & Puchta, H. CRISPR–Cas-mediated chromosome engineering for crop improvement and synthetic biology. Nat. Plants 7, 566–573 (2021).
7. Rönspies, M. et al. Massive crossover suppression by CRISPR–Cas-mediated plant chromosome engineering. Nat. Plants 10, 1153-1159 (2022).

39. Genetic determinants of autonomous endosperm formation in Arabidopsis

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In Angiosperms, seed development starts with the double fertilization of the maternal gametes by two sperm cells. This leads to the formation of two distinct structures, the embryo and the endosperm, surrounded by a maternal seed coat. Some species called apomicts can produce clonal seeds without fertilization. However, this highly desirable agronomical trait is not present in crops. The apomixis process involves three steps: bypassing meiosis, embryo parthenogenesis and autonomous endosperm formation. This project aims at deciphering the molecular mechanisms involved in autonomous endosperm formation. The endosperm starts as a coenocyte, which later cellularizes. Hormonal treatments with auxin or mutations in components of the Polycomb Repressive Complex 2 (PRC2) induce the first step of autonomous endosperm formation, but its growth and cellularization are still a limiting factor. Among PRC2 mutants, *fie* leads to the formation of big autonomous seeds, whereas *fis2* produces small autonomous seeds. Thus, we employed a genetic suppressor screen to identify the genetic determinants of the large autonomous endosperm of *fie* mutants. On the other hand, paternally-expressed imprinted genes (PEGs) have been shown to restore endosperm cellularization in interploidy crosses. We will thus test if mutations in these genes also have an effect on autonomous endosperm formation. The most promising results will be used to test the induction of autonomous endosperm development in barley.

40. Secondary wall formation in xylem as a model system to uncover principles of cytoskeletal patterning in *Arabidopsis thaliana*

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The vascular tissue allows plants to efficiently transport water and plays a crucial role during early seedling development. The vasculature of young *Arabidopsis thaliana* roots is composed of Proto- and Metaxylem vessels. These vessel types can easily be distinguished by their characteristic cell wall patterning. The underlying patterning processes are partially known for the holey metaxylem cell walls but remain largely elusive for the spiral-like protoxylem wall pattern.

Our research aims to contribute to bridge this knowledge gap. So far, we used co-expression network analysis on published transcriptomic data to identify potential players that have not been studied under the aspect of protoxylem patterning before. Homozygous mutants of the respective genes had been screened. For subsequent image analysis we're using a script that measures band / gap width on micrometer scale. This precise processing enables us to detect even the smallest changes.

Further, we attempt to alter the cell wall pattern by tissue-specific expression of cytoskeletal remodeler to investigate its influence on the patterning. In this context, we're aiming to also focus on the physiological role and explore to what extent altered protoxylem patterning influences the water flow within the vessels.

41. Chloroplast ascorbate peroxidases and their impact on plant immunity after prior cold exposure

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Cellular protection against reactive oxygen species (ROS) but also ROS-dependent signaling pathways are crucial for plants to cope with many environmental stress situations. Emerging questions are how abiotic environmental stressors impact on plant-pathogen interactions and which cellular components are involved in the cross-talk. Recently, we showed that the *ROS*-scavenging stroma-localized ascorbate peroxidase (sAPX) and the thylakoid ascorbate peroxidase (tAPX) contribute to enhanced resistance against virulent *Pseudomonas syringae* pv. *tomato* DC3000 *(Pst)* in *Arabidopsis thaliana* after an up to five days earlier cold pretreatment (4 °C, 24 h). Here, we wanted to elucidate the cold-primed immune signaling pathways and responses controlled by sAPX and tAPX. Hence, we analyzed and compared transcripts of pathogen- and ROS-responsive genes using different pathogen immune triggers and identified sAPX- and tAPX-dependent transcript variations after prior cold treatments. In addition, we found that an immediate cold pretreatment, however not an earlier cold exposure, lowered the susceptibility of *Arabidopsis* against necrotrophic *Botrytis cinerea* independent of tAPX but with contributions from sAPX. Our next goal is to identify the connecting signaling hubs between the chloroplast peroxidase system and pathogen defense pathways.

Griebel T, Schütte D, Ebert A, Nguyen HH, Baier M. Cold Exposure Memory Reduces Pathogen Susceptibility in *Arabidopsis* Based on a Functional Plastid Peroxidase System. Mol Plant Microbe Interact. 2022 Jul;35(7):627-637. doi: 10.1094/MPMI-11-21-0283-FI

42. Phytochemistry from the Himalayan diversity – from molecular discovery and metabolic analysis to Health applications

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Himalayan region houses a rich biodiversity of medicinal and aromatic plants (MAPs) due to its varied phytogeographical climatic zones at different altitudes. The therapeutic potential and industrial applications of these MAPs are attributed to the bioactive molecules present in their different parts. A range of challenges and research gaps exist in relation to phytochemical profiling, understanding the associated metabolic pathways, and drug discovery. From the Himalayan Medicinal and Aromatic plants (about 100), we profiled a large number of phytochemicals using multi-analytical platforms (NMR, GC-MS, and LC-MS). This allowed us to predict the ADME properties of phytochemicals and is currently assisting in establishing a Himalayan-specific phytochemical database. Further, we mapped the metabolic pathways of the detected diverse secondary metabolites involved in selected plants. Finally, case studies that led us to promise phytochemicals against various applications (in agriculture, industry and health) which we are focusing on will be discussed.

43. Elucidating the role of *SABRE* in coordinated polarity

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The ability to break symmetry and polarize cells is a fundamental property of living systems. Its regulation is at the core of multicellular development, of growth and form. In plants, the coordination of auxin transport, regulating a plethora of developmental programs, is dependent on the establishment of polar PIN protein (auxin efflux carriers) localization. Here we show that *SABRE* (Pietra *et al*., 2013), a gene of unknown function, is involved in the coordination of PIN2 polarity in cortical root meristematic cells of *Arabidopsis thaliana.* At the subcellular level, SABRE (SAB) colocalizes with PIN2 as well cytoskeletal components including different microtubule (MT) arrays. Mutations in the *SABRE* gene result in defective root gravitropic reorientation, a process which is known to be regulated by PIN2 (Luschnig *et al*., 1998; Müller *et al*., 1998; Chen *et al*., 1998).

44. Photosynthetic performance in pea and maize plants under salt stress

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The aim of the present study is to assess the effects of the short salt treatments (5 days) on the functions of the thylakoid membranes from pea (*Pisum sativum* L.) and maize (*Zea mays* L.), grown in a Hoagland solution. The low-temperature chlorophyll fluorescence revealed that NaCl influences the energy transfer between both photosystems as well as in the PSII complex, as a result of its modification. The salt-induced changes in the energy transfer correspond with an inhibition of the photochemical activity of PSI ($DCPIH_2 \rightarrow MV$), PSII ($H_2O \rightarrow BQ$) and an alteration of the kinetic parameters of the oxygen-evolving reactions (initial S_0-S_1 state distribution, misses (α), double hits (β) and blocked centers (S_B)). In addition, total antioxidant and antiradical activity were determined. The data in this work revealed the effect of salt-induced alterations in the energy transfer between pigment-protein complexes and oxygen-evolving complex modification on the degree of inhibition of photochemistry in both photosystems. The study contributes to our understanding of plant tolerance to salt stress.

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45. Role of a formin in *Arabidopsis thaliana* root hair elongation

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Root hairs are epidermal cell outgrowths that increase the root surface area, leading to better nutrient acquisition, plant anchorage and interactions with microbes. The development of root hairs can be divided into an initiation and elongation stage, both of which are known to be affected by several phytohormones (Datta et al., 2011). Recently karrikins, which are smoke-derived compounds thought to mimic phytohormones, were shown to positively regulate both root hair initiation and elongation by Villaecija-Aguilar et al. (2019). In the karrikin receptor mutant *kai2*, the density and length of root hairs is strongly reduced compared to WT plants, whereas karrikin treatment increases density and length. To find more proteins involved in karrikin signaling, we performed a suppressor screen with *Arabidopsis thaliana kai2* mutants using EMS. Via this screen, the *skai1* (*suppressor of kai2 1*) mutant was found, that restored root hair density and length to almost WT levels in a dominant fashion. The *skai1* mutation was mapped to a member of the formin gene family, encoding a group of proteins found across kingdoms, that interact with the actin cytoskeleton and are linked to cytokinesis, cell polarity, cell migration and endocytosis processes (Goode & Eck, 2007). 21 formins have been found in *A. thaliana* and while their ability to act on actin and sometimes microtubules has been confirmed for multiple members, their role in plant development is not well-studied (van Gisbergen & Bezanilla, 2013). Loss-of-function mutants rarely have visible phenotypes without treatments due to likely redundancy, meaning that the dominant *skai1* mutation offers a unique perspective into the role of formins during plant development.

Datta S. et al. (2011). Root hairs: development, growth and evolution at the plant-soil interface. *Plant and Soil*, *346*, 1–14. doi: 10.1007/s11104-011-0845-4.
Goode B. L. & Eck M. J. (2007). Mechanism and function of formins in the control of actin assembly. *Annual Review of Biochemistry*, *76*, 593-627. doi: 10.1146/annurev.biochem.75.103004.142647.
van Gisbergen P. A. & Bezanilla M. (2013). Plant formins: membrane anchors for actin polymerization. *Trends in Cell Biology*, *23*(5), 227-33. doi: 10.1016/j.tcb.2012.12.001.
Villaecija-Aguilar J. et al. (2019). SMAX1/SMXL2 regulate root and root hair development downstream of KAI2-mediated signalling in Arabidopsis. *PLoS Genetics*, *15*(8), e1008327. doi: 10.1371/journal.pgen.1008327.

46. Gene identification and mechanistic analysis of cytoplasmic male sterility derived from *Oryza sativa cv.* Tadukan

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Cytoplasmic male sterile (CMS) plants produce abnormal anthers or pollen because of an expression of a mitochondrial CMS-causing gene. In contrast, nuclear genes, *Restorer of fertility* (*Rf*), suppress an expression of the mitochondrial gene, resulting in fertility recover. We have developed a Tadukan-type CMS line, TAA, and a restorer line, TAR, by successive backcrossing *Oryza sativa* cv. Taichung 65 (T65) to cv. Tadukan. In TAA, mature pollen looks normal, but anthers do not dehisce, resulting in no seed set. We are going to identify a mitochondrial CMS-causing gene and nuclear *Rf* genes to elucidate the mechanism of Tadukan-type CMS.

First, we identified a CMS-causing gene, named *orf312*, by mitochondrial gene knockout using TALEN. *orf312*-knocked out plants recovered to form septum gaps in the connective tissue of the anther, leading to anther dehiscence, while TAA lines were not. RNA-seq analysis revealed that two genes of mitochondrial electron transfer chain (mtETC) complex were down-regulated in TAA. Based on these results, we hypothesized that ORF312 inhibits mtETC function, resulting in dysregulation of reactive oxygen species, which prevents programmed cell death in the anther tissue and thus prevents anther dehiscence.

Map-based cloning and complementation of *Rf* candidate genes revealed that one pentatricopeptide repeat (PPR) protein gene recovered spikelet fertility of TAA. Based on the PPR code prediction, this PPR protein are predicted to bind *orf312* RNA.

47. Rice-ing colors: Metabolite-Genome wide association studies unraveled the antidiabetic and anticancer properties of pigmented rice

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Rice is a vital staple crop for more than half of the world's population, making it essential to understand its metabolite composition and nutritional properties. Screening a diverse panel of rice varieties for their metabolite content is crucial for ensuring the dietary needs of rice-consuming countries. In this study, we conducted a comprehensive metabolomic analysis to assess the variation in bioactive compounds in large panel of pigmented rice varieties. Our findings revealed significant differences in the metabolite profiles of pigmented rice. Purple rice exhibited high levels of flavonols and anthocyanins, while red rice samples showed elevated levels of catechin and procyanidins. Through metabolite genome-wide association studies (mGWAS), we identified the Rc and IPT5 genes as being linked to higher proanthocyanidin levels in red rice. Interestingly, these genes were also associated with a lower glycemic index, indicating potential health benefits. Correlation network analyses revealed that proanthocyanidins play a pivotal role in the anti-colon cancer activities of rice. Additionally, molecular docking simulations indicated the potential interaction of these metabolites with cancer receptors, further highlighting their potential therapeutic value. Overall, our study provides valuable insights into the genetic regulation of phenolic metabolites in rice and offers a framework for screening a diverse range of rice varieties for their nutritional attributes. This knowledge can be utilized to develop rice varieties with enhanced dietary benefits, contributing to improved nutrition and health outcomes for rice-consuming populations.

48. Identification of green lineage osmotic stress pathways uncovers a role for actin during stress acclimation

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Maintenance of water homeostasis is a fundamental cellular process required by all living organisms. Here, we use the single-celled green alga *Chlamydomonas reinhardtii* to establish a foundational understanding of osmotic-stress signaling pathways through transcriptomics, phosphoproteomics, and functional genomics approaches. Comparison of pathways identified through this analysis with yeast and Arabidopsis allowed us to infer their evolutionary conservation and divergence across these lineages. Five genes, acting across diverse cellular pathways, were found to be essential for osmotic-stress tolerance in Chlamydomonas including cytoskeletal organization, potassium transport, vesicle trafficking, mitogen-activated protein kinase and chloroplast signaling. We show that homologs of these genes in the multicellular land plant *Arabidopsis thaliana* have conserved functional roles in stress tolerance and reveal a novel PROFILIN-dependent actin remodeling stage of acclimation that ensures tissue integrity upon osmotic stress. This study highlights the conservation of the stress response in algae and land plants and establishes Chlamydomonas as a unicellular plant model system to dissect the osmotic stress signaling pathway.

49. Exploring the functional diversification of the C4 proteins from geminiviruses

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Among all the six to eight proteins encoded by geminiviruses, devastating plant viruses worldwide, C4 is the most functionally diverse one. It has been proven that C4 is essential for viral full infectivity in all geminiviruses tested to date. C4 is also described as a symptom determinant. However, the complete functional repertoire of geminivirus-encoded C4 proteins as well as the underlying molecular determinants and mechanisms are not fully understood. Here, we investigate the diversity of C4 proteins encoded by a selection of geminiviruses by looking at their properties, subcellular localization, interactome, and potential functions in the context of the infection. We have found that C4 proteins show different subcellular localizations, including plasma membrane, chloroplasts, nucleus, and endosomes. Through targeted functional assays, we have identified both conserved and specific functions, and their potential underlying host interactors. We are currently investigating the effect of these selected C4 proteins on plant development, which underlies symptoms during the viral infection, and defining their proximity interactomes by TurboID-based proximity labelling (PL). Ultimately, we expect to integrate the obtained information on subcellular localization, biological function, and interacting partners, in order to uncover crucial biological processes manipulated by these viral proteins.

50. Mapping of plant organellar RNA binding proteins by targeted RNA editing

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Numerous RNA-binding proteins (RBPs) including PPR protein family have been extensively studied due to their essential functions in post-transcriptional processes within mitochondria and chloroplasts. To fully understand each RBPs' function, their RNA targets in vivo are very important information. However, the RNA ligands of RBPs are poorly understood in plants. STAMP (surveying targets by APOBEC-mediated profiling) was a newly developed method to detect the interactions between RBPs and their target RNAs using APOBEC1 cytidine deaminase enzyme in human cells. Upon binding of the APOBEC1 fused with an RBP, RBP can directly recruit APOBEC1 to its RNA targets and lead to C-to-U editing near binding sites. Therefore, the binding site of RBPs can be detected as C-to-U editing due to the fused APOBEC1 protein. The goal of this work is to establish STAMP in plants as a powerful tool to study the overviews of binding sites for organelles RBPs and understand the relationship between them. As the first pilot analysis, we selected several PPR proteins whose binding sites are already known or predicted and fused with APOBEC1 then introduced them into the knock-out lines to see if editing occurs at the expected sites or adjacent cytidines. One of the pilot experiments with CRR4 successfully edited the original target editing site, ndhD-1, in the *crr4-3* mutant with the help of the fused APOBEC1 protein.

51. Positional isotopologue analysis of aspartate to determine PEPC activity *in vivo*

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Photoautotrophic organisms fix inorganic carbon (Ci) by two important enzymes, ribulose-1,5-bisphosphate carboxylase/oxygenase (RUBISCO), which generates two molecules 3-phosphoglycerate, and phosphoenolpyruvate carboxylase (PEPC), which forms oxaloacetate. While 1,2,3-C of oxaloacetate carbon backbone and respective downstream metabolites (i.e. malate and aspartate) is derived from RUBISCO assimilation, 4-C is specific to PEPC assimilation. Positional isotopologue analysis of aspartate, the major downstream metabolite in *Synechocystis sp*. PCC 6803, allows differentiation between RUBISCO and PEPC assimilation of Ci. Exploring *in source* fragmentation of gas chromatography-electron impact ionization-mass spectrometry (GC-EI-MS) at nominal mass resolution and GC-atmospheric pressure chemical ionization-MS (GC-APCI-MS) at high mass resolution enabled determination of ^{13}C fractional enrichment ($E^{13}C$) in each carbon position of aspartate. Validation was performed by measurements of positional labelled aspartic acid standard mixtures. Combined with dynamic $^{13}CO_2$ labelling of *Synechocystis sp*. PCC 6803 cultures, it was possible to determine PEPC activity *in vivo*. Accurate quantification of aspartate concentration and positional $E^{13}C$ provided molar Ci assimilation rates. In addition, it was possible to reveal the impact of PEPC on total carbon assimilation, i.e. the ratio of Ci fixation by PEPC and RUBISCO.

52. Interrelation between Reactive Carbonyl Species (RCS) and Unfolded Protein Response (UPR) in *Arabidopsis thaliana*

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The UPR is an essential element of ER homeostasis, which is triggered and maintained by environmental stress conditions. Although there are many studies investigating ER stress and related signaling pathways in the literature, a novel perspective about the signaling role of RCS as ROS for growth, development, and stress response in plants is getting lots of attention. Therefore, this study elucidates the induction of the UPR and the role of RCS in ER stress tolerance in *A. thaliana*. The results of Schiff's staining showed that ER stress-induced RCS accumulation and 20 different carbonyl compounds were detected by HPLC analysis. Moreover, the regulatory role of ER stress induction on the transcriptional pathways of RCS scavenging was examined by qRT-PCR. To elucidate RCS involvement in ER stress tolerance, growth parameters and expressions of UPR-related genes were measured by induction of ER stress with different carbonyls and after treatment with carnosine, an RCS scavenger dipeptide. Clearance of RCS has been observed to result in changes in UPR-related genes. Furthermore, time-dependent analyzes of the expressions of UPR-related genes under carnosine treatment were performed to elucidate the transient response to RCS. To summarize, the results concluded that RCS is required for efficient induction of the UPR, and RCS is required for ER stress tolerance in *A. thaliana*.

53. Chloroplast Expression of Analgesic Conotoxins and Mambalgin

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Conventional painkillers are often addictive and have neurotoxic side effects, raising substantial health concerns. Some naturally occurring small polypeptides, including conotoxins and mambalgins, do not have these side effects and are even more potent analgesics. However, due to the low stability of these small peptides in microbial systems, and their complicated and expensive chemical synthesis, there are currently no economical production systems for peptide-based next-generation analgesics available. Plants offer great potential as bioreactors for the inexpensive synthesis of large amounts of recombinant proteins and peptides. Transgenic chloroplasts have received particularly great attention, as they often accumulate much higher levels of recombinant proteins than nuclear-transgenic plants. Unfortunately, small peptides are very unstable also in chloroplasts, most likely due to the presence of proteases that specifically degrade cleaved-off signal peptides. To provide a solution to this problem, we have attempted to synthesize conotoxins and mambalgin as fusion proteins.

We will report on the development of two successful strategies for the expression of five conotoxins and mambalgin. The peptides were expressed in transplastomic plants as cleavable fusion proteins. We show that the fusion proteins can be readily purified, and the peptides can be subsequently released by protease cleavage. The purified peptides are now available for tests of their pharmacological activities as ion channel inhibitors using electrophysiological methods.

Our work provides expression strategies for the production of small polypeptides in chloroplasts and demonstrates the great potential of transplastomic plants to produce next-generation painkillers at low cost and high yield.

54. Synchronization of flower opening: the heterodichogamous species as a case study

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Flower opening is essential for pollination and thus successful sexual reproduction. The vegetative and reproductive floral organs develop until the onset of flower opening, which takes place at different times of the day or night in different plant species. Although there is evidence in several species that a circadian clock regulates the time of flower opening, a detailed understanding of the mechanisms controlling this process is still lacking. In this project I study the heterodichogamous species *Ziziphus jujuba* addressing the knowledge gaps regarding the synchronization of the time of flower opening and development. The findings indicate that there are no significant differences in the time of flower open between control and inverted light/night conditions. These results support my hypothesis about a circadian rhythm that controlled the time of flower opening in both morphs. Hormone profiling evidenced that the accumulation of IAA-Asp (indole-3-acetic aspartate) was significant significantly increases over time in flowers of both morph in normal and inverted light conditions. RNA-seq and qRT-PCR results revealed the genes and pathways related to the circadian rhythm. At the end of this project, we will be able to draw a more comprehensive "picture" of the synchronous process of flower opening. This research will provide a valuable set of findings that will shed light on a fundamental biological process.

55. Targeted A-to-G Base Editing in the Mitochondrial and Plastid genome of Arabidopsis thaliana with Monomeric programmable deaminases

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In plants, plastid and mitochondria are two organelles that essential, yet partially independent, functional components of the cell. Precise base editing in both plastid and mitochondrial genomes would benefit their gene functional analysis as well as crop breeding. Targeted base editing in organellar genomes relies on a protein-based genome editing system that uses the TALE-DNA recognition motif with deaminases. This is because delivery of gRNA for CRISPR/Cas9 systems into organelles is currently almost impossible. Since all base editors used in plant organellar genomes were dimeric types, here, we tried targeted A-to-G base editing in plant organellar genomes with monomeric TALE-based deaminase for easier assembling of vectors. As a result, inheritable targeted A-to-G base editing in ATP6-2 in plant mitochondrial and 16S rRNA in plastid genome of Arabidopsis thaliana was successfully induced by monomeric TALE-based adenine deaminase without off-target mutations. The most efficient editing position from the sequences recognized by the monomeric enzyme was at the 8th T. Phenotypic analysis showed only the A-to-G conversion at 1139A of plastid 16S rRNA conferred significant spectinomycin resistance to plants, but not other two resistant mutations at 11131T and 1137T, predicted from the previous bacterial data. Our study demonstrated the feasibility of monomeric TALE-based adenine deaminases in plant organelles and we look forward to that the monomeric base editors would contribute to the functional analyses of all unknown genes in plant organelles with easier assembling.

Plants and People Conferences started in 2011, with the inaugural theme ‘On Roots and Fruits of Plant Biology’, looking into the history and present-day applications of plant research.

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Our 6th conference in 2023 focusses on the diversity and advances of plant research and showcases career paths in academia and beyond.

We hope you enjoyed this year’s P&P conference!

Our next meeting will be in 2025.
We hope to see you then!

The P&P 2023 organization team

Doctoral researchers of the MPI-MP (left to right):

Jinghan Liu, Esra Karakas, Koki Hayashi, Mustafa Bulut, Josephin Laskowski, Thekla von Bismarck, Fabienne Bürki, Varsha Vasudevan, Diego Pinheiro Brito, Jonathan Huc (not pictured)

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