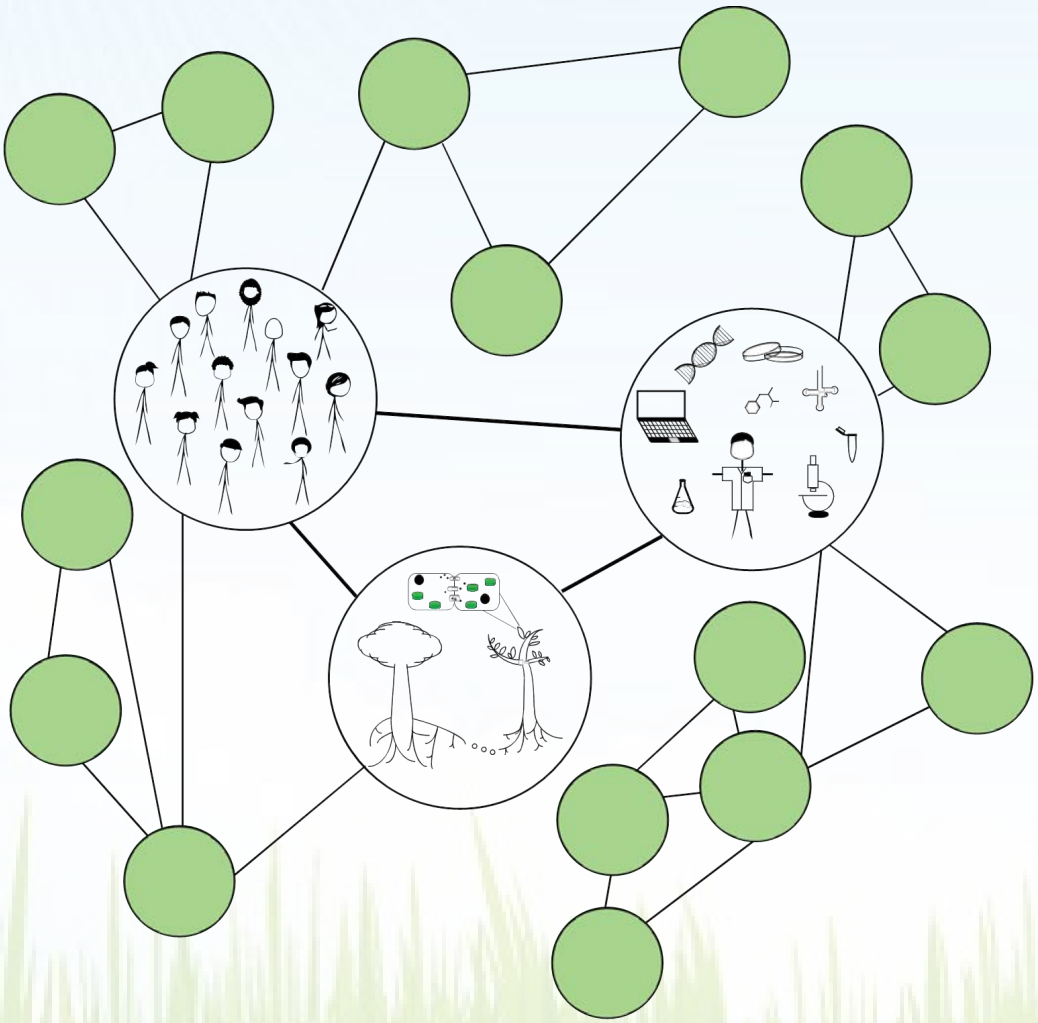
MAX-PLANCK-GESELLSCHAFT

# *Communicating Science – Connecting Worlds*

## 11-12 September 2017

## Max Planck Institute of Molecular Plant Physiology
## Potsdam, Germany



Organized by PhD students

IMPRS
Primary Metabolism and Plant Growth

Universität Potsdam

Max-Planck-Institut für Molekulare Pflanzenphysiologie

Plants and People

# Welcome to Plants and People 2017!

**Plants and People (P&P) Conferences** are organized by the PhD students at the Max Planck Institute of Molecular Plant Physiology in Potsdam-Golm and occur every second year.

Our conferences aim to bring together a unique mixture of high-profile international speakers, to speak not only on their specific research within the plant science field, but also to discuss wider aspects of life and growth within the scientific research world.

Our theme for this year's conference is 'Communicating Science - Connecting Worlds'. Besides our scientific program where speakers from both academia and industry will share their research with us, we have also invited professionals from the field of science communication. As PhD students we feel that it is crucial to communicate science, not only to our colleagues and fellow scientists, but also to non-experts such as stakeholders in politics, economy and the general public.

## Thank you!

Much of our financial support comes from the Max Planck Society, within the funding for the International Max Planck Research School (IMPRS) 'Primary Metabolism and Plant Growth'. IMPRS-PMPG is a joint doctoral programme of the University of Potsdam and the Max Planck Institute of Molecular Plant Physiology.

Thank you to all the helpers on and leading up to the conference days for their support: Dr. Ina Talke for assisting us with her guidance and great experience from previous conferences, Birgit Schäfer and Jacqueline Sommer from the MPI-MP administration for helping us with the internal organization; and Stefan Heinich, web programmer of the Max Planck Campus Golm for establishing the Plants and People website and helping us with technical issues.

Plants and People 2017 thanks the following companies for their support: F1000, Labfolder, LGC Genomics, Roboklon, Targenomix and ThermoFisher Scientific.

The P&P logo was designed by the organization team of the inaugural conference in 2011.

# Contents

## Plants and People Conference 2017
### Communicating Science – Connecting Worlds




Max Planck Institute of Molecular Plant Physiology
Science Park Potsdam-Golm
Am Mühlenberg 1 • D-14476 Potsdam • Germany


http://plants-and-people.mpg.de/

# Conference Programme

## Monday, 11 September 2017

| | |
|---|---|
| **09.00 - 10.00** | **Registration** |
| 10.00 - 10.45 | Ian T. Baldwin (Max Planck Institute for Chemical Ecology, Jena, DE) |
| 10.45 - 11.30 | Kauser Abdulla Malik (Department of Biological Sciences, Forman Christian College Lahore, PK) |
| 11.30 - 12.00 | Ángela Posada-Swafford (Science writer, Florida, USA) |
| **12.00 - 13.30** | **Lunch break** |
| 13.30 - 14.15 | Eva Stöger (Institute of Applied Genetics and Cell Biology, BOKU University, Vienna, AU) |
| 14.15 - 15.00 | Sven Gould (Institute of Molecular Evolution, University of Düsseldorf, DE) |
| **15.00 - 15.30** | **Coffee break** |
| 15.30 - 16.15 | Poul Erik Jensen (University of Copenhagen, DK) |
| 16.15 - 17.00 | Paul Christou (ICREA, University of Lleida, ES) |
| 17.00 - 17.30 | Justin Cherny (Journal of Visualized Experiments (JoVE), Cambridge, MA, USA) |
| **17.30 - 17.45** | **Group picture** |
| **17.45 - 20.00** | **Poster session** |

## Tuesday, 12 September 2017

| | |
|---|---|
| 09.30 - 10.15 | Brigitte Slaats (Seedcare Insecticides and Nematicides Research, Syngenta Crop Protection AG, Basel, CH) |
| 10.15 - 10.45 | Maaike Pols (F1000, London, UK) |
| **10.45 - 11.15** | **Coffee break** |
| 11.15 - 12.00 | Birgit Mitter (Austrian Institute of Technology, Vienna, AU) |
| 12.00 - 12.30 | Lorenzo Mannella (Science writer, University of Bologna, IT) |
| **12.30 - 14.00** | **Lunch break** |
| 14.00 - 14.45 | Eric Kemen (Max Planck Institute for Plant Breeding Research, Cologne, DE) |
| 14.45 - 15.30 | Stefan A. Rensing (Department of Cell Biology, University of Marburg, DE) |
| 15.30 - 16.00 | Dennis Fink (Mediomix, Cologne, DE) |
| **16.00 - 17.15** | **Coffee break + Poster session** |
| 17.15 - 18.15 | Round table moderated by Hanna Berger |
| **18.15 - 18.30** | **Concluding remarks + Poster prize** |
| **18.30** | **BBQ** |

# Conference Venue

## Max Planck Institute of Molecular Plant Physiology

Our institute was established in 1994, with founding director Prof. Dr. Lothar Willmitzer focusing investigations on plant central metabolic pathways and analysis of plant gene function. In the 23 years that have followed, we have grown to include directors Prof. Dr. Mark Stitt and Prof. Dr. Ralph Bock, independent and associated group leaders, and over 300 postdocs, students, technicians and support staff originating from all corners of the world.

The research focus, too, has shifted with the times. Our long-term goal is to develop a comprehensive, systems-level understanding of the plant: to not only understand the underlying genetic factors that drive plant growth, but to also asses the dynamics of plant responses. To achieve this, we combine analyses at multiple levels – integrating functional analysis of individual genes and specific molecular details, with generated 'omics' data sets, network models, and existing biological knowledge.

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

## Travel Information

### Connections between Golm and Potsdam Hauptbahnhof:

| | |
|---|---|
| Bus: | **605** Wissenschaftspark Golm <> S Hauptbahnhof Potsdam |
| | **606** Alt-Golm <> S Hauptbahnhof Potsdam |
| Train: | **RB 21** Bahnhof Golm <> S Hauptbahnhof Potsdam |
| | **RB 22** Bahnhof Golm <> S Hauptbahnhof Potsdam |

### Trains from Berlin central train stations (Friedrichstrasse, Hauptbahnhof, Zoologischer Garten, Charlottenburg):

**RB 21** (to Wustermark or Golm): Direct trains from Berlin to Golm every half hour, approximately between 7:00 and 9:00 in the morning and 15:00 and 18:00 in the afternoon.
At other times during the day, **RE 1** (to Brandenburg or Magdeburg) goes to Potsdam-Hauptbahnhof every 30 minutes. In Potsdam Hbf, you change to the RB 21. The **S 7** goes between Potsdam Hbf and Berlin stations.

It is a 10 min walk between the Golm train station and the Max Planck campus. For further information, please visit our website.

# Max Planck Campus Map


All lectures take place in the lecture hall of the Max Planck campus, located in building 4 (central building: yellow). The poster session will take place in the foyer and first floor seminar room of the central building.

Canteen/cafeteria: Max Planck canteen in building 4
Fraunhofer canteen near building 7

At the Max Planck canteen you pay with a pre-paid card that you can get from the machines at the entrance of the canteen. At the Fraunhofer canteen you can pay in cash.

# Speaker
# Profiles & Abstracts

## Ian T. Baldwin

*Department of Molecular Ecology, Max Planck Institute for Chemical Ecology, Jena, Germany*

Prof. Ian T. Baldwin received an AB from Dartmouth College in 1981, his PhD from Cornell University in 1989, rose through the academic ranks at the State University of New York at Buffalo and in1996 became the founding director of the Max Planck Institute for Chemical Ecology in Jena, Germany, where he heads the Department of Molecular Ecology. He is a member of the National Academy of Sciences, European Molecular Biology Organization EMBO, Nationale Akademie der Wissenschaften Leopoldina, Berlin Brandenburgische Akademie der Wissenschaften, Wissenschaftskolleg Berlin, and has published 450 peer-reviewed papers and one book on the induced defenses of plants.

## Abstract

### On becoming (and remaining) a plant scientist

This talk will have two components:

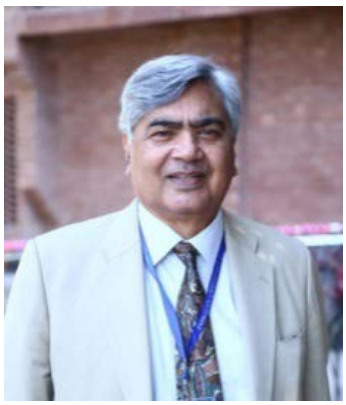
First, it will describe three decades of research into how a native tobacco plant, *Nicotiana attenuata*, that lives in the Great Basin Desert of the SW USA has been developed into a model system for the study of all types of plant-ecological interactions, particularly those biotic interactions that dominate the agricultural niche. This plant recognizes attack from specific herbivore species by the particular chemistry of the herbivore's saliva, and uses this recognition to tailor a complicated 6-layered defense response that requires a remodeling of the plant's transcriptome, metabolome and proteome, as well as some of its life history traits. The science writer, Michael Pollan, inverted the relationship between humans and their domesticated plants to argue that it was plants that domesticated humans, and not vice versa. *Nicotiana attenuata* has had designs more Machiavellian than domestication for the heterotrophs that feed on it and the adage "you are what you eat" is only just the beginning.

Second, it will describe what Baldwin thinks is important for the development of successful scientific career.

## Notes

## Kauser Abdulla Malik

*Department of Biological Sciences, Forman Christian College, Lahore, Pakistan*



Dr. Kauser Malik had his first degree in Botany from Government College, Lahore and PhD in Soil Microbiology from University of Aston, UK. He is an Alexander von Humboldt Fellow and worked at the Institute of Soil Biochemistry at FAL in Braunschweig under Prof. Konrad Haider. In Pakistan he worked at the Nuclear Institute for Agriculture and Biology (NIAB) and was later founder Director of the National Institute for Biotechnology & Genetic Engineering (NIBGE) at Faisalabad. Dr. Malik has been the Chairman of Pakistan Agriculture Research Council, Member of Biosciences at Pakistan Atomic Energy Commission and then Member of Food & Agri of Planning Commission of Pakistan.

Now since 2008, Dr. Malik has been appointed as Distinguished National Professor and Dean of Postgraduate Studies at Forman Christian College (A Chartered University), Lahore.

Researches of Dr. Malik are in the area of Biosaline Agriculture, Bioenergy, Plant Microbe Interactions, Metagenomics and Plant biotechnology with over 200 publications. He has been awarded three civil awards for his contribution to science by the Presidents of Pakistan.

## Abstract

### A Journey with Plants, Microbes and Environment for achieving Food Security

Salinity and sodicity has been the major impediment for the environment and agricultural productivity. Our earlier researches on biological approaches for utilization of salt affected wastelands lead to the development of Biosaline Agriculture Technology. During these studies we got interested in the rhizosphere of plants growing under such extreme conditions of salinity. This resulted in isolation and characterization of several novel bacteria living in tight association with roots of non-legumes and shown to fix atmospheric nitrogen. Further such studies on microbial diversity revealed that these bacteria perform several plant growth promoting functions such as phosphate solubilization, hormone production, bio control of soil borne diseases. This resulted in formulation of a commercial bio fertilizer named BioPower.

With the advent of metagenomic approaches and the use of rRNA technology, extensive studies on microbial diversity based on metagenome analysis of hypersaline environment of salt mines is being carried out. Hyperhalpohylic bacteria have been isolated. It has been shown that the osmoregulatory properties are borne on plasmids. The sequencing of plasmid DNA is underway to determine the osmoregulatory genes.

More recently we focused on Food security which can only be achieved if we can provide nutritious food sufficient to meet the requirement for healthy and active life. It is in this context that the National Nutrition Survey revealed acute deficiencies of iron and zinc in our diet which results in stunting and wasting in children. Wheat being the main staple diet of most of the population of South Asia, is most appropriate candidate for biofortification. Transgenic wheat with endosperm specific phytase protein offers an effective way to increase bioavailability of iron and zinc by degrading phytate which is a powerful chelator; binds with free metal ions to form mixed salts. Using this approach we have been able to

develop transgenic wheat with two fold increase in bioavailability of Fe and Zn. The National Biosafety Committee has approved the biofortified wheat for field trials.

The Journey still continues…

## Notes

## Ángela Posada-Swafford

*Science writer, Florida, USA*

Science, environment and exploration writer, producer, author. Knight Fellow in Science Journalist, MIT/Harvard. US Senior Correspondent, *Muy Interesante* magazine, the largest Spanish-language publication entirely devoted to science for the general reader in the world, edited in Madrid and Mexico. Her stories have appeared in *Scientific American, National Geographic en Español; WIRED, New Scientist, The Miami Herald, The Boston Globe*. Has produced documentaries for Discovery Channel Latin America/Iberia, and radio documentaries for NPR's *Living on Earth*. Twice nominated for regional Emmys in Spanish. Author of *Juntos en la Aventura / Bound by Adventure*, an on-going series of 15 adventure and adrenaline novels for young adults, with science and exploration themes edited by Grupo Planeta in Colombia. Each plot is based on the author's real field trips, following researchers.

## Abstract

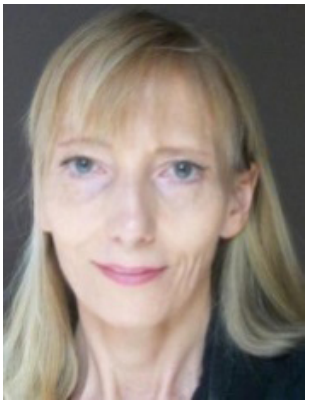
### Science Writing and the Art of Seduction

Whether you are applying for funding, telling a family member about your research or engaging the public, your success will depend on how well you communicate. Science writers and science journalists do their share of communicating and popularizing science. But they should not be the only ones doing so. Who should report on science? The answer is whoever does it well. With science being such a profound part of our daily lives and with its widespread presence in politics, effective and accurate communication of science is now more important than ever. Decisions have to be made in response to big issues such as climate change, declining biodiversity, ocean health and securing adequate food supplies for the growing world population, to name a few. However, most news readers, listeners and viewers have limited or no scientific education on which to base their opinions, and limited knowledge of where and how to find objective information. To make matters worse is the recent cut-back of entire departments specializing in science journalism at major news outlets in the US and elsewhere. Like all journalists, science writers have to know their stuff, have a good eye for the story and know the best sources. But they also have to write better than anyone else, because science is tough to sell. In this short talk I will share the challenges and rewards I have encountered in my 25 years as a science writer, lecturer and book author, as well as offer tips for those scientists who might to dabble in communicating their own research.

## Notes

## Eva Stöger

*Department of Applied Genetics and Cell Biology, BOKU,*
*University of Natural Resources and Life Sciences, Vienna, Austria*



Eva Stöger is currently Professor of Molecular Plant Physiology in the Department of Applied Genetics and Cell Biology at the University of Natural Resources and Life Sciences, Vienna, Austria. After completing her PhD at the University of Vienna she worked at the University of Florida, Gainesville, US, at the John Innes Centre, Norwich, UK, and at the Aachen Technical University (RWTH). She received several awards including the Golden Grain award from the Cerealiers de France and AGPM (France), and the Sofia-Kovalevskaja Prize awarded by the Alexander-von-Humboldt Foundation (Germany). Her main research interests are in the area of cereal biotechnology, intracellular protein trafficking and deposition, endomembrane dynamics and the production of high-value recombinant proteins in seed crops.

## Abstract

### Medicines and more from leaves and seeds

The production of high-value proteins in plants is maturing, as shown by the approval of innovative products and numerous studies that showcase plant-based production systems.

It is obvious however, that plant molecular pharming has emerged mainly as a niche technology for the manufacture of pharmaceutical products that do not readily fit into the current industry-favored model of fermenter-based production, and where product-specific benefits of plant-based systems can be exploited. Such benefits include specific glycosylation patterns as well as bio-encapsulation in endogenous plant polymers and the mucosal delivery of minimally processed topical and oral products. The ease of host cell engineering in plants, recently fueled by the development of gene editing technologies, is increasingly exploited for host cell engineering to produce proteins with tailor-made post-translational modifications, to modulate the spectrum of secondary metabolites and to modify or design storage organelles that may serve as protective shells allowing a slow or even controlled release of recombinant pharmaceuticals. Targeted host plant engineering requires a detailed understanding of the production organism and the use of various tissues and plant species offers additional opportunities for matching specific products with tailor-made production systems.

Although medical products have taken the limelight, the commercially available non-pharmaceutical plant-produced proteins currently still outnumber the medical products of plant molecular farming, reflecting the shorter development times and lower regulatory burden of the former. Non-pharmaceutical products benefit more from the low costs and greater scalability of plant production systems without incurring the high costs associated with downstream processing and purification of pharmaceuticals. Areas where plant-based manufacturing can make a significant impact include the production of antibodies, enzymes, and growth factors that are used as research-grade or diagnostic reagents, and as biosensors or biocatalysts. Examples of high-volume, low-margin proteins will also be discussed.

## Notes

## Sven Gould

*Institute of Molecular Evolution, University of Düsseldorf, Germany*

Sven Gould studied biology in Marburg, completing his PhD in 2006 just there and before moving on to Melbourne, Australia for his first Postdoc. In 2010 he returned to Germany and joined the group of Bill Martin in Düsseldorf, where he received tenure in 2013 and now runs his own small independent group (cellevo.de). They analyze the cell biology of eukaryotes and their compartments on the ground of biodiversity and under the umbrella of evolutionary trajectories. A main theme is trusting the traditional power of observation and subsequent interpretation, from which they synthesize their ideas. The Gould group uses a range of different (model) systems in order to provide empirical evidence for predicted concepts. Their work is characterized by curiosity and often a bird's eye perspective on the inner workings of a cell.

## Abstract

### The role of charge in protein targeting

Protein targeting is as old as the common ancestor of all cellular life. In those cells of prokaryotic nature, there was only the need for targeting to the plasma membrane or beyond. With the advent of the eukaryotic cell through the endosymbiotic integration of an alphaproteobacterial symbiont into an archaeal host cell, that situation changed dramatically. The eukaryotic cell is characterized in particular by its endomembrane system (endoplasmic reticulum, Golgi apparatus, nucleus, peroxisomes, etc.), whose origin hinges on the mitochondrion, the streamlined remnant of the alphaproteobacterial symbiont. That first protist lineage was required to evolve elaborate and specific targeting mechanisms to its many different compartments and it often referred to charged amino acids to solve the problem. The reasons for this will be discussed as well as the complications that arise from them, in particular in algae and plant cells that carry a plastid in addition. The presence or absence of charged amino acids alone can determine localization and comparisons across diverse eukaryotes, and their different types of mitochondria and plastids, uncover unexplored avenues of protein import research that we will discuss.

## Notes

## Poul Erik Jensen

*Copenhagen Plant Science Centre, Department of Plant and Environmental Sciences, University of Copenhagen, Denmark*

Holds a degree in agronomy (1989), a PhD in molecular genetics (1993) and worked as postdoc, in Copenhagen and in Sheffield, UK, with molecular biology and biochemistry before I initiated work on photosynthesis, in particular photosystem I, chlorophyll biosynthesis and chloroplast biology. In 2006 I became independent group leader (http://plen.ku.dk/english/research/molecular_plant_biology/photosyn/). Over the years my work involved elucidation of the function of several subunits of the photosystem I complex, characterized enzymes in chlorophyll biosynthesis and gained expertise in characterizing photosynthetic membrane protein-pigment complexes using biophysical, biochemical and physiological techniques. In recent years, my focus has been on synthetic biology and metabolic engineering in photosynthetic organisms. Specifically we have combined cytochrome P450-dependent biosynthetic pathways and photosystems in both chloroplasts of higher plants and cyanobacteria to achieve redirection of photosynthetic electrons towards new pathways. In these projects, the pathways use light-dependent reducing power generated by photosystem I directly circumventing metabolic energy and redox conversions. Since 2016 I have headed the Copenhagen Plant Science Centre (CPSC, http://cpsc.ku.dk/).

## Abstract

### Using photosynthesis: Engineering of cyanobacteria and chloroplast for production of high-value products

Plants produce a multitude of specialized metabolites with use in the medicinal, fragrance and flavor industries. Cytochromes P450 (P450s) are key enzymes in specialized metabolism and are involved in the formation of terpenoids, alkaloids, cyanogenic glycosides, glucosinolates, and phenylpropanoids like flavonoids, coumarins, and stilbenes. P450s catalyze stereo- and regiospecific hydroxylations, epoxidations, and C–C couplings that are often difficult to accomplish by chemical synthesis. In eukaryotes, P450s reside on the endoplasmic reticulum, and plant genomes often contain several hundred P450-encoding genes. P450s are difficult to express heterologously in active form, and due to their requirement for reducing power in the form of NADPH their use for in vitro and whole-cell production is complicated.

We recently showed that plant P450s can be expressed in chloroplasts and in cyanobacteria, where they will insert into the thylakoid membrane and photosynthesis will support P450 catalytic activity independent of NADPH through the action ferredoxin. Here we show that the genetic fusion of ferredoxin or FMN domains with the plant P450 CYP79A1 is indeed feasible. These fusions allow the P450 to obtain electrons for catalysis directly from photosynthesis by interacting with photosystem I. Furthermore, the electrons captured by the fused ferredoxin or FMN domains are directed efficiently towards the P450 in competition with other ferredoxin requiring enzymes. The fusion strategy overcomes the problem of competition for reduced ferredoxin by endogenous metabolic pathways.

Complete biosynthetic pathways involve usually several enzymes of which some are membrane bound and others are soluble. Scaffolding all the enzymes on the membrane is

one strategy to ensure efficient flow of substrate to the final product without intermediates escaping. We have fused the three enzymes constituting the dhurrin pathway with membrane anchors from TatB and TatC from the twin arginine translocation (TAT) system. Besides ensuring that the P450s are attached to the membrane, the normally soluble glucosyl transferase (UGT) is also associated with the membrane using this strategy. The result is accumulation of less unwanted intermediates and consequently more product. This constitutes an additional strategy to increase productivity.

## Notes

## Paul Christou

*ICREA, University of Lleida, Spain*

I received a 1st Class honors degree in Chemistry (University of London) and a PhD in plant biochemistry (UCL, London) in 1980. Following postdoctoral research at UCL, I joined one of the first plant biotechnology companies, Cetus Madison Corp (subsequently Agracetus, Inc.) Madison WI, USA, where I led a group which achieved the first transformed staple crop (soybean) followed by the development of a variety independent gene transfer method for rice. My work with rice led to an approach by the Rockefeller Foundation (RF), which sponsored a new department under my leadership at the John Innes Center (JIC) to transfer this technology from the private to the public sector (1994–2001). In 2001, I joined the Fraunhofer Institute for Molecular Biotechnology & Applied Ecology (IME) in Aachen/Schmallenberg, Germany, as a full professor. In 2004 I was offered a research professorship (ICREA) by the Catalan government at the University of Lleida as professor and head of the Applied Plant Biotechnology Laboratory.

## Abstract

### Waiting for Godot? Thirty five years of plant biotechnology but still a long way to go

We will discuss defining moments in the development of plant biotechnology from its infancy in the early eighties to the present day. We will highlight key drivers, personalities, achievements and promises of the technology from a personal perspective. A case study from our own lab's research focusing on the development of a portfolio of products targeting nutritionally enhanced (biofortified) staple crops for developing country applications will highlight more recent breakthroughs in multi-gene metabolic engineering and show how synergies and interdisciplinary collaborations give added value to applied research programs. An account of the rise of organized opposition to the technology and underlying reasons will be given. We will conclude with non-scientific challenges that need to be addressed and resolved effectively in order for the benefits of the technology to reach a major segment of its intended beneficiaries, poor and impoverished people in the developing world.

## Notes

## Justin Cherny

*JoVE, Journal of Visualized Experiments,*
*Cambridge MA, USA*

Justin Cherny is Vice President of Operations at JoVE (Journal of Visualized Experiments). Justin obtained an interdisciplinary PhD in biology and computer science from Wesleyan University, which focused primarily on identifying mRNA translation initiation on a transcriptomic scale and the development of novel approaches for quality assessment of peptide searching algorithms on a proteomic scale. Justin joined JoVE in 2013 and is continually motivated by JoVE's mission statement, which coincides perfectly with his passion for adoption of new scientific techniques, interdisciplinary work, innovation, and changing the way science is done.

## Abstract

### The Power of Visualized Science – Connecting Worlds Through Effective Knowledge Transfer

Multiple published reports suggest that scientific research is confronting a reproducibility crisis wherein scientists are unable to reproduce up to 80% of the results found in published studies. We assert that traditional scholarly communication is largely responsible for this crisis as well as the resulting inefficiency, inefficacy, and frustration felt by researchers, professors, and students worldwide. Dr. Cherny will discuss how JoVE has come to revolutionize the way science is communicated through video-based solutions that increase productivity, reproducibility, and knowledge transfer in scientific research and education. Along the way, Dr. Cherny will share insights into the unique career path that led him from early-career scientist to his most recent promotion to Vice President of Operations at JoVE.

## Notes

## Brigitte Slaats

*Seedcare Insecticides and Nematicides Research,*
*Syngenta Crop Protection AG, Basel, Switzerland*

Brigitte Slaats obtained the degree of an Agricultural Engineer (Dipl.-Ing. Agr) as well as her PhD degree in Agricultural Sciences at the Rheinische Friedrich-Wilhelms University of Bonn. Research for her diplom thesis was carried out at the University Riverside, California where she investigated the performance of abamectin, a chemical nematicide applied as a seed treatment to minimize the impact of plant-parasitic nematodes. The topic of her PhD thesis focused on biological control of sugar beet cyst nematodes, in particular, on the efficacy of encapsulated endoparasitic fungus *Hirsutella rhossiliensis*. Research was conducted at the Julius Kühn Intitute in Münster, Germany. Hereafter, in 2007 she joined Syngenta AG as a postdoctoral researcher to launch a new nematicide research program. A year later, in 2008, she was appointed Team Leader for Seedcare Nematicides Research and became responsible for the discovery and optimization of new chemical active ingredients with nematicidal activity for control of a broad range of plant-parasitic nematodes. In 2011 she additionally became Team Leader for Seedcare Insecticides Research, since then she has been managing all Crop Protection Research Biology related activities for Seedcare Insecticides and Nematicides.

## Abstract

### The Search for Innovative Agrochemicals for Seed Treatment Use

A number of current agrochemical products are under regulatory pressure due to a range of environmental or human safety issues. There is a strong societal demand for the discovery and development of new chemical crop protection agents that provide improved human and environmental safety profiles. Syngenta Crop Protection AG is dedicated to the discovery and development of new solutions which work by novel mode of actions, are highly efficacious against the target pest or pathogen and fulfill existing global regulatory hurdles. Next generation crop protection agents should be efficacious, safe, affordable and built into sustainable and integrated production systems. Furthermore due to a growing world population and limited production areas, the demand for higher yields in existing production areas has arisen which is coupled with increased intensification. Such conditions can favor the increase in pathogens and pests making it vital to protect the young seedling against these. Syngenta Seedcare solutions offer triple protection from the day the seed is planted against all relevant soil and seed borne diseases, early season insect pests and plant-parasitic nematodes, as a convenient “in the bag solution”. Within Crop Protection Research, a dedicated screening platform has been established to secure the delivery of next generation seed treatment fungicides, insecticides and nematicides enabling the continuous delivery of novel seed treatments that lead to healthy root development and optimal overall crop establishment, setting the foundation for best yields.

## Notes

## Maaike Pols

*Outreach Manager, Faculty of 1000,*
*London, United Kingdom*

Maaike holds a PhD in Cell Biology from Utrecht University, The Netherlands. She's working as Scientific Outreach Manager for F1000 and F1000Research; F1000's open science publishing platform.

## Abstract

### A new way of writing, discovering and sharing science

The Faculty of 1000 (F1000) is a provider of innovative and unique services that support the work of life scientists and clinicians around the globe.

F1000Research is an Open Science publishing platform that aims to address limitations of the traditional publishing process, such as publication bias towards 'positive' and 'interesting' results; protracted peer-review processes; and lack of source data in publications that reduce the reproducibility of the presented results.

To further support scientists, F1000 launched an authoring tool that will revolutionize the way that researchers write and collaborate. The tool covers all aspects of writing a research article; from literature discovery and reference management to sharing and annotating papers with collaborators in a safe and secure environment. The F1000 Workspace software incorporates over 150,000 article recommendations written by more than 8,000 eminent scientists and clinical researchers who have been systematically surveying the scientific literature over the past decade for the most relevant publications in their fields.

By creating tools for scientists to write, discover and share science, F1000 aims to make science and publishing fast, easy, transparent and reproducible.

## Notes

## Birgit Mitter

*Health & Environment Department, Bioresources Unit,*
*Austrian Institute of Technology GmbH, Tulln, Austria*

Birgit Mitter is microbiologist and molecular biologist with strong experience in the field of beneficial plant-microbe interactions, in particular bacterial endophytes. In her research she is aiming to obtain improved understanding on the interaction between microbial endophytes and plants and to translate basic knowledge into application. She has studied endophytes in a variety of plants including plants of agricultural importance, such as potato, rice and maize but also in wild flowers and tropical trees. B. Mitter applies (meta-)genomic and transcriptomic approaches to elucidate functional roles of (uncultivated) endophytes and to study the genetic background of beneficial plant-microbe interactions.

## Abstract

### Whole transcriptome analysis of the endophyte *Paraburkholderia phytofirmans* PsJN colonizing potato plants and in response to host plant drought stress

Similar to the human gut are plants tightly colonized by complex microbial communities. Microorganisms colonize the plant surface, the rhizosphere and phyllosphere, and establish populations inside plants as endophytes. It is widely accepted that bacterial endophytes actively colonize plants, interact with their host and frequently show beneficial effects on plant growth and health. However, very little is known about the mechanisms of plant-endophyte communication and bacterial adaption to the plant environment. For example, how do bacterial endophytes recognize the plant environment? Do bacteria respond to changing physiological conditions in plants e.g. due to plant stress?

To address these questions we performed whole transcriptome sequencing of *Paraburkholderia phytofirmans* PsJN colonizing potato (*Solanum tuberosum* L.) plants and analyzed *in planta* gene activity and the response of strain PsJN to plant stress. The *in planta* transcriptome of *P. phytofirmans* PsJN showed a broad array of functionalities encoded on the genome of strain PsJN. Transcripts up-regulated in response to plant drought stress were mainly involved in transcriptional regulation, cellular homeostasis and the detoxification of reactive oxygen species, indicating oxidative stress response in strain PsJN.

Differentially expressed genes included genes for extracytoplasmatic function (ECF) group IV sigma factors. These cell surface signaling elements allow bacteria to sense changing environmental conditions and to adjust their metabolism accordingly. TaqMan-qPCR was performed to identify ECF sigma factors in strain PsJN that were activated in response to plant stress. Six ECF sigma factor genes were expressed in strain PsJN colonizing potato plants. The expression of one ECF sigma factor was up-regulated, whereas another one was down-regulated in a plant genotype specific manner when the plants were stressed.

To sum up, our study indicates that endophytic *P. phytofirmans* PsJN cells are active inside plants. Moreover, the activity of bacterial cells is affected by plant drought stress; strain PsJN senses plant stress signals and adjusts its gene expression accordingly.

## Notes

## Lorenzo Mannella

*Communications Officer, University of Bologna, Italy*

Lorenzo Mannella works as communications officer at the University of Bologna. He holds an MSc in Plant-Microbial Biotechnology and a MA in Science Communication. As a journalist and fixer, he contributed to *Galileo, CheFuturo!, Wired, Maker Faire Rome, Motherboard, Medium, Epic Magazine* and *Dailybest*. He is fond of science fiction, storytelling and LARP.

## Abstract

### Science writing vs email reading

Imagine a minute-by-minute daily work schedule displayed on a sheet of paper. An astronaut's schedule would be filled out with instruments maintenance checks, zero-G experiments, Earth watching sessions and extravehicular activities (EVA). On the other hand, scientists, communications officers and most of the world population holding a job would see a recurring activity that spreads all over the week: email handling. While lacking reliable supporting data on a scientific level, the email overwhelm in work activities has a measurable impact on our lives. The number of business emails sent and received per user totals 122 emails per day, according to a 2015 Radicati Group report. On top of that, adults spent five and a half hours a week on social media, according to a 2016 Nielsen Social Media Report. Modern technology consumption resulted in a digital information overload, which has been modelled through multiple stages of software design in email and social media. Indeed, online productivity tools offer affordable solutions to manage our daily work flow, but their set of pervasive desktop and mobile notifications has monopolized our attention span. Despite all drawbacks and time consuming features, scientists and communications officers must turn to emails and social media to send messages and receive professional feedback from colleagues and engage their audience. Following different career paths, we all need to tell what a research project is about, who carries out experiments and why, how project results are exploited to make an impact on society and so on. Is there a way to master communication tools as they evolve? How can we manage our workload without burning ourselves out? Should an artificial intelligence (AI) replace us in repetitive, scalable tasks? Are we science writers or email readers? We will look for possible solutions and discuss about the role of scientists and communications officers in connecting worlds.

## Notes

## Eric Kemen

*Max Planck Institute for Plant Breeding Research,*
*Cologne, Germany*

Eric Kemen completed his PhD in biology at the University of Konstanz in 2007 before he moved to the Sainsbury Laboratory in Norwich UK, where he joined the group of Jonathan Jones, working on plant pathogen genomics. In 2012, Eric Kemen became a research group leader at the MPI for Plant Breeding Research in Cologne, focusing with his group on microbe-microbe and plant-microbe interactions. An important finding was the discovery of 'microbial hubs' that link microbial communities to the host genotype. Goal of the Kemen group is to combine computational modelling with ecology and host/microbe genetics.

## Abstract

### Leaf microbiome structure and dynamics

Plant-associated microorganisms critically affect host phenotypes including growth, disease and reproductive fitness. While the ability to control plant microbial communities is central to ensuring food security by advances in resource-efficient crop production, increased yield and protection, our basic understanding of how microbial communities assemble and how they persist on plants and become robust to perturbation is still very limited.

We addressed this fundamental knowledge gap by simultaneously studying wild and planted *Arabidopsis thaliana* populations in the field and used reconstitution biology in gnotobiotic systems to dissect mechanisms.

Our results indicate that abiotic factors, host genotype and time together have strong effects on plant colonization patterns of bacteria, fungi, oomycetes and other protists. Only a minority of all microbes we identify, however, are strongly interconnected with other microbes and have a severe effect on community structure development. We therefore call those 'microbial hubs'. Those 'hubs' via host-microbe and microbe-microbe interactions transmit host genotypic signatures to the microbial community structure. In depth analyses on 'hub' microbes revealed strong effects on endophytic colonization for specific taxonomic groups from phyllosphere communities that otherwise vary between plants.

The identification of microbial 'hubs' and their importance in phyllosphere microbiome structuring over time has crucial implications for plant-pathogen and microbe-microbe research and opens new entry points for ecosystem management and future targeted biocontrol.

## Notes

## Stefan A. Rensing

*Department of Cell Biology, University of Marburg, Germany*

Stefan A. Rensing is Professor of Plant Cell Biology at the University of Marburg, Germany. He is biologist by training, but has two decades of experience in phylogenetic and comparative genomics methods. His lab is interested in the evolution of land plants, in particular the water-to-land-transition, and involves both wetlab and computer work. Prof. Rensing is best known for his work on the moss model, *Physcomitrella patens*. He is leading the international effort to further improve this US Department of Energy "flagship" genome, and is president of iMOSS, the international molecular moss science community. Rensing is vice speaker for the section on plant molecular biology of the German Botanical society and member of many genome consortia studying plants and algae.

## Abstract

### On the early evolution of plant complexity

The conquest of land by plant life was a singular event occurring ca. 500 Ma ago, in the Ordovician. Some lineages of charophyte freshwater algae share a common ancestry with the land plants (Embryophyta). Synapomorphies that probably already evolved in the water include land plant type cell wall synthesis, cell division and polyplastidy.

Extant representatives of the earliest splits that occurred after the establishment of land plants are the bryophytes (hornworts, mosses and liverworts). Although, like all land plants, they feature the alternation of a haploid and a diploid multicellular generation, the haploid gametophyte represents the dominant phase in bryophytes. By comparison with diploid-dominant flowering plants we unravel more and more gene regulatory networks and key transcription factors that control similar processes in dominant gametophytes or sporophytes. Evolution of land plant complexity thus is rooted in gene networks coopted from gametophytes.

Whole genome duplications, and the increase of transcriptional network complexity, are hallmarks of plant evolution. By comparative genomics we are now able to determine in detail how complexity evolution occurs. I will present examples mainly from the bryophytes and charophytes to illustrate how inference of ancestral states and complexity evolution of the land plants is aided in particular by non-seed plant genomes.

## Notes

## Dennis Fink

*Mediomix, Cologne, Germany*

Dennis Fink graduated in 2011 at the Max Planck Institute for Marine Microbiology in Bremen and afterwards co-founded an agency for digital science communication in Cologne. This step from scientist to science communicator was supported by a stipend from the BMWi and the company mediomix GmbH was founded in 2013. Since then, Dennis Fink has been working with scientists from academia and industry on the communication of their science among each other or to the general public. Projects include the production of digital media (movies, illustrations, animations), social media outreach campaigns, web design and soft skill training workshops for graduate schools. Since 2016, Dennis Fink was also asked to join the board of the Max Planck Alumni Association as General Secretary.

## Abstract

### From scientist to science communicator – The challenge of science communication in the digital age

I would like to share with you my experiences in modern science communication and also the challenges I faced on this special career path. In my PhD, I did not get prepared for a career path in science communication and so I had to learn a lot of things by myself. It was mainly the good supervision and exchange with my former PI that made me realize that my future was not in academia. I will tell you how I made it from scientist to science communicator and what skills I could leverage when leaving academia and starting my own company in Cologne (while becoming a father of 2 kids). You will hear about different projects I worked on during the last 5 years, bringing me to places like Island, Tromsø, the biggest radiotelescope in Europe and massive turbulence facilities like CERN. I will share with you my motivation to communicate science and how I deal with scientists who do not see the benefits of this way of talking about research.

## Notes

## Hanna Berger

*PLANT 2030, Potsdam, Germany*

Dr. Hanna Berger is plant biologist and science communicator. She specialized in photosynthesis and algae research at the Universities of Lund (Sweden), Mainz and Bielefeld (Germany). For Hanna, science management and communication are key elements of successful research.
Today, Hanna supports the PLANT 2030 network of applied plant science in Germany, located at the Max Planck Institute of Molecular Plant Physiology. PLANT 2030 interconnects plant scientists and is a central hub for the interrelation of research, policy, plant breeding and the public.

## Abstract

### Hanna will be moderating the discussion session “Science and Society”.

Science communication is part of the researcher’s everyday life. Besides papers, proposals and talks within the community, the interaction with general public is getting more and more important. Still, science communication is controversial. Do scientists have to legitimize their research by the society? How to communicate difficult topics, such as Genome Editing as a current example? During the Round-Table-Session, representatives from academic science, industry, and communication will discuss these issues, share their experiences, and give best and worst practice examples.

## Notes

# Poster Abstracts

## INDEX

## P01| What causes the inflorescence abnormality in hybrids between *Arabidopsis thaliana* accessions BG-5 and Kro-0?

**Dema Alhajturki[1], Regina Feil[1] , John Lunn[1], Detlef Weigel[2] and Roosa Laitinen[1]**

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When two parents are crossed, their offspring can show greater or lesser fitness than their parents. Superior hybrid phenotypes are known as heterosis while reduced fitness is called hybrid incompatibility or weakness. In *Arabidopsis thaliana*, when accessions Kro-0 (Krotzenburg, Germany) and BG-5 (Seattle, USA) are crossed, the F1 hybrid shows shorter stem internodes and more branches from the rosette in comparison to the parents. Moreover the F2 generation segregates individuals with smaller size and purple coloration, which could be grouped into three distinct phenotypic classes. Interestingly, both F1 and F2 phenotypes were dependent on temperature. Mapping revealed that the F1 inflorescence phenotype is linked to two interacting loci, one on Chr. 2 and one on Chr. 3. The three phenotype classes in the F2 generation were linked to the same loci in a dosage-dependent manner. We have further characterized the mapped region on Chr. 2. This region contains 14 annotated genes that were individually silenced by introducing artificial micro-RNA constructs into one of the parents (Kro-0) and crossing the silenced lines with the other parent. Individual silencing of two genes, AT2G14100 and AT2G14120 rescued both, F1 and F2 hybrid phenotypes. We are currently further analyzing the causal role of these two genes in more detail. In addition to the genetic analysis, investigating the role of sugar metabolism showed that F1 hybrid at the inducing temperature has a different configuration. Altogether, our results give insights into the mechanisms underlying epistatic interactions in plants and the role they could play in plant adaptation.

**NOTES**

## P02| Getting back to nature: a reality check for experiments in controlled environments

**Maria Grazia Annunziata[1], Federico Apelt[1], Petronia Carillo[2], Ursula Krause[1], Regina Feil[1], Virginie Mengin[1], Martin A. Lauxmann[1], Karin Köhl[1], Zoran Nikoloski[1,3], Mark Stitt[1] and John E. Lunn[1]**

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[3] *University of Potsdam, Germany*
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Irradiance from sunlight changes in a sinusoidal manner during the day, with irregular fluctuations due to clouds, and light–dark shifts at dawn and dusk are gradual. Experiments in controlled environments typically expose plants to constant irradiance during the day and abrupt light–dark transitions. To compare the effects on metabolism of sunlight versus artificial light regimes, *Arabidopsis thaliana* plants were grown in a naturally illuminated greenhouse around the vernal equinox, and in controlled environment chambers with a 12-h photoperiod and either constant or sinusoidal light profiles, using either white fluorescent tubes or light-emitting diodes (LEDs) tuned to a sunlight-like spectrum as light source. Rosettes were sampled throughout a 24-h diurnal cycle for metabolite analysis. The diurnal metabolite profiles revealed that carbon and nitrogen metabolism differed significantly between sunlight and artificial light conditions. The variability of sunlight within and between days could be a factor underlying these differences. Pairwise comparisons of the artificial light sources (fluorescent versus LED) or the light profiles (constant versus sinusoidal) showed much smaller differences. The data indicate that energy-efficient LED lighting is an acceptable alternative to fluorescent lights, but results obtained from plants grown with either type of artificial lighting might not be representative of natural conditions.

### NOTES

## P03| Dynamic changes in protein phosphorylation of proteins associated with plant TOR pathway

**Krzysztof Bajdzienko and Patrick Giavalisco**

*Max Planck Institute of Molecular Plant Physiology, Germany*

Target of Rapamycin (TOR) is a central regulator of growth in eukaryotes, integrating signals such as nutrient levels and energy status to promote anabolic processes, while inhibiting catabolic processes. I have adapted and optimized phosphopeptide purification methods for plant tissues. These developments resulted in a reproducible methodological workflow allowing the enrichment of phosphoproteomes from different plant material. The standardized phosphoproteomics method was then used to investigate early kinetics of changes in the Arabidopsis proteome and phosphoproteome in response to AZD-driven inactivation and glucose-driven reactivation of the TOR kinase. My data demonstrates that TOR in Arabidopsis maintains the energy balance by dynamically adjusting abundance and phosphorylation of selected down-stream effectors. Accordingly, I could detect significant changes in both proteome and phosphoproteome. Interestingly, the amplitude of changes in the phosphoproteome was dramatically bigger compared to the changes in abundance observed in the proteome studies. In total, I have identified 2,500 proteins in the proteomic experiment, of which 370 showed significant changes between control and treatment. TOR inhibition resulted in changes in abundance of proteins related to photosynthesis, plastidic translation and response to photooxidative stress. Contrary, the phosphoproteomic experiments led to 1,800 identified proteins, harboring 3,700 phosphorylation sites, of which 400 showed significant difference. This time-resolved phosphoproteomic analysis demonstrated that even after 15 minutes the cellular phosphoproteome is being globally reprogrammed in response to TOR inactivation and reactivation. The most severe changes were observed for proteins related to the regulation of cytosolic translation, cell cycle and protein import to chloroplast.

**NOTES**

## P04 | Arabidopsis REI1-like cytosolic ribosome biogenesis factor homologs suppress premature cold acclimation responses and are required for plant growth and enhanced 60S LSU accumulation upon cold shift

**Olga Beine-Golovchuk and Joachim Kopka**

*Max-Planck-Institute of Molecular Plant Physiology, Germany*
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Plant growth and development requires precise regulation of cytosolic ribosome biogenesis. Control of ribosome availability may be specifically important for stress acclimation, e.g. the cold acclimation process. While cytoplasmic ribosome biogenesis is extensively studied in the model organism *Saccharomyces cerevisiae* (yeast) only a minor fraction of the plant homologs of ribosome biogenesis proteins (RBP) from yeast have been identified.

We recently recognized the *Arabidopsis thaliana* four zinc finger proteins, REI1-LIKE1 (REIL1) and REIL2, that we named after their yeast homologs Rei1 (for Required for isotropic bud growth1) and its paralog Reh1 (for Rei1 homologue1) as late stage RBP homologs that may take part in the cytoplasmic steps of ribosomal maturation. REIL1 and REIL2 apparently share conserved functions with the yeast homologs as was indicated by transcript co-expression and protein-protein interaction studies of REIL1 and REIL2 with selected Arabidopsis homologs of known Rei1 interacting RPBs from yeast. The loss of one or both paralogs was non-essential both, in Arabidopsis and yeast but caused surprisingly similar cold-conditional growth defects of unicellular yeast and the embryophyte Arabidopsis.

The role of yeast Rei1 for cytoplasmic maturation of the 60S LSU is well established not least by a cryo-EM structure that indicates involvement in proof reading of the ribosome peptide exit tunnel. In contrast, the analyses of conserved and potentially new functions of Arabidopsis REIL proteins are in their initial phase. Integrative systems analysis of the Arabidopsis reil1-1reil2-1 double mutant revealed interaction of REIL proteins with cytosolic ribosomes and functional interaction with cytosolic ribosome subunit accumulation. Metabolomic and Transcriptomic profiling demonstrated a hidden acclimation phenotype of the, under optimized temperature conditions, morphologically inconspicuous mutant and compensation responses linked to mutant growth defect at 10°C. These compensation responses indicate that REIL function may extend beyond cytosolic ribosome biogenesis towards translation initiation.

**NOTES**

## P05| Systems Biology approach to investigate the development and degradation of the photosynthetic apparatus during leaf ontogenesis in tobacco (*Nicotiana tabacum*)

**Karolina Belkius, Wolfram Thiele, Tegan Armarego Marriott, Eugenia Maximova, Ralph Bock, and Mark Aurel Schöttler**

*Max Planck Institute of Molecular Plant Physiology, Germany*
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Changes in photosynthetic parameters during leaf ontogenesis have been studied in several species, but they have rarely been systematically correlated to changes in chloroplast structure, leaf metabolism, and gene expression. Using a systems biology approach, we followed all of these parameters during leaf development from leaf initiation to senescence, analyzing the fifth true leaf of tobacco (*Nicotiana tabacum*). Here, we report changes in physiological parameters such as chlorophyll content, leaf assimilation and respiration, photosynthetic electron transport, and the accumulation of the photosynthetic complexes, which we determined twice per week by spectroscopic approaches and gas exchange measurements.

Tobacco leaves were fully expanded after three weeks of leaf development. At the same time, the chlorophyll content peaked, and then immediately started to decrease again. The contents of both photosystems closely followed the changes in chlorophyll content. In contrast, leaf assimilation and linear electron transport capacity began to decrease even prior to full leaf expansion, and this correlated with decreases in chloroplast ATP synthase activity and cytochrome $b_6f$ complex content. After five weeks of development, senescing leaves became photosynthetically inactive. After full leaf expansion, only the contents of the light harvesting complexes increased. This correlated with a drastic increase in grana stacking in senescing leaves, as revealed by electron microscopy. Furthermore, with increasing leaf age, we observed a strong reduction of chloroplast number per cell, indicating that besides of adjustments of the photosynthetic apparatus within each chloroplast, also entire chloroplasts are degraded the autophagy.

**NOTES**

## P06| The PLANT 2030 Competence Network of Applied Plant Research in Germany

**Hanna Berger, Christiane Hilgardt, Henrike Perner and Matthias Arlt**

*Max Planck Institute of Molecular Plant Physiology, Germany*
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Innovative research approaches and forward-oriented crop development – that's PLANT 2030. Several hundred scientists and plant breeders collaborate to address global challenges of nutrition security, sustainable agricultural production and renewable resources. Recent research highlights such as the elucidation of the barley genome [1] underline the success of the initiative of the German Federal Ministry of Education and Research (BMBF).

Currently, PLANT 2030 includes the national programs "Plant Breeding research for the Bioeconomy" and "Innovative Plant Breeding within the Cultivation System" as well as the transnational program PLANT-KBBE [2,3]. As research and communication partner, PLANT 2030 also addresses ethical, legal and socioeconomic issues of genome editing in agriculture [4].

On our poster, we provide insights into the goals and scientific progress within the PLANT 2030 initiative. We introduce the PLANT 2030 Managing Office as the interface between scientists, plant breeders, policy and public. We outline our main activities and show how integrated research coordination, communication and support of young investigators successfully strengthen the applied plant science community.

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[3] www.plant2030.de
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**NOTES**

## P07| Understanding the evolution of $C_4$ photosynthesis in the genus *Flaveria*: a metabolic perspective

**Gian Luca Borghi[1], Stéphanie Arrivault[1], John Lunn[1], Martha Ludwig[2] and Mark Stitt[1]**

[1]*Max Planck Institute of Molecular Plant Physiology*
[2]*University of Western Australia (School of Molecular Sciences)*
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The $C_4$ photosynthetic pathway evolved independently more than 60 times in higher plants [1], but we are only beginning to understand in detail how this $CO_2$ concentrating mechanism arose from $C_3$ ancestors. The genus *Flaveria* (Asteraceae) is an interesting subject for $C_4$ photosynthesis evolution since it has multiple representative species for different evolutionary intermediate stages.

In our study we use 9 different *Flaveria* species: *F. cronquistii* ($C_3$), *F. robusta* ($C_3$-proto-kranz), *F. anomala* and *F. ramosissima* (both $C_2$), *F. brownii*, *F. palmeri* and *F. vaginata* (three $C_4$-like species), *F. bidentis* and *F. trinervia* (both complete $C_4$).

To understand the evolution of $C_4$ photosynthesis in the genus *Flaveria* we are combining metabolite flux analyses done by $^{13}CO_2$ labelling and isotopomer analysis by LC-MS/MS [3] with cell fractionation into bundle sheath and mesophyll cell enriched fractions [2]. This approach will enable us to track the pathway of carbon assimilation in both a spatial and temporal way.

Our investigations have the potential to uncover additional, but so far hidden evolutionary stages, leading to revision or refinement of the consensus model, and ultimately guide biotechnological efforts to introduce the $C_4$ pathway into $C_3$ crops such as rice.

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[2] Stitt, M., & Heldt, H. W. (1985). Biochimica et Biophysica Acta (BBA)-Bioenergetics, 808(3), 400-414.
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**NOTES**

## P08| iPED: an integrative data portal for exploring plant epigenomes

**Dijun Chen and Kerstin Kaufmann**

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In this poster, I would like to show an integrative data portal for exploring plant epigenomes (iPED). We collected huge amount of epigenetic data from an extensive list of plant genomes and processed these data in uniform pipelines. We provided various visualization and analysis tools alongside this web-based resource. Furthermore, we performed in-depth comparative analyses on these data from several plant species to understand the regulation and evolution of chromatin structure and histone modifications in plant development.

**NOTES**

## P09| The HD-Zip class I transcription factor JUB2 modulates growth and development by regulating JUNGBRUNNEN1 in Arabidopsis

**Shuchao Dong and Salma Balazadeh**

*Max-Planck-Institute for Molecular Plant Physiology, Germany*
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An Arabidopsis NAC transcription factor (TF), JUNGBRUNNEN1 (JUB1), has been previously identified as a central regulator of longevity and the interplay between growth and stress responses. Employing yeast-one-hybrid, we identified JUNGBRUNNEN2 (JUB2), a member of HD-Zip class I subfamily of TFs, as a potential upstream regulator of *JUB1*. The goal of my PhD project is to characterize the function of JUB2 and identify JUB2-*JUB1* gene regulatory networks. Our previous results have demonstrated that JUB1 directly and negatively regulates expression of gibberellin (GA) and brassinosteroid (BR) biosynthesis genes. Overexpression of *JUB2* resulted in GA- and BR-deficient phenotypes similar to *JUB1* overexpressors (*JUB1ox*), such as compact rosette, shorter stem, impaired stamen filament elongation, and delayed senescence. Furthermore, *JUB1* mutation rescued growth and developmental defects of *JUB2* overexpression plants *(JUB2ox)*. However, in contrast to *JUB1ox*, treatment with $GA_4$ failed to restore the phenotype of *JUB2ox* suggesting involvement of JUB2 in regulation of GA signaling. In an attempt to identify JUB2 early responsive genes (through inducible overexpression of *JUB2* and gene expression profiling by RNA-seq) we found *GA2OX1*, which encodes an enzyme catalyzing $GA_4$ to bio-inactive GAs, as another candidate target gene of JUB2. Our preliminary data suggest that JUB2 negatively controls $GA_4$ biosynthesis and signaling pathways via *JUB1* and *GA2OX1* regulation, respectively.

**References:**

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**NOTES**

## P10| One billion years of getting out of bed in the morning: analysis of diurnal gene expression of major plant clades

**Camilla Ferrari[1], Sebastian Proost[1], Ann-Cathrin Lindner[2], Jörg Becker[2], Arren Bar-Even[1], Alisdair Fernie[1] and Marek Mutwil[1]**

*[1]Max Planck Institute of Molecular Plant Physiology, Germany*
*[2]Instituto Gulbenkian de Ciência, Portugal*

The number of sequenced plant genomes is growing rapidly, and the resulting data and comparative analyses have revealed the appearance of biological pathways throughout 1600 million years of plant evolution. However, activity of the evolved biological pathways is also under strict transcriptional control, which might not be revealed by genomics. To address this, we are generating dense diurnal expression atlases of *Cyanophora paradoxa* (glaucophyte), *Porphiridium purpureum* (rhodophyte), *Klebsormidium nitens* (charophyte), *Physcomitrella patens* (bryophyte), *Selaginella moellendorffii* (lycophyte), and *Picea abies* (gymnosperm). Together with publicly available data for other plants, these atlases allow us to compare gene expression and daily scheduling of biological processes of ten major plant clades. We found that, despite one billion years of evolution, diurnal transcriptomes of algae are similar, but observed an extensive reprogramming of the transcriptomes in land plants. We also show how the scheduling of biological processes was reprogrammed and how genes that appeared at specific time in evolution are expressed during the diurnal cycle. To conclude, the comprehensive group of diurnal atlases, together with novel bioinformatical approaches, allow us to determine how the establishment of new traits such as multicellularity and terrestrialization, has affected gene expression.

**NOTES**

## P11| Haplotype phasing and de novo genome assembly with 10 x genomics and PacBio Sequel

**Janina Fuss, Kurt Stüber, Bruno Hüttel and Richard Reinhardt**

*Max Planck Genome centre Cologne, Germany*

*De novo* sequencing and assembly of plant genomes poses a number of challenges. Many plants are highly heterozygous, often polyploid and some have extensive genomes with highly repetitive stretches. Those factors make the assembly of genomes from short read (Illumina) data problematic and the size of some plant genomes makes long read sequencing very expensive. In addition to the PacBio Sequel for long read sequencing, we have now established the 10x Genomics Chromium Controller for linked read sequencing at the Max Planck Genome centre Cologne. 10x Genomics offers a platform that contains ~ 4 mio individual barcodes that can be used to track the high molecular weight DNA template of origin. On the Chromium Chip, the template is entrapped in one droplet with a polymerase for isothermal amplification and random hexamers all attached to one barcode sequence. This way, each fragment copied form this template can later be identified as belonging to the same, connected strand of DNA even though it was sequenced with Illumina short reads. We show examples to illustrate the power of both, long reads from PacBio and 10x linked reads.

**NOTES**

## P12| Reduced Complexity, RCO: a leaf sculptor within the Brassicaceae Family

**Mohsen Hajheidari[1], Francesco Vuolo[1], Remco Mentink[1], Daniela Vlad[4], Xiangchao Gan[1], Daniel Kierzkowski[1], Madlen I. Rast-Somssich[1], Carla Galinha[4], Raffaele Dello Loio[2], Richard S. Smith[1], Peter Huijser[1], Angela Hay[1], Donovan Bailey[3], Dmitry A. Filatov[4] and Miltos Tsiantis[1]**

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[2]*Università di Roma, Dipartimento di Biologia e Biotecnologie, Italy*
[3]*New Mexico State University, Department of Biology, United States*
[4] *University of Oxford, Department of Plant Sciences, United Kingdom*
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How morphological diversity emerges and evolves is a long-standing question in biology. Using comparative genetic approaches we discovered that a tandem duplication of the *LATE MERISTEM IDENTITY 1 (LMI1)* gene has given rise to two new copies within the Brassicaceae family. Diversification of the regulatory and coding sequence in one of the copies led to emergence of a novel transcription factor called *Reduced Complexity (RCO)*. However, the second copy was pseusogenized owing to accumulation of deleterious mutations. We first isolated *RCO* in *C. hirsuta* that has complex leaves with distinct leaflets where a loss of function allele results in loss of leaflets. In contrast to *LMI1*, which is expressed in the margins of leaflets, *RCO* is expressed at the base of leaflets and promotes their formation through locally regulating growth. Although *RCO* was fixed in several Brassicaceae species, it was lost in *A. thaliana*, leading to development of the simple leaf of this species. Surprisingly, *RCO* can improve photosynthesis activity in *C. hirsuta* and *A. thaliana* suggesting it may have contributed to adaptive evolution of leaf morphology. The evolutionary trajectory of *RCO* provides an example of how small scale gene duplication drives evolutionary novelty.

**References:**
Vuolo F, *et al*. (2016) Genes & Development, 30: 2370-2375.
Daniela V, *et al*. (2014) Science, 343: 780-783.

**NOTES**

## P13| Characterization of a leaf-specific *Ustilago maydis* α-L-arabinofuranosidase

**Elaine Jaeger[1, 2], Lena Schilling[1], Alexandra Matei[1,2], Amey Redkar[1], Virginia Walbot[3] and Gunther Doehlemann[1,2]**

[1]*Max Planck Institute for Terrestrial Microbiology, Germany*
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Infection by the basidiomycete *Ustilago maydis* causes smut disease and provides an important model for biotrophic host-pathogen interactions. *U. maydis* penetrates the maize epidermis and leads to tumor formation. The infection is commonly observed on all the vegetative and floral organs of the host plant. The different plant tissues infected by *U. maydis* exhibit enormous differences in their cell structure and physiology. Therefore we hypothesized that transformation of different primordia into plant tumors requires organ specific effector proteins. *ara1*, a leaf-induced gene which is required for full virulence in leaves, is predicted to encode an α-L-arabinofuranosidase. Here we investigate the biological function of this enzyme for the pathogenicity of *U. maydis*.

**NOTES**

## P14| 2',3'-cyclic adenosine monophosphates regulates delicate balance between RNA storage and degradation

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2',3'-cAMP is a positional isomer of well-known characterized in animals, secondary messenger 3',5'- cyclic adenosine monophosphate (cAMP). In fact it was only in 2009, when Ren and colleagues (2009) detected 2',3'- cAMP in the biological material. Since than 2',3'-cAMP has been measured in animals, plants and in bacteria. The role of 2',3'-cAMP, other than product of RNA turn-over, is as yet unknown. Intriguingly, in our previous work separating protein bound from free small molecules using size exclusion chromatography (SEC) (Veyel *et al*., 2017) we could demonstrate that 2',3'-cAMP is retained in protein complexes arguing for the existence of 2',3'-cAMP protein receptors. Herein, using combination of biochemical (affinity purification and thermal protein profiling) and biophysical methods (microscale thermophoresis) we present that 2',3'-cAMP, but not 3'5'cAMP, binds to the Arabidopsis RNA binding proteins. These proteins are involved in maintaining the balance between RNA degradation and storage under stress conditions, which fits well 2',3'-cAMP accumulation in heat, darkness and upon wounding and therefore pointing towards 2',3'-cAMP as molecule involved in signal transduction. To our knowledge it is the first report of soluble cAMP receptors in plants.

**References:**
[1] Ren J, *et al*. (2009) J Pharmacol Exp Ther, 328: 855-865
[2] Veyel D, *et al*. (2017) Sci Rep, 7: 42387

**NOTES**

## P15| Increasing our understanding on lipid biosynthesis in *Arabidopsis thaliana* by quantitative genetics approach

**Urszula Luzarowska[1], Lothar Willmitzer[2], Si Wu[2], Alvaro Cuadros Inostroza[2], Marcin Luzarowski[2] and Yariv Brotman[1]**

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Although genes encoding proteins responsible for lipid biosynthesis and regulation have been extensively studied in *A. thaliana*, our knowledge about their genetic basis is not complete. From the currently 700 putatively annotated lipid-metabolism genes, the function of only 40% is biochemically or genetically proven. Therefore, we conducted a genome-wide association study (GWAS) in Arabidopsis using lipid levels as quantitative traits. This will allow to increase the knowledge on genome-level regulation of lipid biosynthesis and to identify novel genes that participate in lipid biosynthesis. The GWAS was conducted on 314 accessions that were grown under control and stress conditions. We could identify a high number of lipid quantitative trait loci (QTL). We observed variation between the genetic loci identified in the control and in the stressed panel, indicating genome plasticity in the regulation of lipid biosynthesis. We thus illustrate a genotype by environment interaction (G×E), showing environment specific regulation of lipid biosynthesis.

**NOTES**

## P16| Affinity purification with metabolomic and proteomic analysis unravels diverse roles of nucleoside diphosphate kinases

**Marcin Luzarowski, Monika Kosmacz, Ewelina Sokolowska, Weronika Jasińska, Lothar Willmitzer, Daniel Veyel* and Aleksandra Skirycz***

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**These authors contributed equally to this work.*

Multiple biological processes are triggered by molecule-molecule interactions. These include interactions between proteins, proteins and nucleic acids, and proteins and small molecules. Discovery and characterization of the role of these complexes are objects of intensive investigation. In recent years, many new techniques allowing analysis of protein-small molecules interactions, also at "omics"-scale, became available [1].

We exploited protein-to-small molecule strategy based on affinity purification method. We adjusted previously available yeast protocol and used IgG antibodies against chimeric proteins consisting of an IgG-binding domain fused to the protein of interest to unravel potential protein-small molecule complexes in native plant lysate [2]. We examined small molecule ligands of three nucleoside-diphosphate kinase proteins (NDPK1-3). Primary role of these multifunctional proteins is to maintain nucleoside triphosphates (NTP) level. They transfer phosphate from ATP to cognate nucleoside diphosphates (NDP) via ping-pong mechanism.

Here we show co-elution of glutathione S-transferases (GSTs) and reduced glutathione (GSH) with the affinity-purified NDPK1 complexes. Following up on this finding, we could demonstrate that NDPK1 undergoes glutathionylation, opening a new paradigm of NDPK regulation in plants. The described results extend our knowledge of NDPKs, the key enzymes regulating NDP/NTP homeostasis.

**References:**

[1] Blancaflor, E.B., *et al* (2014) The Plant Journal. 79(4): p. 568-583.
[2] Havaux, M (2014) The Plant Journal 79(4): p. 597-606.

**NOTES**

## P17| Single cell mapping of transcriptomes and mobile mRNAs

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A surprisingly high number of messenger RNAs (mRNA) have been shown to travel over graft junctions to distant and distinct tissues in *A. thaliana*. Currently, we have a limited understanding regarding the potential signaling role of these mobile mRNAs and how and why they move in specific tissues. Investigating mRNA transport directionality and target cell specificity is challenged by technical limitations to establish the RNA content of specific cells. Also identifying specific cell types is problematic, since the phloem consisting of sieve elements and companion and parenchyma cells are tightly interconnected. In order to overcome these technical constraints we are implementing a new singlecell RNA sequencing (scRNAseq) technology allowing us to identify mobile mRNAs in individual cells. The method we use is based on a microfluidic device that coencapsulates single cells with barcoded beads in aqueous droplets. Within droplets transcripts bind to barcoded oligo-TTT oligonucleotides and a cDNA library is produced carrying cell specific barcodes. This method is based on the Dropseq technology published by Macosko *et al*. (2015, Cell) for mammalian cells. We are showing that this DropSeq system can be applied to protoplasted plant cells. In order to further assess the feasibility and reliability of the DropSeq technology to identify individual plant cells and cell types we use transgenic lines producing cell-type specific fluorescent fusion proteins. Currently we create DropSeq scRNAseq libraries from wild-type and hetero-grafted plants to establish the distribution of mobile transcripts in individual cell types.

**References:**
[1] Macosko *et al*. (2015) Cell 161: 1202-1214

**NOTES**

## P18| Developing a toolkit for barley genebank genomics

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Genomics and biodiversity informatics are rising as pivotal tools to harness genetic resources harbored in germplasm collections, essential albeit mostly untapped reservoirs of genetic diversity for crop research and improvement. The BRIDGE project is characterizing by genotyping-by-sequencing (GBS) more than 20,000 accessions of domesticated (*Hordeum vulgare* ssp*. vulgare*) and wild (*Hordeum vulgare* ssp. *spontaneum*) barley hosted at the German *ex situ* genebank of IPK Gatersleben. Such genome diversity catalog is enabling a more informed classification of our genebank accessions based on non-redundant molecular passports. Moreover, GBS data is being analyzed in context of the barley genomic framework to study population structure, shed light on the historical flow of pedigree haplotypes during breeding practices and mine allelic variation at breeding-relevant traits. A novel warehouse infrastructure will provide a systematic valorization of the genomics data and a link to the passport and phenotypic data accumulated by the genebank conservation management.

**NOTES**

## P19| Investigation of dipeptide function in *Arabidopsis* by combining genomic, biochemical, and systems biology approaches

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Dipeptides are widespread across the cells of all living organisms. Dipeptides are commonly believed to be the product of protein catabolism but some, as for example, the neurotransmitter kyotorphin (L-Tyr-L-Arg), are synthesized from single amino acids. However, dipeptide metabolism and regulation have not been studied systematically in plants so far. Recently we discovered that many dipeptides were bound to different proteins in *Arabidopsis* cell culture extracts suggesting potential novel functions. In addition, published reports showed possible regulatory roles for dipeptides in different organisms.

To uncover the function(s) of dipeptides in plants we decided to employ three strategies. Firstly, we used genome wide association to map possible candidate genes involved in dipeptide accumulation in *Arabidopsis* ecotypes. Secondly, we use biochemical approaches to find protein interaction partners of dipeptides. For this we conducted size exclusion chromatography to conclude that dipeptides are interacting with high mass protein complexes due to their early elution patterns. Currently, we are performing affinity purification experiments with six individual dipeptides to characterize their protein interaction partners. At last but not least, we use a systems biology approach to analyze stress dependent dipeptide accumulation and metabolism. Therefore we integrate metabolomics and transcriptomics data in a comprehensive time-course experiment of *Arabidopsis* plants grown under eight different light and temperature conditions.

The evidences obtained here provide a first, but comprehensive, insight in dipeptide metabolism in *Arabidopsis* and their potential exciting signaling/regulatory functions.

**NOTES**

## P20| Regulation of central carbon and nitrogen metabolism by TORC1 in Chlamydomonas

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Growth signalling in eukaryotes is controlled by a highly conserved complex containing a protein kinase known as Target of Rapamycin (TORC1) that has been reported to control protein synthesis and cell cycle. Although, a number of studies have elucidated the mechanisms of TORC1 activation by leucine and glutamine in mammals and yeast, the understanding of an association between amino acids and TORC1 function is lagging far behind in photosynthetic organisms. Amino acids which act as critical upstream signals of TORC1 have been previously observed to accumulate upon its inhibition in Chlamydomonas. In order to explore the role of TORC1 in regulation of cell metabolism, we followed time course shifts in the metabolome after treatment of cultures with Rapamycin (a potent inhibitor of TORC1) under various conditions (i.e. light dark, nitrogen deprivation). We noted that the inhibition of TORC1 results in an immediate (i.e. within 5-15min) transformation of the primary metabolism. Interestingly, a distinct metabolic phenotype comprising of elevated levels of six amino acids, remained conserved across various tested conditions. Further in depth investigation of the enrichment of labelled carbon and nitrogen revealed that TORC1 inhibition triggers *de novo* amino acids synthesis in Chlamydomonas. Considering our data it is surmised that TORC1 signalling cascade regulates rate limiting enzymes of glycolysis, TCA cycle as well as amino acid biosynthesis in order to ensure elevated amino acid levels. While, *de novo* amino acids synthesis can be deliberated as an approach to favour TORC1 activity that in turn regulates various growth functions.

**NOTES**

## P21| Adaptive mechanical thinning – A new approach to compensate spatial variability in flower set in commercial apple orchards

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Mechanical flower thinning is a major yield regulating measure in sustainable apple production. At rotor speeds > 200 rpm flowers from trees are removed effectively. In practice, mechanical thinning is performed uniformly in the entire orchard with one rotor speed, not considering spatial heterogeneity. Since high variability in flower set occurs, this may cause yield losses at low flower set or reduced fruit quality as a result of underthinning of trees with heavy flower set.

In 2011, 2014 - 2016, the cultivar 'Elstar' was thinned with varying rotor speed. Thinning efficacy, fruit mass, and yield were recorded tree-wise (n = 200 for each year).

The amount of flowers per tree ranged between 0 - 2000 with an average flowering intensity of 568 flowers. The data pointed to linear relationships between crop load, average fruit mass and yield.

Considering flower set < 900 per tree, 280 rpm, 320 rpm and 340 rpm rotor speed increased the average fruit mass. At flower set > 1000, rotor speeds < 280 rpm resulted in small fruit < 65 mm. At flower set > 1400 only 280 rpm and 340 rpm could provide marketable fruit calibers > 65 mm.

To realize marketable quality of fruit compromised with high yield, the crop load of the 'Elstar' trees studied should not fall below 70 and not exceed 150 fruits per tree. In the following work the carbon balance model MALUSIM will be implemented to precise the optimum crop load for different cultivars.

**NOTES**

## P22| Ethical, legal and socio-economical aspects of genome editing in agriculture (ELSA-GEA)

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Ethical, legal and socio-economical aspects of genome editing in agriculture are addressed by a transdisciplinary project consortium. Genome editing is a promising tool to improve the genetic basis of crops and domesticated animals. To date, the techniques have been used in a variety of approaches for the precise editing of genes leading to altered phenotypes for basic research as well as for applied biology. Still, future risk assessment and regulation of organisms generated by genome editing are not defined in Europe. Legislators have to be aware of newly generated knowledge and may alter the current laws. From consumers perspective the right of freedom of choice, with regard to health or environmental benefits, is an important ethical and economical aspect. Therefore the project consortium a) compares international legal situation on biosafety, fundamental rights of biosecurity and consumer protection, b) organizes interviews and workshops on product declaration concerning genome edited organisms, c) evaluates benefits and costs across the agricultural process chain and d) assesses the impact of genome editing using systematic reviews of scientific publications. Project results and related contributions are presented on www.dialog-gea.de throughout the project.

Our work supports a science-based public discussion and provides facts-based information to an interested society.

**NOTES**

## P23| Next generation sequencing service – A case study

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This case study, using different sequencing methods, demonstrates the powerful combination of Illumina, PacBio-Sequel and 10x Genomics methods for next generation sequencing projects.

**NOTES**

## P24| Loss of function of *RAPTOR1B,* Regulatory-Associated *Protein of TOR 1B*, leads to unconventional physiological and molecular changes in *Arabidopsis thaliana*

**Mohamed A. Salem, Yan Li, Krzysztof Bajdzienko and Patrick Giavalisco**

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Plant cell growth and proliferation are controlled by a number of complex signal transduction pathways that connect environmental inputs to development and growth. Target of rapamycin (TOR), an essential high molecular weight Ser/Thr protein kinase, controls one of these central regulatory pathways that is evolutionary conserved among all eukaryotes. *Arabidopsis thaliana* TOR complex (*At*TORC1) contains in its core, next to TOR protein, regulatory-associated protein of TOR (Raptor) and lethal with SEC13 protein 8 (Lst8). To gain more knowledge about TOR complex function, we decided to study the influence of Raptor on growth and metabolism through a detailed phenotypic analysis of *raptor1b* T-DNA insertion knock out lines. Our results reveal that Raptor is involved in most developmental stages from post-embryonic growth to senescence. Accordingly, *raptor1b* mutants showed delay in development of rosette leaves and primary root next to defects in root hairs. Additionally, a delayed vegetative and reproductive growth and delayed senescence could be observed. To better understand the physiological changes involved upon *RAPTOR1B* mutation, we comprehensively profiled the molecular changes in *raptor1b* mutants. These mutants showed significant changes in primary and secondary metabolism next to changes in lipids and hormones. The significant molecular differences reflected the crucial roles of Raptor in regulating growth, metabolism and stress adaptation in plants.

**NOTES**

## P25| Analysis of the role of RNA methylation in intercellular transport

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In plants, mRNAs were shown to be transported from cell to cell via plasmodesmata and over graft junctions to distant tissues, potentially acting as non-cell-autonomous signals. However, a common RNA transport motif or proteins facilitating mRNA mobility have not yet been identified. It was recently shown that tRNA-like structures (TLS) present in approx. 11 % of mobile mRNAs found in *A. thaliana* trigger transport of GUS:TLS fusions in grafted plants. As tRNA structures are known to be targeted by many ribonucleotide modification enzymes, we compared the population of C5-methylated mRNAs, established by methylated RNA immunoprecipitation (MeRIP) and mRNA bisulfite sequencing, with our mobile mRNAs. This analysis revealed a significant correlation between the presence of RNA cytosine methylation and RNA mobility. Here, out of 341 mRNAs harboring C5-methylated cytosines 241 (70%) mRNAs are assigned as graft-mobile. To substantiate these findings we are currently evaluating enrichment of mobile mRNAs in MeRIP samples. We also test the mobility of GUS:TLS fusion constructs and variants thereof in transgenic RNA methyl-transferase double mutants (dnmt2/nsun2b). In addition, TCTP1 is a highly enriched methylated and mobile mRNA with the region carrying the modification(s) narrowed down to approximately 50 nucleotides. We were able to show that deletions associated to methylated TCTP1 regions lead to loss of RNA mobility. Summarized these insights point to a cellular mechanism existing in many organisms that has the capacity to facilitate transport of secondary modified mRNAs to distant tissues.

**NOTES**

## P26| Comparison of seven RNA-seq alignment tools based on experimental data of two *Arabidopsis thaliana* accessions

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Since the completion of the human genome project in 2003 (1) sequencing technologies developed extraordinarily fast. One of those methods is RNA-sequencing (RNA-seq), where detailed analysis pipelines have been published recently (2). While comprehensive comparisons of diverse read aligners for RNA-seq were performed for experimental and *in silico* data, e.g. for mapping primate data on the human genome and transcriptome (3), almost no studies of the performance of read mappers using different members of polymorphic species are available.

Here different algorithmical mappers (bwa, CLC, kallisto, RSEM, salmon, STAR, tophat2) were used to map experimentally generated data of two *Arabidopsis thaliana* accessions (Col-0, N14) under control and cold acclimated conditions. Also, variability of the transcriptome between these two genetically different accessions was analyzed.

All mappers showed similar results for the percentage of mapped reads against the reference. Comparing the number of expressed and differentially expressed genes, tophat2 and STAR were more similar compared to all other mappers. The N14 transcriptome was characterized with RSEM, STAR and tophat2 resulting in approximately 97.000 high quality SNPs compared to Col-0. Additionally, *in silico* analyses showed differences in the mapping behavior between STAR and tophat2.

Finally, all mappers showed similar results and the choice of a mapper will depend on the aim, computing power and time for the analysis.

**References:**
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[2] Conesa *et al*. (2016) Genome Biol 17(1): 13.
[3] Benjamin *et al*. (2014) BMC Genomics 15(1): 570.

**NOTES**

## P27| Towards the discovery of epigenetic regulation during low temperature priming, memory and triggering in Arabidopsis

**Kora Schmitt[1], Ellen Zuther[1], Stephanie Schaarschmidt[1], Axel Fischer[1], Daniel Schubert[2], Dirk Walther[1] and Dirk K. Hincha[1]**

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Plants originating from temperate climate zones can acquire improved freezing tolerance when primed by low, non-freezing temperatures (cold acclimation). Changes at the molecular and metabolic levels during this process have been previously studied and are well understood. On the other hand, barely anything is known about memory of a previous low temperature stress when followed by a later low temperature triggering event. Previous results have shown that Arabidopsis Col-0 plants subjected to cold priming at 4°C for three days, followed by a seven day lag phase at 20°C and a subsequent low temperature triggering event at 4°C, displayed an improved freezing tolerance compared to plants that were only subjected to priming. Epigenetic regulators have been linked to "cellular memory" in plants, a possible involvement in low temperature memory is thus likely. To identify genes encoding epigenetic regulators involved in cold memory plants were harvested at different time points after priming (C28P) and triggering (C28P3L7T) as well as after priming of a developmental control (C35P). The samples were analysed by Illumina-based RNA-Seq as well as qRT-PCR. The data were compared to each other and analysed for expression changes of genes encoding epigenetic regulators. This work marks the beginning of an investigation of an involvement of epigenetic regulation in low temperature memory in Arabidopsis.

**NOTES**

## P28| Cysteine proteases and their inhibitors in microbe-maize root interactions

**Jan Schulze Hüynck[1], André N. Müller[2], Farnusch Kaschani[3], Karina van der Linde[2], Stefanie Gläser[4], Michael Thielen[1], Richard Jacoby[1], Marcel Bucher[1], Johana C. Misas-Villamil[1] and Gunther Doehlemann[1]**

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Plants are associated with a broad spectrum of microbes and outcomes in plant-microbe interaction range from beneficial symbiosis to destructive diseases. Two main events determine whether a plant-microbe interaction can be established: 1) the perception of microbial molecules by the plant and 2) the modulation of plant immune responses. The apoplast or extracellular space of plants plays a critical role in the establishment of the plant-microbe interaction since it is the first interface where plants recognize microorganisms. Plant proteases are key players in microbe perception. Cysteine proteases belong to the most abundant class of proteases found in the plant apoplast [1]. Among them, papain-like cysteine proteases (PLCPs), belonging to the Clan CA, family C1 present structural homology to papain [2]. They have been identified as pivotal components during plant-pathogen interactions [3]. We propose that the modulation of PLCPs displays a conserved mechanism during plant-microbe interactions and that microbes need to overcome plant immunity by inhibiting or modulating PLCP activity for a first encounter with the plant. We aim to investigate the role of PLCPs for plant-microbe interactions and the importance of microbial modulation of these PLCPs. Preliminary data shows that some root associated microbes are capable of modulating maize root PLCPs and that a novel root specific PLCP is present in maize which will be studied further.

**References:**

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[2] Rawlings, N.D., F.R. Morton, and A.J. Barrett, (2006) Nucleic Acids Res. 34(Database issue): p. D270-2.
[3] Misas-Villamil, J.C., R.A. van der Hoorn, and G. Doehlemann (2016) New Phytol 212(4): p. 902-907.

### NOTES

## P29| Mechanisms of quantitative resistance in the maize – *Ustilago maydis* interaction

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The biotrophic pathogen *Ustilago maydis* causes smut disease on maize and induces the formation of tumors on all aerial parts of the plant. Unlike in other biotrophic interactions, no gene-for-gene interactions could be identified in the maize – *U. maydis* pathosystem. As a consequence, resistance of maize to *U. maydis* is a polygenic, quantitative trait. For one *U. maydis* effector, Ara1, a line-specific function has been observed (Jaeger *et al*., unpublished). This suggests that the fungus' effectors intervene with maize QTLs. The molecular basis of quantitative resistance in maize and how *U. maydis* interferes with its components is, however, still mostly unknown.

We assessed *U. maydis* resistance levels in the 26 inbred founder lines of the NAM RILs (Yu *et al.* 2008; McMullen *et al.* 2009) and Early Golden Bantam. Within this set of diverse maize lines, resistance levels ranged from highly susceptible to highly resistant (>94% vs. <35% tumors, respectively). Generally, maize lines of close provenance to the *U. maydis* strain used were more susceptible than those of distant provenance (temperate vs. tropical). In follow-up experiments, we will analyze the transcriptome of *U. maydis* infecting maize lines of different resistance levels by RNA-Seq. Line-specifically expressed effectors will be selected for investigation of their virulence function and isolation of their plant targets.

**References:**

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Yu *et al*. (2008) Genetics 178(1): 539–551
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**NOTES**

## P30| A novel control module for heat stress memory in plants

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Plants have the capacity to *'memorize'* stressful events and protect themselves from future stresses. Furthermore, they are able to *'reset'* or *'forget'* memories of certain stressful situations, which helps to maximize growth after returning to non-stress conditions. A delicate balance between the consolidation of stress memory and the degree of forgetfulness is critical for plant growth and productivity under changing environmental conditions.

Here, we report a novel control module for heat stress memory (thermomemory) in plants. Recently, we identified HSP21, a chloroplast-localized small heat shock protein, as a crucial component of thermomemory. Variation in HSP21 protein level contributes to the differential thermomemory performance of *Arabidopsis* accessions, revealing a strong positive correlation between HSP21 abundance and enhanced thermomemory capacity (Sedaghatmehr *et al.*, 2016). Employing a combined pharmacological/genomics approach, we discovered a plastid-localised metalloprotease, FtsH6, as a protease involved in degradation of HSP21 during the memory phase in Col-0. Furthermore, we now show that, in addition to FtsH6, autophagy contributes to the selective degradation of HSP21 at later stages of the thermomemory phase. Our results thus reveal the presence of a novel HSP21 – plastidial protease – autophagy control module for thermomemory in plants.

**References:**
Sedaghatmehr, M. *et al*. (2016). Nat. Commun. 7:12439
Sedaghatmehr, M. *et al*. (2017) submitted

**NOTES**

## P31| Mass spectrometry as a tool for understanding plant redox regulation

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Molecular signal transduction by redox signaling is a key element in the response of organisms to fluctuating environmental or intracellular conditions. It involves specific and reversible oxidation of redox-sensitive cysteines. In plants, one type of the redox regulation is the thioredoxin system where thioredoxins specifically reduce a target enzyme.

In this study we focus on the role of changes in the global redox-proteome during plant adaptation to changing environmental conditions. We ask how many proteins of the plant proteome are under redox control. In a first approach to answer this question, we use a double-labelling method to differentially tag reduced and oxidized cysteine residues and combine it with SDS-PAGE in which the different labels create a size shift. We then apply a shot-gun proteomics approach on gel-fractions to quantitatively resolve the position of proteins in the gel and thereby reveal their redox state in the cell. As second approach we are using a resin-assisted enrichment of thiols (Guo *et al.* 2014) followed by mass spectrometry analysis. Our preliminary results confirm that both methods are applicable to *Arabidopsis thaliana.* We were able to capture changes in the redox state of proteins in Arabidopsis plants exposed to different light intensities. We also performed a large-scale analysis of metabolites using a thioredoxins M1, M2 and M4 triple mutant (*trxm124*). While thioredoxin M was proposed to regulate enzymes of the TCA cycle, our analysis shows for the first time that loss of thioredoxin M1, M2 and M4 function results in very specific changes on TCA cycle-related metabolite levels with only minor effects on other metabolic processes. We are now performing further experiments to study the *trxm124* redoxome in comparison to WT plants with the aim to identify novel thioredoxin M targets.

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Geigenberger, P. and A. R. Fernie (2014) Antioxid Redox Signal 21(9): 1389-1421.

### NOTES

## P32| Global analysis of protein-small molecule interactions guided by co-fractionation

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Small molecules are not only intermediates of metabolism but additionally have various functions, including energy, structure, signaling, thereby controlling cellular metabolism, growth, and development. Despite a few systematic studies, the true extent of protein-small molecule interactions in biological systems remains unknown. To study protein-small molecules interactions, a non-targeted approach using size exclusion chromatography was established. Assuming that small molecules bound to proteins will co-fractionate, protein-small molecule complexes of Arabidopsis cells cultures were separated by size. Subsequently, fractions were analyzed for co-occurrence of small molecules and proteins by LC-MS. Numerous small molecules co-eluted with proteins strongly suggesting stable complexes. Following evidence of co-elution we could retrieve known small molecules-protein complexes like enzyme-co-factors as well as find novel interactions. Among them we identified Pantothenic acid to interact with the enzyme catalyzing the first step in its pathway, Ketopantoate hydroxymethyltransferase 1 (KPHMT1) with a Kd of 376 µM. This for the first time suggests presence of an end product feed-back mechanism of Pantothenic acid biosynthesis in Arabidopsis. We expect that a deeper identification of the small molecules bound to proteins found here will uncover yet unknown small molecules possessing regulatory roles.

**NOTES**

## P33| Enhancing the properties of plant cell walls for the production of sustainable, carbon-neutral chemicals

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In a sustainable bioeconomy all parts of a plant need to be utilized in an energy efficient manner to be converted to commodity chemicals e.g. via fermentation of plant sugars by microbes. Plants not only contain soluble sugars and starch, but they also contain sugar-rich cell walls. The sugars are locked in the wall in three major classes of polysaccharides (cellulose, hemicellulose and pectin), which are among the planet's most abundant biopolymers (Loque, Scheller & Pauly, 2015). Hemicelluloses represent a third of the plant wall biomass, and contribute to the wall's resistance to degradation. One goal of increasing fermentation yields of wall derived sugars it to increase the abundance of hexose sugars (Pauly & Keegstra, 2008). However, changes in wall sugar composition may affect plant growth and development, and therefore it is advisable to fine-tune the hexose sugar levels in specific plant tissues.

This project aims to alter hemicellulose composition by replacing xylans (pentoses) with mannans (hexoses) in selected *Arabidopsis thaliana* walls. *Arabidopsis* mutant lines showing a strong reduction in xylan (Brown *et al*., 2007) have reduced biomass yields due to collapsed vasculature and dwarfism. To overcome these defects and further increase the hexose/pentose sugar ratio in these lines, mannan-related biosynthetic genes are expressed under the control of cell-type-specific promoters. This strategy provides insight into the biological functions of distinct hemicelluloses, and establishes genetic engineering tools to improve the chemical yields derived from plant wall biomass.

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**NOTES**

## P34| Inducible RNAi repression of galactolipid biosynthesis in tobacco reveals a strict coordination of thylakoid membrane constituent accumulation

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To examine the impact of galactolipid deficiency on the photosynthetic apparatus in tobacco, we used ethanol-inducible RNAi approach against two key enzymes of galactolipid biosynthesis in the chloroplast, MGD1 and DGD1. Using this approach, it becomes possible to track changes in lipid composition and photosynthesis at different time points after RNAi induction. Our studies revealed very similar changes in both MGDG- and DGDG-deficient mutants, however young and mature leaves of transgenic lines behaved differently. While no changes of photosynthetic parameters and minor changes in lipid content were observed in mature leaves of transgenic lines, drastic differences occurred in young leaves after induction: strong reductions in total chlorophyll content and in the accumulation of all photosynthetic complexes; significant changes in content of galactolipids, phospholipids and storage lipids. Because of the reduced demand for membrane lipids in young leaves, fatty acids are repartitioned into storage lipids, as shown by the accumulation of triacylglycerols and the appearance of lipid droplets in the cytosol of the transgenic lines. Collected data indicate that both investigated galactolipids serve as structural lipids since changes in photosynthetic parameters were mostly results of reduced amounts of all photosynthetic constituents. In response to restricted galactolipid synthesis, thylakoid biogenesis is precisely readjusted to keep the proper stoichiometry and functionality of photosynthetic apparatus.

**NOTES**

## P35| Community structure and plant growth-promoting potential of cultivable bacteria isolated from Cameroon soil

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Exploitation of native plant growth-promoting bacteria (PGPB) in Cameroonian agro-ecosystems modulate plant–microbes interactions that may affect ecosystems sustainability and agricultural productivity in an environmental eco-friendly way. Consequently, knowledge about the community structure and the functional PGP diversity of bacteria associated with maize grown in Cameroon is required. In our approach native bacteria from Cameroon soil were isolated, identified by partial 16S rDNA gene sequencing and screened for their abilities to solubilize inorganic phosphate, to fix atmospheric nitrogen, to produce siderophore and to tolerate increasing concentrations of salt. Genetic and functional diversity was characterized according to their phylogenetic affiliation. A total of 143 bacteria were identified and distributed among three phyla (*Actinobacteria*, *Firmicutes* and *Proteobacteria*), 14 families and 19 genera. *Bacillus* (33.56%), *Arthrobacter* (23.07%), *Sinomonas* (7.69%) and *Staphylococcus* (6.29%) were the most abundant genera found among all the isolates. Based on their PGP potential *in vitro* characterization, 50.35 % (72/143) solubilized phosphate, 10. 48% (15/143) were nitrogen fixer, 18.88% (27/143) produced siderophore and 88.11% (126/143) salt tolerant at 2% NaCl whereas only 16.78% (24/143) were able to tolerate 8% NaCl. We found that the occurrence of PGP traits was depended on genus, family and phylum. Six isolates (V1, V39, V54, V62, V64, and V84), affiliated to the most abundant genera, *Bacillus* and *Arthorobacter,* and comprising different PGP abilities were selected and *in vitro* tested on maize seedlings in a germination bioassay. All six strains induced a significant increase in hypocotyl and root length and a higher vigor index of maize seeds compared to the non- inoculated seeds (control). In the next steps bacterial transcriptome analysis and quantification of marker gene expression shall reveal the PGP mechanisms in model experiments. Our results indicate the potential of selected indigenous bacteria from Cameroon soil to enhance maize growth and productivity which finally can be used for bio-fertilizers development.

**NOTES**

## P36| NAC transcription factor JUNGBRUNNEN1 enhances drought tolerance in tomato

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Drought stress is one of the major threats to the agricultural production. Transcription factors (TF) are central regulators of transcriptional reprogramming and expression of many TF genes is affected by drought, including members of the NAC family. Previously, we reported JUNGBRUNNEN1 (JUB1) a NAC TF in *Arabidopsis thaliana* as a master regulator of growth and stress response. Here, we identified JUB1 to be a positive regulator of drought stress in tomato. Expression of tomato *JUB1* (*SlJUB1*) is enhanced by several abiotic stress treatments and in particular to drought. Silencing *SlJUB1* by VIGS (virus induced gene silencing) severely reduces drought tolerance in tomato. In accordance, with an increase in ion leakage, elevation of hydrogen peroxide ($H_2O_2$) levels, and a decrease in the expression of various drought-responsive genes during drought. In contrary, transgenic tomato plants overexpressing AtJUB1 from *A. thaliana* increases tolerance to drought stress, alongside with a higher relative water content and lower levels of MDA and hydrogen peroxide. Moreover, transcripts of *SlDREB1, SlDREB2* and *SlDELLA* were controlled by SlJUB1 during drought stress. Furthermore, we show by *invitro* and *invivo* assays that AtJUB1 can directly bind to the promoters of its tomato homolog target genes (*SlDREB1, SlDREB2 and SlDELLA*) during drought stress. Together, our study highlights the importance of JUB1 in tomato during drought stress and suggests an ideal candidate for breeding stress tolerant tomatoes.

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**NOTES**

## P37| Metabolic pathway assignment based on phylogenetic profiling

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The assignment of gene function is a crucial step following the complete sequencing of a genome. In order to improve functional gene annotation in plants, we applied phylogenetic profiling [1] with the particular goal to identify as of yet unassigned secondary metabolic pathway genes as well as predicting the presence of secondary metabolic pathways in newly sequenced species. While primary metabolites and associated pathways are indispensable and, thus, occur in essentially all plants, most secondary metabolites and their biosynthesis pathways have evolved only in a subset of plant species. Thus, an involvement of genes in a common secondary pathway ought to be reflected by a common presence/absence pattern across different plant species. We calculated phylogenetic profiles for 42,014 metabolic pathway enzymes with KEGG enzyme identifiers from 24 plant species based on sequence and pathway annotation data from KEGG and Ensemble Plants. For the required step of gene family assignment, we included data of all 39 species available at the Ensemble Plants database and established gene families using a network-based approach. For a subset of known metabolic pathways, we were indeed able to show that the phylogenetic profiles of their enzymes cluster together significantly more often than randomly expected. In our tests for pathway assignments of enzymes with known function, best results were achieved in the categories carbon metabolism and biosynthesis of amino acids; i.e. primary metabolism pathways. A successful application to secondary pathway assignments currently appears severely hampered by the paucity of functionally characterized secondary metabolism pathway genes in a broader set of plant species. Nonetheless, our results show that phylogenetic profiling has the potential to improve protein function prediction of unknown enzymes and may contribute to the identification and annotation of plant secondary metabolic pathways.

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**NOTES**

## P38| Dipeptides- novel class of small molecule regulators

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Metabolites are low molecular weight molecules produced in cells during metabolic processes. Those small molecules may interact with proteins not only as a substrates or products, but also as a ligands or cofactors influencing biophysical properties of their protein partners [1]. Metabolite binding might affect protein's activity, influence protein localization and regulate protein-nucleic acid or protein-protein interactions changing thereby activity of some biological pathways [2].

In our research, we used Size Exclusion Chromatography (SEC) that enables separation of molecules based on their size to split free small molecules from those that forms complexes with proteins in native plant lysate [3]. Using mass spectrometry (MS), we measured protein and metabolite content in collected fractions. Surprisingly, we identified ~100 dipeptides (i.e. Gly-Pro) in protein containing fractions what suggests that dipeptides may be more than by-products of protein degradation. Predicted interactors were verified performing Affinity Chromatography (AC) and then the protein-dipeptide binding was tested using MicroScale Thermophoresis (MST) and Thermostability.

Using SEC and AC we found Gly-Pro to be in a complex with fructose 1,6-bisphosphate aldolase (F1,6BP). Performing further experiments we confirmed the binding between Gly-Pro and rabbit or plant F1,6BP. Basing on these results we speculate that Gly-Pro might affect enzyme activity, changing the balance between glycolysis and gluconeogenesis.

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**NOTES**

## P39| Unlinking phloem-mediated protein transport from mRNA transport

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An increasing number of mRNAs were shown to be graft-transmissible and phloem-mobile. However, little is known about RNA mobility motifs or features facilitating their transport and the tissue(s) / cells they are allocated to. We address these questions by using *A. thaliana* plants expressing deletion mutants of a mobile transcript *(TRANSCRIPTIONAL CONTROLLED TUMOR PROTEIN*, *TCTP*) in grafting experiments. This approach allows us to evaluate specificity of *TCTP* mRNA/protein transport and to pinpoint *TCTP* motifs mediating transport of the otherwise non-mobile *YFP* RNA. In addition, we use CALLOSE SYNTHASE (CALS3) overexpressing plants in which companion cell plasmodesmata (PD) are transiently closed to study whether YFP-TCTP unloading dependents on symplasmically connected companion cells. Finally, we ask whether $m^5C$ methylation of *TCTP* mRNA is necessary for its movement from root to shoot. Our data indicate that *YFP* mRNA itself is not mobile. However, *YFP* fused to *TCTP* moves from above ground tissues to roots via the phloem. Although smaller in their size, 5' truncated *YFP – ΔN TCTP* RNAs are not transported over graft junctions whereas the YFP-ΔN TCTP protein moves in a similar fashion as full-length fusion proteins from shoot to root. In addition, we identified a small *TCTP* 5' RNA region essential for RNA mobility and present evidence suggesting that the identified RNA mobility region is a target for RNA $m^5C$ methylation and that this secondary modification is essential for *TCTP* RNA mobility.

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**NOTES**

Plants and People conferences are held every two years. Our inaugural conference in 2011, themed **'On Roots and Fruits of Plant Biology'** looked into the history and present day applications of plant research, while our 2013 conference, titled **'Challenges in Biology – Big Data and Ethics'** focused on advances in biology and addressed ethical challenges that we as scientists have to consider. **'Future Plan[t]s'** in 2015 brought together academic researchers and industry professionals to discuss their science and career paths, offering new ideas and career outlooks to young scientists.

We hope you enjoyed this year's P&P conference

'Communicating Science – Connecting Worlds'

Our next meeting will be in 2019.

We hope to see you then!

## The 2017 organizing team

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

Silvia Martínez Jaime, Umarah Mubeen, Camilla Ferrari,
Eleftheria Saplaoura, Andrés Eduardo Rodríguez Cubillos,
Corné Swart, Fabio Giulio Moratti

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