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Symposium of the Zurich-Basel Plant Science Center

# PLANTS FOR HEALTH

*from research to application*



→ [www.psc2016.eth.ch](http://www.psc2016.eth.ch)

**Symposium of the Zurich-Basel  
Plant Science Center**  
1<sup>st</sup> December 2016, ETH Zurich

# **Plants for Health**

*from research to application*

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# Organization

## Symposium committee

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## Date and Venue

1 December 2016  
ETH Zurich  
Auditorium Maximum (HG F30)  
Rämistrasse 101, 8006 Zurich

## Symposium website

→ [www.psc2016.ethz.ch](http://www.psc2016.ethz.ch)

**Admission is free of charge.**

# Program

09.00 Opening remarks by Samuel C. Zeeman, ETH Zurich

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## Session 1 NUTRITION

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09.15 *Hidden Hunger – seeking solutions with staple crops*  
Herve Vanderschuren University of Liege, Belgium

10.00 *Folate biofortification of crop plants*  
Dominique Van Der Straeten University of Ghent, Belgium

10:45 Coffee

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## Session 2 MEDICINE

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11.00 *Plants as a platform to produce therapeutic glycoprotein*  
Dirk Bosch Wageningen UR, The Netherlands

11.45 *Multipotent natural leads against respiratory tract infections*  
Judith Rollinger University of Vienna, Austria

12:30 Lunch and Poster Session

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## Session 3 ENVIRONMENT

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14.15 *A mass balance approach to quantify interception of fine dust (PM10) by trees*  
Anette Pronk Wageningen UR, The Netherlands

15.00 *Phytoremediation of contaminated soils: facts and challenges*  
Jean-Paul Schwitzguebel EPFL, Switzerland

15.45 Break

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## Session 4 EMBO SCIENCE-POLICY ADDRESS

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16.00 *What and how can plant science contribute to society?*  
Karin Metzloff European Plant Science Organisation

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## Session 4 PANEL DISCUSSION

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16.30 *Natural products: from plant-based production to synthetic biology*

*Panellists:*

*Brian King*

*Ana Deplazes-Zemp*

*Francois Meienberg*

*Herve Vanderschuren*

*Karin Metzloff*

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## 18.00 Closing Remarks and Poster Prizes

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18.15 Aperero

## **Invited speakers**

in speaking order

## Herve Vanderschuren

Professor of Plant Genetics  
University of Liege, Belgium

8 Prof. Herve Vanderschuren holds a MSc in Crop Genetics from AgroParisTech (France). He obtained his PhD in Plant Biotechnology at ETH Zurich (Switzerland). He has led a research team focusing on crop biotechnology at ETH Zurich and has recently been appointed as Professor of Plant Genetics at University of Liège (Belgium). Over the last 10 years, his research activities have been focused on the study of crop responses to biotic and abiotic stresses as well as on the implementation of tools to select and develop cassava and rice with improved traits. Several cassava and rice accessions with increased disease resistance, improved nutritional quality and prolonged shelf life traits have been developed by his team. His group has recently developed and field tested a vitamin B6 enriched rice variety (Li et al, 2015, Nature Biotechnology) and is working on the biofortification of other micronutrients in rice and cassava. Prof. Vanderschuren's team is also actively involved in technology transfer to laboratories in Africa, Asia and South America.

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## Dominique Van Der Straeten

Professor of Functional Plant Biology  
University of Ghent, Belgium

Prof. Dominique Van Der Straeten is a full professor at Ghent University and research director of the Laboratory of Functional Plant Biology. She began her academic career working in ethylene biosynthesis in tomato and Arabidopsis, followed by researching plant stress using remote imaging. She further expanded her research interests working on signal crosstalk of ethylene with other hormones and light. In 2003, aiming to apply basic science to solve societal problems, she initiated research on folate biofortification of crop plants in 2003 leading to a major publication on folate bio-fortification in rice (Blancquaert et al., 2015 Nature Biotechnology).

## Dirk Bosch

Professor  
Wageningen UR, The Netherlands

Prof. Dirk Bosch is an expert concerning bioactive compounds, biochemical pathways, biotechnology and biochemistry. His research group at Wageningen University in the Netherlands is interested in how plant derived substances can serve as medicine, specifically as anti-cancer compounds. Besides this, they are also investigating in a novel type of potato starch, which cannot be fully decomposed. This would be interesting for diet products. Investigation in highly decomposable starch is carried out as well in order to improve animal feed. In another unconventional project they are looking into plant-derived molecules as building blocks for recyclable bottles and for replacement of plastic bottles.

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## Judith Rollinger

Professor of Pharmacognosy  
University of Vienna, Austria

Prof. Judith Rollinger is a professor of Pharmacognosy/Pharmaceutical Biology at the University of Vienna. After her PhD in Pharmacognosy of the University of Innsbruck dealing with crystal polymorphism, she extended her studies to the fields of phytochemistry, ethnopharmacology, and molecular modelling. Her current research focuses on the interdisciplinary field of integrating computational techniques in pharmacognostic research as strategy for the discovery of natural lead structures for treating viral infections, metabolic syndrome and inflammation. Publications resulting from her research appear in highly ranked international journals, as book contributions, and patents.

## **Anette Pronk**

Researcher in Agrosystems  
Wageningen UR, The Netherlands

Dr. Anette Pronk received her Master degree in Agronomy and Crop Science in 1990 and obtained her doctorate in 2004 on the topic "Irrigation and nitrogen use efficiency of *Thuja occidentalis* grown on sandy soils", both at Wageningen University. Dr. Pronk is conducting applied research to enhance farming systems for over 25 years and published several articles and reports. Since 2010, she researches the potential of trees to intercept fine dust particles and thereby enhance local air quality.

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## **Jean-Paul Schwitzguebel**

Senior Scientist  
EPFL, Switzerland

Dr. Jean-Paul Schwitzguebel is a plant and microbial biochemist. After obtaining his PhD at the University of Geneva, he spent postdoctoral time at the ETH Zurich, the Imperial College London and the University of Neuchatel, before he became a senior scientist at the Ecole Polytechnique Fédérale de Lausanne (EPFL). His research focuses especially on phytoremediation and the removal of organic pollutants from wastewater and contaminated sites.

## **Karin Metzloff**

Executive Director  
European Plant Science Organisation (EPSO)

Dr. Karin Metzloff has been the executive director of EPSO since its creation in 2001. She works with the EPSO members and other partners to promote plant research in the European science and science policy arena by overseeing the EPSO Working Groups, providing advice and recommendations to politicians at European, multinational and national level. Karin represents EPSO in the Initiative for Science in Europe, ISE and the Global Plant Council (GPC). She is a member of the European Commission High Level Steering Board on Agricultural Productivity and Sustainability and of the Steering Council and Executive Committee of the European Technology Platform Plants for the Future and. Karin is responsible for all member, observer and association relations of EPSO.

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## **Panel Discussion**

**Natural products: from plant-based  
production to synthetic biology**

## Natural products: from plant-based production to synthetic biology

**A 90-minute discussion on the science, technology, risks, promises and policies surrounding a new technology with great disruptive potential.**

Since the industrial revolution there has been a shift in the production of natural products (drugs, chemicals, dyes, micronutrients etc.) from plant-based production and chemical extraction to de novo synthesis through synthetic chemistry and more recently by synthetic biology techniques.

14 Recent advances in synthetic biology have discovered ways to replace the cultivation of, for example, the anti-malarial drug plant artemisia, poppy and vanilla with yeast fermentation, a process akin to “brewing beer”. These advances often lower the price of natural products and can lead to widespread adoption of life-saving drugs. Biological means of organic chemicals production are also significantly more environmentally friendly compared to petrochemical and wood-pulp based industries. However they may also pit large multinational companies against the interests of small-holder farmers in the developing world. Further, while some of these products are marketed as natural (since they are produced through biological and not chemical means), others feel that this is an attempt to deceive consumers. We propose a discussion around this topic encompassing questions on: the costs vs. benefits of this technological revolution, the role of plant technologies (e.g. biofortification), the impact on biodiversity with the replacement of rare-plant cropping with fermentation, the ethical issues arising from the future replacement of farms with fermenters and the role of the consumer.

## Our panellists

### Brian King

Post-doctoral researcher at the University of Copenhagen and co-founder of TychoBio ([www.tycho.bio](http://www.tycho.bio)). TychoBio is a young company working on industrial production of plant-derived small molecules by introducing new genes into moss.

### Ana Deplazes-Zemp

Dr Ana Deplazes-Zemp is a research associate at the Institute of Biomedical Ethics at the University of Zurich. A doctorate in Biochemistry from ETH Zurich, Ana’s current research interests include the ethical effects of synthetic biology, responsible research and innovation in biotechnology, definitions of life and the boundary between natural and artificial/life and machines.

### François Meienberg

François Meienberg has worked at Public Eye (formerly the Berne Declaration) since 1999, with a focus on Intellectual Property Rights and Agriculture. He has followed Convention of Biological Diversity, Access and benefit sharing and FAO-Treaty negotiations intensely and worked on Joint Projects and Campaigns with different stakeholders to reveal Biopiracy and implement ABS include: the Basmati Patent, Swartzia Madagascariensis, Hoodia, Pelargonium Patent and Rooibos.

### Karin Metzloff

Executive director of EPSO ([www.epsoweb.org](http://www.epsoweb.org)). Karin works with the EPSO members and other partners to promote plant research in the European science and science policy arena by overseeing the EPSO Working Groups, providing advice and recommendations to politicians at the European, multinational and national level.

### Herve Vanderschuren

Professor of Plant Genetics at the University of Liege and an expert in plant biotechnology focusing on applications aimed at improving nutrition-profiles and disease-resistance in staple crops like rice and cassava. Herve has significant experience with technology transfer to developing countries and field-trial deployment of genetically engineered plants in Africa.

## Poster abstracts

ETH Zurich

P1

## Metabolic engineering of carbon pathways to enhance cassava starch yields

Anjanappa Ravi Bodampalli<sup>1</sup>; Rohner Marius<sup>1</sup>; Hirsch-Hoffmann Matthias<sup>1</sup>; Gruissem Wilhelm<sup>1</sup>

<sup>1</sup> ETH Zurich, Switzerland

Cassava (*Manihot esculenta* Crantz), a semi-perennial woody shrub that produces edible starchy tuberous roots is an important staple food crop in Sub-Saharan Africa and also has many industrial applications. Here we seek to produce high-yielding farmer preferred cassava varieties to support the income of small-holder farmers. We are implementing a “push-pull” strategy to increase starch content in cassava storage roots by improving photosynthetic carbon assimilation in source tissue, long-distance transport of assimilates through the phloem and their utilization in sink tissues. We used current knowledge of source-sink relationship from other crop species to select candidate genes for overexpression or downregulation. In addition, we are also generating a promoter library for cassava by isolation and characterization of novel tissue-specific promoters that are considerably relevant, especially for engineering strategies for improving cassava source-sink relationships.

Keywords: Cassava; source-sink; push-pull; promoters; starch; roots

P2

## RNAi control of SLCMV in a commercially important Indian cassava cultivar

Bull Simon E.<sup>1</sup>; Abraham Leen N.<sup>2</sup>; Vijayan Abhilash P.<sup>2</sup>; Vasudevan Kumar<sup>3</sup>; Makesh Kumar Thangaraju<sup>2</sup>; Gruissem Wilhelm<sup>1</sup>; Vanderschuren Herve<sup>3</sup>

<sup>1</sup> ETH Zurich, Switzerland

<sup>2</sup> Central Tuber Crops Research Institute (CTCRI), India

<sup>3</sup> University of Liège, Belgium

Cassava mosaic disease (CMD) is a major constraint to food security and commercial production of cassava (*Manihot esculenta* Crantz) in southern India. In India, CMD is caused by *Indian cassava mosaic virus* (ICMV) and *Sri Lankan cassava mosaic virus* (SLCMV) – species of bipartite begomoviruses (family *Geminiviridae*) that are transmitted by whiteflies (*Bemisia tabaci*). Chimeric RNAi constructs targeting the replication protein coding sequence (AC1; Rep) of the recently sequenced SLCMV strains isolated from Kerala and Tamil Nadu regions have been designed and are being used for *Agrobacterium*-mediated stable transformation of cassava. In addition to the model cassava cultivar 60444, we assessed the capacity of the commercially important H165 to produce friable, embryogenic callus (FEC) required for transformation, as well as their ability to regenerate into healthy plantlets. Successfully transformed independent lines are being characterised.

Keywords: virus; disease; cassava; India; transformation; RNAi; root

P3

## Genetic redundancy and enzymatic compensation in the Calvin-Benson cycle

Carrera Dániel Árpád<sup>1</sup>; Zanella Martina<sup>1</sup>; Bräunlich Stephanie<sup>1</sup>; Streb Sebastian<sup>1</sup>; Zeeman Samuel C.<sup>1</sup>

<sup>1</sup> ETH Zurich, Switzerland

The most important pathway of CO<sub>2</sub> fixation on earth is the Calvin-Benson cycle. Its manipulation is one of the most promising targets to increase total carbon assimilation. The cycle involves three phases: CO<sub>2</sub> fixation, reduction of 3-phosphoglycerate, regeneration of ribulose 1,5-bisphosphate (RuBP). The latter can be considered more as a pool of reactions to rearrange carbon skeletons into RuBP, rather than a straightforward, fixed sequence of reactions. Moreover, not all genes encoding the major enzymes for each step have been unambiguously assigned so far. Several key enzymes of the regenerative phase (fructose 1,6-bisphosphate aldolase, sedoheptulose 1,7-bisphosphatase, fructose 1,6-bisphosphatase and phosphoribulokinase) are being investigated to assess redundancy and specificity.

Keywords: Calvin-Benson cycle; isoforms; FBA; SBPase; FBPase; PRK

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P4

## Research into the function of RubisCO in green seeds

Deslandes Gabriel<sup>1</sup>; Zanella Martina<sup>1</sup>; Herrfurth Cornelia<sup>2</sup>; Feussner Ivo<sup>2</sup>; Zeeman Samuel C.<sup>1</sup>

<sup>1</sup> ETH Zurich, Switzerland

<sup>2</sup> Georg-August-University Göttingen, Germany

Seeds from a great number of plants, including many grown for agricultural purposes are green during their development. The aim of the project is to test genetically a pathway that was proposed to improve efficiency of lipid synthesis during the development of green seeds.

Keywords: Calvin-Benson cycle; lipid; *Arabidopsis thaliana*

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P5

## Molecular diversity of cassava mosaic geminiviruses in farmer fields in Ghana

Elegba Wilfred<sup>1</sup>; Gruissem Wilhelm<sup>1</sup>; Vanderschuren Herve<sup>2</sup>

<sup>1</sup> ETH Zurich, Switzerland

<sup>2</sup> University of Liège, Belgium

Cassava mosaic disease (CMD) is a major constraint to cassava production in Ghana and Africa. CMD is caused by at least nine distinct CMG species, which have evolved to become one of the most damaging crop pathogens. In this study, we report the complete genome sequencing and characterization of 80 full-length CMG clones (79% DNA-A genomes and 29% DNA-B genomes) isolated from sampled cassava leaf material in farmer fields. The newly identified CMG clones share 95 to 99% nucleotide sequence identity to three prevalent African cassava mosaic (ACMV) isolates; ACMV-Nigeria, ACMV-Ivory Coast and ACMV-Uganda. The detection of three different CMG variants in samples collected from 5 out of 8 sampling locations supports the high propensity of recombination of CMG species in the field. The characterisation of diversity that exist among CMG isolates, strains or variants in the field is important for developing durable and broad spectrum solutions to achieve resistance in the field.

Keywords: cassava; geminiviruses; diversity; Africa

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P6

## Management matters: Testing a mitigation strategy of nitrous oxide emissions on managed grassland

Fuchs Kathrin<sup>1</sup>; Hörtnagl Lukas<sup>1</sup>; Eugster Werner<sup>1</sup>; Koller Patrick<sup>1</sup>; Käslin Florian<sup>1</sup>; Merbold Lutz<sup>2</sup>

<sup>1</sup> ETH Zurich, Switzerland

<sup>2</sup> ILRI Nairobi, Kenya

The magnitude of greenhouse gas (GHG) exchange between managed grasslands and the atmosphere largely depends on management practices. While natural or extensively managed grasslands are known to function as GHG sinks intensively managed grasslands are often characterized by substantial nitrous oxide (N<sub>2</sub>O) emissions and therefore act as net GHG emitters. One potential approach to mitigate N<sub>2</sub>O emissions is a decrease in fertilizer inputs by replacing the needed N input by biological nitrogen fixation via legumes. However, the effect of legumes on nitrous oxide fluxes is still uncertain. In this study we aim at quantifying net GHG fluxes from two management strategies under field conditions in relation to the productivity of the fields (yield estimates). Furthermore, we aim at revealing direct drivers of N<sub>2</sub>O exchange and developing suggestions for a more sustainable grassland management in the future.

Keywords: GHG; mitigation; N<sub>2</sub>O; grassland

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P7

## Organic wheat farming improves grain zinc concentration

Helfenstein Julian<sup>1</sup>; Müller Isabel<sup>1</sup>; Grüter Roman<sup>1</sup>; Bhullar Gurbir<sup>2</sup>; Mandloi Lokendra<sup>3</sup>; Papritz Andreas<sup>1</sup>; Michael Siegrist<sup>1</sup>; Schulin Rainer<sup>1</sup>; Frossard Emmanuel<sup>1</sup>

<sup>1</sup> ETH Zurich, Switzerland

<sup>2</sup>Research Institute of Organic Agriculture, FiBL, Switzerland

<sup>3</sup>bioRE India, India

Zinc (Zn) nutrition is of key relevance in India, as a large fraction of the population suffers from Zn malnutrition and many soils contain little plant available Zn. In this study we compared organic and conventional wheat cropping systems with respect to DTPA (diethylene triamine pentaacetic acid)-extractable Zn as a proxy for plant available Zn, yield, and grain Zn concentration. We analyzed soil and wheat grain samples from 30 organic and 30 conventional farms in Madhya Pradesh (central India), and conducted farmer interviews to elucidate sociological and management variables. Total and DTPA-extractable soil Zn concentrations and grain yield (3400 kg ha<sup>-1</sup>) did not differ between the two farming systems, but with 32 and 28 mg kg<sup>-1</sup> respectively, grain Zn concentrations were higher on organic than conventional farms ( $t = -2.2$ ,  $p = 0.03$ ). Furthermore, multiple linear regression analyses revealed predictors of a) DTPA-extractable soil Zn, b) wheat yield, and c) grain Zn conc.

Keywords: interdisciplinary farming systems comparison; biofortification; wheat; zinc deficiency; farmer interviews

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P8

## Does Arabidopsis regulate protein levels by differential translation or protein degradation?

Ihmor Phillip<sup>1</sup>; Gruissem Wilhelm<sup>1</sup>; Robinson Mark<sup>2</sup>; Baerenfaller Katja<sup>1</sup>

<sup>1</sup> ETH Zurich, Switzerland

<sup>2</sup>University of Zurich, Switzerland

Stimuli induce tightly regulated changes in protein levels. Many studies rely on transcriptional data as a proxy for these changes, although protein and transcript dynamics correlate only moderately. Clearly, this is caused by further regulatory mechanisms at the level of translation and degradation. In our study, we quantified Arabidopsis' non-transcriptional response to biotic stress in a combinatorial multi-omics approach. We obtained 4 quantitative time-courses data sets on 1) transcription with RNA-Seq, 2) translation with Ribo-Seq, 3) protein abundances with SILAC-MS, and 4) protein degradation with pulse-chase dynamic SILAC-MS. All data were obtained from the identical Arabidopsis cell culture, which got treated with either a mock solution or with flg22, a well-described bacterial PAMP. The individual data sets show substantial genome-wide gene expression regulations, but only their combinations show the truly interesting post-transcriptional regulatory pattern.

Keywords: translation; degradation; protein turnover; half life; ribo-seq; systems biology

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P9

## Chromosome-level assembly of farmer preferred cassava varieties using single – molecule sequencing (SMRT) technology and Chromosome-Conformation Capture

Kuon Joel<sup>1</sup>; Qi Weihong<sup>2</sup>; Gruissem Wilhelm<sup>1</sup>; Vanderschuren Hervé<sup>3</sup>

<sup>1</sup> ETH Zurich, Switzerland

<sup>2</sup>Functional Genomics Center Zurich, Switzerland

<sup>3</sup>University of Liège, Belgium

Cassava is an important food security crop for the poorest communities in sub-Saharan Africa. Here we present a high quality de novo genome assembly of farmer preferred cassava varieties. Through the combination of SMRT PacBio sequencing and high-throughput chromosome conformation capture sequencing (Hi-C), three cassava genomes have been sequenced and assembled to a high degree of completeness. Starting with 7.13 million PacBio reads, we integrated the FALCON assembler and the Quiver genome finishing tool to produce assemblies each composed of approximately 5700 contigs with a contig N50 size of 212 Kb. The genomes were scaffolded with the composite genetic map of African cassava varieties. Finally, cis-chromosome associations were determined by Hi-C, yielding complete reconstructions of all 18 chromosomes into single scaffolds. The three new high quality assemblies enable novel comparative insights into the genome evolution of cultivated African cassava varieties.

Keywords: genomics; PacBio; cassava; HiC

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P10

## The pleiotropic phenotype of a *Bradyrhizobium diazoefficiens* $\Delta$ ecfG mutant under free-living and symbiotic conditions

Ledermann Raphael<sup>1</sup>; Müller Barbara<sup>1</sup>; Wülser Janine<sup>1</sup>; Couzigou Jean-Malo<sup>1</sup>; Michel Anja<sup>1</sup>; Vorholt Julia A.<sup>1</sup>; Fischer Hans-Martin<sup>1</sup>

<sup>1</sup> ETH Zurich, Switzerland

The general stress response (GSR) in  $\alpha$ -proteobacteria regulates responses that result in decrease of stress-induced damage. Typically, the GSR confers cross-protection by integrating a variety of different stress signals. Core elements of the response involve the  $\sigma$ -factor EcfG, its cognate anti- $\sigma$ -factor NepR and the anti-anti- $\sigma$ -factor PhyR. Previously it was shown that a *B. diazoefficiens*  $\Delta$ ecfG mutant is more susceptible to stresses, and the symbiotic interaction of this mutant with soybean is impaired. We have performed a detailed phenotypic characterization of the  $\Delta$ ecfG mutant under symbiotic conditions. We found that the symbiotic defect of the mutant is first manifested by the restricted formation of infection threads. Also, mutant strains lacking components of the upstream signaling cascade to PhyR were constructed and tested under symbiotic conditions. Preliminary results indicate functional redundancy in the sensing segment of the GSR network.

Keywords: legumes; symbiosis; nitrogen; *bradyrhizobium*

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P11

## Natural variation, molecular determinants and genetic engineering of vitamin B6 biosynthesis in staple crops

Mangel Nathalie<sup>1</sup>; Fudge Jared<sup>2</sup>; Li Kuan-Te<sup>1</sup>; Moulin Michael<sup>2</sup>; Albersen Monique<sup>3</sup>; Verhoeven-Duif Nanda<sup>3</sup>; Ma Qiuxiang<sup>4</sup>; Zhang Peng<sup>4</sup>; Wu Ting-Ying<sup>1</sup>; Takayuki Tohge<sup>5</sup>; Fernie Alisdair<sup>5</sup>; Szurek Boris<sup>6</sup>; Fitzpatrick Teresa<sup>2</sup>; Gruissem Wilhelm<sup>1,4</sup>; Vanderschuren Hervé<sup>7</sup>

<sup>1</sup> ETH Zurich, Switzerland

<sup>2</sup> University of Geneva, Switzerland

<sup>3</sup> University Medical Center Utrecht, The Netherlands

<sup>4</sup> SIBS-ETH Shanghai Center for Cassava Biotechnology, China

<sup>5</sup> Max-Planck-Institute for Molecular Plant Physiology, Germany

<sup>6</sup> Institut de Recherche pour le Développement, France

<sup>7</sup> University of Liège, Belgium

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Vitamin B6, primarily derived from plant sources, is a vital metabolic cofactor in several key enzymatic reactions. Humans cannot synthesize it and therefore need to acquire this compound from their diet. Acute deficiency in vitamin B6 is associated with various chronic diseases, particularly in developing countries where populations often do not have diverse diets and access to supplementation strategies. Cassava and rice rank amongst the five most produced food crops in the world and constitute the most important sources of calories in tropical and subtropical regions. However, both crops contain insufficient levels of vitamin B6 to meet human daily requirements in populations heavily relying on these crops in their diet. In order to improve the nutritional quality of these two major staple crops, we investigated natural diversity and molecular determinants of vitamin B6 accumulation in cassava and rice, and increased vitamin B6 content in both crops via genetic engineering.

Keywords: rice; staple food crop; natural diversity; pyridoxine; vitamin B6; vitamers; genetic engineering; bioavailability; dietary sufficiency; cassava; rice; crop; diversity; pyridoxine; vitamin; vitamer; engineering; bioavailability; sufficiency

P12

## Lab to field - engineering geminivirus resistance in cassava

Mehta Devang<sup>1</sup>; Gruissem Wilhelm<sup>1</sup>; Vanderschuren Hervé<sup>2</sup>

<sup>1</sup> ETH Zurich, Switzerland

<sup>2</sup> University of Liège, Belgium

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Cassava is a starchy, root crop that forms a staple food for an estimates 800 million people globally. The majority of all cassava production occurs in Africa where it is grown for domestic food consumption, industrial starch and biofuel production. However, in Africa, cassava production is constrained by the cassava mosaic disease (CMD). Caused by cassava mosaic geminiviruses (CMGs), this disease leads to severe yield losses averaging 28% annually, and in some cases causes complete harvest loss. Various transgenic approaches to combat this disease have been developed in labs across the globe, but these approaches have not yet been validated in field settings. We have recently completed a confined field trial of first generation virus-resistant transgenics in Kenya, and are developing new strategies to engineer geminivirus resistance. In this poster we present results from the field trial and new synthetic biology technologies under development for virus resistance.

Keywords: transgenic; cassava; field; virus; resistance; RNAi; PACBIO; CRISPR/Cas9

P13

## Investigating the molecular mechanism behind the self-incompatibility response in grasses

Pellegrini Marina<sup>1,2</sup>; Manzanares Chloe<sup>1</sup>; Thorogood Danny<sup>2</sup>; Bosch Maurice<sup>2</sup>; Studer Bruno<sup>1</sup>

<sup>1</sup> ETH Zurich, Switzerland

<sup>2</sup> Aberystwyth University, United Kingdom

Angiosperms evolved genetically determined self-incompatibility (SI) mechanisms which prevent selfing and inbreeding depression. The molecular mechanisms regulating SI are highly divergent between families. In the grasses (*Poaceae*), it was shown that SI is controlled by two multi-allelic loci, S and Z. Gene candidates for S and Z pollen and stigma components have been identified in perennial ryegrass (*Lolium perenne* L.). We aim to understand how S and Z interact by performing a functional characterisation of SI genes in *Lolium*. RNAi will be used to knockdown expression of gene candidates. Temporal and spatial expression of these genes will be studied to deduce the synergistic activity of S and Z. Mutants will be identified from a TILLING population and protein interactions will be investigated. Knowledge of SI systems will facilitate breeding programmes and simplify the production of hybrids and thus the exploitation of heterosis for the generation of superior fodder crops.

Keywords: Perennial ryegrass (*Lolium perenne* L.); self-incompatibility; RNAi; TILLING

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P14

## Elucidating the molecular basis for the role of protein degradation in defence response

Petersen Sebastian<sup>1</sup>; Gruißem Wilhelm<sup>1</sup>; Bärenfaller Katja<sup>1</sup>

<sup>1</sup> ETH Zurich, Switzerland

Protein levels inside cells are partly regulated by specific protein degradation by the Ubiquitin-26S proteasome system (UPS). This system is large and complex, occupying nearly 6% of the coding capacity of the *A. thaliana* genome. The largest class of proteins involved in the UPS are the E3 ubiquitin ligases, which are responsible for mediating the transfer of the activated ubiquitin to the respective target proteins. The plant U-box E3s (PUBs) are a class of E3s that are considered to be important in mediating plant-specific processes. Several of the PUBs in *Arabidopsis* have been associated with a role in defense response, but few target proteins could be identified so far. Using different pub mutant *Arabidopsis* lines coupled with protein-protein interaction detection assays (TAP- & BioID) and methods to identify the sites of ubiquitylation we aim to elucidate the molecular basis of different PUBs in defense response, and to gain novel insight into this biological process.

Keywords: proteasome; ubiquitin; defense-response

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P15

## Recreating the synthesis of starch granules in yeast

Pfister Barbara<sup>1</sup>; Sánchez-Ferrer Antoni<sup>1</sup>; Diaz Ana<sup>2</sup>; Lu Kuanjen<sup>1</sup>; Zeeman Samuel C.<sup>1</sup>

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32 Starch is the major nutritional component of our staple crops and a feedstock for industry. It is composed of glucose polymers that form massive semi-crystalline granules. Its precise structure and composition determine its functionality and thus applications; however, there is no versatile model system allowing the relationships between the biosynthetic apparatus and glucan properties to be explored. Here, we expressed the core *Arabidopsis* starch-biosynthesis pathway in *Saccharomyces cerevisiae* purged of its endogenous glycogen-metabolic enzymes. Systematic variation of the set of biosynthetic enzymes illustrated how each affects glucan structure and solubility. Expression of the complete set resulted in dense, insoluble granules with a starch-like semi-crystalline organization, demonstrating that this system indeed simulates starch biosynthesis. Thus, the yeast system has the potential to accelerate starch, providing a basis for the targeted biotechnological improvement of crops.

Keywords: starch; amylopectin; *Arabidopsis thaliana*; *Saccharomyces cerevisiae*

P16

## Development of high energy red clover

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33 Red clover (*Trifolium pratense* L.) is one of the most important forage legumes worldwide for feeding ruminant livestock. Although red clover has a relatively high biomass potential, it lacks the high-energy carbohydrates required to meet the productivity potential of modern livestock breeds. Therefore, forage-based diets are supplemented with high-energy corn, cereals and soy that are often derived from unsustainable foreign supply chains. Although, red clover accumulates starch in its leaves during the day as a temporary carbon store of photosynthesis, leaf starch content has yet to be exploited as an agronomic trait in forage crops. By characterizing leaf starch content in red clover, we found it has the genetic potential to accumulate up to one third of its dry mass as starch. Here we proposed a strategy to exploit this energy content as a trait. Such a trait would provide a feed source to improve the economic and environmental sustainability of ruminant livestock production.

Keywords: forage; starch; livestock

P17

## In silico identification of candidate genes for fertility restoration in cytoplasmic male sterile perennial ryegrass (*Lolium perenne* L.)

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Cytoplasmic male sterility (CMS) is a widely applied mechanism to control pollination for hybrid seed production. CMS systems have been identified in perennial ryegrass but they are yet to be fully characterised. We have developed a bioinformatics pipeline for efficient detection of candidate *restorer of fertility* (*Rf*) genes for CMS. From a draft of the perennial ryegrass genome, 25 *restorer of fertility-like pentatricopeptide repeat* (*RFL*) genes were identified. These *RFL* genes were further investigated identifying three clusters of perennial ryegrass *RFLs*. These three groups likely represent genomic regions of active *RFL* generation and identify the probable location of perennial ryegrass *PPR-Rf* genes. This pipeline allows for the identification of candidate *PPR-Rf* genes from genomic sequence data and can be used in any plant species. This will facilitate map-based cloning of *Rf* genes and enable the use of CMS as an efficient tool to control pollination for hybrid crop production.

Keywords: cytoplasmic male sterility (CMS); hybrid breeding; pentatricopeptide repeat (PPR) proteins; perennial ryegrass (*Lolium perenne* L.); restoration of fertility; *restorer of fertility-like PPR* (*RFL*)

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P18

## Leaf transcriptomics reveals differing responses of *Arabidopsis* to colonization by ubiquitous phyllosphere colonizers with potential implications for plant health upon pathogen encounter

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Plants are colonized by a variety of microorganisms, the plant microbiota. We examined the transcriptional response of *Arabidopsis thaliana* leaves to colonization by representatives of the bacterial phyllosphere core microbiota in a gnotobiotic system. *Arabidopsis* responded differently to colonization by the model bacteria *Sphingomonas melonis* Fr1 and *Methylobacterium exotruquens* PA1. Whereas PA1 only marginally affected the expression of plant genes, Fr1 colonization changed the expression of almost 400 genes. The transcriptional response to Fr1 partly overlapped with the one elicited by the pathogen *Pseudomonas syringae* DC3000. As Fr1 is known to confer protection against *P. syringae*, we tested whether plant protection is affected in different plant hormone signaling and immune system mutants. Our experiments demonstrate that the plant responds to its microbiota and a subset of commensals may increase expression of defense-related genes and contribute to plant health and performance.

Keywords: biocontrol; commensals; protection; transcriptomics; microbiota

35

P19

## Starch modification in staple crops

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Starch is the most widespread and abundant storage carbohydrate in plants. Based on the study of starch metabolism in model plant *Arabidopsis thaliana*, fundamental knowledge about how plants make and degrade starch has been obtained. This knowledge could be utilized to improve our staple crops. Here we focus on two crops: *Eragrostis tef* (tef) and *Manihot esculenta* Crantz (Cassava). Tef is the main cereal crop in Ethiopia, which is able to tolerate adverse conditions compared with rice and wheat. However, it has low yield and lacks diversity in its grain properties. The aim of this project is to modify the starch properties in seeds to diversify its functionality.

Cassava is an important starch crop in the tropics and subtropics also used in paper manufacturing. As starch with high phosphate level is desired in paper making, my second project focuses on the modification of starch phosphorylation in cassava storage roots.

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P20

## Novel strategy for iron biofortification of rice with focus on iron trafficking in grain

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Iron deficiency is a serious problem affecting around 30% of world's population. To address this issue, iron-biofortified rice has been considered as a possible and solution. However, there is less evidence on engineering intracellular iron transporter to enhance grain iron content. The vacuoles serve as essential cell compartments for metal storage. The member of the NRAMP family is suggested to play a central role in exporting iron from the vacuoles to cytosol. In this study, we expressed *AtNRAMP3* in combination with *AtNAS1* and *PvFER* to improve iron intracellular translocation together with iron transport and storage in rice grains. Iron content of up to  $12.67 \pm 0.32 \mu\text{g/gDW}$  was obtained in the polished grains, with no increases observed for cadmium in transgenic plants. Moreover, we demonstrated that the transgenic plants enhanced the tolerance against low iron condition. Combination of *AtNRAMP3*, *AtNAS1* and *PvFER* is therefore a valuable strategy for iron biofortification programs.

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Keywords: rice; biofortification; iron; *AtNRAMP3*; *AtNAS1*; *PvFER*

## Poster abstracts

University of Zurich

P21

## Environment-dependent homeolog expression in an allopolyploid in *Cardamine flexuosa*

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40 Whole genome duplication (polyploidy) is pervasive in plants. Little is known about ecology and genomics of allopolyploids (polyploids originated from different parental species) in field, including their habitat environment and whether they exhibit environmental-dependency in gene expression and expression ratio of homeologs (sets of genes derived from the different parental species). We found that an allopolyploid *Cardamine flexuosa* occurred along soil moisture gradient and coexisted with either of the parental species in dry or wet extremes in native areas in Switzerland. Total expression level and the ratio between homeologs of known water-responsive genes differed between habitats. Furthermore, the pattern of expression varied at different time points. The results suggest that *C. flexuosa* utilises homeologs in response to environmental fluctuation, and that the genus *Cardamine* is a useful system to study the molecular basis of adaptive significance of allopolyploidy in wild plants.

Keywords: allopolyploid; homeolog expression ratio; RNA-seq; *Cardamine*; habitat environment; field observation

P22

## Altered expression of *Lr34* in barley mediates resistance without negative effects

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41 Plant diseases are a serious threat to crop production. The most promising strategy to reduce yield losses caused by plant pathogens is through exploiting disease resistance mechanisms. *Lr34* is a durable resistance gene from wheat that confers partial resistance to several fungal pathogens. *Lr34* was stably transformed into barley and was shown to be functional. The *Lr34*-resistance is accompanied by a senescence-related phenotype known as leaf tip necrosis. *Lr34* is active at adult stage in wheat but highly expressed in barley already at seedling stage. Transgenic barley plants are strongly affected in growth vigor and seed production. Here we present data that altered expression of *Lr34* does avoid these negative effects while maintaining *Lr34*-mediated resistance. We fused the pathogen-inducible *Ger4c* promoter to *Lr34* and analyzed regarding resistance to leaf rust and powdery mildew. Growth parameters were assessed under standard glasshouse and semi-field conditions.

Keywords: *Lr34*; resistance

P23

## Characterization of *rol* genes or factors and their role in cell wall development in *Arabidopsis thaliana*

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The cell wall that surrounds each plant cell is one of the major factors for plant growth and development and largely determines cellular morphogenesis. A family of cell wall specific proteins called LRX (LRR-extensin) were found to be associated with proper cell wall development. The *lrx1* mutant develops aberrant root hairs which frequently abort, swell, or branch. During whole genome sequencing, a number of *rol* mutants were identified which suppress the *lrx1* mutant phenotype. The aim of this project is to functionally characterize four *rol* mutants (*rol16* and *rol23*) and investigate their role in cell wall development. The identification of mutations and co-segregation analysis have led to the identification of candidate genes in these *rol* mutants, which most likely cause suppression of the *lrx1* mutant phenotype. Some of them are potentially functionally linked to LRX1 and/or its regulation and might, thus, help us to understand the function of LRX1 in cell wall.

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P24

## Adaptive reduction of male gamete number in a selfing species

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The number of male gametes is critically important for reproductive success, and its reduction in response to recent breeding-system changes has been reported in both plants and animals. However, little is known about the molecular basis of this quantitative trait. Through a genome-wide association study of pollen number in the predominantly selfing model plant *Arabidopsis thaliana*, we identified the *GENJI* (*GEN1*) gene to be associated with variation in male gamete number. Analyses of *gen1*-null mutants in standard and nonstandard accessions generated using the CRISPR-Cas9 system revealed that the natural variants affect cell proliferation in the male germline. Signatures of selective sweeps at *GEN1* and other loci underlying pollen number variation support an adaptive role of male gamete reduction in recent evolutionary time.

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Keywords: pollen number; GWAS; *Arabidopsis thaliana*; CRISPR/Cas9

P25

## The importance of strigolactone transport in plant nutrient uptake and biomass production

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44 Strigolactones (SL) are newly discovered carotenoid-derived phytohormones. They play a plethora of functions in plant architecture formation and development. For instance, SLs were characterized to regulate bud out growth, leaf senescence, lateral root and adventitious root formation, plant-rhizosphere interactions. In a previous work, we identified an ABC transporter (PDR1) from *Petunia hybrida* as a cellular SL exporter, which is present in the plasma membrane of hypodermal passage cells (HPCs). HPCs are the cells through which SLs are exuded to the soil and the entrance points for mycorrhizal fungi into the plant. Intriguingly, our results indicate that PDR1 and hormones regulate the identity and/or maintenance of HPCs. What's more important is that we found SLs to be crucial for the uptake of some nutrients, e.g., Magnesium. Moreover, our results demonstrated that the overexpression of PDR1 results in increased SL exudation to the rhizosphere and leading to a faster mycorrhization, which finally resulted in a significant raising of plant biomass under low nutrient condition. This could be a promising approach to improve plant nutrient uptake on barren ground, at least for certain plant species.

Keywords: strigolactone; transporter; plant-nutrition; mycorrhization

P26

## Tissue morphodynamics of *Arabidopsis* and *Oryza* ovules using light sheet microscopy

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45 One of the unresolved questions in Plant Developmental Biology is to understand how plants initiate germline differentiation from somatic, floral tissue. At the tip of the ovule primordium inside the carpel of the flower, a single sub-epidermal cell undergoes the somatic to reproductive fate transition and forms a spore mother cell (SMC). To elucidate the role of tissue patterning and positional information in SMC specification, we aim at establishing a morphodynamic atlas of cell division and elongation in the developing ovule primordium in *Arabidopsis* and *Oryza* (rice), a dicot and monocot (crop) model system, respectively. Currently, the development of ovules ex planta is not possible impeding on live imaging. Yet, we use light sheet microscopy to record static images of ovule primordia in whole-mount carpels sampled at consecutive time points to collect replicates at large scale.

Keywords: ovule; morphodynamics; LSFM

P27

## Mechanistic of sex: Lessons from *Arabidopsis* pollen mutants

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46 During sexual reproduction pollen tubes (PT), conveying sperm cells to the ovule, exert invasive forces on the female reproductive tissue by establishing a fine balance between turgor pressure and cell wall elasticity. The fine-tuning of the mechanics for invasive growth remains an unelucidated subject. Here we combined a range of techniques to study PT mechanics and simulate growth in the *xtt1 xtt2* and *LRR-Extensin (lrx)* mutants. TEM and biochemical studies revealed striking ultrastructural differences between wild-type and mutant PT cell walls. CFM and FEM analyses of mechanical properties revealed three key biomechanical criteria relevant to predict growth: (i) the absolute values of, (ii) the ratio between, and (iii) the variations in turgor pressure and cell wall elasticity. These results provide new biomechanics explanatory concepts for PT invasive growth during sexual reproduction, and new possibilities to explain cell growth dynamics within vegetative tissues.

Keywords: cell; wall; turgor; young's; modulus; TEM; CFM; FEM

P28

## Unravelling traits contributing to salinity tolerance in *Arabidopsis thaliana* using high-throughput phenotyping

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47 Major developments in high-throughput phenotyping systems have made possible to capture plant traits in a non-invasive way, facing the phenotyping bottleneck. In the context of changing climate conditions, salinity tolerance represents a critical abiotic stress tolerance trait. Using high-throughput non-invasive imaging platform developed at the Photon Systems Instruments (PSI, Czech Republic), we established a quantitative phenotyping protocol suitable for investigating early stress responses to salinity stress of soil-grown *Arabidopsis thaliana*. RGB and kinetic chlorophyll fluorescence imaging revealed that salinity stress significantly affects growth-related parameters, leaf color index and photosystem II efficiency. The data presented are one of the first successful examples of integrative approach, in which the simultaneous analysis of different phenotypic traits by multiple sensors provides insights into the dynamics of plant responses to environmental stress (Awlia et al, 2016).

Keywords: *Arabidopsis thaliana*; high-throughput phenotyping; salinity tolerance; sugars

P29

## Zinc hyperaccumulation, differential expression and diversity in the allopolyploid *Arabidopsis kamchatica*

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48 A feature that makes gene duplication through allopolyploid hybridization (diploid hybridization without chromosome reduction) interesting compared to that of autopolyploidization (autosomal duplication within a single diploid ancestor) is that homeologous copies are not ancestrally identical but have unique evolutionary histories as a result of each diploid progenitor's evolution and their respective adaptations. Ancestral gene copies therefore have the potential to result in the retention of phenotypes that were present in either of these parents. Using a newly developed bioinformatics pipeline to separate homeologous RNAseq reads, we have demonstrated that zinc accumulation in *A. kamchatica* is largely the result of transcriptional patterns and polymorphism derived from the diploid hyperaccumulating ancestor *A. halleri* despite hybridization with a non-accumulating *A. lyrata* ancestor.

Keywords: allopolyploid; homeolog; hyperaccumulation; metaltolerance; evolution; diversity

P30

## The effect of the TOR (target of rapamycin) pathway on cell wall development

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49 The target of rapamycin (TOR) signaling network integrates information on nutrient availability and growth factors to modulate cell growth. Its central coordinator, the TOR kinase, is specifically inhibited by rapamycin and other TOR-specific inhibitors. In a previous study it has been shown that modulation of the TOR kinase activity leads to changes in the plant cell wall structure. Since knock-out mutations in the *TOR* gene are embryo lethal, the application of alternative strategies is required for functional genetic studies of this crucial protein and the signaling pathway connected to it. In former studies RNAi silencing lines and overexpression lines have been used to alter the *TOR* gene expression. The aim of this study is to investigate the function of the TOR kinase / TOR pathway in regulating carbon partitioning and cell wall development. This will be analyzed by modification of the TOR activity with the help of newly identified tor alleles.

P31

## Composition and evolution of Beta-amylases in green plants

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50  $\beta$ -Amylases are key enzymes of plastidial starch turnover and have been extensively studied in the model plant *Arabidopsis thaliana*. However, little is known about their function in other species. To determine the level of conservation amongst different species we analysed the  $\beta$ -amylases of 111 land plants. Despite overall high conservation, our analysis revealed clear differences between *Arabidopsis* and many crop plants. Notably, a novel subgroup of  $\beta$ -amylases which is absent in *Arabidopsis* was found in virtually all angiosperms and gymnosperms, except the *pinaceae* family. Conversely, we found that BAM4 – an essential protein in *Arabidopsis* – is not found in many important crops species, including all cereals. Moreover, duplications of  $\beta$ -amylases were observed in many species or even whole families, indicating sub- and neofunctionalisation of those genes.

Keywords: evolution; phylogeny; starch

P32

## A cultivar-specific long-range chromosome assembly enables rapid isolation of a disease resistance gene in hexaploid wheat

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51 Isolation of agriculturally important genes in cereals is hampered by their large and complex genomes. Moreover, gene order and content, as well as gene sequences can differ dramatically between cultivars of same species and this represented one of the major obstacles for gene isolation projects in the past. Here, we combined a lossless genome complexity reduction with Chicago long-range linkage to rapidly and inexpensively generate a high quality de novo assembly harboring the broad-spectrum *Lr22a* leaf rust resistance gene from wheat. We identified a single 6.39 Mb scaffold that contained both *Lr22a* flanking markers. *Lr22a* was validated as intracellular immune receptor with homology to the Arabidopsis RMP1 protein using five EMS mutants that lost the *Lr22a*-activity. Our study demonstrates that it is now feasible to develop high-quality de novo assemblies for genomic loci of interest even in species with complex genomes to facilitate cloning of agriculturally important genes.

Keywords: *Lr22a*; wheat; chicago long-range scaffolding; de novo assembly

P33

## ***Lycium* spp. : A cross-cultural study of its use as medicine and food**

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Many species of the genus *Lycium* have been widely used as medicine in Asian countries for thousands of years, while nowadays some are also advertised as superfood in Europe and America. However, the history of their uses are unclear, as well, the knowledge evolution under a cross-cultural background is missing. This study aims to reveal the use history of *Lycium* spp. by the existing herbals, including the historical traditional Chinese medicine herbals, ethnic herbals and herbals in an international scale, as well as local legends. Therefore, we find that *Lycium* spp. has a medical use history of around 2000 years, and its food use history is ca. 1500 years. Usages diversified along the time goes. The used species, plant parts and usages differ under different culture background. Nowadays, they are accepted in many countries as medicine, but with different quality criterion. The folk legends may deliver the similar traditional knowledge as the herbals.

Keywords: *Lycium*; traditional medicine; ethnobotany; cross-cultural; healthy food

P34

## **Loss of self-incompatibility in the allotetraploid *Arabidopsis kamchatica* by degradation of the male component**

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Polyploids, which are commonly found in plants, are suggested to self more frequently than their diploid relatives, although the underlying mechanism is still largely unknown. Here, we study the loss of self-incompatibility (SI) in *Arabidopsis kamchatica*, which is a self-compatible allotetraploid species, originated through allopolyploidization between two predominantly outcrossing diploid species, *Arabidopsis halleri* and *Arabidopsis lyrata*. We applied high-throughput sequencing to isolate the male component, *S-locus cysteine-rich protein* (*SCR*) genes. Moreover, transgenic method was developed to transform functionally restored *SCR* into *A. kamchatica* bearing functional female components. SI was recovered in transformed *A. kamchatica*, indicating that the degradation of *SCR* is primarily responsible for the loss of SI in *A. kamchatica*. Moreover, dominance hierarchy among different S-haplogroups may be involved in the evolutionary loss of SI in allotetraploid *A. kamchatica*.

Keywords: allopolyploid; self-incompatibility; transgenic

## **Poster abstracts**

**University of Basel**

P35

## Stem diameter variations of six temperate European forest tree species reflect the species' water status

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56 Assessing a trees' stem water potential is essential to evaluate its performance during drought. However, for mature trees it is extremely hard to monitor water potential throughout the growing season because of the difficulty of canopy access. Daily variations of stem diameter (SDV) could provide a powerful alternative. SDV have been shown to incorporate both radial growth and the diurnal shrinkage and swelling of bark tissue at a time. During dry periods, bark tissue that is depleted in water cannot entirely refill at night, leading to a progressive overall shrinkage of the tree's stem diameter allowing to calculate values for tree water deficit (TWD). Comprehensive tests, if SDV-based values for TWD reflect values for a tree's stem water potential are yet missing. We calculated an SDV-derived TWD for six Central European forest tree species during one moist (2014) and one exceptionally dry (2015) growing season and compared these values to the trees' stem water potential.

Keywords: tree water deficit; drought; water relations; stem shrinkage

P36

## Seasonal droughts and their different effects on grassland productivity

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57 The effects of drought events on ecosystem functions are of high interest. Grassland productivity follows a distinct seasonal pattern with high biomass productivity at the time of flowering and lower productivity during vegetative growth. If the sensitivity of grassland productivity to drought varies throughout the growing season remains, however, unclear. To test the effects of drought events that occur at different times of the growing season on grassland productivity we installed a large field experiment where we simulated drought events in three seasons (spring, summer, fall) and determined the effects on productivity of different European grassland species. We designed our experiment with six harvests evenly distributed over the entire growing season allowing us to disentangle (i) immediate drought effects on the productivity and (ii) effects of seasonal droughts on the productivity over the entire growing season.

P37

## Century long assessment of herbaceous plants' physiological responses to climate change in Switzerland

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The isotopic analysis of archived plant material offers the exceptional opportunity to reconstruct the physiological activity of plants over long time periods and thus, to assess plant responses to environmental changes during the last centuries. In addition, the stable isotope analysis of herbarium samples offers the opportunity to reconstruct the physiological processes of a large range of different plant species and from different environments. Interestingly, only few studies have to date assessed these archives. We will present a novel analysis of leaf nitrogen and carbon isotope ratios of more than a thousand herbarium specimen from the unique herbaria hold at the University of Basel. The objective of our study was to assess century-long physiological responses of herbaceous plant species to climate change and to test if these responses differ in different plant functional groups and in plants that live in different habitats across Switzerland.

Keywords: isotopes; herbarium; water relations; nitrogen

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P38

## The influence of snow cover duration on plant phenology

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The growing season of alpine plant species is controlled by the duration of snow cover. At the same time snow acts as an insulation layer for the vegetation and soil during cold winter months and allows for soil processes to continue beneath it. Photoperiodism can prevent plants from profiting from prolonged season lengths due to earlier snow cover release and from nutrient release during snowmelt. Delayed snowmelt on the other hand shortens the length of the growing season and time for reproduction. In a unique snow and precipitation manipulation experiment in alpine grassland, the influence of advanced and delayed snow melt on plant phenology was assessed at seven times during the growing season. A first analysis of the results revealed different responses of functional groups to advanced / delayed snowmelt. While differences in phenology of graminoids were observable mostly at the beginning of the growing season, for forbs these differences persisted until later in the season. Legumes did not react to shifted snowmelt dates.

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P39

## Controls of carbon reserves in temperate trees at long-term carbon limitation

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Non-structural carbohydrates (NSC, i.e. free sugars and starch) are regarded as freely available carbon (C) reserves in plants. They are often quantified to estimate a plant's C-balance, assuming that NSC are controlled by the net-balance between photo-assimilation and C-usage (respiration, growth and other sinks). Within this project, we investigate the extent to which C-reserves (NSC) can be formed against prevailing C-sink demands under C-limitation. We use permanent shading on tree saplings to test, if C-storage in tree saplings can occur in competition with sinks. After three months exposure to only 5 % of full sunlight, trees show a reduction in stored C, but no reduction in sink activities (yet). Photosynthesis shows strong acclimatization to the low light conditions. NSC concentrations follow the C-source-sink balance during the first half of the growing season, but they might be actively up-regulated against C-sinks in the following seasons.

Keywords: sugar; starch; forest; storage; sink; respiration; NSC

P40

## Linkage of root morphology to anatomy with increasing nitrogen availability in six temperate tree species

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Responses of fine root morphological traits, such as diameter, to soil nitrogen (N) enrichment showed large discrepancies among tree species in forest ecosystems, but the reason for this remains unclear. We installed in growth cores in six plantations, *Juglans mandshurica* Maxim., *Fraxinus mandschurica* Rupr., *Phellodendron amurense* Rupr., *Larix gmelinii* Rupr., *Pinus koraiensis* Sieb., and *Picea koraiensis* Nakai, in northeastern China. After fertilization with N, we sampled root tips (i.e., first-order roots) from two soil depths (0–10 cm, 10–20 cm) and analyzed the association of variabilities of morphological traits with anatomical traits among tree species in the context of increasing soil N availability. In the surface soil layer, N fertilization significant increased root diameter and stele diameter, and significant decreased specific root length in all species, but the changes of cortical thickness after N fertilization varied with species. The increment of root diameter after N fertilization close related with the increments of stele diameter and cortical thickness, and can explained 82% and 65% variations of root diameter, respectively. But these effects in the subsurface were not observed. The changes in fine root morphological traits such as diameter after N fertilization were strongly associated with changes of anatomical traits in woody plants.

Keywords: conifers; hardwoods; ingrowth core; nitrogen fertilization; root tips; root form and function

## **Poster abstracts**

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## Genomic tools to assess biodiversity in grasslands

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Grasslands are ecosystems of great natural and societal importance. They cover more than 40% of Earth's land, making them important nutrient sources and sinks on a global scale. Multi-species pastures and meadows not only provide the basis for sustainable ruminant nutrition, but they also contribute to the maintenance of biodiversity, fulfill a range of ecological services, and harbor valuable genetic resources for the genetic improvement of forage crops. This work aims to explore and develop tools to assess the diversity within and between grassland plant species, using species specific barcode sequences and methods such as Genotyping by Sequencing. Ultimately, these tools will assist scientists and decision makers to assess the value of genetic resources in grasslands.

Keywords: genomics; biodiversity; grassland

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## Impact of *Fusarium* infections on $\beta$ -glucans in barley grains

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Barley grains can provide elevated quantities of  $\beta$ -glucans, recognized to provide benefits for health. Barley plants are also hosts for *Fusarium* pathogens, causing FHB disease and accumulating mycotoxins in grains. This study aims at investigating modifications of  $\beta$ -glucan content in grains in case of infections. For that, 6 barley varieties were infected in field trials with a DON producing strains of *F.graminearum*. Success of infection was controlled by FHB symptoms on spikes. Thousand Kernel Weight (TKW) were compared between infected and non-infected grains to evaluate changes in morphological properties of grains due to the infections. DON accumulation was measured as well as  $\beta$ -glucan content in both infected and non-infected grains. Our results indicate that  $\beta$ -glucan content decreased with infection. The decrease was correlated with TKW losses in infected grains and stronger in susceptible varieties. In grains with elevated  $\beta$ -glucan content, we detected lower DON accumulation.

Keywords: barley; fusarium-head-blight; resistance; beta-glucan; deoxynivalenol

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## Transcriptome analysis in *Fusarium* infected wheat spikes

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*Fusarium* is one of the most destructive diseases of wheat. Comparison of transcriptomes between infected and non-infected wheat spikes unravels response mechanisms against the disease. The genes and the signaling pathways involved in the early response of wheat on *Fusarium* infection have been detected in two Expressed Sequence Tag (EST) libraries from both inoculated and non-inoculated wheat spikes. Differentially expressed contigs were identified. The corresponding proteins were annotated by BLASTX against Arabidopsis and classified into 18 functional categories. Majority of genes were assigned into 2 functional groups: Proteins with binding and with catalytic activity. These groups include up or downregulated stress factors. Most of these proteins are involved in the defense response, in the regulation of programmed cell death and to prevent diffusion of the pathogen in the spike.

Keywords: *Fusarium* Head Blight; bioinformatic; transcriptomics; wheat; phytopathology

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## Landscape connectivity analysis to reduce cocoa swollen shoot virus disease (CSSVD) in Ghana

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Cocoa (*Theobroma cacao* L.) productivity in Ghana is limited by the Cocoa Swollen Shoot Virus Disease (CSSVD). Since CSSVD spreads through mealy bug (*Pseudococcidae*) vectors, fragmented landscapes may decrease CSSVD spread. However, no systematic studies on landscape connectivity have been carried out so far. The Cocoa Health and Extension Division has mapped all the cocoa areas and CSSVD presence between 2010 and 2013. Using this data, we are investigating the potential of fragmented cocoa landscapes to reduce CSSVD spread on a scale of several hundreds of thousands of hectares. Preliminary results from about 5'000 ha show that high connectivity sites (> 85% of area covered with cocoa) are highly affected by CSSVD (> 75% of cocoa area diseased) while CSSVD incidences in low connectivity sites (< 60% of area covered with cocoa) are much rarer (< 2% of cocoa area diseased). The expected results may provide crucial insights for Ghanaian policy makers to design sustainable cocoa landscapes.

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## Epigenetic variation in albino plants of *Agave angustifolia* Haw.

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68 The role of DNA methylation in albinism development during in vitro culture of *Agave angustifolia* Haw. is not completely understood. During *A. angustifolia* Haw. micropropagation process, we found three different phenotypes of: green (G), variegated (V) and albino (A). Those phenotypes do not present genome differences and each one maintains a particular degree of global DNA methylation percentage, suggesting an epigenetic control of this variation. In order to understand the role of DNA methylation in phenotypic variation, we had obtained and analyzed differentially methylated regions in the genomes of G, V and A phenotype using Methylation-sensitive Representational Difference Analysis (MS-RDA) technique, founding the genome sections that are regulated epigenetically by DNA methylation mark and those would be associated with the phenotypic variation.

Keywords: MS-RDA; variation; albinism; DNA; methylation

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## Genetic diversity of *Ramonda serbica* (*Gesneriaceae*) in Bulgaria

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69 Even though the Balkan Peninsula is a biodiversity hot spot in southeastern Europe harboring many endemic plants, very little is known about the genetic diversity of the endemics there. *Ramonda serbica* Panč. is one of the European Gesneriads occurring in this region. This species has been a subject of many studies concerning its distribution, ecology and physiology, but its genetic diversity has not been investigated to date. The populations of *R. serbica* appear to be stable, except in Bulgaria, where the subpopulations range from a few tens to a few hundreds of individuals with a tendency of declining distribution points. The current study represents the first molecular approach to describe the genetic diversity of *R. serbica* in Bulgaria. Our findings stress that it is imperative to protect the species' habitats and to avoid either exploitation or disturbance of its populations. This work was supported by EMREF Research Grant provided to G.P. by the Gesneriad Society Inc. USA.

Keywords: *Ramonda*; ISSR; diversity

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## Blue mood for superfood

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The term superfood refers to food with high levels of nutrient or bioactive phytochemicals with human health benefits. Plant traits in phytochemical production are tightly bound with the genome while modified markedly by the environmental conditions. The results of our study indicated doubled or higher increases in the accumulation of several species-specific phenolic acids or flavonoids under supplemental blue light exposure.

Keywords: blue light; LEDs; phytochemicals; superfood