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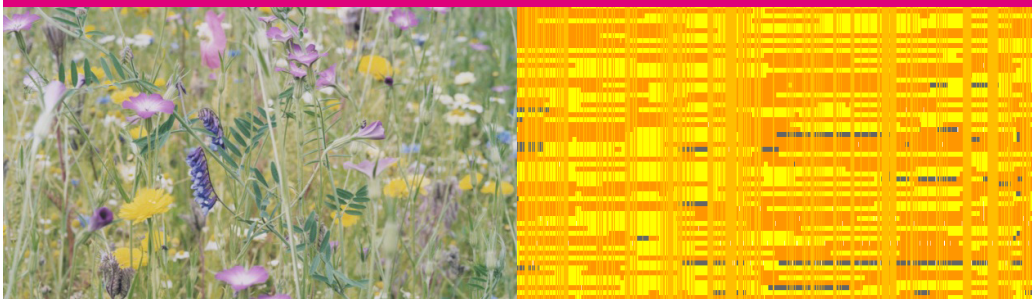
Zurich-Basel Plant Science Center

Symposium of the Zurich-Basel Plant Science Center

3 December 2015, ETH Zurich



Unlocking the potential of diversity

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Symposium of the Zurich-Basel Plant Science Center
3 December 2015, ETH Zurich

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ETH Zurich
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Rämistrasse 101, 8006 Zurich

Symposium website

→ www.plantsciences.ch/symposium

Admission is free of charge.

Program
Thursday, 3 December 2015

09.00	Opening remarks by Bernhard Schmid, University of Zurich
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	Ecole Normale Supérieure, Lyon, France
	Flower power – why and how plant science and geopolitics meet
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	Gregor Mendel Institute of Molecular Plant Biology, Vienna, Austria
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10.10	Michael Lenhard
	Potsdam University, Germany
	Evolution of flower morphology after the outbreeding-to-selfing transition in Capsella
10.40	Alex Widmer
	ETH Zurich & Zurich-Basel Plant Science Center, Switzerland
	Genetic diversity and adaptation in natural populations
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	Wageningen University, The Netherlands
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	Universidad Rey Juan Carlos, Mostoles/Madrid, Spain
	Linking plant diversity at multiple levels with microbial diversity and ecosystem multifunctionality in global drylands
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	Novel competitors shape plant species persistence with climate change
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15.15	Susan McCouch
	Cornell University, Ithaca, USA
	Linking genome wide association studies (GWAS) and plant breeding to better utilize natural variation in rice
15.45	John Pickett
	Rothamsted Research, Harpenden, UK
	Evidence for the wider value of diversity in plant secondary metabolism from the agro-ecological system, push-pull
16.15	Dani Zamir
	Hebrew University of Jerusalem, Rehovot, Israel
	Yield canalization in crop plants
16.45	Poster awards and concluding remarks by Samuel Zeeman, ETH Zurich, PSC president
17.00	Apéro and poster session

Symposium

Talks by invited speakers

in alphabetical order

Gerlinde De Deyn

Wageningen University, The Netherlands
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Illuminating the soil black box to unlock its potential

Soils host a tremendous biodiversity which governs functions essential for sustaining plant productivity and diversity. Decomposers in the soil ensure the release of plant growth-limiting mineral nutrients, and mutualistic symbionts can facilitate nutrient acquisition, while plant pathogens reduce plant growth. Different plant species develop different soil communities in their rhizosphere and thereby develop plant-species specific plant-soil feedback (PSF) effects that selectively suppress or stimulate the growth of specific plant species. To date, it remains hard to predict PSF effects, yet it is expected that soil biota respond to plant traits such that plant traits can be indicative for the PSF a plant develops. The development of negative PSF appears to be most common so that plant species combinations in space or time could promote plant productivity via the release of negative PSF. We tested the hypotheses that 1) plant traits indicative for high resource acquisition (high RGR, SLA, SRL, low % AMF colonisation) trade-off with more negative PSF, and that 2) the higher yield in plant species mixtures as compared to in monocultures can be (at least in part) explained by the dilution of negative PSF. We used the long-term Jena grassland biodiversity experiment, quantified plant species-specific plant traits and PSF values of 49 plant species, and related the species-specific PSF to plant species-specific relative yield and to the diversity effects in the species-rich plant communities in the field. We found that PSF across species ranged from negative to positive and that SRL and % AMF colonisation played a significantly role in PSF, even when accounting for plant functional groups. In contrast to our expectations, species with neutral to positive PSF contributed most to overyielding and to complementarity effects. These results point at the importance of beneficial soil organisms not only to support plant productivity in monoculture but also in species mixtures.

Michael Lenhard

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Evolution of flower morphology after the outbreeding-to-selfing transition in *Capsella*

A frequent evolutionary transition in flowering plants is the change from animal-mediated outbreeding to selfing. This is often accompanied by a suite of morphological and functional changes to the flowers, termed the selfing syndrome. While self-incompatible, outbreeding plants in general form large and conspicuous flowers to attract animal pollinators, derived selfing species show much smaller, less open and less attractive flowers. This phenomenon allows addressing two basic evolutionary questions: Given that leaf and flower size are controlled by a common growth-regulatory machinery, how has evolution specifically changed flower size, while keeping leaf size constant in many examples of the above transition? How constrained is the evolution of size, i.e. have the same growth-regulatory genes been modified in many cases of flower-size reduction, or are there many different genetic paths available to natural evolution to change flower size?

We are using the model genus *Capsella* (Shepherd's purse) to begin addressing these questions. In this genus, the transition from animal-mediated outbreeding to selfing has occurred at least twice, most recently from the self-incompatible *C. grandiflora* to the self-compatible *C. rubella.* Using a population of recombinant inbred lines derived from a cross between the two species, we have mapped QTL underlying the reduced flower size, flower opening and scent production in *C. rubella* compared to the ancestral *C. grandiflora*. Zooming in on individual QTL by fine-mapping has allowed identifying plausible candidate genes, some of which have been confirmed by reciprocal transformation. Population-genetic analyses are being performed to address the origin of the small-flower alleles. Also, we are using *C. orientalis*, a third species that represents an independent transition to selfing, to determine whether the same genes as in *C. rubella* have been modified to reduce flower size.

Jonathan Levine

ETH Zurich & Zurich-Basel Plant Science Center, Switzerland
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Novel competitors shape plant species persistence with climate change

Climate change can have direct effects on species phenology, ecophysiology and demography, as well as indirect effects mediated by interactions with other species, including their competitors. While previous studies have investigated how climate alters competition among species that co-occur today, some of the largest climate change impacts are likely to arise as new species enter communities through migration. These effects have so far been neglected because of uncertainty regarding the species composition of future communities, and the challenges of simulating such communities under realistic future climate scenarios. To test the effect of novel competitors on plant performance, we transplanted focal alpine species and communities of competitors along an elevation gradient in the Swiss Alps. We specifically simulated different scenarios for the competitive environment that a focal alpine species will encounter following climate change. Results showed that when the focal species failed to migrate, their performance in a warmer climate depended strongly on the identity of the community with which they competed; specifically, their growth, survival, and flowering were strongly reduced by the presence of competitors that could migrate upwards from lower elevation versus their current alpine competitors. However, community identity did not influence performance in scenarios where the focal species migrates to track climate change. These results suggest that explicitly accounting for novel competitors could underpin our ability to accurately predict species responses to climate change.

Fernando T. Maestre

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Linking plant diversity at multiple levels with microbial diversity and ecosystem multifunctionality in global drylands

Substantial research efforts are being devoted to understand how plant species richness affects ecosystem functioning and multifunctionality (the simultaneous provision of multiple functions and services by natural ecosystems). However, the links between the diversities of plants and microbes such as fungi and bacteria, which largely control key ecosystem processes such as organic matter decomposition, and their relative importance as drivers of ecosystem multifunctionality, are poorly understood in natural ecosystems. Therefore, much remains unknown on the interplay between plant diversity, microbial diversity and ecosystem multifunctionality. This is particularly true for ecosystems such as drylands (arid, semi-arid and dry-subhumid areas), which cover over 41% of the total land surface and host ~38% of the global population.

I will summarize the results of recent and ongoing studies evaluating the relationships between plant diversity, microbial diversity and multifunctionality in drylands, and how these relationships are affected by climate change drivers such as global warming and expected increases in aridity. These studies use multiple experimental approaches (manipulative and natural experiments), biotic communities (vascular plants and biocrusts dominated by mosses, lichens and cyanobacteria) and spatial scales (from local to global).

We found that the relative importance of plant diversity as driver such as plant cover or species richness as modulators of ecosystem responses to GEC drivers varies with the spatial scale considered, being more important at local and regional (~400 km) scales. At the global scale, abiotic variables such as annual temperature or aridity largely explained multifunctionality, but attributes such as species richness explained significant fractions of this variation. These effects, however, seems to be indirect and mediated by the positive effects of plant diversity on microbial diversity, which exerted a strong positive effect on multifunctionality. Overall, our results indicate that plant diversity plays a key role as a driver of ecosystem functioning in drylands, and that may partially buffer negative effects of climate change on multifunctionality.

Susan McCouch

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Linking genome wide association studies (GWAS) and plant breeding to better utilize natural variation in rice

Understanding the relationship between genotypic and phenotypic variation lies at the heart of the study of genetics and is also critically important to applications in plant breeding. Here we present a genome-wide association study (GWAS) based on genotyping a rice diversity panel with a high-density SNP array and systematically phenotyping the panel for a range of agronomic, physiological and morphological traits. Seeds conserved in global germplasm repositories, including wild rice ancestors, ancient landrace varieties and modern elite cultivars provide insight into a wide range of natural genetic variation that remains underutilized in modern rice genetics and breeding. Using high throughput sequencing and genotyping technologies, we examine genome-wide patterns of variation and document deep sub-population structure within *Oryza sativa*. We use GWAS to identify common variants influencing complex traits and demonstrate heterogeneity of genetic architecture across subpopulations and environments. This work establishes an open-source translational research platform for genome-wide association studies in rice that directly links molecular variation in genes and metabolic/regulatory pathways with the germplasm resources needed to accelerate varietal development and crop improvement for diverse environments.

Ioan Negrutiu

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Flower power – why and how plant science and geopolitics meet. From flower evo-devo to biomass geopolitics

Developmental genetics and "backwards evolution" experiments with flowering plants revealed (1) a large morphological spectrum ranging from domestication mimicry to ancestral trait "reconstruction" and (2) the role resource reallocation strategies and developmental robustness play in making angiosperms both "biomass and sex bombs". Plants are sequential modular heterochronic living beings. With their extraordinary toolbox of evo-novelties and optimizations, flowering plants are the matrix and engine of land ecosystems. Such ecosystems are highly efficient in terms of productivity and diversity, and are resilient. As such, they singularly support sophisticated human societies and civilizations. Integrating the morphological and biochemical evolutionary trees of land plants tells us the story of where from we come and where we possibly can go.

Plants, as the primary resource system on land (coined net primary production), constrain and calibrate cultural and political (developmental) options. Terrestrial ecosystems exhibit nowadays increasing ecological deficits (with biomass as an early marker) through overexploitation (i.e., forcings and debt syndromes). On those lines I argue that the next 10 years are critical in designing sustainable societies. For these and other reasons, building a socio-ecosystemic resilient world becomes an extremely demanding enterprise. In terms of research, there is a need to more precisely measure and anticipate the extent of (agro)ecosystem state shifts produced by the general rush on natural resources and the global game of resources geopolitics. This, in turn, requires - to name just one urgency, a strong and smart science on plant Eco-Evo-Devo.

References – a starter

de Bossoreille de Ribou S, Douam F, Hamant O, Frohlich MW, Negrutiu I. 2013. Plant science and agricultural productivity: Why are we hitting the yield ceiling? Plant Science 210: 159– 176.

Skidmore AK, Pettorelli N. 2015. Agree on biodiversity metrics to track from space. Nature 523, 403-405.

Magnus Nordborg

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Epigenetic diversity in *Arabidopsis*

Epigenome modulation in response to the environment potentially provides a mechanism for organisms to adapt, both within and between generations. However, neither the extent to which this occurs, nor the molecular mechanisms involved are known. Here we investigate DNA methylation variation in Swedish *Arabidopsis thaliana* accessions grown at two different temperatures. Environmental effects on DNA methylation were limited to transposons, where CHH methylation was found to increase with temperature. Genome-wide association mapping revealed that the extensive CHH methylation variation was strongly associated with genetic variants in both cis and trans, including a major trans-association close to the DNA methyltransferase CMT2. Unlike CHH methylation, CpG gene body methylation (GBM) on the coding region of genes was not affected by growth temperature, but was instead strongly correlated with the latitude of origin. Accessions from colder regions had higher levels of GBM for a significant fraction of the genome, and this was correlated with elevated transcription levels for the genes affected. Genome-wide association mapping revealed that this effect was largely due to trans-acting loci, a significant fraction of which showed evidence of local adaptation. These findings constitute the first direct link between DNA methylation and adaptation to the environment, and provide a basis for further dissecting how environmentally driven and genetically determined epigenetic variation interact and influence organismal fitness.

John Pickett

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Evidence for the wider value of diversity in plant secondary metabolism from the agro-ecological system, push-pull

Botanical diversity is the basis for the push-pull system typified by removal of constraints to sub-Saharan small holder cereal production by companion planting. Originally using the forage legume *Desmodium uncinatum* as intercrop and *Pennisetum purpureum* as perimeter crop and now, against problems associated with climate change, other *Desmodium* species that are drought tolerant, and the apomictic hybrid *Brachiaria Mulato II* as the perimeter crop, insect pests and parasitic weeds are controlled, plant nutrition is enhanced and, for zero grazing farm animal husbandry, forage is supplied on farm. The crop protection in the push-pull is provided by release of stress related semiochemicals against the pests and rhizosphere allelopathy against the weeds. Greater botanical diversity is also evidenced via use of open pollinated varieties (OPVs) of maize rather than hybrids. Certain local OPVs, more closely related to the ancestral teosintes, recognise egg laying by pests and respond systemically by signalling to egg and larval parasitoids via volatile semiochemicals. Tens of thousands of regional farmers are already practising push-pull and there are lessons for industrial agriculture in designing new GM strategies for pest management.

Alex Widmer

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Genetic diversity and adaptation in natural populations

Genetic diversity is considered a prerequisite for natural populations to adapt to their biotic and abiotic environment and to changing environmental conditions. Studies of genetic diversity within and among natural populations inform us about population history, levels of present-day standing genetic variation, and may help us to assess the future adaptive potential of populations. Here I outline how population genomic analyses shape our understanding of genetic diversity in natural populations and explore current evidence for parallel adaptation, adaptation from standing genetic variation, and the age of adaptive variants. Recent studies of natural populations reveal that they harbor a treasure of genetic diversity and adaptive variation. Unlocking this potential will require that we prevent further loss of natural diversity and improve our understanding of adaptive changes in natural and managed populations.

Dani Zamir

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Yield canalization in crop plants

Plant development represents a balance between phenotypic stability and plasticity in response to genetic and environmental perturbations. This balance was termed canalization - the property of a developmental process of being to some extent modifiable but to some extent resistant to modification. In light of global climatic changes and the need to maintain our current crop productivity rates we aim to better understand the factors that regulate phenotypic canalization. We explored the pattern of canalization of 16 "homologous" traits in 31 varieties of tomato, pepper, eggplant, melon, watermelon, sunflower and maize. We found remarkable similarity in trait canalization patterns where those associated with reproduction and yield were plastic and the rest were consistently stable in all crops. For a particular genotype the highest variation was found for seed number produced per plant while single seed weight was the most stable trait for all entries. These conserved ancestral canalization patterns in higher plants indicated that tomato is as good a system as any to investigate the genetic basis of canalization. Meta analysis of 20 years of "historic" tomato data which is publically available via ‘Phenome Networks’ led to the identification of a number of quantitative trait loci (QTL) of *Solanum pennellii* origin that affected yield stability. In some hybrids heterosis was shown to be a factor that induced yield stability, an observation that is well documented in modern agriculture. Validation of the effect of these historic QTL was done using a new experimental design that generates multiple estimates of the coefficient of variation of traits as well as their reaction norms in optimal and water stress environments. For example, the introgression line IL10-2-2 did not affect mean yield but doubled its stability in three years of consecutive trials as well as in fine mapping analysis. This 2 Mbp genomic segment is the first QTL identified for yield stability in any plant and we hope that further studies of stable and plastic genotypes will allow us to address the long-standing question of the genetic basis of Waddindton’s theory of canalization.

Poster abstracts

Institute of Agricultural Sciences ETH Zurich

in alphabetical order

P1

Melanie Abt, David Seung, Samuel C. Zeeman
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The importance of protein targeting during starch biosynthesis

Starch represents one of the most important resources of energy, not only in human nutrition, but also for the production of everyday items such as paper and textiles. It is composed of glucose subunits in two distinct polymers, the branched amylopectin and the linear amylose. While we do not fully understand how starch is produced in plants, it is promising that new aspects of starch biochemistry are still being unraveled, going beyond the biosynthetic enzymes that produce the polymers. Recent findings in our lab suggest that there are mechanisms to target enzymes to starch granules. Such a mechanism might ensure that the correct enzymes are targeted to the appropriate substrate during starch biosynthesis at the right time. The PROTEIN TARGETING TO STARCH (PTST) protein in Arabidopsis was demonstrated to target the enzyme responsible for amylose synthesis, GRANULE BOUND STARCH SYNTHASE (GBSS), to developing starch granules. GBSS cannot localise to starch in the Arabidopsis ptst mutant, and amylose synthesis is consequently disrupted. Currently, we are evaluating the role of several candidate proteins that may also play a starch-targeting role in Arabidopsis leaves. Using in vitro experiments and analysis of Arabidopsis mutants, we will investigate the function of these proteins in starch biosynthesis or degradation. Furthermore, we aim to assess the importance of protein targeting in starch biosynthesis in amyloplasts of staple crops. A cross-species analysis of the orthologs of these proteins is being performed in agriculturally important crops such as potato and rice. These experiments will shed further light on this previously uncharacterised process, and the findings obtained during this project may have a significant impact on future biotechnological studies and applications.

P2

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Investigating the nuclear ß-amylases signalling pathway in *Arabidopsis thaliana*

Plant growth is underpinned by carbohydrate metabolism. The balance between carbon partitioned into utilization and storage is important for plant survival and requires a continuous monitoring and adjustment of nutrients availability. In this scenario, sugars not only act as nutrients but also as signalling molecules. Carbon partitioning needs a tight regulation, which is partly provided by proteins able to sense sugar-derived metabolites.

We have recently identified two members of the ß-amylase protein family, BAM7 and BAM8, which unlike the other isoforms of the family do not catalyse starch breakdown in the chloroplast, but modulate plant development acting as transcription factors (TFs) in the nucleus. Their structure is remarkable in that they couple a ß-amylase domain to an N-terminal DNA-binding domain of the BZR-family type. Given these structural features, BAM7 and BAM8 are referred to as BZR1-BAMs.

In the nucleus BAM7 and BAM8 recognise an eight-letter DNA motif, the BZR1-BAMs Responsive Element (BBRE), containing two known cis-regulatory elements that mediate responses to light and brassinosteroid, respectively. Deregulation of the BZR1-BAMs causes transcriptional changes of genes possessing the BBRE in their promoters with consequences on plant architecture. The role as TFs and the two-domains structure makes of BAM7 and BAM8 possible factors linking perception of energy availability, via the BAM domain, to developmental responses. Despite a body of information is available on the function of BAM7 and BAM8 as TFs, little is known about how this is regulated and how the BZR1-BAMs signalling pathway integrates with signals derived from other internal and external cues. By mass spectrometry analyses we have mapped several phosphorylation sites in BAM7 and BAM8 protein sequence. Using a combination of methods that include site-directed mutagenesis, in vitro kinase assays and transactivation assays, we seek to understand how this post-translational modification affects protein activity, possibly regulating their stability and interactions with other cellular factors.

With this study we want to identify the cellular components that allow to coordinate responses to energy availability and to other internal and external cues, such as those triggered by hormones and light, in order to understand how the crosstalk participates in shaping plant development.

P3

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The FBA junction in *Arabidopsis thaliana*

Fructose-bisphosphate aldolase (FBA) enzymes have key functions in sucrose biosynthesis, glycolysis, gluconeogenesis and the Calvin cycle. They catalyze the reversible condensation of triose-phosphates to fructose 1,6-bisphosphate. Additionally, plastid FBAs (pFBA) are known to catalyze the condensation of erythrose 4-phosphate and dihydroxyacetone phosphate to sedoheptulose 1,7-bisphosphate. Therefore, pFBAs have dual substrate specificity, with potential to control photosynthetic carbon flux through the cycle.

Arabidopsis has eight annotated and identified FBA genes. Three proteins encoded by this gene family are localized in the plastid (FBA 1-3). So far it is unknown why higher plants have three pFBA isoforms and what their potential specific roles might be. First, we isolated single knock-out mutants (fba1, fba2, fba3) and studied them phenotypically. Surprisingly, growth rates differed extremely between all three mutants, suggesting varying contributions in the Calvin cycle. Fba1 mutants are indistinguishable from wild-type plants. Fba2 mutant plants have a reduced growth and starch synthesis. Fba3 mutants show an even more severe reduced-growth phenotype but now with high starch content. These differences do not correlate with the relative contribution of each pFBA to total FBA activity. The knock-out plants of FBA2 have reduced FBA activity, whereas fba1 and fba3 mutants have unchanged total FBA activity. These finding are not in agreement with the current model that the pFBAs are redundant in their function. Instead, we hypothesis that the three pFBAs conduct different functions in the chloroplast with partially redundancies. For example; fba1 and fba2 single mutants are viable, whereas loss of FBA1 and FBA2 together results in not viable plants. In the future we will elucidate the role of each pFBA in detail by determining their enzyme properties and specificities. This will allow us to define their true functions in the Calvin Cycle and carbohydrate metabolism.

P4

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Efficient doubled haploid production in perennial ryegrass

Hybrid breeding has contributed significantly to the enormous yield increases that many major crops have undergone during the previous century. Its success relies on the exploitation of heterosis, which is the superior performance of an F1 hybrid compared to its inbred parents. Attempts to implement hybrid breeding in forage grasses, such as perennial ryegrass (*Lolium perenne* L.), are hampered by its highly effective self-incompatibility system as well as its sensitivity to inbreeding depression. It is therefore difficult in practical terms to develop homozygous inbred lines through the classical method of repeated selfing.

Here, we report an efficient method to obtain homozygous genotypes of perennial ryegrass using doubled haploid (DH) induction. By means of anther culture, completely homozygous lines were obtained within one generation cycle. A highly genotype dependent response was observed for traits such as the number of embryos/calli per 100 cultured anthers and the percentages of green and albino plants regenerated. Transgressive segregation, indicative of heritable and polygenic control of the traits, was also found.

We aim to develop a molecular marker system to select for high responsiveness and to facilitate the introgression of this trait into advanced breeding germplasm. Segregating mapping populations will be phenotyped during anther culture and genotyped via a genotyping-by-sequencing (GBS) approach. Family-based association mapping will be used to identify marker-trait associations. In this way, an efficient breeding tool to screen germplasm for DH induction capacity will be developed. Our work will significantly accelerate forage grass breeding and constitute the first step towards efficient production of grass hybrids.

P5

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Integration of sugar signals into other signaling pathways

Plant growth and development depends on the plant's ability to keep an appropriate balance between generation, consumption and storage of its resources. The monitoring process of this equilibrium is essential, yet mechanistically barely understood. Sugars likely act as indicators of the plant's nutritional status, which in turn reflects the plant's resource status. However, the nutritional status is not the only determinant of plant performance. Many other cues such as prevalent light conditions, seasonal changes, biotic and abiotic stresses are also very important. To achieve an optimal response to prevalent conditions, internal (such as nutritional status) as well as external cues have to be integrated.

The domain structure of the two ?beta-amylase derived proteins BAM7 and BAM8 make them potential components in sugar sensing. They contain a catalytically inactive BAM-domain, which is suggested to have kept the ability to bind to a carbohydrate. Furthermore, the N-terminal BZR1-domain renders them active as transcription factors. Interestingly, their preferred DNA binding motif (BZR1-BAM responsive element, BBRE) overlaps with the Brassinosteroid Responsive Element (BRRE), which is bound by brassinosteriod responsive transcription factors and the G-box, a commonly known light responsive motif. This leads to the speculation that the BAM7 and BAM8 are involved in the convergence of sensing mechanisms incorporating light, hormone and nutritional cues.

Our approach to substantiate the hypothesis that BAM7 and BAM8 are involved in sugar sensing and signalling is to look for the potential (sugar) ligand. By site-directed mutagenesis of residues in the BAM domain of BAM8 we found that BAM8's function as transcriptional activator requires an intact substrate binding site (Soyk et al., 2014). Furthermore, preliminary results from an interaction study using Surface Plasmon Resonance identified some sugar-phosphates as promising potential ligands. The physical protein-sugar interaction was further assessed by Microscale Thermophoresis. The impact of one potential substrate (trehalose 6-phosphate) on BAM8 transcription factor activity was tested in an in vivo protoplast reporter gene assay.

P6

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Linking non-destructive measurements to investigate temporal niche complementarity in a grassland biodiversity experiment

The relationships between biodiversity (often defined as plant species richness), plant productivity and ecosystem functioning have emerged as a central issue in ecological and environmental sciences during the last two decades. Within this context, the concept of niche complementarity is expected to play a key role for plant species coexistence. Niche complementarity refers to a mechanism by which plant species in high-diverse communities jointly exploit available resources more efficiently than a monoculture or a low-diversity mixture, resulting in higher productivity (biomass production), higher resilience against disturbances and higher ecosystem functioning in general. Temporal niche complementarity, arising from phenological diversity, is expected to extend the growing season because it might distribute peak phases of vegetative development, and therefore resource requirements, more evenly throughout the season. Still, temporal niche complementarity has rarely been studied in a biodiversity ecosystem functioning context. Within the framework of the Jena Grassland Biodiversity Experiment in Germany, we continuously monitored phenological adaptions of 13 temperate grassland species distributed over 92 experimental plots characterized by a diversity gradient ranging from monocultures to eight-species mixtures for two consecutive years. We hypothesize that offsets in key phenophases allow high-diverse communities to exploit resources over an extended period of time (‚time-filling') and are therefore of significant importance for ecosystem functioning. By combining advanced non-destructive imaging techniques, including high definition-timelapse photography, thermal infrared imaging and laser scanning, we were able to track inter- and intra-seasonal changes in above-ground plant phenology, plant growth and resource acquisition along a biodiversity gradient in high-temporal and -spatial resolutions for the first time in a grassland experiment.

P7

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A gene encoding a DUF247 domain protein co-segregates with the S self-incompatibility locus in perennial ryegrass

The grass family (Poaceae), the fourth largest family of flowering plants, encompasses the most economically important cereal, forage and energy crops, and exhibits a unique gametophytic self-incompatibility (SI) mechanism that is controlled by at least two multi-allelic and independent loci, S and Z. Despite intense research efforts over the last six decades, the genes underlying S and Z remain uncharacterised.

Here, we report a fine-mapping approach to identify the S-locus in perennial ryegrass (*Lolium perenne* L.) and provide strong evidence that a domain of unknown function 247 (DUF247) gene is involved in its determination. Using a total of 10,177 individuals from seven different mapping populations segregating for S, we narrowed the S-locus to a genomic region containing eight genes, the closest recombinant marker mapping at a distance of 0.016 cM. The S-locus region was compared to other sequenced Poaceae genomes and showed small-scale genome rearrangements compared to rice (*Oryza sativa* L.) and Brachypodium (*Brachypodium distachyon*). Of the eight genes co-segregating with the S-locus, a highly polymorphic gene encoding for a protein containing a DUF247 was fully predictive of known S-locus genotypes at the amino acid level in the seven mapping populations. Strikingly, this genes showed a frame-shift mutation in self-compatible darnel (*Lolium temulentum* L.), whereas all of the self-incompatible species of the Festuca-Lolium complex were predicted to encode functional proteins.

Our results represent a major step forward towards understanding the gametophytic SI system in one of the most important plant families and will enable the identification of additional components interacting with the S-locus.

P8

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Development of red clover as a model to understand carbon partitioning and growth

Red clover (*Trifolium pratense* L.), like many plants accumulates starch in its leaves during the day as a temporary carbon store of photosynthesis and remobilizes it to support metabolism and growth at night. Although plant leaves were first reported to accumulate starch over a century ago, leaf starch content has yet to be exploited as an agronomic trait in crops such as forages, where a high starch trait would be beneficial as a high energy feed source. To understand why high leaf starch content has been an elusive trait to select in red clover breeding programs, several genetically distinct genotypes were analyzed for diurnal leaf starch content. Although some of these genotypes resemble model systems such as *Arabidopsis*, which accumulate starch during the day and degrade it at night, other genotypes were observed to forgo nighttime starch mobilization and sequester starch in the leaves during the night. This nighttime sequestration appears to be dependent on daytime light intensity, as starch is fully mobilized at night in the sequestration genotypes when grown at lower light intensities during the day. In a larger genetically diverse population, both starch content and starch sequestration was observed to have a high degree of natural variation. Given this natural variation in carbon usage and storage and its unique growth architecture, red clover offers an interesting model to study how starch metabolism couples photosynthesis with growth. Moreover, with the recent publication of the red clover genome, development of modern genetic resources, and advances in modern sequencing technologies, red clover also has potential as a genetic model system, which is amenable to approaches such as genome wide association studies (GWAS). Ultimately, knowledge from this project is envisioned to direct a breeding strategy for a high starch trait in red clover as well as guide farming practices to maximize forage energy content.

P9

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Cowpea inoculation for improved yields in small holder farms in Kenya

Cowpea (*Vigna unguiculata* L. Walp) is the most important pulse crop in the dry lands of Eastern and Coastal Kenya. Challenges to production include mainly low soil fertility (mainly N and P deficiency) among others thus, resulting to poor grain yields (on average 150 kg ha-1) in smallholder farms. This legume forms root nodules with rhizobia that symbiotically fix atmospheric nitrogen via the Biological Nitrogen Fixation (BNF) process. Through exploiting this symbiotic relationship to optimize BNF, yields and soil fertility can be improved. The overall aim of this research is to improve cowpea yield for smallholder farmers in two different agro-ecologies [Kilifi (Coastal lowland) and Mbeere (Lower midland)] in Kenya through inoculation with effective and competitive *Bradyrhizobia* strains. The first study objective entails isolation and characterization of *Bradyrhizobia* nodulating cowpea in both agro-ecologies from sites characterized by diverse soil types and land management practices (Objective 1). A novel approach for rapid and accurate identification of bacteria; Matrix Assisted Laser Desorption/ionization Time of Flight (MALDI-TOF) mass spectrometry (MS) will be used for identification of isolates. After characterization, genetically distinct strains will be selected for screening for symbiotic effectiveness and competitiveness in two phases; (i) growth chamber screening (Objective 2) using axenic conditions by inoculating individual strains to cowpea and a mixture of the strains to assess their competitiveness by nodule occupancy using MALDI-TOF MS; (ii) on farm field screening of 4 best performing strains (Objective 3) selected from Objective 2, MALDI-TOF MS to assess nodule occupancy for competitiveness of our inoculated strains (versus indigenous strains). Finally, functional gene analysis will be done on selected symbiotic genes to investigate their role in efficient BNF and competitiveness of *Bradyrhizobia* strains (Objective 4). Through *Bradyrhizobia* isolation and rigorous growth chamber and field screening of the same, the use of newly developed techniques to elucidate genes involved in the BNF process, yields and soil fertility status can be hopefully improved to enhance food security of smallholder cowpea farmers in Kenya.

P10

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Composition of soil microorganisms harboring the *phoD* and *phoX* alkaline phosphatase genes as affected by land-use type, climate and soil type

Phosphatase enzymes, like PhoD and PhoX alkaline phosphatases, are responsible for much of the organic phosphorus recycling in soil and, yet, our knowledge on these microbial functional genes remains very limited. Here, we explore the composition of the *phoD*- and *phoX*-harboring community in 30 soils across 3 land-use types (arable, grassland and forest), 3 climate zones and 6 soil types using 454-sequencing. *phoD* was investigated using recently published primers (Ragot *et al*, 2015, Appl Environ Microbiol), and a new set of primers was designed to study *phoX*. The *phoD* gene was found in 1 archaeal, 13 bacterial and 2 fungal phyla, and the phoX gene in 1 archaeal and 16 bacterial phyla. Land-use type changed the relative abundance of *phoD*-harboring Cyanobacteria, which were more abundant in grassland than in arable and forest soils, and of *phoD*-harboring Firmicutes, which were significantly lower in forest than in arable and grassland soils. Additionally, land-use type influenced the relative abundances of 6 *phoX*-harboring phyla, including Actinobacteria, Chloroflexi and Proteobacteria, which were all more abundant in grassland than in arable and forest soils. Climate influenced the relative abundances of 6 *phoD*- and 4 *phoX*-harboring phyla including *phoD*-harboring Firmicutes, which were more abundant in temperate climate, and *phoX*-harboring Chloroflexi, which were more abundant in arid climate. Soil type affected the relative abundances of 9 *phoD*-and 6 *phoX*-harboring phyla. The *phoD*-harboring community was composed by the same dominant phyla in all soils. In contrast, dominant *phoX*-harboring phyla varied greatly between soils. Our results suggest that land-use type, climate and soil type affect the relative abundances of some dominant *phoD*-and *phoX*-harboring phyla specifically. This study gave new insights into the microbial key players in organic phosphorus recycling in soil.

P11

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Advanced breeding of high energy red clover for sustainable ruminant livestock production

Red clover (*Trifolium pratense* L.) is one of the most important forage legumes worldwide and like other forage legumes, it offers a highly sustainable feed source for ruminant livestock production. Although red clover has a relatively high biomass potential, its content in fermentable, high-energy carbohydrates is insufficient 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 monoculture-based foreign supply chains. Although highly beneficial as a trait, leaf energy content has been a complex and elusive trait to breed. The goal of the High Energy Red Clover (HERC) project, is to utilize the recently published red clover genome sequence and our current understanding of leaf carbohydrate metabolism from the model plant *Arabidopsis*, to direct an advanced breeding approach based on Targeting Induced Local Lesions in Genomes (TILLING). Specifically, the project is targeting enzymes required for starch degradation to identify alleles, which are expected to sequester carbon in the leaf. To maximize allele discovery, seeds of a genetically diverse red clover population were mutagenized with nitro-methyl-urea, and a mutation frequency similar to the model system *Arabidopsis thaliana* was observed. Given this mutation rate, a population of 2000 genotypes was collected to obtain adequate mutation coverage in the target genes. These mutant alleles will be used to develop a high-energy variety. The expected outcome is a variety that can be readily integrated into local and global farming and food systems, and will provide a feed source to significantly improve the economic and environmental sustainability of ruminant livestock production.

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Investigation of the post-embryonic function of plastidial NAD-dependent malate dehydrogenase in *Arabidopsis thaliana*

Malate dehydrogenases (MDH) catalyse the reversible interconversion of malate and oxaloacetate, using NAD(H) or NADP(H) as a cofactor. Plant tissues contain multiple isoforms of MDH, and are claimed to play an important role in balancing the availability of redox equivalents between different cellular compartments. Of the nine MDH isoforms in Arabidopsis, only two are plastidial - one is NADP-dependent, while the other is NAD-dependent (pdNAD-MDH). The pdNAD-MDH isoform shows by far the most severe knockout phenotype among all the MDH isoforms. We could show that a pdnad-mdh-null mutation is lethal (Beeler *et al*, 2014): pdnad-mdh embryos arrest in the globular-to-heart transition stage and therefore, pdNAD-MDH is essential for embryo development in Arabidopsis. The constitutive silencing line, miR-mdh-1, with strongly reduced pdNAD-MDH levels, is dwarfed, shows a disturbed chloroplast ultrastructure, and exhibits severe pleiotropic effects compared to the wild type. Since these effects are alleviated as the plants grow, we wondered whether they result from developmental defects during embryogenesis, or specifically due to pdNAD-MDH silencing after germination. To specifically investigate the post-embryonic function of pdNAD-MDH, we expressed pdNAD-MDH under control of the embryo-specific ABI3 promoter in the pdnad-mdh knockout line. Embryo-specific expression of pdNAD-MDH rescued embryo-lethality, however, growth of the pABI3a::pdNAD-MDH lines was even more severely reduced than that of miR-mdh-1. Furthermore, these plants failed to develop any chlorophyll, and while they initiated true leaves, they did not develop further and died within a few weeks. Exogenous supply of various substrates to diminish potential energetic or redox effects slightly improved the growth phenotype in some cases, but the plants still failed to reach the reproductive stage. These findings suggest that pdNAD-MDH is not exclusively essential for embryogenesis, but that it also plays a crucial role for the establishment of mature plants.

P13

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Effect of N and K mineral fertilizers on growth and yield of water yam (*Dioscorea alata*)

Water yam (*Dioscorea alata*) is known to be very demanding in term of soil fertility. The effect of N and K in mineral fertilizers on the growth of yams, however, has not yet been studied in Sri Lanka. A field study was carried out at Field Crops Research and Development Institute, Mahailluppallama, Sri Lanka for two consecutive years in 2013/14 and 2014/15. The experiment design was a randomized complete block design with four replications. There were six N: K mineral fertilizer ratios added as follows: T1 (0 N: 0 K) Control, T2 (90 N: 0 K), T3 (0 N: 105 K), T4 (90 N: 105 K), T5 (180 N: 105 K), T6 (90 N: 210 K) kg/ha. The N, P2O5 and K2O rates (kg/ha) are 90, 70 and 105 (for 1N 1P 1K) as recommended by the Department of Agriculture, Sri Lanka and applied at 1:1:1 ratio as 2 splits, to determine how different N and K ratios effects on Leaf Area Index (LAI), shoot biomass, final fresh tuber yields (FTY) and harvesting index (HI) of *Dioscorea alata*. The highest LAI, shoot biomass and FTY were observed in T5 treatment than the control treatment T1 in both seasons. There were 34% and 28% yield drop in T1 treatment, than the T5 treatment, respectively in two seasons. Correlation analyses showed significant relationship between the mean LAI at tuber bulking stage and the final fresh tuber yields, suggesting that the development of leaf area is determining the growth rate of the tuber. These results suggested that application of double quantity of N had an effect for tuber formation in *D. alata*.

P14

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Starch granule initiation in chloroplasts requires the co-ordination of glucan biosynthesis and degradation enzymes

Starch biosynthesis in leaves provides a crucial energy reserve that plants need to fuel growth and metabolism at night. Starch is composed of polymers solely containing glucose subunits, and the arrangement of these polymers give rise to semi-crystalline, insoluble granules. It is produced in chloroplasts during the day from photosynthates - *Arabidopsis* leaf chloroplasts typically accumulating five to seven granules, which are almost completely degraded during the subsequent night. It is currently poorly understood how the synthesis of each granule is initiated, and how starch granule number is determined within each chloroplast. *Arabidopsis* mutants lacking the glucosyltransferase, STARCH SYNTHASE 4 (SS4) is impaired in its ability to initiate starch granules, with chloroplasts containing either no starch, or one large granule. ss4 mutants also have reduced growth compared to wild type and a pale appearance due to the accumulation of the substrate for starch synthesis, ADP-Glucose. In this study, we identified a suppressor mutation that can complement the pale phenotype of the ss4 mutant, restoring normal growth and increasing the number of starch granules produced in each chloroplast. The suppressor mutation can also restore starch synthesis in the starchless ss3 ss4 double mutant, which lacks STARCH SYNTHASE 3 (SS3) in addition to SS4, and is unable to initiate any starch granules. Unexpectedly, the suppressor mutation abolishes the activity of a known starch hydrolase, involved in starch degradation at night. The suppressor mutation alone causes no obvious phenotype under normal growth conditions, and has normal starch granule numbers in the chloroplast. These results suggest that the initiation of starch granules requires the balanced activities of enzymes involved in starch biosynthesis and degradation. It also appears that SS3 and SS4 enzymes are not strictly required to initiate starch granules as previously thought, but may rather alter the substrate in a way that prevents premature degradation by starch hydrolases.

P15

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Fertility restoration of cytoplasmic male sterility in perennial ryegrass (*Lolium perenne* L.)

Exploitation of the phenomenon of heterosis through hybrid breeding has been one of the most influential factors for increasing yields from agriculturally important plants. An integral aspect of any hybrid breeding scheme is an effective pollination control mechanism, such as cytoplasmic male sterility (CMS), to ensure complete outcrossing of hybrid lines. In order for CMS based hybrid breeding schemes to be successful, the genes that restore fertility to CMS affected plants need to be identifiable, often through the use of molecular markers, to ensure that the CMS phenotype can be maintained within breeding populations. We have developed a bioinformatics pipeline for rapid identification of candidate fertility restorer (Rf) genes for CMS. This pipeline utilises orthologous clustering methods to identify a subset of the pentatricopeptide repeat (PPR) proteins - the restorer of fertility-like PPR (RFL) proteins simultaneously from multiple plant species. Further investigation of these RFL proteins through phylogenetic analyses reveals that the most related RFLs are found at the same genomic locus within an individual species. This is exemplified through the use of sequence data from perennial ryegrass (*Lolium perenne* L.), where detected RFLs were analysed, identifying three groups 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. In perennial ryegrass this data will be augmented through the analysis of a population of CMS affected plants segregating for fertility restoration using several molecular genetics tools. A classical QTL analysis will be performed through Genotyping by Sequencing, Bulk Segregant Analysis will identify genomic differences between restored and sterile plants and transcript analysis will pinpoint the expression changes of the identified RFL genes. This will lead to the development of functional markers for PPR-Rf genes 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.

P16

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Light-dependent regulation of Calvin-Benson cycle, studying photosynthetic acclimation in *Arabidopsis thaliana*

As photoautotrophic organisms plants are capable of using light energy to convert water and atmospheric CO_2 into carbohydrates, which serve as a primary energy source not only for the plant itself but also for heterotrophic organisms. Photosynthesis dominates leaf metabolism and it is conveniently divided into energy-capturing reactions, where the photochemical electron transport chain provides energy for ATP synthesis and NADPH reduction; and the carbon-fixing reactions (the Calvin-Benson cycle) where the energy freed by the cleavage of P from ATP and the reducing power of NADPH are used to fix CO_2 into triose and hexose phosphates. In order to keep metabolism effective, an intimate link between CO_2 assimilation and light-dependent reactions is necessary. The fine tuning of the two processes relies on numerous regulatory mechanisms among which the light-dependent redox signaling, which modulates the activity of certain enzymatic steps in the Calvin-Benson cycle, is one of the more studied and yet not completely understood. Although the structural basis for this regulatory pathway are well known, the significance of the redox control exerted on the Calvin-Benson cycle and its in vivo quantification in comparison to other parallel regulatory mechanisms (e.g. end-product feedback or pH-dependence) remain largely to be uncovered. Our aim is to investigate the effects, in terms of photosynthetic performance, of uncoupling the redox-regulation of the Calvin-Benson cycle enzymes using the model plant *A. thaliana*. Redox-insensitive forms of the regulated enzymes fructose 1,6-bisphosphatase (FBPase), sedoheptulose 1,7-bisphosphatase (SBPase), glyceraldehyde-3-phosphate dehydrogenase (GAPDH) and phosphoribulokinase (PRK), have been generated by cysteines/serines substitutions; these mutated proteins, transformed into *Arabidopsis* lines lacking the endogenous genes, provides redox-insensitive plants unable to inactivate the Calvin-Benson cycle enzymes upon light/dark transition and in response to light intensity variations. Also, the observations conducted on the single knock-outs for FBPase and SBPase raised our awareness about the possibility of alternative carbon fluxes through the cycle, potentially emerging in specific philological conditions. This project will provide new insight into carbon metabolism and its regulation and will generate data for developing a mathematical model of photosynthetic light acclimation. This knowledge will be of value for agronomy and crop science, currently facing looming challenges in terms of providing food, fiber and fuel for an increasing world population.

Poster abstracts

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in alphabetical order

P17

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How is the abundance of plant beneficial pseudomonads influenced by soil characteristics in Swiss agricultural soils?

Many bacterial strains belonging to *Pseudomonas* spp. are known to be antagonists of soilborne pathogens and are used as biocontrol agents. Beneficial pseudomonads have different mechanisms for the suppression of fungal diseases, the most important is the production of antifungal metabolites, such as phenazines (PHZ) and 2,4-diacetylphloroglucinol (DAPG). PHZ and DAPG producing plant beneficial pseudomonads are naturally present in the rhizosphere of plants in suppressive soils, where no disease symptoms develop on plants although pathogens are present. However, little is known about the abundance of plant beneficial pseudomonads across a wide range of soils with different physical and chemical characteristics.
In this study, soil and wheat root samples were collected from 10 field sites in Switzerland with different soil composition. Resistance of soils against soilborne pathogens due to the natural flora was tested. The host-pathogen systems used were *Pythium ultimum*-cucumber and *Gaeumannomyces graminis* var. *tritici*-spring wheat. Genes involved in the biosynthesis of antifungal compounds were quantified by qPCR in the DNA extracted from root washes. Moreover, the composition of the rhizosphere microbiome was characterized by 16s rRNA amplicon sequencing. Soils collected at different field sites showed different degrees of resistance to the two pathogens tested. DAPG producers could be detected in all soils, while PHZ producers could be detected in 9 of 10 soils. DAPG producers tended to be more abundant in soils resistant to *G. graminis* var. tritici. However, soil characteristics were the most important factor shaping the rhizosphere microbiome. Abundance of *Pseudomonas* spp. was highest in the rhizosphere of plants grown in soils with neutral pH, high organic carbon content and high macro- and micronutrient content. Knowledge on the abundance of beneficial pseudomonads in a wide range of soils could help farmers to implement conservation biocontrol strategies.

P18

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Understanding hybrid seed failure in wild tomatoes: phenotypic and transcriptomic signatures

Hybrid seed failure is a common reproductive barrier between plant species. For plant breeders, it represents a major obstacle to introgression of desirable traits from wild to domesticated species. Postzygotic barriers to hybridization have been well-documented among wild tomato species, and histological work showed that endosperm failure is the main cause of seed abortion. Based on an updated phylogeny of the tomato clade, we addressed hybrid seed failure between three taxa, namely *Solanum peruvianum*, *S. chilense* and *S. arcanum* var. maranon). We characterized mature seed size and viability in a large number of crosses and conducted endosperm-specific RNAseq experiments using six reciprocal crosses within and between the three taxa. The crossing design was chosen to detect expression pattern differences with regard to overall and parent-of-origin-specific expression (i.e. imprinting). Reciprocal interspecific crosses involving *S. peruvianum* yielded no viable seeds and were classified as having a ‚strong' barrier. Crosses between *S. chilense* and *S. arcanum* var. maranon were characterized by variable levels of seed viability as well as asymmetric outcomes in some reciprocal crosses, here classified as a ‚soft' barrier. Seed size was significantly reduced with *S. peruvianum* in the maternal role in hybrid crosses, compared to crosses within this species. Transcriptome analyses shows drastic expression changes when comparing intraspecific crosses with normally developing endosperm and among-species crosses with abnormal endosperm. We propose imprinting disturbance as a mechanism contributing to hybrid seed failure, but ongoing work will further characterize molecular pathways possibly involved in this reproductive barrier and its variability.

Poster abstracts

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in alphabetical order

P19

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Habitat segregation in an allopolyploid and its parent species in Cardamine

Whole genome duplication (polyploidy) is pervasive in plants. Polyploids are generally expected to have intermediate and broader environmental distributions than diploids. However, empirical data on environment of polyploids and its diploid parents in field are limited. We quantified habitat environment of diploids *C. hirsuta* and *C. amara* and the allopolyploid *C. flexuosa* originated from *C. hirsuta* and *C. amara* in their native area in Switzerland in order to examine whether habitat environment differs among species. The diploids *C. hirsuta* and *C. amara* segregated in that *C. hirsuta* occurred in dry, bright, and nutrient-rich habitat in contrast to *C. amara*, while the allopolyploid *C. flexuosa* occurred in intermediate and fluctuating environment. These findings provided evidence that the parent species occurred in extreme environments, while the allopolyploid occurs in intermediate environment. They also suggest that the *C. amara*, *C. hirsuta*, and *C. flexuosa* serve as a useful system to study the molecular basis of adaptive significance of allopolyploidy in wild plants.

P20

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Asynchronous species fluctuations are the main driver of community stability in experimental plant communities

A predominant effect of biodiversity on ecosystems is the temporal stability of species-rich plant communities. However, which biotic and abiotic factors are responsible for the increased stability of more diverse communities, is still an open question. In this study we used species specific aboveground biomass measured for a 10-year period in the Jena Experiment, Germany, to investigate temporal patterns of community stability. We first calculated community stability and identified five potential drivers of it: species richness, temporal species fluctuations, environmental fluctuations, community structure and functional diversity. We then used general linear and structural equation modelling to quantify the contributions of these drivers and their interactions to community stability.

Our results showed that asynchronous temporal fluctuations of species populations were mainly responsible for the increased stability of more species-rich communities. Furthermore, community structure and functional diversity both acted directly on community stability and indirectly via the asynchronous species fluctuations. Environmental fluctuations had little effects on community stability. Finally, different drivers affected community stability at different time intervals, partly compensating each other influence. These results are congruent with postulates of an insurance effect of diversity and with niche theory. They support the hypothesis that compensatory dynamics originating at the species level are able to stabilize aboveground biomass production at the community level.

P21

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Feedback of soil organisms in 12-year old grassland monocultures and mixtures

Accumulation of species-specific pathogens in plant-monoculture soils is a widely known phenomenon in agriculture. When monoculture communities are exposed to specialized soil organisms over several years, it is likely that selection favors plant individuals with traits such as better defense against pathogens or increased capability to benefit from mutualists. In recent studies, progeny of grassland plants which had undergone 8 years of selection in the Jena Experiment in either monoculture or mixture communities, showed differential growth responses to "home" soil and soils with which they had no history. The effect of home soil was negative for plants with mixture-community history but positive for plants with monoculture-community history. However, the mechanisms behind the differential growth responses remain unclear. In this study, we set up soil-feedback experiments to test the effects of soil mutualists and pathogens on plants selected in monoculture ("monoculture types") or mixture communities ("mixture types") over 12 years. Moreover, we test whether monoculture types have increased investment in resistance against soil pathogens in contrast to mixture types. We hypothesize that monoculture-type plants are selected for increased pathogen resistance or increased beneficial associations with soil mutualists compared to mixture-type plants in response to, respectively, the accumulation of species-specific pathogens or mutualists under plant monocultures and dilution of these under plant mixtures.

P22

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Cis-trans regulation detecting pipeline development on SUSHI

Gene expression in allopolyploid hybrid species depends on both cis and trans regulatory factors that influence parentally inherited gene copies. In hybrids, cis-expression divergence must evolve by selection on surrounding non-coding regulatory regions to enhance homeolog specific expression. We have integrated a statistical framework for detecting cis-trans regulation in polyploid species using SUSHI, a web-interface platform available for users of the Functional Genomics Center Zurich sequencing facility. SUSHI is a pipeline framework of Supporting User for SHell-script Integration developed on the Ruby on Rails Web-application framework. The cis-trans regulation is detected in several steps: 1. Mapping polyploid RNAseq data on parental genome reference(s), 2. Mapped reads classification into either parental homeolog, 3. Quantifying diffierential homeolog expression ratio genes relative to parental expression using HomeoRoq, 4. Detecting differentially expressed genes between polyploid homeologs using EdgeR, and 5. Classifying genes into cis- or trans-regulated genes. Using an *Arabidopsis* allopolyploid species and its parental diploid species, we detected 3868 cis and 395 trans genes in synthetic F1's and 8950 cis and 408 trans in a natural allopolyploid. The nearly twice difference in cis genes detected in F1's compared to the natural allopolyploid suggests strong cis-regulatory divergence among homeologs over evolutionary time. Using silent substitutions in coding sequences and non-coding 5' and 3' flanking regions, we will estimate the strength of selection on cis-regulatory regions using a MacDonald-Kreitman framework. SUSHI on iPad will be demonstrated at the front of the poster on the day.

P23

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Resources or enemies – which have greater influence on plant diversity productivity relationships in subtropical forest?

Aboveground primary productivity is one of the most important ecosystem functions in forest and has been found to increase with plant diversity in many studies. Many experiments have been carried out in grassland to identify complementary effects, selection effects and effects of soil microbes on this relationship. However, there is little knowledge about the relationship in subtropical forest. Here, we show first results from a newly established large forest biodiversity ecosystem functioning experiment in JiangXi Province, China (BEF-China). We analyzed 6 biodiversity levels, which were designed to represent random extinction scenarios from 24 to 16, 8, 4, 2 and finally 1 species per plot. Experimental treatments included pathogen exclusion, herbivore exclusion, weeds admission, phosphorus fertilization and control. This allowed us to test whether the positive effect of biodiversity on aboveground primary productivity resulted from a reduced pressure from host-specific predators and pathogens at high diversity or from resource-based niche complementarity. Our results provide evidence for both and contribute to a mechanistic understanding of plant diversity productivity relationships in subtropical forest.

P24

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The genetic basis of pollen number variation revealed by a genome-wide association study in *Arabidopsis thaliana*

Although self-fertilization (selfing) has independently evolved numerous times in flowering plants, selfing species tend to share numbers of floral traits collectively known as the ‚selfing syndrome', which involves a reduced pollen number instead of increased ovule number, i.e., changes in so-called pollen/ovule ratio.
Despite a wealth of knowledge about the ecological significance of the changes, the molecular genetic mechanisms are still poorly understood. To reveal the genes that are involved in pollen number variation, we first performed a genome-wide association study (GWAS) using world-wide natural accessions of *Arabidopsis thaliana*. GWAS identified several loci that are significantly associated with pollen number variation, and some of them encompass genes that have already been reported to be important for pollen function, suggesting the validity of our GWAS scan. GWAS also identified several unknown genes, including one we named Reduced Pollen Number 1 (RDP1). Secondly, we confirmed that mutant lines of RDP1 show a significant reduction in pollen number as well as reduced expression of RDP1 compared to wild type lines.

P25

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Facilitative interactions increase stability of plant-plant networks under different environmental change scenarios

There is unequivocal evidence that environmental changes are affecting the stability of ecosystems. Plant-plant interactions are fundamental processes structuring plant communities and an important mechanism governing the response of plant species and communities to environmental changes. Thus, understanding the role of plant interaction networks in modulating the impact of environmental change on plant community structure is crucial. In an observational and simulation study we assessed the robustness of a plant–plant network to four environmental change scenarios, and we evaluated the role of facilitative interactions for species persistence through avoidance of secondary extinctions. We recorded the abundance and three functional traits of plant species growing alone and associated with three foundation species (*Arenaria tetraquetra* spp. *amabilis*, *Plantago holosteum* and *Festuca indigesta*) in the dry high-elevation ecosystem of the Sierra Nevada Mountains (Spain). Using network analysis, we simulated primary species loss based on plant response traits that were expected to be susceptible to on-going climate change, and we explored the plant communities robustness. Under scenarios of increasing summer temperature and drought, and under increasing nitrogen availability, our simulations suggest that foundation species reduce extinctions by up to 50%. Under scenarios of increasing summer temperature and summer precipitation simulation models suggest that foundation species reduce extinctions by up to 35%, similarly to a random extinction model. Scenarios of increased soil nitrogen depletion produced no secondary extinctions. Overall, facilitative interactions, by increasing species survival, reduced the impact of environmental changes on species composition of the plant community and supported community stability.

P26

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Zinc accumulation and transcriptional response in the allopolyploid *Arabidopsis kamchatica*

In allopolyploid species, ancestral gene copies can result in the retention of phenotypes that were present in either of the diploid parents. Heavy metal hyperaccumulation in plants represents a highly tractable quantitative trait that has tremendous potential for detailed analyses of gene regulation between diploid and polyploid relatives. While most studies of additive or non-additive expression following polyploid hybridization have analyzed differential expression between diploid orthologs and homeologs from base line expression, heavy metal treatments allow for quantifiable differential responses of gene expression among species and hybrids. *Arabidopsis kamchatica* is an allopolyploid species derived from the metal hyperaccumulator *A. halleri* and non-metal accumulator *A. lyrata* diploid species. We have developed a bioinformatics pipeline to separate homeologous RNAseq reads and have demonstrated that zinc hyperaccumulation in *A. kamchatica* appears to be the result of gene regulation and polymorphism derived from the diploid hyperaccumulating ancestor *A. halleri* despite hybridization with a non-accumulating *A. lyrata* ancestor. Several candidate metal homeostasis genes show strong expression bias favoring the *A. halleri* derived copies. Specifically, the zinc transporter ATPase gene HMA4 shows 15 70 fold increased expression in *A. halleri* vs. *A. lyrata* derived copies in the allopolyploid and a large genomic region (290 kb) surrounding this locus shows significantly different patterns of sequence diversity consistent with relaxed selective constraint on the *A. lyrata* derived homeologs and strong constraint or hitch-hiking on the *A. halleri* derived HMA4 region.

P27

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Integrating climate change drivers and biodiversity

Global change is a term that refers to the group of processes from natural and anthropogenic origins that affect the Earth´s environmental system and possibly its capacity to sustain life. These processes affect biodiversity, ecosystems services, politics, economics, and culture. Understanding and predicting global change is thus a highly interdisciplinary and complex undertaking. The aim of my PhD is to build towards an understanding of how interactions and feedbacks are patterned among physical, biological, and human entities.

P28

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Is there evidence for rapid evolution in a long-term grassland biodiversity experiment?

Previous studies have shown that plants that survived for eight years in species mixtures have been selected for better performance in the species mixtures than in monocultures, and vice versa. Better performance of mixture phenotype plants in species mixtures is likely due to selection pressures sorting out individuals that use overlapping niches, leading to increased complementarity between plant species in terms of character displacement and resource use, and finally, increased biodiversity effects over time. Thus, high- and low-diversity communities result in selection for plant traits leading to different phenotypes. Arguably, differences between mixture and monoculture phenotypes may be due to genetic divergence, a process called rapid evolution. However, it is possible that epigenetic factors also play an important role.

To test this, we will measure both genetic and epigenetic variation in the offspring from plants from monocultures and mixed communities (from the Jena Experiment) which were propagated in experimental monocultures and mixed communities. For the genetic and epigenetic analysis of the mixture and monoculture phenotypes, we make use of a reduced representation bisulfite sequencing (RRBS) technique that enables us to screen both genetic and epigenetic variation in a cost-efficient and highly detailed way. Furthermore, we study selection for combining ability, or the ability to function more complementarily with coexisting species, of the monoculture versus mixture selected plant types. With this project, we want to start the exploration of the role of epigenetic and genetic processes in the coexistence of species, a prime mechanism in conservation biology.

P29

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Identifying discrete genetic elements underlying diversity effects in conspecific plant communities

Recent research has frequently found a positive relationship between species diversity and ecosystem functioning, e.g. the productivity or stability of communities. Reports have further suggested that also within-species genetic diversity can promote ecosystem functioning (sometimes to a similar extent as species diversity), but little is know about the genetic principles underlying such diversity effects. A possible mechanism that can explain overyielding in more diverse communities is complementarity through niche partitioning amongst individuals in a community. Here, we describe an approach to "screen" for positive interactions between genotype pairs of *Arabidopsis thaliana* and subsequently use a quantitive genetic approach to identify discrete genetic elements underlying positive community-levels properties. Preliminary results suggest that positive effects can be caused by allelic diversity at dicrete loci. The identification and "mendelization" of such discrete genetic elements could provide a proof-of-concept for a new approach to breeding (i.e. diversity breeding), in which selection happens not for a given allele in individuals, but for a given allele diversity in a conspecific community. Cloning of the respective loci in future projects might provide insights into the mechansims that underlie niche differentiation in conspecific plant communities.

P30

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

The genetic basis of the evolutionary transition from outcrossing to selfing has been a major focus in evolutionary biology. Selfing, most commonly, evolved through the breakdown of the self-incompatibility (SI) system. Sporophytic SI system consists of the male specificity component, S-locus cysteine-rich protein (SCR), the female specificity component, S-locus receptor kinase (SRK) and genes that are involved in the downstream signaling pathway. SCR is expressed at the pollen coat and acts as the ligand of SRK, a transmembrane serine/threonine receptor kinase that expresses on the stigma. Interaction between SCR and SRK from the same S-haplogroup triggers downstream mechanism to inhibit pollen tube germination on the stigma.
Polyploidization is common in plant genomes and it has been suggested that polyploids self more frequently than their diploid relatives. However, the underlying mechanisms associating self-compatibility and polyploidization are still largely unknown. We are interested in elucidating the molecular mechanisms involve in the loss of SI in *Arabidopsis kamchatica*. It is a self-compatible allotetraploid species, originated through allopolyploidization of multiple individuals from two diploid species, *Arabidopsis halleri* and *Arabidopsis lyrata* that are predominantly outcrossing. Previous study shows that SRK and genes involved in the downstream signaling pathway are still functional in some *A. kamchatica* accessions. On the other hand, SCR is not functional in all *A. kamchatica* accessions. In order to isolate the short and polymorphic SCR genes, we performed next-generation sequencing of the anther cDNA of *A. halleri*. Potential SCR gene of S-haplogroup A, B and D, respectively were isolated. Mutations disrupting the function or expression of the potential SCR genes were identified in *A. kamchatica*. These indicate that the degradation of the male component, SCR, is responsible for the loss of SI in *A. kamchatica*.

Poster abstracts

Institute of Plant Biology
University of Zurich

in alphabetical order

P31

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ALMT4 – A Vacuolar Membrane Regulatory Anion Channel Subunit?

Aluminium Activated Malate Transporters (ALMT) are a family of ion channels unique to plants. In *Arabidopsis thaliana*, six members of this family localise to the tonoplast. ALMT9 has been shown to be a malate-activated chloride channel required for efficient stomatal opening. By contrast, nothing is known about the role of vacuolar ALMT channels during stomatal closure. Here we present data characterising a member of the vacuolar ALMT family as a channel that regulates solute fluxes during stomatal closure. Mutant plants lacking the channel protein show reduced stomatal closure in response to the drought stress hormone abscisic acid and increased sensitivity to drought. Electrophysiological data demonstrate that this channel is inactive when phosphorylated at a c-terminal motif and able to mediate malate efflux from the vacuole in a dephosphorylated, active state. Furthermore, the channel forms heteromers with other ALMTs to modulate channel gating characteristics and effectively 'shut-down' vacuolar malate uptake during stomatal closure.

P32

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FLAVONOL SYNTHASE 1(FLS1): Beyond flavonol biosynthesis, a novel mechanism of action to modulate cell growth

Flavonoids represent one of the ancestral, biggest, and most diversified families of plant secondary metabolites. Flavonols, a subgroup of flavonoids, are known to influence biological processes and play a plethora of functions in plants, from UV protection, pigmentation and modulation of hormone transport to regulation of cell growth. The last enzymatic step of flavonol biosynthesis is attributed to a single enzyme, FLAVONOL SYNTHASE 1(FLS1).

Although flavonols appeared to be in different locations both interior and exterior of the cell, biosynthesis machinery has long been thought taking place exclusively in the cytoplasm. Recent studies have shown that not only flavonoids, but also at least two of the biosynthetic enzymes, are situated in the nucleus in many cell types in Arabidopsis thaliana. This raises questions about the functional roles of nuclear localization of these enzymes. We present evidence that FLS1 and Flavonols modulate cell growth and that nuclear localization of FLS1 is of importance for this effect. Furthermore, nuclear FLS1 induces gene expression of key enzymes in flavonoid biosynthesis, suggesting a possible novel mechanisms of action of this enzyme along with its flavonol biosynthesis activity.

P33

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Identification of new rol genes or factors and their role in cell wall development in *Arabidopsis thaliana*

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. Suppressors of lrx1 were identified called rol (repressors of lrx1) mutants and whole genome sequencing was performed on them to identify a number of genes. The aim of this project is to functionally characterize four rol mutants (rol6, rol13, 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. These candidate genes could give new insights into the process of cell wall development. 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.

P34

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Evidence in powdery mildew of effector diversity as a means to evade resistance responses in wheat

One way many cereal crops defend themselves against infection by mildews is with large allelic series of resistance genes. These alleles have can evolve to recognize different factors from the fungus and thereby induce a resistance response. One such case is the Pm3 allelic series in wheat (*Triticum aestivum*), which confers race-specific resistance against wheat powdery mildew (*Blumeria graminis*). Much is known about the molecular basis of the interaction on the Pm3 side, but in this study we explored the genetics of avirulence in wheat powdery mildew in response to each of six Pm3 alleles. We found a complicated genetic interaction involving three loci in the mildew, one of which is involved in all interactions with the tested Pm3 alleles.

We generated two mapping populations and combined high-throughput, genome-wide SNP genotyping using KASP technology with bulk segregant analysis, illumina re-sequencing of target genetic intervals, de novo gene prediction, and fine mapping to identify and clone two effector genes, one from the locus common to all interactions (Bcg1), and one with a specific interaction with the Pm3a and Pm3f alleles (pu_7). Transient protein expression in *Nicotiana benthamiana* and particle bombardment in wheat provided functional validation of the recognition of pu_7 by the Pm3a and Pm3f. The genetics of the interaction provided evidence that Bcg1, the effector common to all interactions, is in fact a suppressor of recognition of avirulence effectors by Pm3 alleles. This hypothesis is supported by assays in *Nicotiana* and wheat.

A closer look into the natural variation of the pu_7 avirulence effector in wheat powdery mildew isolates from around the world revealed a diverse collection of haplotypes with evidence of purifying selection. We propose that this diversity in protein sequence is a mechanism employed by the fungus to retain the virulence function of this effector, while evading recognition by the Pm3a and Pm3f resistance gene alleles.

P35

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Pollen tube cell wall mutants as a tool for investigating plant cell growth and cell wall dynamics

Plant cells are surrounded by a cell wall that regulates growth and provides mechanical strength. While significant progress has been made in studying the chemical structure of individual cell wall components, little is known regarding the role of the constituents and arrangement of cell wall materials in regulating both cell growth and rheology. We have developed a set of approaches to characterise biochemical, biophysical, growth, and ultrastructural features at the single cell level (pollen tubes) in wild-type and different cell wall mutants. A vast array of biochemical probes including antibodies have been used to study the biochemistry of mutants and wild-type pollen tube cell walls. In addition, the cellular force microscope (CFM) has been built to investigate the biophysical properties (notably the apparent stiffness) of pollen tube cells. Furthermore, finite element method based modelling has enable the recapitulation of the behaviour of biological samples, but most importantly to obtain meaningful insight about the contribution of different biophysical players such as turgor, cell geometry, and the cell wall to the mechanical properties. While light microscopic techniques have enable the study of the growth behaviour, transmission electron microscopy (TEM) has enabled the visualization of ultrastructural changes in mutants compared to the wild-type. The gap in our knowledge of cell biophysics has played a major setback to our understanding of the immense data set obtained from cell physiology and molecular genetic studies. The approach taken here has successfully integrated different techniques enabling to advance the bridging of this gap. It offers a unique way to a comprehensive understanding of the major players in plant cell biology, and particularly the cell wall and its components.

P36

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The impact of the TOR pathway on cell growth, cell wall development and partitioning of assimilated carbon

The target of rapamycin (TOR) pathway is a major controller of eukaryotic cell growth. It is able to sense the presence of nutrients, stress signals, and growth factors, and relays this information to control processes such as translation, ribosome biogenesis and cytoskeleton dynamics. The TOR kinase, which is the central component of the TOR pathway, is specifically inhibited by rapamycin and other inhibitors. In plants, a number of TOR pathway components have been described. In a previous study it has been shown that modulation of the TOR kinase activity leads to changes in the 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 and ectopic expression of the TOR gene in *Arabidopsis*.

P37

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Mechanisms and role of linker histone dynamics in plant reproduction

Chromatin organization is important for the function of transcription, mRNA export, replication and DNA repair.1 H1 linker histone variants are among the critical factors involved in the nuclear organization of the chromatin. H1's bind the nucleosomes and the linker DNA to confer a "beads-on-a-string" sub-structure, which compaction level defines a higher-order organization to the chromatin. H1 dynamics influence not only chromatin structure but also gene expression via influencing accessibility to the transcription machinery, nucleosome positioning, histone- and DNA methylation[1]. There is increasing evidence that developmental phase transitions in *Arabidopsis thaliana* are associated with dynamic events of nuclear reorganizations. For instance, it has recently been shown, that the somatic-to-reproductive fate transition in *Arabidopsis* is accompanied by transient depletion of H1 linker histone variants[2]. While eviction is mediated by the proteasome-degradation pathway, the precise mechanisms and role of this process in development and cellular reprogramming is unknown. In this PhD project we aim to (i) elucidate the molecular mechanisms that regulate cell-specific H1 eviction in megaspore mother cells (MMCs) in *Arabidopsis* and (ii) determine the developmental function of the transient H1 eviction and its impact on the epigenetic and transcriptional status of the gametophyte. To answer those questions we will engineer conditional genetic mutations and H1 dominant negatives, and express them in reproductive tissues, to test whether H1 dynamics is moderated by histone chaperones, post-translational modifications (PTM) or a combination of both. We will monitor the impact of altered H1 dynamic in the MMC on immediate (i.e. meiosis) or mid/long term processes (i.e. gametogenesis, embryogenesis) using molecular and cell biology approaches. We expect that our results will give deeper insights on the role of H1 dynamics in plant cell reprogramming in the reproductive lineage.

References: [1] Misteli T. Concepts in nuclear architecture. BioEssays: news and reviews in molecular, cellular and developmental biology 27, 477-487 (2005), [2] She W, Grimanelli D, Rutowicz K, Whitehead Marek WJ, Puzio M, Kotlinski M, Jerzmanowski A and Baroux C. Chromatin reprogramming during the somatic-to-reproductive cell fate transition in plants. Development 140, 19 4008-4019 (2014)

Justine Sucher[1], Simon G. Krattinger[1], Liselotte L. Selter[1], Harsh Chauhan[1], Bo Zhou[2], Mingzhi Tang[3], Narayana M. Upadhyaya[4], Delphine Mieulet[5], Emmanuel Guiderdoni[5], Denise Weidenbach[6], Ulrich Schaffrath[6], Evans S. Lagudah[4], Beat Keller[1]

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The functional transfer of the wheat gene *Lr34* into rice and its resistance against rice blast

Lr34 is a wheat gene which confers a durable, partial and broad-spectrum resistance to plants. *Lr34* exists in two different alleles: a susceptible version and a resistant one which evolved after the wheat domestication about 1000 years ago. Wheat is the only species carrying such a resistance gene and this is why using it in other crop species such as rice would provide a great advantage to agriculture.
Lr34 resistant allele was transformed into the rice cultivar Nipponbare and four homozygous lines were identified. All expressed the gene, and showed resistance against multiple isolates of one of the most important rice diseases: rice blast (Magnaporthe oryzae). The different lines developed the leaf tip necrosis (LTN) phenotype which is associated with *Lr34res*. Three of them, which had seedling stage *Lr34res* expression comparable to adult expression levels, showed an early and strong phenotype, resulting in a compromised development of the plant.
Interestingly, one line, which had a significantly lower expression of the gene at seedling stage showed a late LTN phenotype and did not have negative effects on plant development. Thus it was possible to obtain one resistant line without yield penalties or fitness cost. *Lr34res* showed partial resistance against the hemi-biotrophic fungus rice blast, increasing the spectrum of resistance provided. *Lr34res* was previously only known to be efficient against biotrophic fungi such as rust or mildew. *Lr34res* might be a very useful tool to improve rice resistance and protect the plants against devastating fungi and reduce yield losses.

Reference: Krattinger *et al* (2015) The wheat durable, multipathogen resistance gene Lr34 confers partial blast resistance in rice. Plant Biotechnol.J., doi: 10.1111/pbi.12491

Poster abstracts

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P39

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Selection on floral volatiles in sister species of Alpine orchids (*Gymnadenia*)

Pollinator-mediated reproductive isolation is a major factor in driving the diversification of flowering plants. Studies of floral traits involved in reproductive isolation have focused nearly exclusively on visual signals, such as flower color. The role of less obvious signals, such as floral scent, has been studied in detail only recently. *Gymnadenia densiflora* and *G. rhellicani* (Orchidaceae) are closely related species that represent a striking transition in floral forms within the genus *Gymnadenia*. Multiple floral traits are divergent in this system, including color, inflorescence size and shape, nectar spur length, and floral scent. Both species emit a complex blend of volatiles, with limited overlap. Previous work has shown multiple floral volatiles found in these species to be important in pollinator neural response and behavior. Together, the two species produce 44 volatile compounds, of which 29 are bioactive; emission of these compounds is tightly correlated in *G. densiflora*, but largely uncorrelated in *G. rhellicani*. Using data from field studies in 2014, we have shown that volatiles in *G. densiflora* are under phenotypic selection, while selection on volatiles is absent in *G. rhellicani*. The diversity of floral volatiles in this system, along with the evidence of differing selection on floral volatiles, suggests a complex evolutionary history of scent in the genus *Gymnadenia*.

P40

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A floral colour polymorphism in *Gymnadenia rhellicani* (Orchidaceae)

Selection of novel, adaptive mutations is the main process behind the incredible diversity of organisms on this planet. In entomophilous plants, adaptation to specific pollinating insect taxa led to the evolution of flowers of an enormous variety of shape and colour. Understanding the evolution of floral traits therefore requires both knowledge about molecular mechanisms behind mutations and adaptive values of the induced phenotypic alterations. We are investigating the evolution of floral colour polymorphisms in the alpine orchid species *Gymnadenia* (= *Nigritella*) *rhellicani*. While flowers of *G. rhellicani* are usually dark red, some populations are highly polymorphic with 1-40% light red to entirely white inflorescences. Our work focuses on molecular and ecological experiments to highlight mechanisms and consequences of this phenomenon. Preliminary data suggest a genetic cause of colour variation and a potential linkage to differences in the floral scent bouquet. We aim to characterize the underlying molecular mechanisms in a forward genetics approach. Phenotypic traits such as levels of different anthocyanins are quantified for the different morphs. A comparison with RNA-seq data should later identify candidate genes for targeted sequencing. Selection pressure on different morphs will be assessed with pollinator behavioural studies and manipulation experiments under artificial and natural conditions.

Poster abstract

University of Bern

P41

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Potential of rapid genetic evolution for adaptation to lower biodiversity

The current biodiversity crisis results in a rapid change in plant community structure, and local environment. As sessile organisms plants have limited migration potential to move into remaining suitable habitats. There is therefore a strong need for adaptation to a changing environment. Specifically adaptations in response to changed light availability are in focus of this study. We assume that this environmental factor changes the most with decreasing level of biodiversity. A possible pathway of adaptation is rapid genetic evolution. However the pace of this pathway, and how strongly phenotypic plasticity mitigates it remains widely unknown. The aim of this study is to find out whether apparent differences of plant traits between communities of the Jena Biodiversity Experiment are the result of plastic adaptation to the local environment or rapid genetic evolution. We use progeny of 18 plant species which have been growing in communities with different plant diversity since 2002, and thus might have experienced different selection pressures. Currently the plants are raised from seed in a common garden experiment located in Bern. In 2016 plant traits (phenology, inflorescences, plant height, leaf size, and biomass) will be measured and compared within species with respect to their original community in the Jena Experiment.