



PSC & Syngenta Symposium 2021



Sysphinx pescadori (Saturniidae) caterpillar
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PROGRAM

KEYNOTES

Chair: Bruno Studer, ETH Zurich

10:00-10:10

Welcome and introductory words

Bruno Studer, ETH Zurich

10:10-10:30

Chemical innovation for sustainable agriculture by investing in soil health

Claudio Srepaniti, Syngenta

10:30-10:50

Plant-insect interactions with focus on plant chemical compounds with defensive properties

Tobias Züst, University of Zurich

10:50-11:10

Plant-insect chemical communication in ecological communities: an information theory perspective

Pengjuan Zu, ETH Zurich

11:10-11:30

Discussion: Questions & Answers

FELLOW PRESENTATIONS

Chair: Sylvain Bischof, University of Zurich

11:30-11:50

Plant life history influences the criteria used to reward mutualistic AMF

Sören Weber, University of Zurich, PhD-Fellow

11:50-12:10

Improved measurements of plant transpiration for sustainable agricultural water use

Dr. Eugénie Paul-Limoges, University of Zurich, Postdoctoral Fellow

12:10-13:45

Lunch Break

13:45-14:00

Influence of plant genes on microbial abundance in Arabidopsis phyllosphere

Jana Mittelstrass, University of Zurich, PhD-Fellow

14:00-14:15

Action of essential bacterial effectors on conserved plant receptor kinases: towards strategies for durable and broad-spectrum disease resistance

Laura Herold, University of Zurich, PhD-Fellow

14:15-14:30

Effects of microbial endosymbionts on the transmission of plant pathogens by aphid vectors

Patricia Sanches, ETH Zurich, PhD-Fellow

14:30-14:45

Deciphering plant exudate and root microbiota dynamics during pathogen attack

Charlotte Joller, University of Basel, PhD-Fellow

14:45-15:00

Epiploidy: An epigenetic approach to increasing the utility of polyploidy as a crop improvement tool

Miguel Wentz, University of Zurich, PhD-Fellow

15:00-15:30

Coffee Break

KEYNOTES

Chair: Willy Rueegg, Syngenta, Head CPRB

15:30-16:00

Develop new frameworks to improve the understanding of societal perception around technologies in plant science / agriculture

Angela Bearth, ETH Zurich

16:00-16:30

Syngenta Sustainability Agenda

Kelly Racette, The Nature Conservancy (TNC), NGO

16:30-16:50

Discussion: Questions & Answers

16:50-17:00

Summary and Final Remarks

Willy Rueegg, Syngenta, Head CPRB

WEDNESDAY, November 3th, 2021 Hybrid event

Registration: <https://www.plantsciences.uzh.ch/en/research/fellowships/syngenta/symposia/registrationsyngenta.html>



Deciphering plant exudate and root microbiota dynamics during pathogen attack

Klaus Schläppi (University of Basel) & Joëlle Schläpfer (University of Zurich)

Charlotte Joller, PhD student

Plants under pathogen attack adjust the composition of their microbiome and thereby, enrich for beneficial strains with protective functions. However, it is currently unclear how plants modulate their microbial communities. Metabolites exported from roots are nutrients and signaling compounds to the microbial community. We

hypothesize that altering the exudation of specific compounds presents the mechanistic link between microbe recognition and changes in the composition of plant-associated microbial communities. The objective of this project is to understand how plants alter exudation under pathogen attack, resulting in a modulated root microbiome. To accomplish this, we employ a reductionistic approach by growing *Arabidopsis thaliana* in sterile microcosm systems, by simulating pathogen attack by the application of elicitors, and studying the effects on a synthetic bacterial community. We first establish an experimental setup permitting parallelized metabolic and microbial analyses, then we identify candidate metabolites changing in response to immune stimulation, validate their effects on microbes and finally, we reassess the relevance of these key exudate compounds under natural conditions. With this project, we will make a step towards understanding the mechanistic link between a plant host and its microbiome during pathogen attack. The identification of such key exudate metabolites will permit future breeding towards cultivars with 'disease-protective microbiomes' as sustainable solution to control pathogen burden.



Epioidy: An epigenetic approach to increasing the utility of polyploidy as a crop improvement tool

Sylvain Bischof (University of Zurich), Kirsten Bomblies (ETH Zurich)

Miguel Wente, PhD student

In the context of a changing climate, stress tolerance of our crop species is critical. Genetic approaches to improving crop stress tolerance are effective, but time consuming and expensive. Whole genome duplication, which gives rise to polyploids, is a promising tool in crop improvement because new polyploids immediately have increased tolerance to multiple stresses relative to their diploid progenitors. This has several key advantages including that it is rapid, non-transgenic, and reliably provides multiple stress tolerance. However, polyploidy is hampered as a crop improvement tool by the fact that most neo-polyploids have low fertility, limiting their breeding potential, our ability to propagate them, and/or the production of fruits or grains. Overcoming this limitation requires fixing problems that occur during meiotic chromosome segregation. While this is likely a complex problem, nature has solved it many times and thus provides guidance. Several studies of different natural polyploids have shown that genes that affect chromatin compaction are targeted by natural selection in polyploid lineages. In addition, we know that in *Arabidopsis arenosa*, chromosomes are more compacted during meiosis in tetraploids than diploids. This raises the hypothesis that increased chromatin compaction is an important feature of tetraploid meiosis. This is the hypothesis we will test, both in *A. thaliana*, where we can easily alter the extent of chromatin compaction, and in tomato (*Solanum lycopersicum*), where we can test its applicability in a crop. Our aim is to manipulate chromatin compaction in diploids of both species and test the outcome for meiotic stability, and fertility, upon genome duplication.



Effects of microbial endosymbionts on the transmission of plant pathogens by aphid vectors

Mark Mescher, Clara Sanchez-Rodriguez, Consuelo De Moraes (ETH Zurich), Anke Buchholz (Syngenta)

Patricia Sanches, PhD student

Endosymbiotic gut bacteria are well-known for mediating aphid interaction with host plants and natural enemies; however, little is currently known about the potential effects of aphid endosymbionts on disease transmission. To address this knowledge gap, we explore how endosymbionts shape aphid-plant-virus interactions. Specifically,

we investigate how aphid association with different suites of gut bacteria influences: (i) aphid preferences for and performance on infected plants; (ii) infected and healthy plant defenses; (iii) aphid susceptibility to natural enemies; and (iv) the acquisition, retention, and transmission of plant viruses by aphid vectors. Results of the objective (i) reveal that the biology and behavior of aphids is influenced by the interaction between the virus infection of host plants and species of aphid symbionts. In migration experiments, only aphids harboring *Regiella insecticola* or *Hamiltonella defensa* bacteria exhibited a plant choice, with viruliferous individuals preferentially settling on healthy plants. Interestingly, aphid biomass and population density were enhanced only for colonies harboring one of these bacterial species. In the host plant, virus infection increased levels of sugars and amino acids in phloem tissue. Further metabolomics assays with aphids revealed that colonies with *H. defensa* and *R. insecticola* had distinctly high levels of some of these amino acids and/or sugars. Taken together, these results reveal that enhanced aphid fitness and modification of their behavior favoring virus transmission depend on the composition of bacteria species and strains in aphid's gut. Furthermore, the specificity of the interaction between the plant virus and the symbiotic bacteria *R. insecticola* or *H. defensa* uncovers a potential novel mutualism.



Action of essential bacterial effectors on conserved plant receptor kinases: towards strategies for durable and broad-spectrum disease resistance

Cyril Zipfel (University of Zurich), Giovanni Brogginì (ETH Zurich), Euiwhan Chung (Syngenta)

Laura Herold, PhD student

Crop losses caused by pathogens and pests threaten food security. Using chemicals to control the ensuing diseases imposes significant monetary and/or environmental costs. A more sustainable approach is to use genetics to increase disease resistance against important pathogens in crops. This however requires a more detailed understanding of the molecular mechanisms controlling the interaction between pathogens and their host plants. This project is based on the characterization of conserved, essential proteins that are injected within plant cells by pathogenic bacteria. These proteins, called effectors, are key determinant of virulence and thus of disease establishment and/or progression. A phylogeny-based approach using the model plant *Arabidopsis thaliana*, the crop maize and the fruit crop apple identified four clusters of receptor kinases as putative targets of a broadly conserved and pathologically important bacterial effector family. These candidates are screened for their interaction with this effector by yeast two-hybrid and split-luciferase assays. Positive interactions will be confirmed in planta using co-immunoprecipitation. The impact of the effector on these candidates will be characterized as well as the role of these proteins in plant immunity (or other processes). Additionally, knock-out mutants in *Arabidopsis* and apple using CRISPR/Cas9 are currently generated and will be investigated for increased disease resistance against phytopathogenic bacteria. This comparative study between different plant species will provide scientific insights and potential practical applications for crop protection.



Improved measurements of plant transpiration for sustainable agricultural water use

Alexander Damm (University of Zurich), Nina Buchmann, Johan Six (ETH Zurich)

Eugénie Paul-Limoges (Postdoc)

As agriculture substantially contributes to freshwater withdrawals, shortages and changes in water availability will be a predominant stress to food security in upcoming years. Reducing water losses in agriculture needs a solid understanding of when evaporation (E) losses occur and how much water is used through crop transpiration

(T) to develop smart water management practices, design irrigation systems, and calculate crop yields. Quantifying ecosystem T is however challenging, and even more so when it comes to low-statured crops, where many standard methods cannot be applied. In our study, we combined biometeorological measurements with a SPA-Crop model to estimate T at a Swiss cropland over two crop seasons with winter cereals. We compared our results with the Transpiration Estimation Algorithm (TEA) model and the Zhou model. Our results showed that the available energy reaching the soil through the crop canopy can highly vary depending on growth and climatic conditions. Despite large differences in the productivity of both years, the T/ET ratio had similar seasonal and diurnal dynamics, and averaged to 0.72 and 0.73 for both crop seasons. Our measurements combined with a SPA-Crop model provided T estimates similar to the TEA model, while the Zhou model underestimated T even when the soil and leaves were dry. T was strongly related to the leaf area index, but additionally varying due to weather and physiology. The most important climatic drivers controlling T were found to be the photosynthetic photon flux density ($R^2=0.84$ and 0.87), and vapor pressure deficit ($R^2=0.86$ and 0.70), while air temperature and soil water content played a less important role. Our results suggest that site-specific studies can help establish T/ET ratios, as well as dominant climatic drivers, which could then be used to partition T from reliable ET measurements.



Identifying the plant genes that shape the leaf metabolome and microbiome

Matt Horton (University of Zurich), Julia Vorholt (ETH Zurich)

Jana Mittelstrass, PhD student

In nature, plants are colonized by a wide variety of microbes. Although it is well understood that these communities influence the health of their hosts, the rules of community assembly remain poorly understood. In particular, the question whether and how plants shape their microbial communities remains unanswered, although defense genes and plant chemistry are known to play important roles. If so, the host genes that are involved in these or other related plant traits are strong a priori candidates in microbiome assembly. Earlier, we identified plant genes which were associated with different components of the *Arabidopsis* microbiome. Here, we compare the microbiomes of wild-type *Arabidopsis* plants with the microbiomes of mutant genotypes to understand the effects of these genes on plant microbiome diversity in field conditions. The discovery that not all of the tested plant genes showed predicted effects on selected microbial traits stimulates the discussion about host effects in the context of genotype-by-environment (GxE) effects. In addition, by confirming that certain genes affected microbial traits, this study illustrates that gene mapping approaches can be a suitable tool in identifying genes involved in microbiome formation.



How does the plant-AMF mutualism scale from pairwise interactions to complex networks? An analysis combining theory and experiments

Pascal Niklaus, Jordi Bascompte (University of Zurich), Ansgar Kahmen (University of Basel)

Sören Weber, PhD student

Arbuscular mycorrhizal fungi (AMF) are mutualists of plants, and their diversity has a large effect on plant community assembly and ecosystem functioning. A predominant role of AMF is the transfer of phosphorous to plants in exchange for sugars and fatty-acids. Previous

research has demonstrated that both AMF and plants can trade resources reciprocally. However, it is unclear how this preferential trade within complex assemblages of AMF and plant taxa mediates the observed positive effects of AMF diversity on plant community diversity and productivity. Using radioactive isotope labels of carbon and phosphorus, we have found that AMF adjust their resource 'costliness' in response to competing AMF by changing the amount of phosphorus they transfer to plants. In turn, these changes in resource costliness increase the total amount of plant foliar phosphorus. Additionally, this effect of AMF competition on phosphorus transfer to plants becomes stronger with increasing AMF species richness.