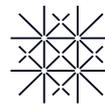




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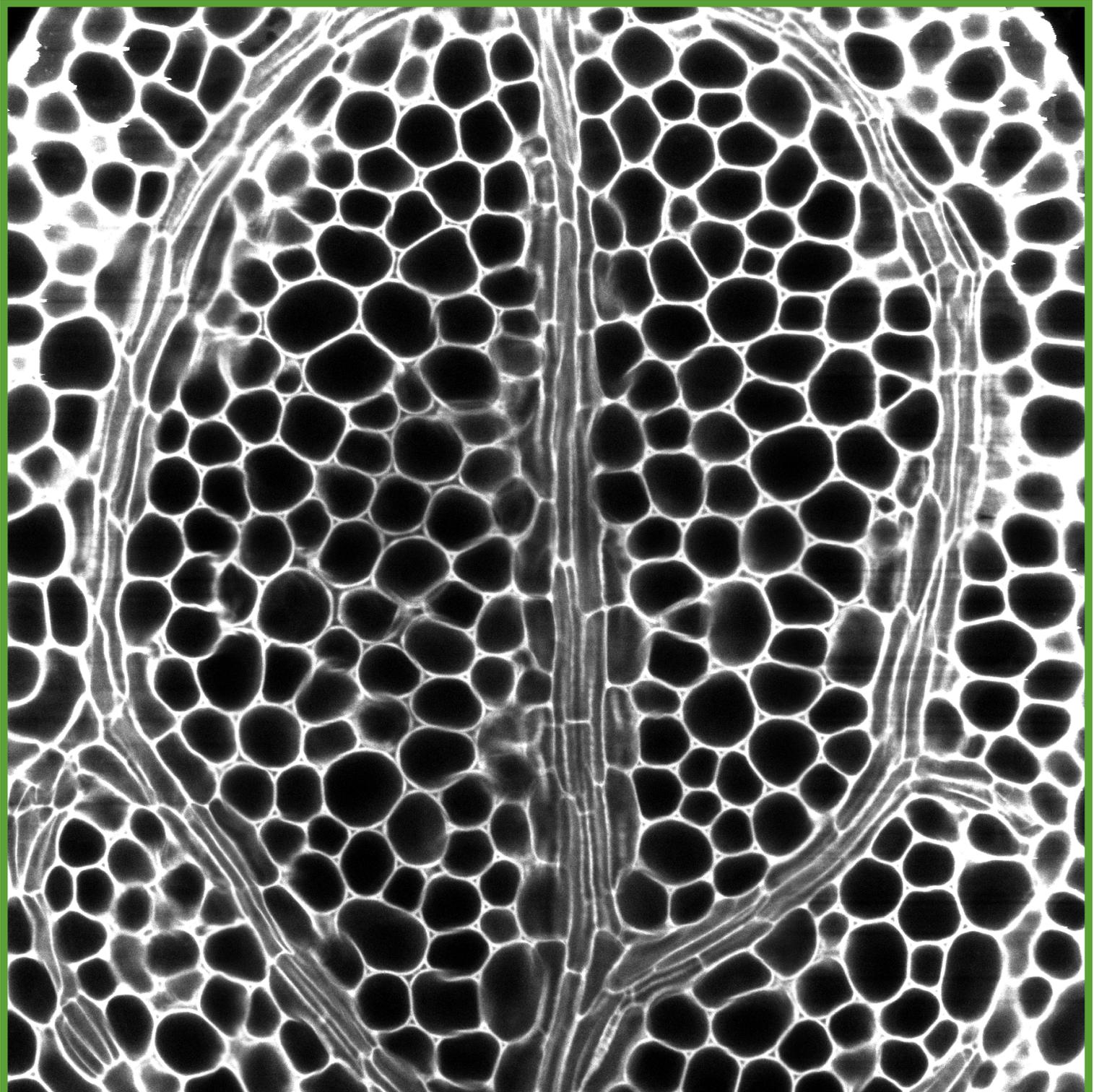


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Zurich-Basel Plant Science Center

PlantScienceNews

No 41, Spring 2022



Editorial

Dance of agency

In the pursuit of scientific understanding, technologies have evolved to fulfill researchers' requirements. In 1995, Pickering coined the term “dance of agencies” describing a combination of material, conceptual and disciplinary agency. In light of the global challenges we face, the agency of the scientist is not only located in their handling of concepts and practices, but in their directing this dance in pursuit of broader goals and purposes.

Digital technologies have been deemed powerful tools for fulfilling the Sustainable Development Goals. However, technological innovation can intersect with values, norms, and moral commitments and thus fail environmental, economic or societal improvements. A new PSC course introduces the concept of value-sensitive innovation to teach students about the ethical considerations associated with the use and development of emerging technologies. It will equip young scientists with a value-based innovation approach, which they will benefit from when they enter today's increasingly digitalized society. The course will offer not only a body of knowledge, but a set of toolkits for students to use in their own domains of research. Recently joining our team, education specialist for value-based design, Ning Wang, co-designed the course with us.

In this edition, we also warmly welcome Janneke Hille Ris Lambers in our PSC network. Janneke is studying the impacts of climate change on plant communities.

Enjoy reading.

Sincerely,
Manuela Dahinden & Melanie Paschke, PSC Managing Directors

Pickering, A. (1995). The mangle of practice: Time, agency, and science. University of Chicago Press.

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PSC Managing Office: **Manuela Dahinden**, managing director research and outreach; **Melanie Paschke**, managing director education and science-society dialogue; **Romy Kohlmann**, finances, events and fellowship program coordinator; **Luisa Last**, coordinator PSC PhD programs & RESPONSE Doctoral Program; **Yvonne Möller-Steinbach** (interim) coordinator PSC PhD programs; **Barbara Templ**, education specialist for data science; **Ning Wang**, education specialist for value-based design; **Daniela Gunz**, feminno program coordinator; **Juanita Schläpfer**, outreach manager; **Ulrike von Groll**, project coordinator: Nachtaktiv; **Dubravka Vrdoljak**, project coordinator: Dialog im Quartier; **Franziska Suter**, teacher and project assistant: PlantScience@School; **Marina Eva Stirnemann**, project assistant: Climate Garden 2085; **Sylvia Martinez**, coordinator Basel & Swiss Plant Science Web.

Open call

PSC-SYNGENTA FELLOWSHIP PROGRAM

This funding scheme promotes bottom-up and innovative research in plant sciences focusing on: **Climate change – challenges and opportunities in agriculture (or crop production)**. Topics may include:

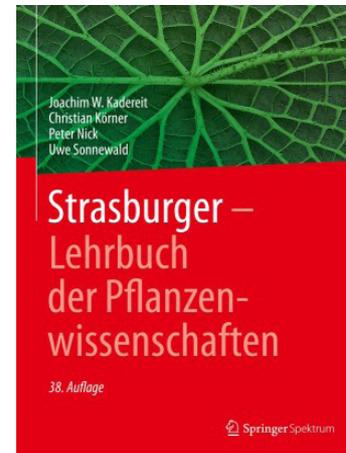
- Develop knowledge & tools to better predict the effects of climate change on agriculture systems (at different spatial and temporal scales).
- Advance on fundamental & applied plant science to mitigate adverse climatic events and secure crop protection and crop production.
- Unearth new discoveries and inventions to feed the innovation process in sustainable crop protection / production.

Proposals for PhD or Post doc fellowships can be submitted until November 1, 2022. Acceptance of research projects include a financial support of either CHF 225,000 for a PhD student (with an expected 4-years PhD duration) or CHF 175,000 for a Post doc (max. 24 months). Research costs / consumables need to be co-founded by the applicants. A maximum of CHF 450,000 funding will be available. Two projects will be selected. Please take into consideration that applicants of approved projects will have to accept the terms and conditions of the agreement between the three PSC partner universities and Syngenta Crop Protection AG. One proposal per applicant is recommended.

Contact: **Manuela Dahinden**, mdahinden@ethz.ch

www.plantsciences.ch/research/fellowships/syngenta.html

Selected book



Strasburger – Lehrbuch der Pflanzenwissenschaften, 2021
Joachim W. Kadereit, Christian Körner, Peter Nick, Uwe Sonnewald

Springer-Verlag GmbH Deutschland, part of Springer Nature
Hardcover ISBN 978-3-662-61942-1
eBook ISBN 978-3-662-61943-8

<https://link.springer.com/book/10.1007/978-3-662-61943-8>

Awards

We congratulate the following PSC members for being among **the Clarivate Highly Cited Researchers 2021**:

Agriculture:

Johan Six, ETH Zurich

Cross-Field:

Jordi Bascompte, University of Zurich
Christian Körner, *emeritus*, University of Basel

Klaus Schläppi, University of Basel
Marcel van der Heijden, University of Zurich & Swiss Fed Res Stn Agroscope

Plant & Animal Science:

Enrico Martinoia, *emeritus*, University of Zurich

Cyril Zipfel, University of Zurich

Post-doctoral fellow Hiroyuki Kakui received the Presentation Award of the 140th meeting of the Japanese Society of Breeding. Title: "PRIMA (Probe-induced heteroduplex mobility assay) for rapid and cost-efficient detection of 1-bp DNA difference", (Kentaro Shimizu group, University of Zurich).

Andrea Carminati received together with Mathieu Javaux the ISCM Publication Award 2021 for the paper "Soil rather than xylem vulnerability controls stomatal response to drought", *Trends in Plant Science*, 25: 868–880.

Kristýna Kantnerová received the Atmospheric Chemistry and Physics (ACP) Award 2021 and the the Chorafas Award 2021 for her PhD thesis "Analysis of clumped isotopes of nitrous oxide: method development and first applications", (Johan Six group, ETH Zurich).

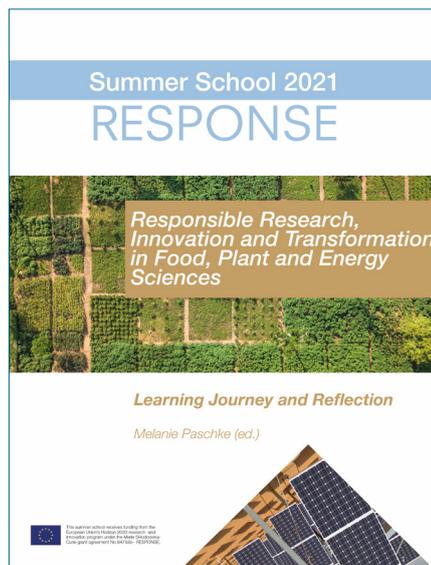
The PSC Symposium Poster Award 2021 was presented to three equal winners: **Zoe Bernasconi** et al., for her poster "Unravelling the molecular basis of wheat powdery mildew virulence patterns through ultraviolet mutagenesis" (Beat Keller group, University of Zurich); **Danli Fei**, for her poster "Chromatin-based controls in the reproductive lineage" (Celia Baroux group, University of Zurich); and **Marie-Louise Schärer** for her poster "Soil nutrient processes and not plant physiological properties are the main drivers of post-drought yield outperformance in *Lolium perenne*" (Ansgar Kahmen group, University of Basel).

RESPONSE Doctoral Program

At a glance

The RESPONSE Doctoral Program (DP) is a joint doctoral program of ETH Zurich, University of Zurich and University of Basel. RESPONSE DP is centrally managed by the PSC in collaboration with the ETH competence centers: the World Food System Center and the Energy Science Center. Since the program's launch in February 2020, 28 students have started their PhD projects. In this newsletter we introduce four fellows who started in Call 4.

www.plantsciences.uzh.ch/en/research/fellowships/response.html



Proceedings of Summer School

The 5-day RESPONSE Summer School built an environment for participants to work through case studies and to expand from a scientific to a society-inclusive perspective. The participants had the opportunity to follow a structured process which guided them towards the development of a group project and to tackle one of the following problems: Digital technologies for urban micro farms, circular approaches in the food system, vertical farming, sustainable and resilient energy, food and biodiversity landscapes, stewardship of land use change – how can drones offer support?

In the first part of the reflective report, you can explore the five case studies and follow the individual learning journey of the groups. In the second part the speaker's abstracts are summarized.

Response Summer School «Responsible Research, Innovation and Transformation in Food, Plant and Energy Sciences» Learning Journey and Reflection. Melanie Paschke (ed.). Zurich-Basel Plant Science Center, 2021.

With contributions by: Manuel Belanche Guadas, Linda Brodnicke, Dusan Denic, Danli Fei, Linda Frattini, Laurent Giguère, Reah Gonzales, Monika Katarzyna Goralczyk, Katharina Jung, Xeniya Kim, Simon Landauer, Yuanyuan Liang, Alberto Linares Quiros, Simone Markoff, Bessie Noll, Dabwiso Sakala, Fei Wu, and Francesca Zuffa.

<https://doi.org/10.3929/ethz-b-000523545>

Upcoming

2nd Annual meeting

Wednesday, March 16, 2022

EU Midterm Review, online

Thursday, March 17, 2022

PhD Retreat, online

Friday, March 18, 2022

Mentoring Workshops (ETH Zurich, CLA J1) and Board Meetings, online

Mentoring Workshop 1 Problem-Framing

Dr. Christian Pohl (TdLab, ETH Zurich)

This workshop aims at developing and strengthening students ability to integrate disciplines and related knowledge for joint knowledge production. It aims at supporting the formulations of questions that are of societal relevance within each participant's own research project.

Mentoring Workshop 2 Impact analysis and generation

Dr. Sibylle Studer (Swiss Academy of Sciences, SCNAT)

This workshop will help students to evaluate the impact of their research projects. They will practice various tools to formulate clearly stated, explicit and measurable indicators of project impact at the science-policy or science-innovation interface for their research projects.



This program receives funding from the European Union's Horizon 2020 research and innovation program under the Marie Skłodowska-Curie grant agreement No 847585 – RESPONSE.

Monitoring the effect of deforestation and reforestation on vertebrate diversity using river environmental DNA (eDNA)

Forest loss and degradation jeopardizes the provisioning of essential ecosystem services to society. Restoration projects, which often involve a mix of planting native vegetation and assisted natural regrowth, aim to bring these ecosystems back to the reference condition of old-growth forests. To ensure their success, one of the crucial aspects of forest restoration is to enable recovery of faunal communities. Unfortunately, this task is often undermined by the limited empirical evidence on species responses to forest loss and regeneration, making it difficult to adopt effective management and restoration strategies.

To address this knowledge gap, we will use a novel approach of quantifying biodiversity through environmental DNA (eDNA) to compare vertebrate diversity between forests at different stages of succession: from old-growth tropical forest through degraded pasture to recently restored forest. Coupled with environmental data, information on catchment-level biodiversity will help improve understanding of the mechanism of habitat selection by forest-dwelling communities in the context of forest loss and restoration.

Beyond understanding of the drivers of biodiversity loss and recovery, in order to adapt effective management and restoration strategies, policymakers need tools for rapid biodiversity assessment and long-term monitoring. Several studies confirm that the analysis of eDNA for terrestrial biodiversity assessments is more time- and cost-effective than traditional methods (such as, e.g., camera traps and mist netting). However, the application of eDNA in biodiversity monitoring, especially in terrestrial ecosystems, remains largely unexplored. To this end, one of the overarching aims of this project is to apply a range of laboratory and computational techniques to contribute to the standardization of eDNA-based methods in monitoring of terrestrial biodiversity.

The secondment partner organization, World Wildlife Fund for Nature (WWF), has a long history of working towards the conservation of threatened wildlife and ecosystems. With their expert help, we aim to use the knowledge gathered in this project to advance the existing indicators of biodiversity. Improved tools for monitoring changes in biodiversity will facilitate the implementation of restoration and conservation projects in line with the global strategic efforts for restoring nature.



Fellow: Monika Golarczyk

PI: Prof. Loïc Pellissier, Department of Environmental Systems Science, ETH Zurich

Project partners: Arnaud Lyet, WWF US and Dr. Tony Dejean, SPYGEN (France)



Animals leave traces of DNA in the water which are carried downstream. Sampling of river eDNA allows us to characterize wildlife of the entire catchment.

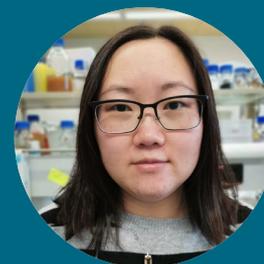
© Monika Golarczyk

Application of plant peptides for the sustainable improvement of crop resistance to biotic and abiotic stresses ('PEPSTRESS')

Massive crop losses occur annually due to diseases and abiotic factors. Attempts to reduce the impact of biotic and abiotic stresses traditionally involve breeding and the extensive use of chemicals. Development and use of agrochemicals require an urgent rethink, due to novel regulations surrounding their development and use. Currently, many chemicals are being increasingly banned, and the EU is aiming for a 'zero-residue' agriculture. The new sustainability and intensification challenges that agriculture is currently facing call for a careful evidence-based evaluation of the solutions that could be implemented to sustain food and feed production. There is therefore a regained interest in 'natural' plant-derived products, as these would be aligned with an increasingly restrictive registration legislation, and could be utilized by both conventional and organic agriculture. While the importance of plant peptides in all aspects of plant biology – including responses to environmental stresses – is increasingly becoming important, their potential use has not been yet fully evaluated. PEPSTRESS directly aims at filling this gap, and capitalizes on the complementary expertise of our group in peptide-based signaling and of Syngenta in crop protection. The project is built on our recent identification of novel families of stress-responsive plant peptides.

In my PhD project, I aim to decipher the mode-of-action of these peptides in activating stress responses, study the regulation and evolution of such peptides, and test the efficacy of peptide treatments on crops' stress resistance. Since it was reported that some peptides inhibit the growth of some plant pathogens, the direct antimicrobial/antifungal activity of the whole peptide family will be assessed.

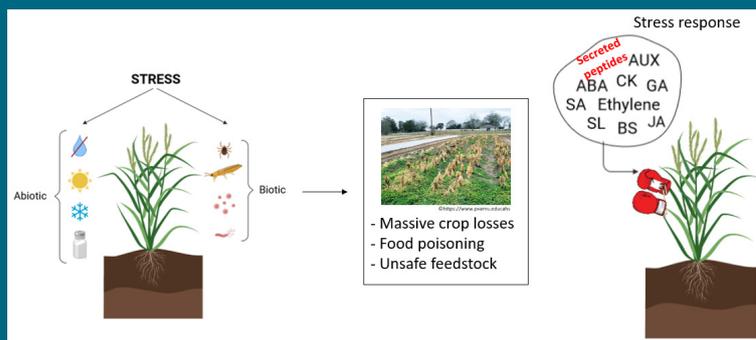
This project will fill (1) a societal need for more sustainable crop management products, (2) a regulatory need for products with negligible impact on the environment and proven human safety, and (3) an industrial need for efficient complementary or alternative technologies to current controversial chemical or genetic solutions. As such, PEPSTRESS will inform academia, industry and policymakers of the potential use of peptides as novel natural crop improvement treatments, and will also lead to potential development of commercial products by the industrial partner.



Fellow: Xeniya Kim

PI: Prof. Cyril Zipfel, Department of Plant and Microbial Biology, University of Zurich

Project partners: Dirk Balmer and Katrin Hermann Syngenta Crop Protection AG – Biological Science, Switzerland



Plants constantly face biotic (e.g., pathogens and pests) and abiotic (e.g., heat, cold, drought, salt) stresses which may lead to undesirable consequences. Central to stress responses are plant hormones. Classical hormones, such as gibberellic acid (GA), abscisic acid (ABA), ethylene or salicylic acid (SA), have been widely studied, and their derivatives are often used in agriculture. In the past decade, it became evident that plant genomes encode a myriad of secreted peptides. While the functions of many of them are still unknown, plant peptides are now being recognized as plant hormones, given the key roles already assigned to several of them in growth, development and responses to the environment.

© Xeniya Kim

Inferring legacy of human activities on tropical forest plant diversity with spatial genetics and remote sensing



Humans have transformed tropical forests dramatically through the acquisition and changes of resources dynamics and modification of conditions, bringing about change in Earth’s surface, both in current and early times of human occupation. Recent research points out that long term human modification explains some present-day patterns of biodiversity because human activities, past plant management and agricultural practices could have a lasting effect on plant diversity in tropical forests. Yet, a lack of integrated studies that connect past land systems with modern vegetation has left unanswered questions about the legacy of long-term land use on the current plant composition and diversity in rainforests. However, how long human-driven effects on forest plant species and traits persist, and what kind of patterns emerge in genetic diversity, remain unknown.

My PhD project aims to unveil patterns and effects of the legacy of human presence on plant species, traits, and genetic diversity in Borneo tropical forests. We hypothesize that with long-term and increasing human presence and intensity, species richness increases until an inflection point is reached, after which a decrease in species richness (along with functional and genetic diversity) is expected. We predict that such effects occur along a gradient of distance to human settlement. I use a novel combination of remote sensing with field data and genetic analyses, expecting to detect persistent effects of long-term human presence on species and functional diversity, even if dampened by natural restoration and forest resilience. Recognizing the long-term human shaping of global biodiversity is key to understanding contemporary and future ecosystems and their restoration.

Fellow: Nathalia Perez Cardenas

PIs: Prof. Maria J. Santos, Department of Geography, University of Zurich and Prof. Dr. Meredith Schuman, Departments of Geography and Chemistry, University of Zurich

Project partner: Dr. Mikey O’Brien, South East Asia Rainforest Research Partnership – SEARRP

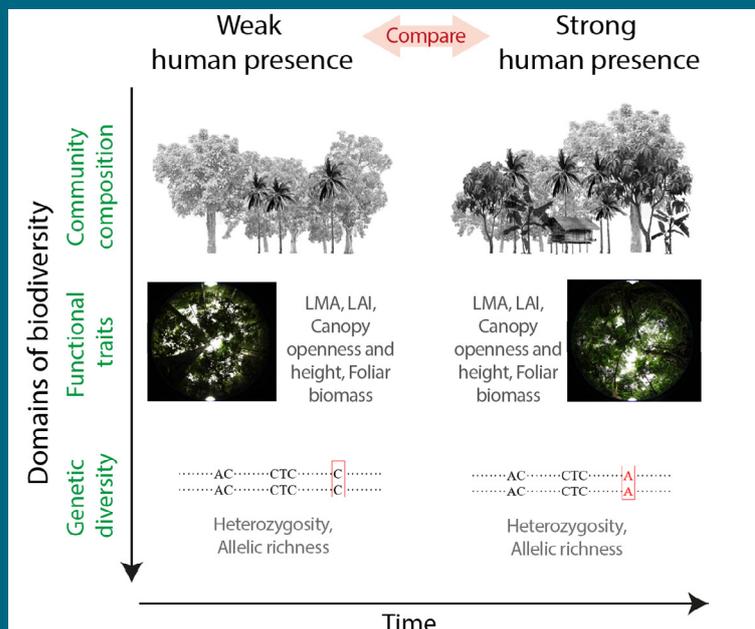


Diagram representing the relationship between the differences in human presence, and the different diversity domains considered in the project, namely community composition, functional traits and genetic diversity.

© Nathalia Perez Cardenas

Sustainable storage hydropower for a resilient future energy system

For decades, hydropower has been an important pillar of the electric power system in Alpine regions, providing both generation of electric energy and storage of energy by high-altitude impoundments of water; and it is still today.

Simultaneously to the future deployment of new renewables including solar and wind as part of the energy transition, hydropower facilities will require a transformation to maintain their role as the backbone of an increasingly volatile and extended electric power system. In 2019, the Swiss Federal Office of Energy published an updated edition of its hydropower potential study, stating that considerable efforts are necessary to maintain and extend today's hydropower capacities to meet the requirements set out in the Swiss Energy Strategy 2050. Among other factors, the study specifies reservoir sedimentation as a negative impact on hydropower storage capacities in Switzerland. An estimated loss of 7% of the seasonal storage capacity in Swiss reservoirs is anticipated until 2050. In many reservoirs, the sedimentation rate is much more acute, creating operational and dam safety problems. The project aims at reducing the uncertainties related to the assessment of long-term reservoir sedimentation under the effect of climate change. This will lead to better information of the future availability of Swiss hydropower's storage capacities. Incorporated in upcoming editions of the hydropower potential study, these results may directly influence policy decisions shaping the development of prospective Swiss energy systems. Therefore, the hydropower section of the Swiss Federal Office of Energy is involved as a partner organization. Numerical modelling will be applied to simulate the effects of different sediment management strategies. Besides engineering challenges, environmental and consequently also societal issues arise by the questions to be dealt with.

This fellowship is hosted by the Energy Science Center.



Fellow: Sudesh Dahal

PI: Prof. Robert Boes, Laboratory of Hydraulics, Hydrology and Glaciology VAW, ETH Zurich

Project partner: Dr. Christian Dupraz, Swiss Federal Office of Energy BFE



Sedimentation in Griessee reservoir.

© Ehrbar/VAW 2018

Machine learning in plant sciences

In this contribution we present two applications of machine learning addressing important research questions such as how plants interact with water and how plants respond to environmental change.

Tracing plant water sources using machine learning

by Daniel B. Nelson

Understanding how water moves through the environment, and when and where it is available for plants is an important research topic. Meteorological data form the foundations of our knowledge in this area, but we still often lack information on many processes that are important for plants. For example, plants may use water from different depths in the soil that contain water from precipitation that fell months earlier. This can mean that the relative importance of precipitation from different seasons is not always clear. To more completely understand how plants interact with water in the environment, measurements of the distributions of water isotopologues provide a useful tool to distinguish between water from different sources or time periods. However, use of water isotopologues as a chemical fingerprinting tool can be complex, and this is an area where machine learning can make an important contribution.

Isotopes in the water cycle

Water isotopologues are water molecules made up of different combinations of oxygen and hydrogen isotopes. All water molecules consist of two hydrogen atoms and one oxygen atom, but the isotopic composition of these hydrogen and oxygen atoms vary among water molecules - these are the isotopologues of water. Water isotopologues all behave in generally the same way, but slight differences in mass mean that heavier isotopologues require slightly more energy to evaporate from liquid to gas, and need to lose slightly less energy to

condense from gas to liquid than the more common lighter isotopologues. This causes differences in the oxygen and hydrogen isotopic composition of precipitation around the world and over time. The underlying mechanisms are complex, but simply knowing what the oxygen or hydrogen isotopic composition of precipitation was over time and space allows these values to be used to understand process that take place after the precipitation falls. This is the starting point for most applications in plant sciences and an area where machine learning can make an important contribution.

The International Atomic Energy Agency has operated the Global Network of Isotopes in Precipitation (GNIP) for more than 60 years, and now manages a database consisting of thousands of monthly average precipitation oxygen and hydrogen isotope values from around the world. Although impressive in its extent, from the viewpoint of a researcher conducting work at a single location, the availability of historic data in this database is often insufficient for the types of questions that they are seeking to address. For example, a researcher might want to know the oxygen isotopic composition of rain at their forest site for the five years leading up to the point when they began their study, but the nearest station in the GNIP database might be 200 km away, and may have only reported data for a few years in the 1970s. Fortunately, we know from work on the mechanisms that control the oxygen and hydrogen isotopic compo-

sition of rain, that these values are strongly related to climate variables that are more routinely measured, such as air temperature, relative humidity, precipitation rate, and others.

The role for machine learning

We sought to improve on the availability of historic precipitation isotope values by taking advantage of the rapidly expanding array of machine learning tools. Specifically, we developed and trained a model using additive regression trees to predict precipitation isotope values from GNIP data using climate variables available from several datasets (Figure 1). Additive regression trees make predictions by splitting the dataset into subcategories based on values for given input predictor variables, with each split creating a branch point in how the data are grouped. Each such procedure forms a single regression tree, and while the predictions from any individual tree do not usually yield accurate predictions for unknown samples, the mean prediction from many such trees can be very accurate. The process by which new trees are produced, added, or removed gives rise to the names of the various models that fall within this broad category of algorithms, such as random forest, gradient boosting, or extreme gradient boosting (xgboost), which is the algorithm at the foundation of our work (Nelson, Basler, Kahmen, PNAS 2021 Vol. 118 No. 26). A primary goal of this work was to generate an accessible tool that could be easily used by interested researchers and students. We therefore

developed a simple web application for this model, which we named Piso.AI (<https://isotope.bot.unibas.ch/PisoAI/>). The web interface provides the ability to generate a time series of predictions at any location within the model area. It can also be used through an application programming interface (API), with instructions on GitHub (<https://github.com/nelsondb/PisoAI>).

Lessons learned

We began this work with the general goal of exploring the potential of machine learning to make better predictions of the oxygen and hydrogen isotopic composition of precipitation. Challenges included identifying an appropriate modeling algorithm for our target problem, selecting data that could be used as predictor variables, deciding what types of preprocessing procedures to use, and determining the optimal

space and time range over which to construct our model. We also had to evaluate different options for splitting the data into testing and training datasets to ensure that the model predictions were as accurate as possible in new locations. These types of challenges are common among many machine learning applications, and there are few universal answers. Each dataset is different, and the overall research goals, as well as the strengths and weaknesses of the available data must be carefully considered in each case. Many of these decisions are best answered with consideration not only of the machine learning approach being used, but also scientific knowledge specific to the question that is being addressed. This highlights the need for researchers in individual scientific disciplines to add basic working knowledge of machine learning to their skill set and training.

Reference

Daniel B. Nelson, David Basler, Ansgar Kahmen (2021). Precipitation isotope time series predictions from machine learning applied in Europe. PNAS, 118 (26) e2024107118. <https://doi.org/10.1073/pnas.2024107118>

Daniel is Senior researcher and Stable Isotope Laboratory Manager in the lab of Ansgar Kahmen at the Department of Environmental Sciences, University of Basel.

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<https://ppe.duw.unibas.ch>

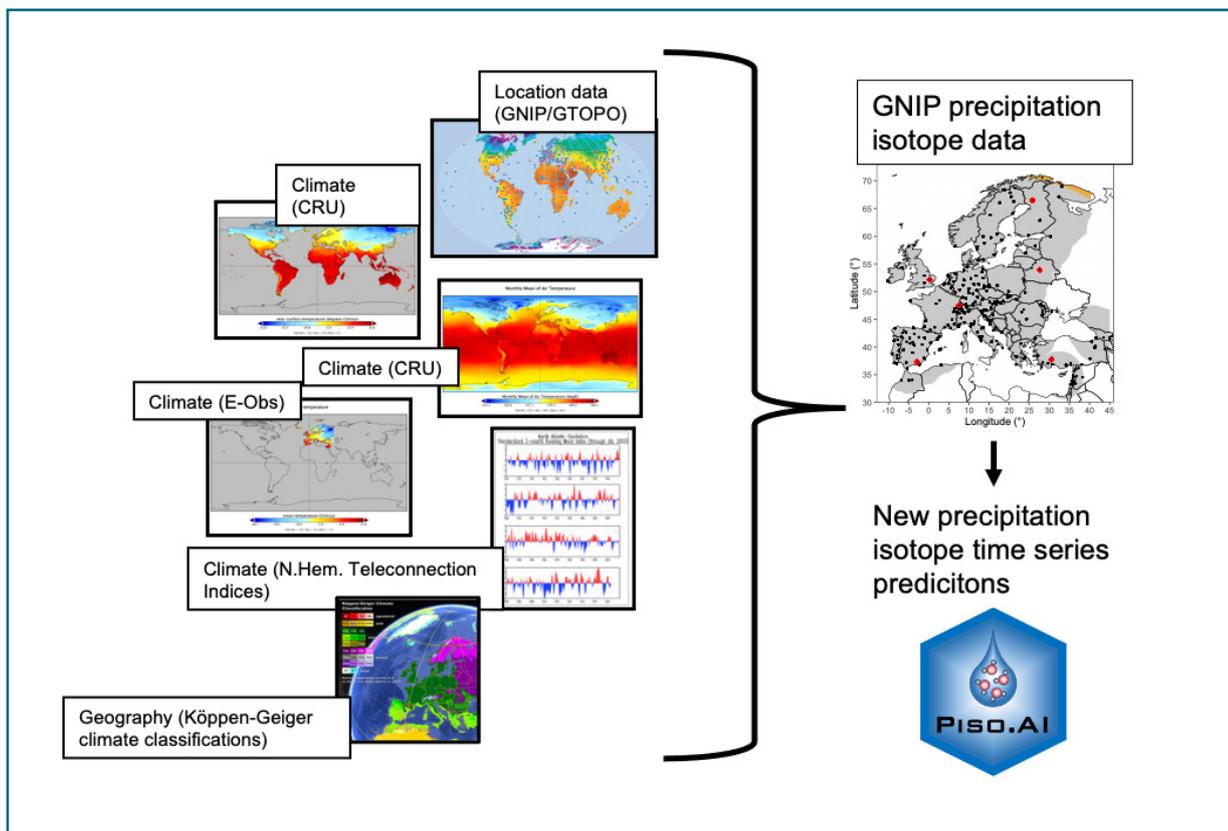


Figure 1: Conceptual workflow for developing a machine learning model to generate time series of isotope data in precipitation. Datasets on the left side of the figure were used for input variables to predict values for precipitation isotope data from the Global Network of Isotopes in Precipitation (GNIP). The model product, Piso.AI, can be accessed at: <https://isotope.bot.unibas.ch/PisoAI/>. For more details, see the original publication.

Time-series image analysis in fluctuating field conditions using machine learning

by Reiko Akiyama

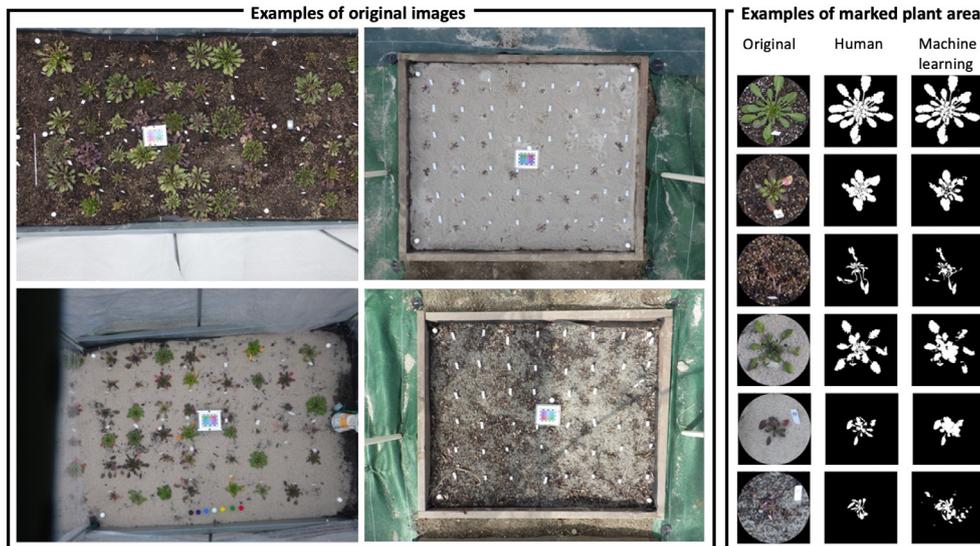


Figure 1: Examples of original images and marked plant area. The original images exemplify the variation in our dataset. Clockwise from top left: relatively large plants in soil background, relatively small plants in sand background, relatively small plants in a mixture of sand and humus background under strong light, and relatively large plants in sand background. In all images, shape and colour of the plants vary. The examples of marked plant area embody typical examples of a green plant in soil background, a plant with green and red leaves in soil background, a red plant in soil background, a green plant in sand background, a red plant in sand background, and a red plant in a mixture of sand and humus background (from top to bottom). For each plant, the original image (left), the 'ground truth' marked by human (middle), and the area marked by the algorithm (right) are shown.

We use machine learning to understand how plants thrive in seasonal environments. Some plants produce red pigments (anthocyanins) in response to climatic factors such as low temperature, or drought. This response can be recorded by regularly photographing the plant. Therefore, by monitoring climatic factors and plant colours throughout plant life cycle, we can approach our goal.

For image analysis, we mark the plants, e.g., using the tool *labelme* in python. Because of the large size of our image dataset, marking the plants by hand is too laborious. This is where machine learning helps. By training an algorithm to mark the plant, the image analysis can be performed fast and efficiently on large datasets (Mou et al., 2021).

One technical challenge is to prepare an efficient training dataset. Our images from outdoor across seasons show variation in plant colour, size, shape, brightness, background colour, and texture (Fig. 1: Examples of original images). If a training dataset contains only plants in a soil background, the algorithm has difficulty in recognizing plants in a sand background. Therefore, a training dataset should cover all the variation in

the dataset. To achieve this without increasing manual marking effort, we can for example synthesize manually marked plants in the soil background with the sand background.

From the plant areas marked by the algorithm (Fig. 1: Examples of marked plant area), we can extract colour information. We use the $L^*a^*b^*$ colour space, where the axis a^* changes from green to red, matching the colour gradient of our plants. With time series data of a^* on different genotypes and species, we will be able to address questions such as: How does the seasonal colour fluctuation vary among different genotypes and species? If so, does it relate to where they originated from?

Trends of a^* can be examined visually by plotting the rolling average of the samples, or the output of dimension reduction, where each sample is indicated by one datapoint representing its trend over time. PCA (principal component analysis) or MDS (multidimensional scaling), among others, are used for such a dimension reduction. Together with time-series data on climatic factors, we could ask: Do green plants turn red in winter when temperature is low and air is dry, and become green again in spring

when the climate is milder? To address this question, we use Granger causality test or generalized linear models.

Reference

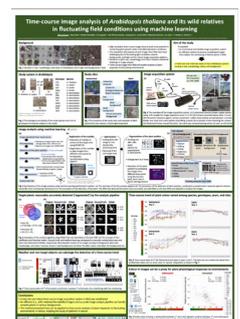
Mou et al. (2021) CS2-Net: Deep learning segmentation of curvilinear structures in medical imaging. *Med Image Anal*;67:101874. <https://doi.org/10.1016/j.media.2020.101874>

Reiko is a Postdoctoral Researcher (Oberassistentin) in the lab of Kentaro Shimizu at Department of Evolutionary Biology and Environmental Studies, University of Zurich. She studies evolutionary ecological genomics of plants with particular focus on environmental responses in polyploid systems.

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[Poster download](#)



Nature Biotechnology (2021)<https://doi.org/10.1038/s41587-021-01058-4>**Population genomic analysis of *Aegilops tauschii* identifies targets for bread wheat improvement**Gaurav, Kumar; Arora, Sanu; Silva, Paula; Sanchez-Martin, Javier; Horsnell, Richard; et al.

Exploring the diversity of the wild progenitor of the wheat D subgenome allows for rapid trait discovery. *Aegilops tauschii*, the diploid wild progenitor of the D subgenome of bread wheat, is a reservoir of genetic diversity for improving bread wheat performance and environmental resilience. Here we sequenced 242 *Ae. tauschii* accessions and compared them to the wheat D subgenome to characterize genomic diversity. We found that a rare lineage of *Ae. tauschii* geographically restricted to present-day Georgia contributed to the wheat D subgenome in the independent hybridizations that gave rise to modern bread wheat. Through k-mer-based association mapping, we identified discrete genomic regions with candidate genes for disease and pest resistance and demonstrated their functional transfer into wheat by transgenesis and wide crossing, including the generation of a library of hexaploids incorporating diverse *Ae. tauschii* genomes. Exploiting the genomic diversity of the *Ae. tauschii* ancestral diploid genome permits rapid trait discovery and functional genetic validation in a hexaploid background amenable to breeding.

Science (2021)<https://doi.org/10.1126/science.abg0929>**Lipid exchanges drove the evolution of mutualism during plant terrestrialization**Rich, Melanie K.; Vigneron, Nicolas; Libourel, Cyril; Keller, Jean; Xue, Li; et al.

Symbiosis with arbuscular mycorrhizal fungi (AMF) improves plant nutrition in most land plants, and its contribution to the colonization of land by plants has been hypothesized. Here, we identify a conserved transcriptomic response to AMF among land plants, including the activation of lipid metabolism. Using gain of function, we show the transfer of lipids from the liverwort *Marchantia paleacea* to AMF and its direct regulation by the transcription factor WRINKLED (WRI). Arbuscules, the nutri-

ent-exchange structures, were not formed in loss-of-function wri mutants in *M. paleacea*, leading to aborted mutualism. Our results show the orthology of the symbiotic transfer of lipids across land plants and demonstrate that mutualism with arbuscular mycorrhizal fungi was present in the most recent ancestor of land plants 450 million years ago.

Nature Climate Change (2021)<https://doi.org/10.1038/s41558-021-01068-9>**Global patterns of geo-ecological controls on the response of soil respiration to warming**Haaf, David; Six, Johan; Doetterl, Sebastian

While soil respiration is known to be controlled by a range of biotic and abiotic factors, its temperature sensitivity in global models is largely related to climate parameters. Here, we show that temperature sensitivity of soil respiration is primarily controlled by interacting soil properties and only secondarily by vegetation traits and plant growth conditions. Temperature was not identified as a primary driver for the response of soil respiration to warming. In contrast, the nonlinearity and large spatial variability of identified controls stress the importance of the interplay among soil, vegetation and climate parameters in controlling warming responses. Global models might predict current soil respiration but not future rates because they neglect the controls exerted by soil development. To accurately predict the response of soil respiration to warming at the global scale, more observational studies across pedogenetically diverse soils are needed rather than focusing on the isolated effect of warming alone.

Understanding the temperature sensitivity of soil respiration is critical to determining soil carbon dynamics under climate change. Spatial heterogeneity in controls highlights the importance of interactions between vegetation, soil and climate in driving the response of respiration to warming.

Nature Sustainability (2021)<https://doi.org/10.1038/s41893-021-00791-7>**Mycorrhizal fungi-mediated uptake of tree-derived nitrogen by maize in smallholder farms**Dierks, Janina; Blaser-Hart, Wilma J.; Gamper, Hannes A.; Six, Johan

Trees within farmers' fields can enhance systems' longer-term productivity, for example, via nutrient amelioration, which is indispensable to attain sustainable agroecosystems. While arbuscular mycorrhizal fungi (AMF) are known to improve plant access to soil nutrients, the potential of AMF to mediate nutrient uptake of tree-derived nitrogen (N) by crops from beyond the crops' rooting zones is unclear. We hypothesized that AMF quantitatively contribute to the crop uptake of tree-derived N. We set up root- and AMF-exclusion and control plots around *Faidherbia* trees (*Faidherbia albida*) and used the N-15 natural abundance technique to determine the magnitude of AMF-mediated uptake of tree-derived N by maize from beyond its rooting zone in smallholder fields. We further tested whether AMF-mediated N uptake decreases with distance from tree. We show that within one cropping season, maize obtained approximately 35 kg ha⁻¹ biologically fixed N from *Faidherbia*. One-third of tree-derived N in maize leaves was attributed to AMF-mediated N uptake from beyond the maize rooting zone and two-thirds to N from tree leaf litter, regardless of distance from tree. As hypothesized, maize grown close (1 m) to *Faidherbia* obtained significantly more tree-derived N than that at farther distances (4 and 5 m). Thus, the *Faidherbia*-AMF association can enhance agroecosystem functioning.

Soil fungi can form beneficial associations with plant roots. This study finds that arbuscular mycorrhizal fungi can increase crop uptake of nitrogen derived from common trees in African smallholder maize fields, sustainably enhancing these agroecosystems.

Molecular Cell (2021)<https://doi.org/10.1016/j.molcel.2021.07.029>**Molecular mechanisms of early plant pattern-triggered immune signaling**

DeFalco, Thomas A.; Zipfel, Cyril

All eukaryotic organisms have evolved sophisticated immune systems to appropriately respond to biotic stresses. In plants and animals, a key part of this immune system is pattern recognition receptors (PRRs). Plant PRRs are cell-surface-localized receptor kinases (RKs) or receptor proteins (RPs) that sense microbial self-derived molecular patterns to regulate pattern-triggered immunity (PTI), a robust form of antimicrobial immunity. Remarkable progress has been made in understanding how PRRs perceive their ligands, form active protein complexes, initiate cell signaling, and ultimately coordinate the cellular reprogramming that leads to PTI. Here, we discuss the critical roles of PRR complex formation and phosphorylation in activating PTI signaling, as well as the emerging paradigm in which receptor-like cytoplasmic kinases (RLCKs) act as executors of signaling downstream of PRR activation.

Trends in Ecology & Evolution (2021)<https://doi.org/10.1016/j.tree.2021.06.011>**The cold range limit of trees**

Körner, Christian

At high elevation or latitude, trees reach low-temperature range limits. In attempting an explanation, the range limits of individual tree species (set by freezing tolerance) and the general limit of the life-form tree (set by thermal growth constraints) need to be distinguished. The general cold edge of the fundamental niche of trees is termed the treeline, by definition, the lower edge of the alpine belt, a most important bioclimatological reference line. Trees can be absent from the treeline due to disturbances or biotic interactions. The actual local edge of tree distribution, the delineation of the realized niche, is driven by stochastic effects. Therefore, treeline theory and hypothesis testing are inevitably tied to the fundamental niche concept.

Nature Microbiology (2021)<https://doi.org/10.1038/s41564-021-00997-7>**Protective role of the *Arabidopsis* leaf microbiota against a bacterial pathogen**

Vogel, Cristine M.; Potthoff, Daniel B.; Schäfer, Martin; Barandun, Niculò; Vorholt, Julia A.

Systematic analysis of bacterial phyllosphere isolates and their ability to protect *A. thaliana* plants against infection, with the model pathogen *Pseudomonas syringae* pv. tomato DC3000, identified protective isolates such as Rhizobium Leaf202, whose activity involves direct interaction with the pathogen. The aerial parts of plants are host to taxonomically structured bacterial communities. Members of the core phyllosphere microbiota can protect *A. thaliana* against foliar pathogens. However, whether plant protection is widespread and to what extent the modes of protection differ among phyllosphere microorganisms are not clear. Here, we present a systematic analysis of plant protection capabilities of the At-LSPHERE, which is a collection of >200 bacterial isolates from *A. thaliana*, against the bacterial pathogen *P. syringae* pv. tomato DC3000. In total, 224 bacterial leaf isolates were individually assessed for plant protection in a gnotobiotic system. Protection against the pathogen varied, with ~10% of leaf microbiota strains providing full protection, ~10% showing intermediate levels of protection and the remaining ~80% not markedly reducing disease phenotypes upon infection. The most protective strains were distributed across different taxonomic groups. Synthetic community experiments revealed additive effects of strains but also that a single strain can confer full protection in a community context. We also identify different mechanisms that contribute to plant protection. Although pattern-triggered immunity coreceptor signalling is involved in protection by a subset of strains, other strains protected in the absence of functional plant immunity receptors BAK1 and BKK1. Using a comparative genomics approach combined with mutagenesis, we reveal that direct bacteria-pathogen interactions contribute to plant protection by Rhizobium Leaf202. This shows that a computational approach based on the data provided can be used to identify genes of the microbiota that are important for plant protection.

Nature Plants (2021)<https://doi.org/10.1038/s41477-021-00913-1>**A general non-self response as part of plant immunity**

Maier, Benjamin A.; Kiefer, Patrick; Field, Christopher, M.; Hemmerle, Lucas; Bortfeld-Miller, Miriam; Emmenegger, Barbara; Schäfer, Martin; Pfeilmeier, Sebastian; Sunagawa, Shinichi; Vogel, Christine M.; Vorholt, Julia A.

Plants, like other multicellular lifeforms, are colonized by microorganisms. How plants respond to their microbiota is currently not well understood. We used a phylogenetically diverse set of 39 endogenous bacterial strains from *Arabidopsis thaliana* leaves to assess host transcriptional and metabolic adaptations to bacterial encounters. We identified a molecular response, which we termed the general non-self response (GNSR) that involves the expression of a core set of 24 genes. The GNSR genes are not only consistently induced by the presence of most strains, they also comprise the most differentially regulated genes across treatments and are predictive of a hierarchical transcriptional reprogramming beyond the GNSR. Using a complementary untargeted metabolomics approach, we link the GNSR to the tryptophan-derived secondary metabolism, highlighting the importance of small molecules in plant-microbe interactions. We demonstrate that several of the GNSR genes are required for resistance against the bacterial pathogen *Pseudomonas syringae*. Our results suggest that the GNSR constitutes a defence adaptation strategy that is consistently elicited by diverse strains from various phyla, contributes to host protection and involves secondary metabolism.

Microbes induce an immune response in plants that includes transcriptional changes and biosynthesis of defence molecules. Analysis of both transcriptome and metabolome output to multiple bacteria identifies a common non-self response to microorganisms.

Systematic Biology (2021)<https://doi.org/10.1093/sysbio/syaa041>**The origin of the legumes is a complex paleopolyploid phylogenomic tangle closely associated with the Cretaceous-Paleogene (K-Pg) mass extinction event**

Koenen, Erik J.M.; Ojeda, Dario I.; Bakker, Freek T.; Wieringa, Jan J.; Kidner, Catherine; Hardy, Olivier J.; Pennington, R. Toby; Herendeen, Patrick S.; Bruneau, Anne; Hughes, Colin E.

The consequences of the Cretaceous-Paleogene (K-Pg) boundary (KPB) mass extinction for the evolution of plant diversity remain poorly understood, even though evolutionary turnover of plant lineages at the KPB is central to understanding assembly of the Cenozoic biota. The apparent concentration of whole genome duplication (WGD) events around the KPB may have played a role in survival and subsequent diversification of plant lineages. To gain new insights into the origins of Cenozoic biodiversity, we examine the origin and early evolution of the globally diverse legume family (Leguminosae or Fabaceae). Legumes are ecologically (co-)dominant across many vegetation types, and the fossil record suggests that they rose to such prominence after the KPB in parallel with several well-studied animal clades including Placentalia and Neoaves. Furthermore, multiple WGD events are hypothesized to have occurred early in legume evolution. Using a recently inferred phylogenomic framework, we investigate the placement of WGDs during early legume evolution using gene tree reconciliation methods, gene count data and phylogenetic supernetwork reconstruction. Using 20 fossil calibrations we estimate a revised timeline of legume evolution based on 36 nuclear genes selected as informative and evolving in an approximately clock-like fashion. To establish the timing of WGDs we also date duplication nodes in gene trees. Results suggest either a pan-legume WGD event on the stem lineage of the family, or an allopolyploid event involving (some of) the earliest lineages within the crown group, with additional nested WGDs subtending subfamilies Papilionoideae and Detarioideae. Gene tree reconciliation methods that do not account for allopolyploidy may be misleading in inferring an earlier WGD event at the time of divergence of the

two parental lineages of the polyploid, suggesting that the allopolyploid scenario is more likely. We show that the crown age of the legumes dates to the Maastrichtian or early Paleocene and that, apart from the Detarioideae WGD, paleopolyploidy occurred close to the KPB. We conclude that the early evolution of the legumes followed a complex history, in which multiple auto- and/or allopolyploidy events coincided with rapid diversification and in association with the mass extinction event at the KPB, ultimately underpinning the evolutionary success of the Leguminosae in the Cenozoic.

Nature Ecology & Evolution (2021)<https://doi.org/10.1038/s41559-021-01485-1>**The global distribution and environmental drivers of aboveground versus belowground plant biomass**

Ma, Haozhi; Mo, Lidong; Crowther, Thomas W.; Maynard, DS; van den Hoogen, J; Stocker, Benjamin D.; Terrer, César; Zohrer, Constantin M.

A poor understanding of the fraction of global plant biomass occurring belowground as roots limits our understanding of present and future ecosystem function and carbon pools. Here we create a database of root-mass fractions (RMFs), an index of plant below- versus aboveground biomass distributions, and generate quantitative, spatially explicit global maps of RMFs in trees, shrubs and grasses. Our analyses reveal large gradients in RMFs both across and within vegetation types that can be attributed to resource availability. High RMFs occur in cold and dry ecosystems, while low RMFs dominate in warm and wet regions. Across all vegetation types, the directional effect of temperature on RMFs depends on water availability, suggesting feedbacks between heat, water and nutrient supply. By integrating our RMF maps with existing aboveground plant biomass information, we estimate that in forests, shrublands and grasslands, respectively, 22%, 47% and 67% of plant biomass exists belowground, with a total global belowground fraction of 24% (20-28%), that is, 113 (90-135) Gt carbon. By documenting the environmental correlates of root biomass allocation, our results can inform model projections of global

vegetation dynamics under current and future climate scenarios.

The fraction of plant biomass in aboveground versus root tissues has implications for carbon storage and dynamics. Here the authors collate a dataset on root-mass fractions and use these data to explore large scale patterns of belowground plant biomass.

Nature Ecology & Evolution (2021)<https://doi.org/10.1038/s41559-021-01450-y>**Limited protection and ongoing loss of tropical cloud forest biodiversity and ecosystems worldwide**

Karger, Dirk Nikolaus; Kessler, Michael; Lehnert, Marcus; Jetz, Walter

Tropical cloud forests (TCFs) are one of the world's most species- and endemism-rich terrestrial ecosystems. TCFs are threatened by direct human pressures and climate change, yet the fate of these extraordinary ecosystems remains insufficiently quantified. With discussions of the post-2020 biodiversity framework underway, TCFs are a defining test case of the success and promise of recent policy targets and their associated mechanisms to avert the global biodiversity crisis. Here we present a global assessment of the recent status and trends of TCFs and their biodiversity and evaluate the efficacy of current protection measures. We find that cloud forests occupied 0.4% of the global land surface in 2001 and harboured similar to 3,700 species of birds, mammal, amphibians and tree ferns (similar to 15% of the global diversity of those groups), with half of those species entirely restricted to cloud forests. Worldwide, similar to 2.4% of cloud forests (in some regions, more than 8%) were lost between 2001 and 2018, especially in readily accessible places. While protected areas have slowed this decline, a large proportion of loss in TCF cover is still occurring despite formal protection. Increased conservation efforts are needed to avert the impending regional or global demise of TCFs and their unique biodiversity.

A global assessment of the status of tropical cloud forests shows that they have declined overall by similar to 2.4% since 2001, with much of this occurring despite formal protection and with up to 8% loss in some regions.

Nature Communications (2021)

<https://doi.org/10.1038/s41467-021-27151-5>**Coalescence and directed anisotropic growth of starch granule initials in subdomains of *Arabidopsis thaliana* chloroplasts**Burgy, Leo; Eicke, Simona; Kopp, Christophe; Jenny, Camilla; Lu, Kuan Jen; Escrig, Stephane; Meibom, Anders; Zeeman, Samuel C.

Starch is the major form of energy storage in plant cells and forms discrete, semi-crystalline granules within plastids. Here the authors use electron tomography and nanoSIMS to show that *Arabidopsis* starch granules initiate in stromal pockets between thylakoid membranes that coalesce before growing anisotropically.

Living cells orchestrate enzyme activities to produce myriads of biopolymers but cell-biological understanding of such processes is scarce. Starch, a plant biopolymer forming discrete, semi-crystalline granules within plastids, plays a central role in glucose storage, which is fundamental to life. Combining complementary imaging techniques and *Arabidopsis* genetics we reveal that, in chloroplasts, multiple starch granules initiate in stromal pockets between thylakoid membranes. These initials coalesce, then grow anisotropically to form lenticular granules. The major starch polymer, amylopectin, is synthesized at the granule surface, while the minor amylose component is deposited internally. The non-enzymatic domain of STARCH SYNTHASE 4, which controls the protein's localization, is required for anisotropic growth. These results present us with a conceptual framework for understanding the biosynthesis of this key nutrient.

Nature Communications (2021)

<https://doi.org/10.1038/s41467-021-20932-y>**Perception of a divergent family of phyto cytokines by the *Arabidopsis* receptor kinase MIK2**Rhodes, Jack; Yang, Huanjie; Moussu, Steven; Boutrot, Freddy; Santiago, Julia; Zipfel, Cyril

Plant genomes encode hundreds of receptor kinases and peptides, but the number of known plant receptor-ligand pairs is limited. We report that the *Arabidopsis* leucine-rich

repeat receptor kinase LRR-RK MALE DISCOVERER 1-INTERACTING RECEPTOR LIKE KINASE 2 (MIK2) is the receptor for the SERINE RICH ENDOGENOUS PEPTIDE (SCOOP) phyto cytokines. MIK2 is necessary and sufficient for immune responses triggered by multiple SCOOP peptides, suggesting that MIK2 is the receptor for this divergent family of peptides. Accordingly, the SCOOP12 peptide directly binds MIK2 and triggers complex formation between MIK2 and the BRASSINOSTEROID INSENSITIVE 1-ASSOCIATED KINASE 1 (BAK1) co-receptor. MIK2 is required for resistance to the important root pathogen *Fusarium oxysporum*. Notably, we reveal that *Fusarium* proteomes encode SCOOP-like sequences, and corresponding synthetic peptides induce MIK2-dependent immune responses. These results suggest that MIK2 may recognise *Fusarium*-derived SCOOP-like sequences to induce immunity against *Fusarium*. The definition of SCOOPs as MIK2 ligands will help to unravel the multiple roles played by MIK2 during plant growth, development and stress responses. Secreted peptides and cell-surface localized receptor kinases allow plants to modify growth and development according to external cues. Here, Rhodes et al. show that the MIK2 receptor perceives the SERINE RICH ENDOGENOUS PEPTIDE (SCOOP) family of phyto cytokines and is capable of recognising *Fusarium*-derived SCOOP-like peptides.

Nature Communications (2021)

<https://doi.org/10.1038/s41467-021-24827-w>**Diffusion-mediated HEI10 coarsening can explain meiotic crossover positioning in *Arabidopsis***Morgan, Chris; Fozard, John A.; Hartley, Matthew; Henderson, Ian R.; Bomblies, Kirsten; et al.

In most organisms, the number and distribution of crossovers that occur during meiosis are tightly controlled. All chromosomes must receive at least one 'obligatory crossover' and crossovers are prevented from occurring near one another by 'crossover interference'. However, the mechanistic basis of this phenomenon of crossover interference has remained mostly mysterious. Using quantitative super-resolution cytogenetics and math-

ematical modelling, we investigate crossover positioning in the *Arabidopsis thaliana* wild-type, an over-expressor of the conserved E3 ligase HEI10, and a *hei10* heterozygous line. We show that crossover positions can be explained by a predictive, diffusion-mediated coarsening model, in which large, approximately evenly-spaced HEI10 foci grow at the expense of smaller, closely-spaced clusters. We propose this coarsening process explains many aspects of *Arabidopsis* crossover positioning, including crossover interference. Consistent with this model, we also demonstrate that crossover positioning can be predictably modified *in vivo* simply by altering HEI10 dosage, with higher and lower dosage leading to weaker and stronger crossover interference, respectively. As HEI10 is a conserved member of the RING finger protein family that functions in the interference-sensitive pathway for crossover formation, we anticipate that similar mechanisms may regulate crossover positioning in diverse eukaryotes.

Microbiome (2021)

<https://doi.org/10.1186/s40168-021-01049-2>**Specific and conserved patterns of microbiota-structuring by maize benzoxazinoids in the field**Cadot, Selma; Guan, Hang; Bigalke, Moritz; Walser, Jean-Claude; Jander, Georg; Erb, Matthias; van der Heijden, Marcel G. A.; Schlaeppi, Klaus

[...] Results: Our analysis showed that BX secretion affected the community composition of the rhizosphere and root microbiota, with the most pronounced effects observed for root fungi. The impact of BX exudation was at least as strong as the genetic background, suggesting that BX exudation is a key trait by which maize structures its associated microbiota. BX-producing plants were not consistently enriching microbial lineages across the three field experiments. However, BX exudation consistently depleted Flavobacteriaceae and Comamonadaceae and enriched various potential plant pathogenic fungi in the roots across the different environments.

Conclusions: [...], this study identifies the BX pathway as an interesting breeding target to manipulate plant-microbiome interactions.

Professor Janneke Hille Ris Lambers, ETH Zurich



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The position of treeline and the timing of peak wildflower blooms are driven by climate at Mt. Tahoma. © Janneke Hille Ris Lambers

Janneke Hille Ris Lambers started as a Professor of Plant Ecology in the Institute of Integrative Biology at the Department of Environmental Systems Sciences at ETH Zurich in 2020. She moved to Switzerland from University of Washington (Seattle, USA), where she was the Doug and Maggie Walker Professor of Natural History. She received her PhD from Duke University in 2001, working with James S. Clark on seed and seedling traits of temperate tree species. She completed her first postdoc at University of Minnesota, where she worked with David Tilman to identify mechanisms underlying the positive diversity-productivity relationship. She worked with Jonathan Levine at UCSB for a second postdoc, assessing why introduced Mediterranean grasses came to displace diverse California native annuals. She started her independent research career as Assistant Professor at University of Washington in 2006.

Janneke is working on the mechanisms that structure plant communities, and how these mechanisms can help us predict the ecological impacts of global change. In early work with Peter Adler and Jonathan Levine, they introduced a new framework for understanding and quantifying the contribution of niche and fitness differences to diversity maintenance. A follow-up study combined theoretical models and field experiments and was among the first to empirically demonstrate that niches strongly promote diversity in Californian annual plant communities. She started studying the impacts of climate change on plant communities in 2006, after starting her position at University of Washington. There, she initiated extensive observational and

experimental studies on Mt. Tahoma, an ideal natural laboratory for climate change research due to its large climatic gradients. She and her group have demonstrated a strong role for climate in driving upper range limits of trees and the timing of the peak flowering for Alpine plants. However, her work also demonstrates that factors like species interactions complicate climate change responses, and can lead to lagged range shifts and novel communities.

Janneke has a keen interest in communicating climate change impacts to the general public. She has done so by establishing a large community science program at Mt. Tahoma (MeadoWatch – see MeadoWatch.org), which has involved 500+ volunteers in the collection of wildflower phenology data since 2013. She received a prestigious US National Science Foundation Career Award in 2010 and was elected an Ecological Society of America Fellow in 2018 in recognition of her scientific and outreach work.

In addition to ongoing studies of forest regeneration and wildflower phenology at Mt. Tahoma, Janneke and her ETH group are establishing new study sites and projects in Switzerland. For example, she has initiated regeneration monitoring at several forest sites (in collaboration with WSL researchers) to assess the importance of seed and seedling stages (the regeneration niche) for the current and future distribution of Swiss trees.

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<https://plantecology.ethz.ch>



Field census of tree seedlings at Mt. Tahoma. @ Elizabeth Wolkovich

PhD Courses in spring 2022

Chlorophyll Fluorescence – Principles and Applications

17.01.2022 – 19.01.2022, 3 days

Introduction to R

20.01.2022 – 27.01.2022, 2 days + work in between

Teaching Science at University

27.01.2022 – 04.03.2022, 7 half days

Scientific Writing Practice II

10.02.2022 – 17.02.2022, 3 days

Microbiomics I: The Microbiome of the Plant-Soil System

24.02.2022 – 02.06.2022, every Thursday in Semester

Crop Phenotyping

25.02.2022 – 24.06.2022, every Friday + 24.06.2022 full day - Field work

Responsible Conduct in Research

10.03.2022 – 05.05.2022, 2 days

Project Management for Research

14.03.2022 – 15.03.2022, 2 days

Advanced Course on 3D-Microscopy Imaging of Plant Tissues and Image Processing

04.04.2022 – 06.04.2022, 3 days

Statistical Modelling

06.04.2022 – 08.04.2022, 3 days

Value-based Design: Enhancing Value-sensitivity in Use and Development of Emerging Technologies

13.04.2022, 18.05.2022, 15.06.2022, 3 days + self-learning phases in between.

Scientific Presentation Practice

20.04.2022 – 03.05.2022, 2 days

Advanced Data Management and Manipulation using R

09.06.2022 – 16.06.2022, two full days + work in between

General Linear and Linear Mixed Models in R

13.06.2022 – 30.06.2022, 6 days

Microbiomics II: Metabarcoding - from Bioinformatics to Statistics

13.06.2022 – 16.06.2022, 4 days

Managing your Publication Workflow and your Open Data

14.06.2022 – 16.06.2022, 2 days

Genetic Diversity: Analysis

20.06.2022 – 01.07.2022, 5 days

Reporting using R Markdown & Shiny

07.07.2022 & 14.07.2022, 2 days

Science & Policy Courses

Introduction to Political Sciences

04.03.2022 & 15.03.2022, 2 days

Stakeholder Engagement

26.04.2022 – 28.04.2022, 3 days

Building Political Support

10.05.2022 – 17.06.2022, 3 days



Alpine Plant Ecology
Summer School on Alpine Plant Life
Swiss central Alps, 17-23 July 2022

Erika Hiltbrunner, Christian Körner, Sabine Rumpf (UNIBAS) and Gianalberto Losapio (UNIL)

This graduate course is offered by the University of Basel and the Zürich-Basel Plant Science Center (PSC) for advanced biology students with basic plant science training. Course topics include micro-climatology, ecophysiology, biodiversity, reproductive biology, vegetation and ecosystem ecology. The course will include lectures, field excursions and project work. Participation is limited to 24 students.

Location:
ALPFOR Alpine Research and Education Station
Furka Pass, 2440 m a.s.l.
www.alpfor.ch

Registration: PhD students register at franziska.grob@unibas.ch, UNIBAS-students (MSc and PhD) at MOiA; PhDs in «Plant Sciences / Science and Policy» at PSC: www.plantsciences.unizh.ch/en/teaching/phdplantscience/coursecatalogue.html. Pre-registration (with motivation letter) until 28 February 2022. Acceptance information: 04 April 2022, confirmed registration: 31 May 2022. Full board costs are CHF 400 (excl. travel expenses).

PSC course registration

www.ethz.ch/services/en/service/courses-continuing-education.html

Select: Plant Sciences

Contact:
psc_phdprogram@ethz.ch

Digital skills Courses

Advanced Course on 3D-Microscopy Imaging of Plant Issues and Image Processing

Lecturers: PD Dr. Celia Baroux (University of Zurich), Dr. Alexis Maizel (University of Heidelberg)

Overview of available microscopy imaging solutions depending on applications such as confocal laser scanning microscopy imaging, high-resolution two-photon microscopy. Learn to cope with specific constraints (speed, viability, bleaching and signal diffraction levels in fresh vs. fixed tissues). Discover how to exploit the benefits of 3D imaging at the qualitative and quantitative level.

Statistical Modelling

Lecturers: Dr. Matthias Templ (ZHAW) and Dr. Barbara Templ (ETH Zurich)

In statistical modeling, the relationships between a response variable and one or more explanatory variables are estimated. We consider the theory of linear regression with one or more explanatory variables and study robust methods and nonlinear models. Several numerical examples will illustrate the theory to get hands-on experience by performing regression analysis and the use of the statistical software R.

Advanced Data Management and Manipulation using R

Lecturer: Dr. Jan Wunder

Big Data is becoming increasingly important in science and elsewhere. Learn how to use R to manage and manipulate large data sets (to sort, merge, subset, aggregate and reshape data). Solve several data quality issues (missing values, outliers, zeros, normalization etc.) and highlight the underlying theoretical foundations and computational frameworks to obtain high-quality data. For advanced data manipulation novel developments such as dplyr, the pipe operator and data.table will be used. Have a closer look at R-data base connections, SQL queries and the creation of new data bases from R.

General Linear and Linear Mixed Models in R

Lecturer: Prof. Pascal Niklaus (University of Zurich)

Analyse experimental and observational data with general linear and linear mixed models. Important concepts and exercises will be introduced. Learn to recognize the essential structure of data sets and to implement them adequately in statistical models with fixed and random effects. Deal with issues of experimental design, analysis of variance, hypothesis testing, variance components, models with multiple error terms as well as balanced and unbalanced data.

Reporting using R Markdown & Shiny

Lecturer: Dr. Jan Wunder

R Markdown and Shiny are powerful R packages for static and dynamic reports, publications and dashboards that can be created fully reproducible using a highly intuitive notebook interface. Learn to create Markdown documents consisting of code, text and the YAML header. Shiny will be introduced for interactive web applications, shinythemes and htmlwidgets. Learn how to embed Shiny into R Markdown docs.

Genetic Diversity Analysis

Lecturers: Dr. Jean-Claude Walser and Dr. Niklaus Zemp (GDC, ETH Zurich)

Hands-on training for advanced students in various aspects of genomic data analysis. The focus is on high-throughput sequencing applications and data analysis, with an emphasis on reproducibility and report writing. We cover the fundamentals of biocomputing. Exercises are an important part and will help to better understand the theory.

Microbiomics I: The Microbiome of the Plant-Soil System

Lecturer: Dr. Martin Hartman (ETH Zurich)

The plant-soil microbiome is an essential component of agroecosystems, regulating crop growth, nutrient use efficiency, stress resilience, and disease resistance. While microorganisms shape the functioning of the plant-soil system, the ecosystem management and global changes influence diversity and functioning of these microbial systems. How might be the microbiome managed to improve sustainable agricultural production? The course focuses on a methodological toolbox to study microbes in the environment including different next-generation DNA sequencing applications such as metabarcoding and metagenomics.

Microbiomics II: Metabarcoding – from Bioinformatics to Statistics

Lecturer: Dr. Martin Hartman (ETH Zurich)

Application of next-generation sequencing techniques to analyze the diversity of microbial communities with focus on the metabarcoding technique. Topics range from bioinformatic processing of sequencing data to the most important approaches in multivariate statistics – the computational steps from processing raw sequencing reads down to the final statistical evaluations.

New course

Value-based design: Enhancing value-sensitivity in use and development of emerging technologies

Lecturers: Dr. Melanie Paschke, Dr. Ning Wang

April 13, May 18, June 15, 2022, 3 days + self-learning phases in between.

This course introduces the concept of value-sensitive innovation to inform students about the ethical considerations associated with the use and development of emerging technologies. It will equip young scientists with a value-based innovation approach, which they could bring with them when they enter today's increasingly digitalized society. The course will transmit not only a body of knowledge, but a set of toolkits that students can use in their own domains of research.

The blended-learning course with face-to-face block course elements, self-learning phases and case studies is at the intersection between technology ethics, value-based design and responsible innovation. Participants will prepare one design or innovation project, which they are currently, or might potentially, working on. In addition, they will explore core concepts in the context of the following case studies:

CASE I –

Drones used in humanitarian aid

Drones represent the first wave of robotic technology applied in the aid sector, demonstrating its remarkable capacity to speed up humanitarian responses and to optimize aid supply operations. However, along with enthusiasm comes uncertainty. Technological innovation intersects with values, norms, beliefs and various moral commitments. For instance, in the aid sector, the use of novel technology may challenge the principle of 'Do No Harm', may raise questions related to sovereignty, and may negatively affect equality and access for at-risk populations in disaster zones and remote areas. Additionally, innovation may also disrupt relationships between various actors including introducing new players (e.g., private for-profit companies and networks of digital volunteers), may widen inequality between those with access and those without, and may lower security and privacy risks disproportionately affecting the already vulnerable.

CASE II –

Drones designed for land stewardship

Drones can be used in varied ways to help protect the environment and can also facilitate or cause biodiversity harm. Small drones have a number of remarkable socio-economic impacts. For instance, images collected by drones can fill a gap between expensive, weather-dependent, and low-resolution images provided by satellites, or car-based images limited to human-level perspectives and the accessibility of roads. Sensors and cameras attached to drones allow managers of natural land to continuously enable land monitoring in real time. However, when we embed land stewardship concepts into the drone development, there are important questions arising: e.g., when environmental and human needs are in conflict, what could be the underlying moral decision-making framework and who should make the decisions? Could we use the technologies for observation of for example littering, illegal logging etc. or would this not be acceptable and in what context?



Ning is an ethicist and political scientist joining the PSC for this project. Her research interest is the ethical assessment and responsible governance of new and emerging technology, such as artificial intelligence, robotics, and autonomous systems. She obtained her PhD from the University of Zurich.

Contact: Ning Wang
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The course development receives funding through the UZH teaching fund.



Picture was created with wombo.art with "machine learning in plant sciences" as entry.

Summer School 2022

Application of Machine Learning in Plant Sciences

The 10th PSC Summer School will take place in Einsiedeln 12–16 September 2022.

The Summer School will provide an overview of current machine learning (ML) techniques, their challenges and opportunities. ML is a type of artificial intelligence (AI) that allows software applications to become more accurate at predicting outcomes without being explicitly programmed to do so.

The Summer School is especially aimed at participants with a background in plant sciences. You will gain an understanding of the concept of ML and insights into its potential and possible applications. You will learn how ML is being used in research fields of soil science, microbiology, ecology, biodiversity, agriculture, plant breeding, and plant pathology.

The Summer School will bring together a multidisciplinary group of participants and facilitate project-based teamwork to strengthen collaborations in different fields and to foster networking.

We plan to hold a face-to-face event. An overview of the program will be announced in March 2022.

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Invited speakers

more to be confirmed

Dr. Carol Alexandru, University of Zurich. Topic: The basics of phyton programming.

prof. Aalt-Jan van Dijk, University of Wageningen, The Netherlands. Topic: ML in plant breeding.

Prof. Manuel Günther, University of Zurich. Topic: The fundamentals of ML.

Dr. Gert Kootstra, Wageningen University, The Netherlands. Topic: Agricultural robotics.

Sharada P. Mohanty, AI Crowd. Topic: Deep Learning for image-based plant disease detection.

Dr. Madlene Nussbaum, University of Bern. Topic: Using ML for spatial mapping demonstrated with soil maps.

Prof. Fernando Perez Cruz, ETH Zurich and SDSC. Topic: The fundamentals of Deep Learning.

Dr. Michael Rzanny, Max Planck Inst. for Biogeochemistry. Topic: Deep Learning for Plant Identification (online).

Prof. Benjamin Stocker, ETH Zurich. Topic: ML in ecosystem science.

Dr. Hai Wang, China Agricultural University, Beijing, China. Topic: Crop improvement using Deep Learning (online).

Prof. Jan Dirk Wegner, University of Zurich and EcoVision Lab at ETH Zurich. Topic: Exciting projects in Plant Sciences using ML.

Prof. Niklaus Zimmerman, WSL and ETH Zurich. Topic: Data mining and ML in macro-ecological research.

feminno– Career program for innovative women

We started well into round 5 in September 2021, with 17 female PhDs and postdocs with research topics from personalized medicine to phenotyping plants. Company visits complemented the six-months training in innovation management and idea generation. Female role models from DSM and CSL Behring shared their work experience and inspired the participants to pro-actively mature their ideas and with this their personal development. The company visits provided an overview on the companies' missions, hiring procedures, and job opportunities. The feminno program not only supports women in becoming entrepreneurs, but also companies are interested more than ever to hire employees with an entrepreneurial mindset, the intrapreneurs. We are closing the call 5 on March 3 with an on-campus event, when feminno participants will pitch their spin-off/start-up idea.

Next Call

Call 6 will start in September 2022, with application process starting in June 2022. Please promote this program and let your female co-workers know about it. Stay up-to-date and follow us on [LinkedIn](#)

www.feminno.ch

Contact: Daniela Gunz
daniela.gunz@uzh.ch

swissuniversities – Equal opportunities and diversity program

As of January 2022, feminno is part of a larger initiative called FEMSPIN funded by the swissuniversities equal opportunities and diversity program (P-7 Diversität, Inklusion und Chancengerechtigkeit in der Hochschulentwicklung, 2021–2024). FEMSPIN will focus on female academic entrepreneurship at Swiss universities, including ETH Zurich, EPFL, Paul Scherrer Institute, University of Zurich and University of Basel, as well as the Swiss universities of applied sciences in Western (HES-SO), Southern (SUPSI) and Northwestern Switzerland (FHNW). The initiative aims at promoting equal opportunities by fostering competencies and developing structures of spin-off promotion for female academics.

Being part of the initiative will allow us to have three more feminno calls in the upcoming years. feminno also will expand to other Swiss universities including additional faculties such as business, tech, and law. It will increase the diversity in the program, and foster innovation and accelerate spin-off founding.



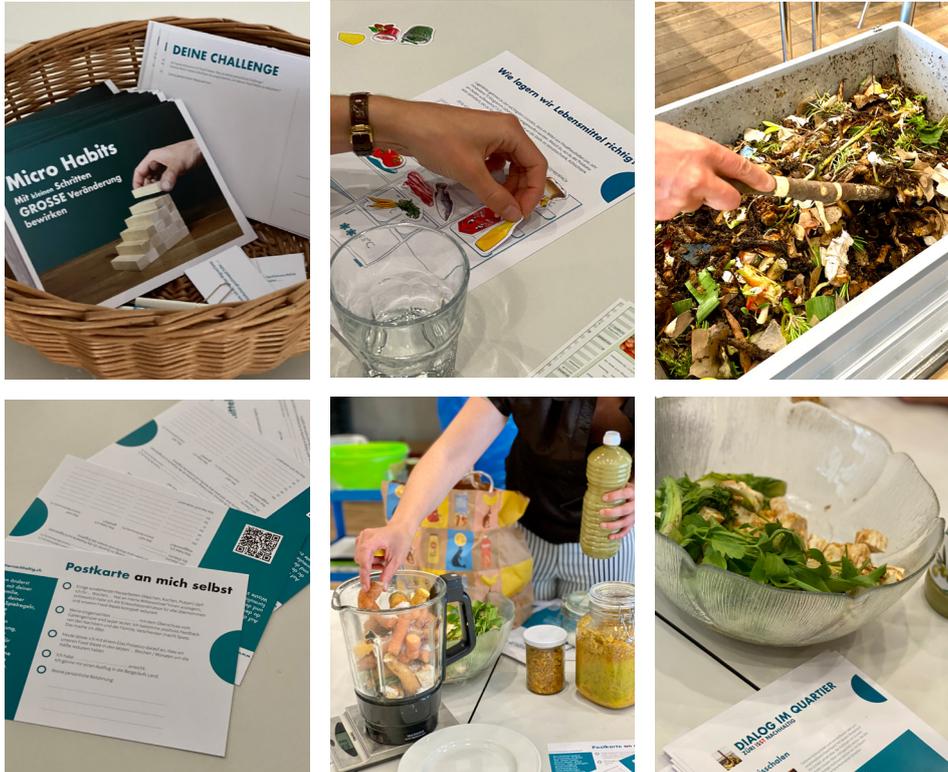
Participants of round 5. © Daniela Gunz



Career retreat in September 2021. © Daniela Gunz

Dialog im Quartier

- How do sustainable changes in food consumption occur in households?
- How can eating habits be consistently changed to be in line with the planetary health diet?
- How to support closed food cycles with no food waste?
- How to support sustainable local food systems?



Impressions of the workshop materials © PSC

Workshop formats: With different social interactions and methods, participants reflect their values and norms related to food habits. They track their own food habits (including food waste), learn and share strategies to avoid food waste in shopping, cooking and storage. They also go on an imagination journey to co-design their neighborhood with local and closed food cycles. In doing so, they build on what already exists, get to know like-minded people and role models, and draw on knowledge and experience from experts. At the end of the event, participants formulate an action in a letter to themselves that include an accomplishment they would like to attempt and implement in their daily lives. We accompany the achievements over a period of time through newsletters and in a challenge. We celebrate successes and share ideas and the obtained knowledge with the participants.

Successful in Basel in 2021 and back in Zurich in 2022

Between October and December 2021 'Dialog im Quartier' held four successful participatory events in Basel. Participants analyzed the local food system in their neighborhood and defined their needs. They worked on their individual access to the planetary health diet (eatforum.org) and analyzed their food waste habits. Among the local food systems ideas of interest in Basel were: Edible landscapes in and around the city, including fruit trees and agroforestry patterns.

<https://deinquartiernachhaltig.org/resultate-lokale-ernahrung/>

In the first half of 2022, we will be back in Zurich collaborating with the Umwelt- und Gesundheitsschutz Zürich (UGZ) and the Ernährungsforum Zürich to be present in different community centers. Dates will be announced soon:

<https://deinquartiernachhaltig.org/veranstaltungen/>

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With financial support of the 3fo Foundation, Christoph Merian Foundation and Amt für Umwelt und Energie (AUE).



Community center Schindlergut. © PSC



Call for participation

On 24th of June 2022, PSC will offer a Nachtaktiv event at the Succulent Collection Zurich. The theme of the evening is plant genetics and plant reproduction and we are looking for students, who can present their work in an entertaining way, preferably with hands-on experiments.

Contact: Ulrike von Groll
ulrike.vongroll@usys.ethz.ch

Nachtaktiv – Scientainment for youth

Nachtaktiv is a scientainment program for youth aged 16–25. It is a new format of science communication where entertainment, art and knowledge transfer are combined. Once per month on a Friday evening, PSC organizes a party-style event in a museum. Science activities are led by students of ETH Zurich, University of Zurich and University of Basel. Selected Spin-offs enrich the program with their inventions. Each event focuses on a different theme.

www.nachtaktiv.live

This program receives funding from the Gebert Rüf Foundation (2020–2022).



Impressions of Nachtaktiv: Healthy Weeds, that took place on 28th of January 2022. Big thanks to our host KULTURAMA Zurich. The museum's current exhibition "HEALTH – 7000 years of healing art" gives insight into diseases and various treatment methods. Contributing scientists: Ina Schmidt, Pharmaceutical Sciences, Department of Chemistry and Applied Biosciences, ETH Zurich; Yasemin Güner, Department of Systematic and Evolutionary Botany, University of Zurich; Camille Brioschi, Plant Ecology, Department of Environmental Systems Science, ETHZ; Georg Aichinger, Toxicology, Department of Health Sciences and Technology, ETZH; Eduard Bruderer, Plant Breeding, Puregene; Dr. Thomas Zumbrunn, ETH Startup CustomSurg AG; DJ Juliette Perroud (helvetiarockt). © Joanna Lesniewska



Visiting the Department of Plant and Microbial Biology at University of Zurich. © PSC

Art-Science internships

Since 2018, PSC offers internships for art students. In collaboration with the Zurich University of Arts (ZHdK), students of the Bachelor of Art Education (BAE) visit PSC science labs, and based on this input, they create plant-related art activities for youth or adults. See examples in our DIY-Book below. In September 2021, students visited the Department of Plant and Microbial Biology at University of Zurich. The inputs from Jordi Bascompte und Cyril Zipfel certainly gave the students plenty of material to work with. Jordi addressed ideas of functionalism versus structuralism, network structures – the architecture of biodiversity. He also made fascinating comparisons to theories in biology and chronologically parallel developments in art.

Cyril elucidated on plant response to danger and warned from the widespread idea of plant intelligence, emphasizing that they rather respond to inputs. He also presented the work from his lab currently looking at calcium pathways.

Three BAE students currently undertake an 11-weeks internship at the PSC. This internship includes many more lab visits and exchanges with researchers followed by ideating immediately afterwards, to document and discuss the images and metaphors which arose.

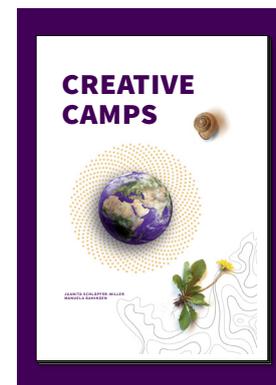
Contact: Juanita Schläpfer
juanita.schlaepfer@usys.ethz.ch



This day aims to recall that plant science is of critical significance to social, environmental and economic issues that affect our Earth today and in the future. **Join us** by organizing interactive events engaging the public on May 18th or around that day.

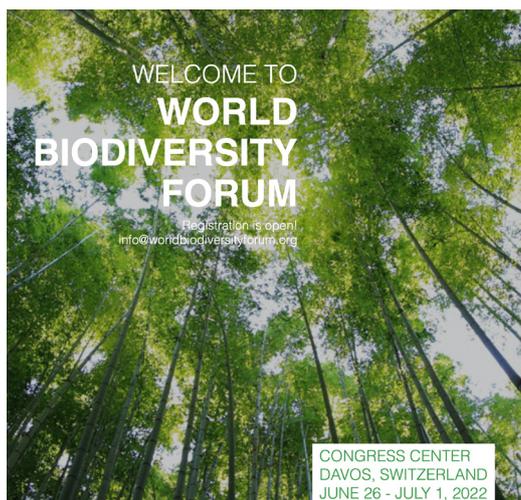
Fascination of Plants Day runs under the umbrella of the European Plant Science Organisation (EPSO). <https://plantday18may.org/>

Contact: Sylvia Martinez, sylvia.martinez@unibas.ch
 National coordinator for Switzerland



Juanita Schläpfer-Miller und Manuela Dahinden, Hrsg. (2020). **Creative Camps – Verknüpfung von Kunst- und Wissenschaftsvermittlung**. Mit Beiträgen von Gianna Brühwiler, Giulia Donati, Christian Ginzler, Oskar Hagen, Sabrina Flütsch, Joyce Kalumba, Mina Karrer, Renate Lerch, Alexandra Rosakis. ISBN: 978-3-907234-04-4

<https://doi.org/10.3929/ethz-b-000421727>



World Biodiversity Forum 2022

26 June – 1 July 2022, hybrid event, Davos Congress Centre, Switzerland.

Under the theme *Inspiration for Action*, the second World Biodiversity Forum will bring together researchers across all disciplines of biodiversity science with practitioners and societal actors in a forum that offers inspiration and examples for actions and solutions to conserve biodiversity – setting us on a path towards transformation for sustainability.

<https://www.worldbiodiversityforum.org>



EPSO General Meeting

13–15 June 2022 in Bordeaux / FR, hosted by the University of Bordeaux and INRAE

The European Plant Science Organisation (EPSO) is an independent academic organisation that represents more than 200 research institutes, departments and universities from 31 countries. EPSO's mission is to improve the impact and visibility of plant science in Europe. PSC is an institutional member of EPSO since its foundation in 2000. As a PSC member, you can apply for a free personal EPSO membership <https://epsoweb.org/join-epsos/> and thus, join the working groups and EPSO events.

Contact: Karin.Metzlaff@epsomail.org

www.epsoweb.org



International Conference on Arabidopsis Research: ICAR2022

20–24 June 2022, Belfast, Northern Ireland

The International Conference on Arabidopsis Research (ICAR) is an annual gathering of up to 1000 scientists whose primary research organism is the model plant *Arabidopsis thaliana*. Topics of six Plenary Sessions include Epigenetics and Chromatin Biology, From Models to Crops, The Dynamic Proteome, Robustness in Genetic Networks, Photobiology and Optogenetics, and Principles of Morphogenesis.

<http://icar2022.arabidopsisresearch.org/>



Plant Vascular Biology Conference 2022

17–21 July 2022, Berlin, Germany

The plant vascular system, comprised of phloem and xylem, is responsible for the delivery of all the organic and inorganic resources and signaling molecules including RNAs, proteins, Ca^{2+} , ROS throughout the plant body. Therefore, the vascular system plays pivotal roles in long-distance signaling, regulating growth and development, crop yield, forest production, and stress responses. It provides important opportunities to exchange novel research on the evolution of long-distance communication, development, structure, biochemistry and physiology, and modelling of xylem and phloem biology. The scope will also encompass loading and unloading mechanisms, regulation of transport, and short and long distance signaling in tissue differentiation processes and response to environmental challenges.

<https://www.pvb2022.org>

More plant science events

<https://swissplantscienceweb.unibas.ch/en/events/>

Thursday 15 & Friday 16 September 2022
University of Basel, Old Town of Basel, Switzerland

International Symposium in Honour of Caspar Bauhin (1560–1624)

400 Years Botanical Collections Implications for Present-Day Research

**Inspiring and show-casing
herbarium-based scientific
research, in the broadest sense,
celebrating 400 years since
Bauhin's pioneering
Flora of Basel.**

Two keynote lectures

15-20 contributed / invited talks
No parallel sessions

Group discussion, poster session
Bauhin herbarium visit

Public lecture by

Prof. Richard Primack, Boston University:
Climate change effects on wildflowers,
trees and birds. Building on the observations
of the famous American environmental philo-
sopher Henry David Thoreau, author of «Walden»

Registration opens 1 March 2022
Abstract deadline 15 June 2022

Organizers
Herbaria Basel, Dept Environmental
Sciences, University of Basel
Basel Botanical Society

Contact
Expression of interest or to receive
notifications: bauhin2022@unibas.ch

Bauhin2022.ch



This international Symposium will trace 400 years back from the origin of local floras and botanical collections to their significance for present-day research in Evolution, Systematics, and Global Change.

Caspar Bauhin, (1560–1624) was the first professor of Botany at the University of Basel, and one of the most prominent plant systematists of his time, a forerunner of Linnaeus. He also founded one of the first University Botanical Gardens and collected a herbarium of thousands of plants that survives to today. He published his pioneering Flora of Basel *Catalogus Plantarum circa Basileam sponte nascentium* exactly 400 years ago – one of the first comprehensive local floras.

Please submit your abstract for talks and posters. We particularly encourage contributions that make use of specimens in non-standard ways and that push the boundaries of what is currently possible.

Organizers:

Jurriaan de Vos, Jürg Stöcklin

Sylvia Martinez

Herbaria Basel, Department of Environmental Sciences & Botanical Society Basel

bauhin2022@unibas.ch

swissPLANT Symposium

Postponed from January 2022, the conference will be held from 13–15 June in the Parkhotel du Sauvage in Meiringen.

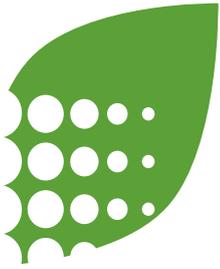
You are cordially invited to submit an abstract, participate, and register before 15 May 2022.

Contact: sylvia.martinez@unibas.ch

<https://swissplantscienceweb.unibas.ch/en/swissplant/>

Scientific committee: Roman Ulm, Emilie Demarsy, Michael Hothorn, Luis Lopez-Molina, Yamama Naciri, University of Geneva.





www.plantsciences.ch

The Zurich-Basel Plant Science Center is a competence center linking and supporting the plant science research community at ETH Zurich, University of Zurich and University of Basel. The center promotes plant and environmental research, education and outreach. It provides platforms for interactions with peers, policymakers, industry, stakeholders, and the public.

PSC MEMBER INSTITUTIONS

ETH Zurich

Department of Environmental Systems Science
Department of Biology
Institute for Environmental Decisions

University of Zurich

Department of Evolutionary Biology and Environmental Studies
Department of Geography
Department of Plant and Microbial Biology
Department of Systematic and Evolutionary Botany
Institute of Evolutionary Medicine

University of Basel

Department of Environmental Sciences

Zurich-Basel Plant Science Center, Managing Office

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Pictures

Courtesy of PSC staff or indicated.
Front image: This is a cotyledon from a mature embryo extracted from a *Arabidopsis thaliana* seed and stained with modified propidium iodide (mPS-PI staining). © Antia Rodriguez-Villalon

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