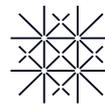




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Zurich<sup>UZH</sup>

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University  
of Basel

# PlantScienceNews

*Newsletter of the Zurich-Basel Plant Science Center*

**No 38, Fall 2020**



# Editorial

## Connectivity

The term connectivity relates to wireless networks and other ICT advancements. This year's topic of the PSC Symposium explores plant-related connectivity and the networks building upon the interactions of plants, microbes and insects. Ranging from molecular to environmental levels those interactions are indispensable for plant growth, plant reproduction, nutrient exploitation and disease resistance. Currently, computational advances and high-throughput technologies bring us new paths to study plant-based networks. Studying plant connectivity in a more contextual way and combining different disciplines, is key to moving forward in our understanding of plant systems. The results can be integrated in frameworks where optimal management of nature's ecological functions and biodiversity improve agricultural system performance, efficiency and farmers' livelihoods. Applications include agricultural biologicals such as biostimulants, biopesticides and biofertilizers. They are largely viewed as a more sustainable way to boost yields and crop protection.

Sustainability is also the key topic of our EU-funded RESPONSE Doctoral Program. In this newsletter, we introduce the first six fellows. By 2021 we expect 35 fellows to be part of this vibrant program – connecting plant, environmental and energy sciences with policy-relevant applicants for sustainable food and energy system as well as land use decisions.

In our Focus section we explore the potential of bioinformatics and its contribution to evolutionary plant sciences. Comparative and functional genomics connect plant data with computational thinking and thus reconstruct phylogenies. But beyond clever computing, phylogenetic trees embody biologists' thinking. In light of this, we warmly welcome Kirsten Bomblies to the PSC network. Kirsten is a professor of plant evolutionary genetics at the Department of Biology, ETH Zurich. Her research group studies the causes and consequences of the adaptive evolution of meiosis with relevance for plant breeding and crop adaptation to climate change.

Our new outreach program *Nachtaktiv* explores the connections of science, technology, art and design in an entertaining way for youth. We invite you to be part of it, creating some unforgettable science nights at the museums of Zurich.

Sincerely,  
Manuela Dahinden & Melanie Paschke, PSC Managing Directors

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**PSC Managing office:** **Manuela Dahinden**, Managing Director Research, Communications and Fundraising; **Melanie Paschke**, Managing Director Education, Science in Society and Fundraising; **Romy Kohlmann**, Finances and PlantHUB Coordinator; **Luisa Last**, Coordinator PSC PhD Programs & RESPONSE DP; **Dubravka Vrdoljak**, Assistant Coordinator PSC PhD Programs; **Juanita Schläpfer**, Outreach Manager; **Alexandra Rosakis & Ulrike von Groll**, Outreach Program Assistants; **Daniela Gunz**, *feminno* Program Coordinator; **Sylvia Martinez**, Coordinator Basel & Swiss Plant Science Web.

# At a Glance

## Open calls

### PSC-JRC COLLABORATIVE DOCTORAL PROGRAM

The PSC invites its members to submit project ideas in collaboration with the EU Joint Research Center (JRC). The JRC's mission is to support EU policy and decision-making. ETH Zurich and University of Zurich can host PhD students in the topics «Soil and land use change» and «Bio-economy and forests». PhD candidates are jointly selected and supervised for the duration of their stay at the JRC (maximum of two years). Salary and research costs during the stay at JRC will be funded by the JRC. Participating PhD students will be enrolled in the *PhD Program Science and Policy* coordinated by the PSC.

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[www.plantsciences.uzh.ch/en/research/fellowships/jrc](http://www.plantsciences.uzh.ch/en/research/fellowships/jrc)

### RESPONSE DOCTORAL PROGRAM (DP)

RESPONSE DP combines inter-sectoral research with the empowerment of 35 new PhD students to interact with stakeholders, policymakers and the public in the fields of «Sustainable food system», «Sustainable transitions in the energy sector» and «Sustainable land use decisions». PhD students will be enrolled in the *PSC PhD Program Science and Policy* and will collaborate with a partner organization at the science / policy / society interface or with a private organization (enterprise) – a secondment of 3 to 12 months is mandatory. This program receives funding from the EU's Horizon 2020 research and innovation program under the Marie Skłodowska-Curie grant agreement No 847585 – RESPONSE.

#### 4th open call for research project submission from 15 Sep until 30 Nov 2020

Relevant documents and research proposal templates are available on the *RESPONSE* website.

#### 3rd open call for PhD candidate applications from 1 Sep until 1 Dec 2020

Open positions are announced on the *RESPONSE* website.

Applications have to be submitted via the application platform of the Life Science Zurich Graduate School (<https://join.lszgs.uzh.ch/>), Choose: *PhD Program Science and Policy*.

Contact: Luisa Last, llast@ethz.ch

[www.plantsciences.uzh.ch/en/research/fellowships/response](http://www.plantsciences.uzh.ch/en/research/fellowships/response)

### PSC-SYNGENTA FELLOWSHIP PROGRAM

Applications for PhD and postdoc fellowships can be submitted by 1 Nov 2020. The funds are intended to promote innovative research in plant sciences. Research co-operation within PSC is an important criterion in the project selection. This call is reserved for PSC professors and group leaders. PhD students funded by the program enroll in the *PSC PhD Program Plant Sciences*.

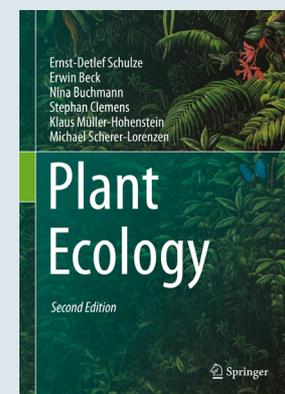
Contact: Manuela Dahinden, mdahinden@ethz.ch

[www.plantsciences.ch/research/fellowships/syngenta](http://www.plantsciences.ch/research/fellowships/syngenta)

## Awards

As of July 2020, **Professor Marcel van der Heijden** (University of Zurich & Agroscope) has been elected president of the International Mycorrhiza Society (IMS).

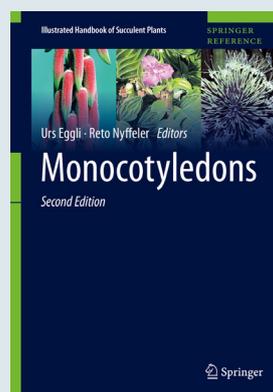
## Books



### Plant Ecology

Schulze, E.-D., Beck, E., Buchmann, N., Clemens, S., Müller-Hohenstein, K., Scherer-Lorenzen, M.  
Springer-Verlag Berlin Heidelberg, 2019  
ISBN 978-3-662-56231-4  
ISBN 978-3-662-56233-8

[www.springer.com/gp/book/9783662562314](http://www.springer.com/gp/book/9783662562314)



### Monocotyledons – Illustrated Handbooks of Succulent Plants

Eggli, Urs, Nyffeler, Reto (Eds.)  
Springer Berlin Heidelberg, 2020  
ISBN 978-3-662-56484-4

[www.springer.com/gp/book/9783662564844](http://www.springer.com/gp/book/9783662564844)

# RESPONSE Doctoral Program

## At a glance

The RESPONSE Doctoral Program (DP) «RESPONSE to society and policy needs through plant, food and energy sciences» is funded by the European Union's Horizon 2020 Marie Skłodowska-Curie Actions. RESPONSE is a joint doctoral program of ETH Zurich, University of Zurich and University of Basel and their competence centers: the Zurich-Basel Plant Science Center, the World Food System Center and the Energy Science Center. RESPONSE DP is centrally managed by the PSC. RESPONSE DP started in February 2020.

## PhD training

PhD students will be enrolled in the PSC PhD Program Science and Policy. They will be trained in different fields such as: communication of scientific evidence to policymakers and the public; involvement of different stakeholder groups in a participative process to co-produce knowledge; policy development and endorsement in Europe and at global level; establishing contacts to policy-implementing organizations, industry, national and international NGOs, GOs and IGOs; and development of a high standard of scientific responsibility and responsiveness towards the needs of the public. RESPONSE DP aims to become a flagship example of inter-sectoral research, underpinned with a dedicated training curriculum to foster awareness, knowhow, expertise and competence in Responsible Research and Innovation (RRI).

## Stakeholder engagement

PhD students will collaborate with a partner organization at the science / policy / society interface or with a private organization (enterprise) and will spend a mandatory secondment of 3–12 months. With their partner organization and stakeholders, PhD students will co-create societally relevant and desirable research and innovation outcomes. Each PhD student will contribute to one Stakeholder Meeting and one Citizen Consensus Conference.

*In this newsletter, we introduce six fellows from the first call. The PhD students have started their projects between March and June 2020. Challenged by the Corona virus pandemic, everyone has finally settled into his or her new research group. By the end of 2020, another eight PhD students will have started their research projects.*

*RESPONSE DP combines inter-sectoral research with the empowerment of 35 new PhD students to interact with stakeholders, policymakers and the public in the fields of «Sustainable food systems», «Sustainable transitions in the energy sector» and «Sustainable land use decisions».*

## Upcoming Events

**First Annual Meeting, March 10–12, 2021**

**Citizen Consensus Conference on sustainable food systems led by the World Food System Center, tbd**

**RESPONSE Summer School, September 13–17, 2021**



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.

## Strategies for improving forage productivity under future climates

Climate change increases the occurrences of unpredictable weather conditions, intense drought events, and has detrimental effects on food production and security. Drought stress significantly limits crop yields. In previous studies, quantitative trait loci (QTLs) regulating transpiration rate and leaf elongation had strong positive effects in association with drought tolerance in wheat. Furthermore, extensive research in maize revealed that the efficiency of photosynthesis is hampered under drought stress. The physiological and genetic mechanisms involved in the response of forage grasses to drought stress are not well understood, indicating the need for precise modulation of growth under drought stress.

In this project, we aim to unravel the physiological and genetic mechanisms involved in the response of forage grasses to drought stress. To achieve this aim, in co-operation with Royal Barenbrug Group (Mas-grenier, France), we will screen populations of *Lolium perenne* and *Festuca arundinacea* for drought responses on a high throughput phenotyping platform as well as under field conditions. The phenotyping platform is a novel precise method of determining the points at which the drought stress slows and arrests leaf elongation, a physiological measure of genotype-specific adaptability to drought stress. A diverse panel of individuals with contrasting responses to drought will form the basis for the development of a segregating F2 population. The F2's will be screened for drought responsive traits on the high throughput phenotyping platform as well as under field conditions. The same plants will be genotyped-by-sequencing and QTL analyses will be conducted to identify regions in the genome associated with drought tolerance. Identified QTLs will form the basis for the development of Kompetitive allele specific PCR (KASP) markers for use in marker-assisted breeding for drought tolerant forage grasses, ensuring sustainable production under future climates.



Fellow: Reah Gonzales

PI: Prof. Bruno Studer, Institute of Agricultural Sciences, ETH Zurich

Partner: Stephane Charrier, Station Manager / Breeder, Royal Barenbrug Group, France



Precise high throughput (left), rainout shelter (middle) and field (right) phenotyping of perennial ryegrass under drought stress conditions.

© Dr. Steven Yates, Stéphane Charrier and Reah Gonzales

## Energy transition and the transport sector – assessing the impact of European and national policies on future drive technology mixes, energy use and emission pathways

The transport sector is one of the largest energy consumers and plays a crucial role in mitigating climate change. With recent cost reductions for battery electric vehicles, a fundamental transformation of the predominant drive technologies towards low-carbon technologies seems possible. However, there is great uncertainty about the speed and outcome of the transition, since a variety of drive technologies still compete for low-carbon road mobility and transport and with increasing modal shifts towards rail. To address this challenge, we will develop a novel model for global projections of technology mixes for mobility and transport until 2040. Embedding a probabilistic discrete choice model within a system-dynamic model architecture, we will consider feedbacks between technology deployment, cost improvement and further factors, and thus contribute to policy advice.

Specifically, this project will address uncertainty in freight transport decarbonization. As evidenced by increasing global demand for goods and services, the freight sector represents a critical analysis point for emissions reduction and an anticipated option for electrification given the likely definitive trend towards total electrification in the passenger transport sector. Entry barriers for alternative fuel freight vehicles in the market, however, include high cost of infrastructure and high capital investment as the technologies required to power long-range road transport, for instance, are not yet cost effective. The developed model will therefore address the positive economic feedback effects of technological development and deployment but perhaps more importantly, identify policy intervention points that would effectively assist a shift from conventional to alternative fuel drive-train technologies. In collaborating with the Swiss Energy Foundation (SES), avenues and best practices for policy intervention will be readily experienced and discussed first-hand by Bessie during the secondment and can thus be incorporated in the model architecture and assessment.

Finally, upon completion, quantitative results as well as the model itself will be open sourced for future researchers to build upon and for other relevant industry stakeholders to reference.



Fellow: Bessie Noll

PI: Ass. Prof. Tobias Schmidt, Department of Humanities, Social and Political Sciences – Energy Politics Groups, ETH Zurich

Partner: Nils Epprecht, General Manager, Schweizerische Energiestiftung (SES), Zurich



The highly anticipated Tesla Cybertruck – one of many battery electric truck offerings coming to the market. A harbinger of what will likely be mainstream in the near future.

© Tesla, Inc.

## Wheat responses in changing climates studied in Asian varieties as underexploited genetic and genomic resources

Bread wheat is one of the three major crops in the world, but its yield is projected to be reduced by rapid climate changes. To create sustainable food systems, the critical mission of breeding centers, including the International Maize and Wheat Improvement Center (CIMMYT), is breeding for anticipated climates. The paucity of genomic information, caused by the large genome size and allohexaploidy, has been a major obstacle in the genetic research on bread wheat, but recently the assembly and analysis of the complex genome was accomplished: the 10+ Wheat Genomes Project completed the *de novo* assembly of ten world-leading varieties. A recent study (Balfourier et al. (2019), *Science Advances* 5(5): eaav0536) reported that, despite harboring large amounts of ancient genetic variation, Asian landraces and traditional varieties are largely unexploited.

Therefore, this project will focus on the variation of 25 representative lines composed of landraces and old cultivars from Asia established by the National Bioresource Project – Wheat of Japan. First, by applying the expertise of CIMMYT, the variation of traits that are important for climate changes, such as disease resistances or stress tolerances, will be measured within the 25 varieties. Second, novel promising traits will be mapped using the nested association mapping (NAM) lines, constructed from the crossing of the 25 core lines, combining the advantages of quantitative trait locus mapping with association mapping. The mapped chromosomal regions will be used for breeding in response to climate changes. The results will be published in open access journals and made available to the general public. Field data will be sent to breeders inside and outside CIMMYT using CIMMYT global network.



Fellow: Katharina Jung

PI: Prof. Kentaro Shimizu, Department of Evolutionary Biology and Environmental Studies, University of Zurich

Partner: Masahiro Kishii, Senior Scientist, International Maize and Wheat Improvement Center (CIMMYT)



Testing of different wheat lines at the experimental station Toluca (CIMMYT) in Mexico.

© Masahiro Kishii

## Developing a source-to-sink value chain for Swiss industrial carbon dioxide via a holistic approach

The scientific community recognizes the key role that carbon dioxide (CO<sub>2</sub>) capture and storage (CCS) systems will play as part of the efforts to mitigate climate change, either to mitigate emissions today or to enable negative emissions in the future. CCS is available and feasible from a technological point of view. Nevertheless, the public acceptance, the political support and the regulatory feasibility of CCS are very limited in many countries, particularly in Europe, including Germany and Switzerland. In this context, my project aims at tackling this question: Is the vision of a source-to-sink value chain for Swiss industrial CO<sub>2</sub> feasible, what are the hurdles to make this vision real, from a technical, economic, regulatory, political, social perspective, and how can these be tackled?

The key challenge in this project is indeed its interdisciplinary nature, whereby technical and scientific knowledge and social sciences expertise have to be integrated. The way we intend to address this is by exploiting the main PI's network of collaborations at ETH Zurich, as well the Energy Science Centre network in order to cover the different scientific domains effectively. Furthermore, Linda will take two secondments at the GeoForschungsZentrum Potsdam, Germany and at Bellona Europa, Belgium – two of the most active and prestigious foundations working on different aspects of the CO<sub>2</sub> value chain. Interacting with such a pool of experts, Linda will design a source-to-sink value chain for Swiss industrial CO<sub>2</sub>. Indeed, the project will deliver: (i) a blueprint of a CCS value chain for Swiss waste-to-energy operators, and for other sectors such as cement or gas-fired power generation; (ii) a cost-benefit analysis of the same, with the identification of possible business models; (iii) an understanding of societal perception about CCS, and a new narrative on how to communicate about CCS; (iv) an assessment of political and regulatory interventions necessary to enable the whole CCS value chain above.

The outcome will consist of 1–2 scientific publications, material for the public, workshops with stakeholders, panel discussions involving students, lectures at ETH Zurich and in high schools. Moreover, we will formulate policy-recommendations (e.g. policy brief, blog article, etc.) based on stakeholder meetings.

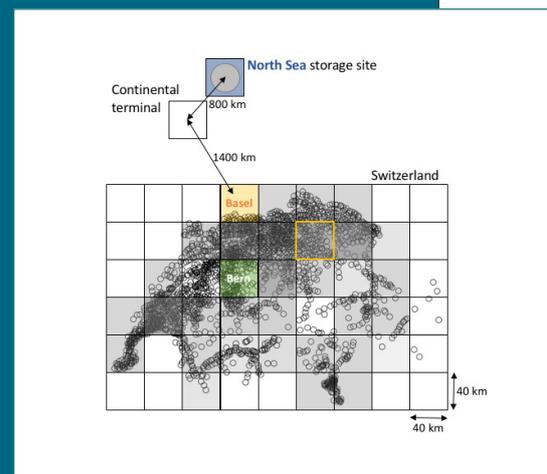


Fellow: Linda Frattini

PI: Prof. Marco Mazzotti, Department of Mechanical and Process Engineering, ETH Zurich

Partner 1: Dr. Cornelia Schmidt-Hattenberger, Senior Research Scientist, Group Leader Geological Storage, Deutsches GeoForschungsZentrum GFZ Potsdam

Partner 2: Dr. Jan-Justus Andreas, Policy Manager Industry, Bellona Europa (Brussels, Belgium)



Realistic system configuration representing Switzerland, with possibility of storing CO<sub>2</sub> in the North Sea (gray circle). Hydrogen demand described by the gray tones of the cells.

Retrieved from: P. Gabrielli, F. Charbonnier, A. Guidolin, M. Mazzotti (2020). Enabling low-carbon hydrogen supply chains through use of biomass and carbon capture and storage: A Swiss case study. *Applied Energy*: 275, 115245.

<https://doi.org/10.1016/j.apenergy.2020.115245>

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## The role of biodiversity in sustainable energy transitions for charcoal

Global demand for charcoal is increasing mainly due to urban population in developing countries. More than half the global population now lives in cities, and urban-dwellers are restricted to charcoal use because of easiness of production, access, transport, and tradition. Growing demand for charcoal, however, may lead to increasing impacts on forests, food, and water resources, and may even create additional pressures on the climate system. The project will for the first-time link trait-based approaches and ecosystem models to the case of charcoal production in the tropics. Its findings will contribute to the fields of functional diversity (within ecology), social ecological systems, complexity science and energy science. Specifically, this project will build on an existing project in the lab looking into the livelihood impacts and drivers of charcoal production in Tanzania. We will build on this expertise to integrate the role of biodiversity in sustainable energy transitions for charcoal, namely through integration with societal drivers of charcoal use, which are dependent to some extent on traits for charcoal production but determine trait evolution as well. The project will review and embed the social, economic and cultural components of the history and evolution of charcoal use with trait evolution to determine their contribution to carbon cycling. The secondment partner Nitidae will hereby provide connection to local conditions and advancement of capacity in the project areas. This integration is fundamental and will enhance the relevance of the project beyond earth system and natural sciences, towards other disciplines.

This project is highly relevant for society because a large fraction of urban populations in sub-Saharan Africa already depend on charcoal for their energy and cooking needs, and this is projected to grow. The demand from these urban populations is extremely linked to rural population livelihoods, biodiversity loss, and carbon cycling and accounting. One of the outcomes will be a White paper (e.g. policy recommendations for biodiversity and livelihood enabling charcoal sector or best practices for nature-based solutions for the charcoal sector). The results from the project will benefit societal groups in the target countries by providing results on the carbon and livelihood effects of charcoal production, fundamental to inform carbon and biodiversity policies, indicator reporting at national and subnational scales, as well as sustainable development objectives and goals that meet both poverty alleviation and biodiversity and climate change goals.



Fellow: Dabwiso Sakala

PI: Prof. Maria Joao Ferreira dos Santos, Department of Geography, University of Zurich

Partner: Clovis Grinand, Researcher / Project Manager, Nitidae France



Remains of a charcoal production site after harvest in a miombo forest in Tanzania. Transforming wood into charcoal involves a slow pyrolysis or carbonisation process in charcoal kilns resulting in greenhouse gasses, soot, fine charcoal, and ash as by products. Intensive charcoal production modifies forest structure and reduces above ground biomass which can lead to forest degradation overtime. This includes loss of soil organic carbon at production sites with major changes in soil physical, chemical and microbial properties.

© Hanneke van't Veen

## Unlocking epigenetic variation to breed sustainable crops in a changing climate

Agricultural productivity needs to be significantly increased by 2050 to meet the needs for food, feed, fibre, and fuel production. The long-term goal of this project is crop improvement through unlocking the potential of epigenetic variation. Apart from genetically modified crops, the development of new cultivars has largely relied on classical breeding, which is based on genetic variation in the primary gene pool. Unfortunately, very little is known about how stable epigenetic variation, so-called epialleles, are inherited over generations, how they are influenced by genetic background, and how they respond to environmental influences. This project will investigate these aspects in the model plant *Arabidopsis thaliana* with a focus on DNA-methylation, a prominent epigenetic mark that can easily be assessed. By analyzing public data from 87 accessions of *A. thaliana*, ~100 loci with a high anticorrelation of gene expression and DNA-methylation were identified. The accessions clearly fell into two groups, some of which also show a correlation with an associated phenotype. We will follow the DNA-methylation status of 20–30 loci over several generations in different F1 hybrids and recurrent backcrosses in *A. thaliana* plants to assess the stability of epialleles across generations and their dependence on genetic background.

This knowledge will help the seed and agroindustry to make decisions regarding the inclusion of epigenetic variation in breeding programs. This may influence policy decisions with regard to epigenetic modifications, and contribute to the development of more resilient, sustainable cultivars in the long term.

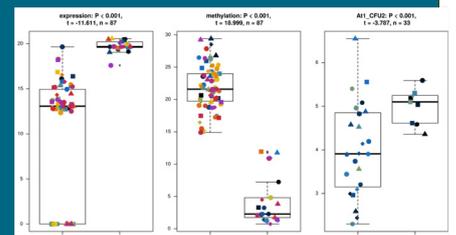
The success of the project relies on combining various disciplines, including genetics, molecular biology, ecology, and – through the secondment – statistics and bioinformatics. A secondment of 3 months is foreseen at MWSchmid GmbH (MWS) with expertise in experimental design, statistics, bioinformatics, data analysis, and data presentation. The unique competences of MWS are essential for optimal data analysis and exploitation of the results. It will also provide insights into small business operations. Throughout the project, MWS will participate in regular meetings to monitor and discuss progress and possible adjustments. The results of the project will be published in open-access journals that are respected in the field and presented at international conferences.



Fellow: Dusan Denic

PI: Prof. Ueli Grossniklaus, Department of Plant and Microbial Biology, University of Zurich

Partner: Marc W. Schmid, Director, MWSchmid GmbH (MWS), Zurich



Variation in DNA-Methylation at At1g52905. Above: part of the gene showing 5/21 demethylated (DA) and 5/76 methylated alleles (MA). Left: box-plots showing expression levels (left graph), levels of methylation (middle graph) of DA and MA groups, and phenotypic data for 33/87 accessions (colony forming units, CFU), unpublished.

Data was extracted from:

[https://archive.gramene.org/db/literature/pub\\_search?ref\\_id=54874](https://archive.gramene.org/db/literature/pub_search?ref_id=54874)

<https://pubmed.ncbi.nlm.nih.gov/23467092/>

# Evolutionary bioinformatics

*Comparative and functional genomics lead to more rapid identification of underlying mechanisms of evolutionary forces. Here we present three case studies that highlight the contribution of bioinformatics in better understanding how species have evolved.*

## Chromosome-scale genome assembly of the heterostylous *Primula veris*

**Giacomo Potente, Department of Systematic and Evolutionary Botany, University of Zurich**

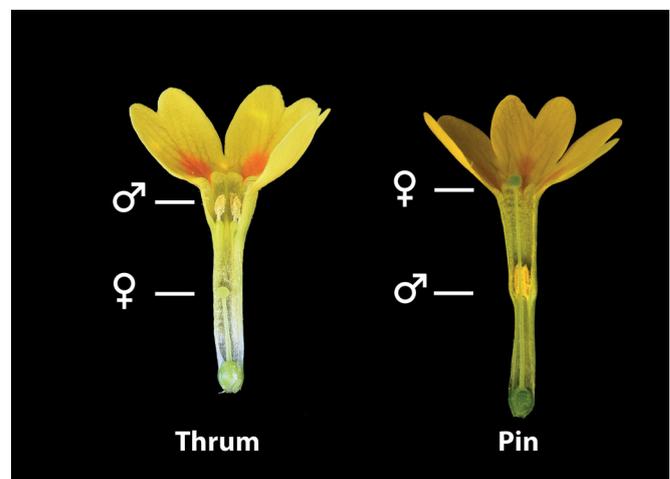
Flowering plants are an extraordinary model to study the evolution of reproduction, as they display a wide variety of reproductive strategies often aimed at increasing outcrossing and reducing inbreeding. A compelling example of a plant reproductive strategy is heterostyly, in which a self-incompatibility mechanism is associated with a floral dimorphism. Heterostylous species produce two forms of flowers, known as ‘pin’ and ‘thrum’, differing in the reciprocal positioning of male and female sexual organs: pins have a long style and low anthers, while the thrums have a short style and high anthers (Figure 1). Such a floral architecture promotes animal-mediated pollen transfer from pin anthers to thrum stigmas and vice versa. In addition, a sporophytic self-incompatibility system prevents self- and intramorph-fertilization. Intriguingly, both aspects of heterostyly are controlled by a single genomic locus, the S-locus supergene.

The genus *Primula* (primroses) has been the model for studying heterostyly since Charles Darwin, who was the first scientist to describe heterostyly. Despite being studied for more than 150 years, knowledge of the molecular mechanisms that gave origin to the heterostyly supergene is scarce and the highly fragmented genome assemblies for heterostylous species currently available make it impossible to address these open questions.

I started my PhD project in September 2017, supervised by Professor Elena Conti and Dr. Péter Szövényi. The project is a collaboration between the University of Zurich and the biotech company BaseClear BV, based in Leiden (The Netherlands), as part of the PlantHUB doctoral program coordinated by the Zurich-Basel Plant Science Center. As a first step to gain a better understanding on the evolution of the S locus, we assembled the genome of the heterostylous *Primula veris* (cowslip). This was achieved by combining state-of-the-art DNA sequencing (third-generation sequencing using Oxford Nanopore), scaffolding strategies (chromosome conformation capture with Chicago and Hi-C libraries) and assembly algorithms (the Trio Binning module of the Canu assembler). This resulted in the first chromosome-scale, haplotype-phased genome assembly of any

heterostylous species. We identified the S locus as a 264-kb genomic region – substantially shorter than the *Primula vulgaris* S locus – containing seven genes and being present only in thrum individuals. We also detected the signatures of an ancient whole-genome duplication specific to the genus *Primula*, which might have played a role in the origin of the S-locus genes. Further analysis to disentangle the steps in the evolutionary origin of the S locus are ongoing. In conclusion, our study will allow us to gain a better understanding of the origin of the S-locus supergene and, more generally, shows once again the importance of high-quality genome assemblies in addressing key questions in modern evolutionary biology.

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**Figure 1:** The two floral morphs of *P. veris* and their genotypes. Pin and thrum individuals differ by having male and female sexual organs reciprocally positioned in their flowers. © A. Bernhard



This project received funding from the European Union's Horizon 2020 research and innovation program under the Marie Skłodowska-Curie GA No 722338 – PlantHUB.

## Mapping genomic landscape of gene flow and natural selection in plant speciation

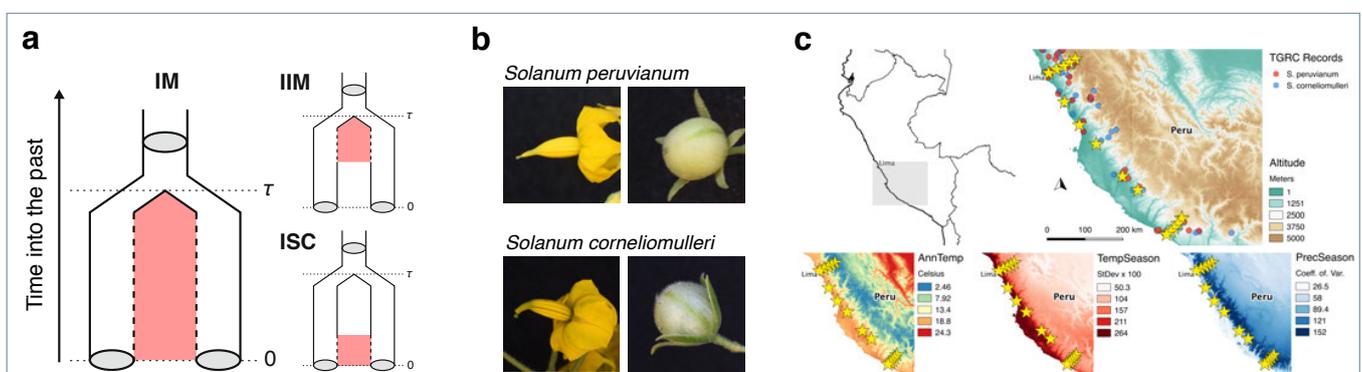
Simon Aeschbacher, Department of Evolutionary Biology and Environmental Studies, University of Zurich

Quantifying evolutionary forces leading to reproductive isolation (RI) is a long-standing issue in speciation research. The evolution of RI among geographically isolated (allopatric) populations is widely seen as the most plausible speciation mode. However, theory predicts that RI evolves between geographically adjacent (parapatric) and even fully overlapping (sympatric) populations if natural selection against gene flow is strong enough. Empirical evidence shows that RI has repeatedly evolved in the face of gene flow. Yet, it remains challenging to quantify when and in what direction gene flow acted. It is also difficult to identify strength and genomic targets of natural selection opposing gene flow. To address these challenges, we rely on bioinformatics to extract information from next-generation sequencing (NGS) data and to make population genomic inference. In a recent project, we developed an approach for co-estimating the strength of gene flow and genome-wide divergent selection in an isolation-with-migration (IM, Figure 1a) model from NGS data and recombination maps. We applied this approach to pairs of allopatric and sympatric populations of the yellow monkeyflower (*Mimulus guttatus*) and its sister species *M. nasutus* in Western North America. We found that the extent of divergent selection varied with the geographic context (Aeschbacher et al. 2017 PNAS 114(27)). Removing blocks from the *M. guttatus* genome that recently introgressed from sympatric *M. nasutus* populations (Brandvain et al. PLoS Genet 10(6):e1004410, 2014), we no longer found a signal of selection against gene flow. This result suggests that natural selection maintains a reproductive barrier between the two species at locations where they have come into secondary contact after independent range

expansions. Our study provides a proof of concept for the co-estimation of fundamental evolutionary forces involved in speciation. However, the approach we used has little power to distinguish between the IM model and alternative scenarios of speciation. To overcome this limitation, we are working on a more sophisticated approach that integrates the distribution of within- and between-species coalescence times with migration–selection theory. We use this approach to study the genetic basis and evolutionary history underlying complex patterns of geographic and reproductive isolation in two species complexes of wild tomato (*Solanum* sect. *Lycopersicon*; Figure 1b). To maximise the resolution of our approach, we require long-range phased haplotypes. We use bioinformatics to determine these haplotypes from whole-genome sequences of parents and progeny of crosses between inbred maternal lines and focal paternal lines. Bioinformatics is essential in two more ways: first, to construct chromosome-level *de novo* genome assemblies from the latest generation of long-read sequencing and optical mapping technologies, and second, to transfer information about function and selective constraint of genetic variants from the well-annotated cultivated tomato genome. Our next challenge is to incorporate spatial and ecological information. To this end, we collected wild tomato tissue along altitudinal and latitudinal gradients in Peru (Figure 1c). Bioinformatics will thus not only help us map variation in the strength of RI among wild tomato species along the genome, it will also allow us to make sense of this variation in a geographical and ecological context, and thus better understand the importance of allopatric, parapatric, and sympatric speciation in nature.

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**Figure 1:** Demographic scenarios of speciation explored (a). Flower and fruit phenotypes in *Solanum peruvianum* and *S. corneliomulleri* (b), two of the wild tomato taxa studied and occurring along the coast and western Andean slopes in Peru and Chile (c, top). Tissue was collected in 2019 along altitudinal and latitudinal gradients (stars) capturing environmental variation across habitats (c, bottom). IM: isolation with migration, IIM: isolation with initial migration, ISC: isolation with secondary contact, AnnTemp: mean annual temperature, TempSeason: temporal seasonality, PrecSeason: precipitation seasonality, TGR: C.M. Rick Tomato Genetic Resource Center, UC Davis. Pictures in (b) by T. Grubinger; altitudinal and bioclimatic data in (c) from <http://srtm.csi.cgiar.org> and <http://worldclim.org/bioclim>.

## Evolutionary functional genomics of selfing and polyploid speciation

**Kentaro K. Shimizu, Department of Evolutionary Biology and Environmental Studies, University of Zurich**

Polyploid species are common among natural and crop plants, but genetic and genomic studies of these species have been difficult because of the high sequence similarity between duplicated genes, referred to as homeologs. We developed bioinformatic workflows to sort sequence reads into each subgenome of allopolyploid species, and showed that the error rate of mapping was markedly reduced by our methods – HomeoRoq and EAGLE-RC (Figure 1 from Kuo et al. *Brief Bioinf* 21:395, 2020). These bioinformatic methods enabled high-quality analysis of the genome-wide polymorphisms, transcriptomes, and epigenomes of allopolyploid species.

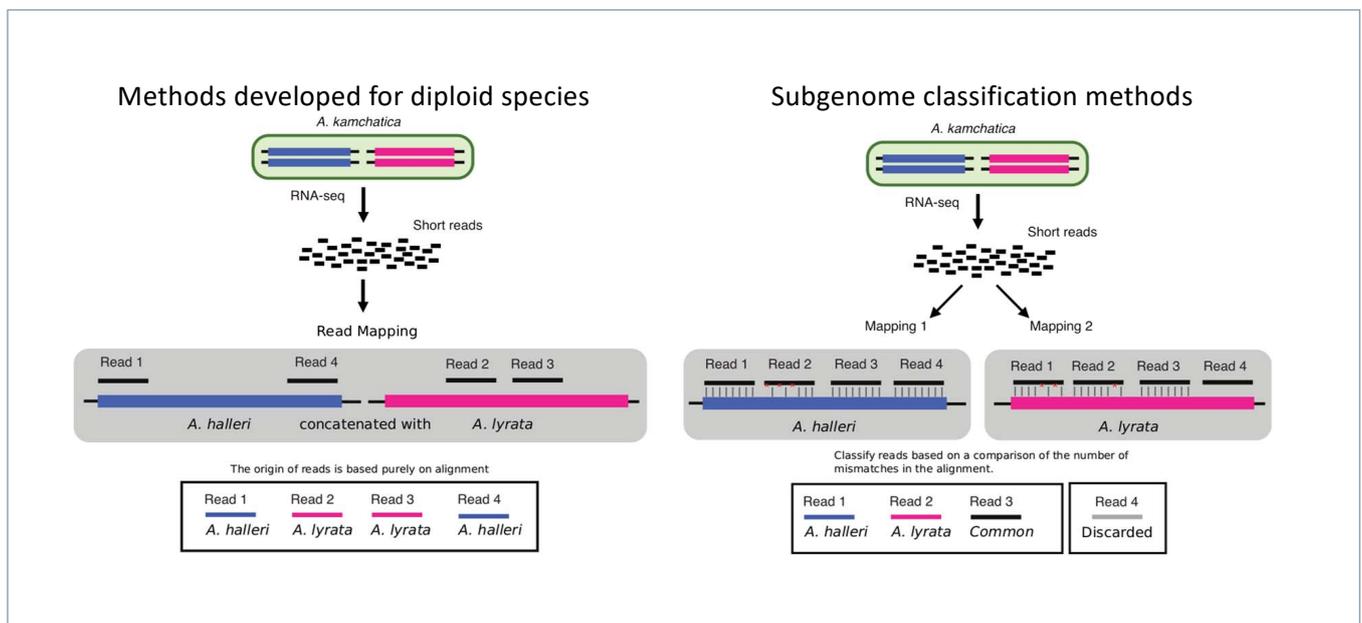
An emerging pattern is that allopolyploid species combine different parental adaptations to obtain broader environmental responses to factors such as cold, heavy metals, drought, and submergence. Consistent with such a division of labor between homeologs, genome-wide polymorphism analysis of the model polyploid *Arabidopsis kamchatica* and the crop bread wheat demonstrated that the homeologs underwent different evolutionary trajectories (Paape et al. *Nature Comm* 9:3909, 2018; in press *Nature* 2020). As a textbook example of contemporary speciation during the past 150 years, we studied the new polyploid species

*Cardamine insueta* in Urnerboden, Switzerland (Sun et al. *Front. Genet*, 10.3389/fgene.2020.567262). Transcriptomic studies that distinguished homeologs showed that the new species combined parental adaptations such as the vivipary of *C. rivularis* and the submergence tolerance of *C. amara* to adapt to human-made new habitats.

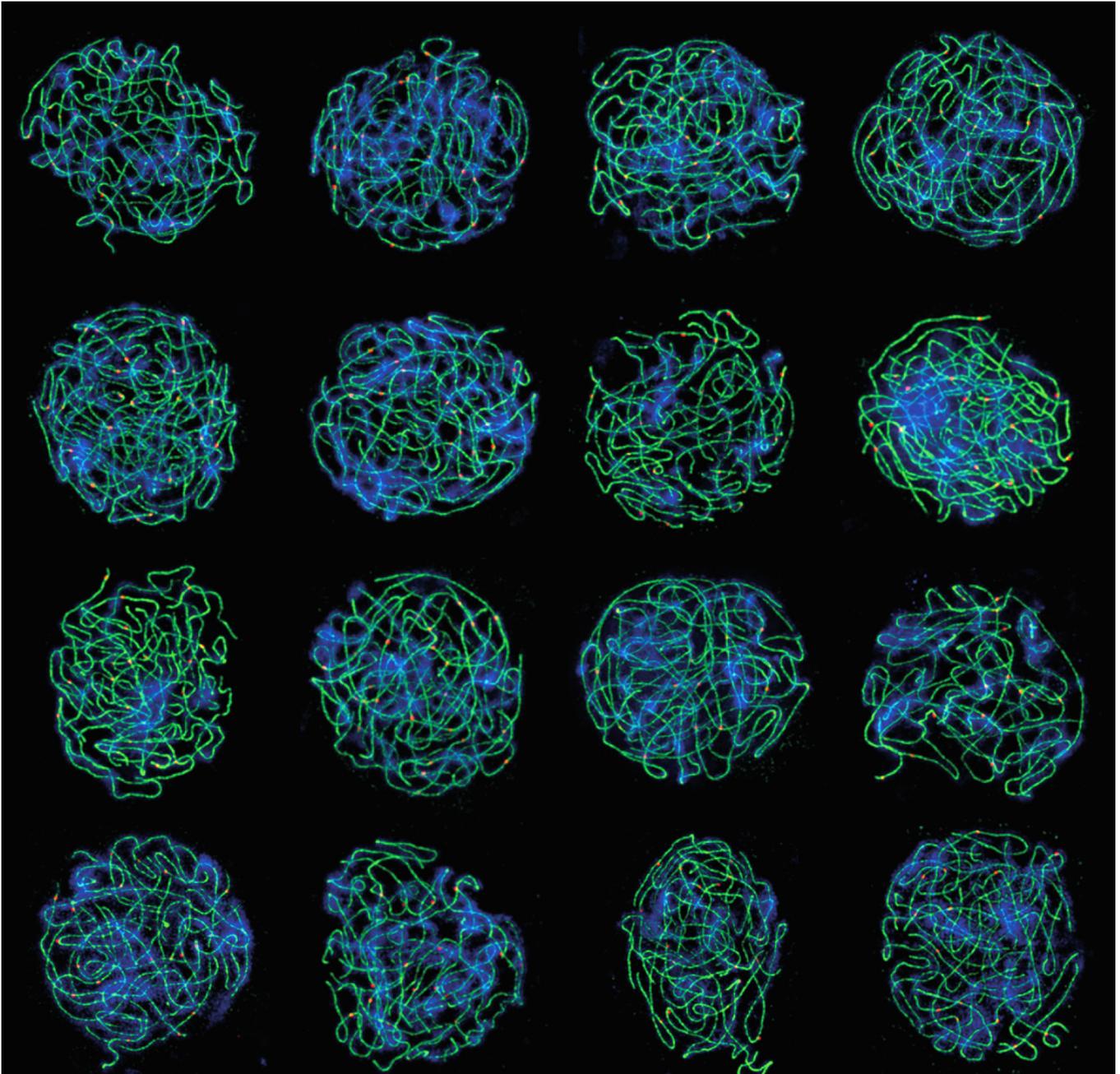
The evolution of self-fertilization is also a widespread transition in natural and crop plants. Self-fertilizing species typically produce a reduced number of pollen grains, or male gametes, but little was known about the molecular basis and signatures of selection. We performed a genome-wide association study of the pollen number in the diploid selfing plant *A. thaliana*, and identified the *REDUCED POLLEN NUMBER1* (*RDP1*) gene that encodes a ribosome-regulating factor. To verify its subtle quantitative allelic effect, we established a new method to test quantitative complementation employing CRISPR/Cas9-based genome editing. Strong selection of loci responsible for pollen number supported theoretical predictions suggesting that a reduced investment in male gametes is advantageous in predominantly selfing species (Tsuchimatsu et al. *Nature Comm* 11:2885, 2020). These studies will provide a pathway to investigating why self-fertilization is common in polyploid species.

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**Figure 1:** Left. A read is mapped to the polyploid genome as if it is a diploid. Right. A read of the allotetraploid *A. kamchatica* is mapped separately to each subgenome (*A. halleri* and *A. lyrata*) and then classified.



Cytological images showing meiotic cells (in a stage called Pachytene) from tetraploid *A. arenosa*. The green marks a meiosis-specific structure called the synaptonemal complex, which forms between homologs and thus marks paired chromosomes. Blue marks the less-condensed DNA. Red dots indicate recombination events. All images: Chris Morgan, postdoc in the Bomblies lab.



A wild tetraploid *Arabidopsis arenosa* plant growing on a disused slate quarry near Bacharach, Germany. © Kirsten Bomblies

## Professor Kirsten Bomblies, ETH Zurich



In March 2019, Kirsten Bomblies started as Professor of Plant Evolutionary Genetics at the Institute of Molecular Plant Biology in the Department of Biology at the ETH Zurich. She began her independent research career in 2009 as an Assistant Professor and later Thomas D. Cabot Associate Professor at Harvard University, and then moved to ETH after a brief stay at the John Innes Centre in Norwich, UK (2015–2018). For her postdoc she was an NIH NRSA fellow in Detlef Weigel's lab at the MPI in Tübingen, Germany (2004–2009), where she worked on plant autoimmunity. She did her PhD in Genetics with John Doebley at the University of Wisconsin, Madison (1999–2004) working on a gene implicated in maize domestication. In 2008 she received a prestigious MacArthur Fellowship from the MacArthur Foundation (USA). She was born in Germany, but grew up in Colorado, USA.

She is a recognized leader in plant evolutionary genetics and has spent the last ten years developing *Arabidopsis arenosa* as a new model for studying the mechanisms of adaptive evolution, especially but not exclusively to polyploidy. After moving to the UK in 2015, she secured a European

Research Council Consolidator Grant to fund her work on meiotic evolution in polyploids (2016–2021). The lab is currently pursuing several different research avenues, but the main focus is on understanding the causes and consequences of the adaptive evolution of meiosis. Some years ago, the lab used a genome-scanning approach to study what genes were under selection in a polyploid lineage of *A. arenosa* (which they estimated to trace to a single event about 30,000 generations ago).

Core structural meiosis genes were dramatically over-represented. This finding spawned an ongoing collaboration with meiosis expert Nancy Kleckner (Harvard University) that has led to novel understanding about what the challenges that polyploids face actually are. Further work in the lab has continued to exploring how the genes under selection in *A. arenosa* tetraploids contribute to meiotic stability, and recent work showed that derived alleles of two of the genes under selection do in fact contribute measurably to the meiotic stability in the tetraploid. Another important recent discovery was that adaptation to the tetraploid state serves as a pre-adaptation for generating higher ploidies. The lab is also exploring additional genes under selection in tetraploids, which has led to exciting collaborations with Sylvain Bischoff (University of Zurich) and Samuel C. Zeeman (ETH Zurich). Another research angle focuses also on understanding the temperature-sensitivity of meiosis, and how tolerance evolves in warm-adapted populations. The lab uses a combination of approaches, ranging from gene sequence analyses, to cytology, super-resolution microscopy, molecular biology and protein biochemistry. Though the lab focus is on fundamental research, there is also applied

relevance: there are new insights about how recombination rates and locations can be altered, which is of interest in plant breeding, the lab's work on temperature effects is relevant in maintaining crop fertility in the context of a warming climate, and polyploidy is a promising breeding tool whose widespread application is commonly hampered by the low fertility of induced polyploids.

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<https://impb.ethz.ch/research/research-evo.html>

## Science (2020)

doi: 10.1126/science.aay0496

**Bumble bees damage plant leaves and accelerate flower production when pollen is scarce**Pashalidou F; Lambert H; Peybernes T; Mescher M; De Moraes CM

Maintaining phenological synchrony with flowers is a key ecological challenge for pollinators that may be exacerbated by ongoing environmental change. Here, we show that bumble bee workers facing pollen scarcity damage leaves of flowerless plants and thereby accelerate flower production. Laboratory studies revealed that leaf-damaging behavior is strongly influenced by pollen availability and that bee-damaged plants flower significantly earlier than undamaged or mechanically damaged controls. Subsequent outdoor experiments showed that the intensity of damage inflicted varies with local flower availability; furthermore, workers from wild colonies of two additional bumble bee species were also observed to damage plant leaves. These findings elucidate a feature of bumble bee worker behavior that can influence the local availability of floral resources.

## Science (2020)

doi: 10.1126/science.aay4490

**Active restoration accelerates the carbon recovery of human-modified tropical forests**Philipson CD; Cutler MEJ; Brodrich PG, et al.

More than half of all tropical forests are degraded by human impacts, leaving them threatened with conversion to agricultural plantations and risking substantial biodiversity and carbon losses. Restoration could accelerate recovery of aboveground carbon density (ACD), but adoption of restoration is constrained by cost and uncertainties over effectiveness. We report a long-term comparison of ACD recovery rates between naturally regenerating and actively restored logged tropical forests. Restoration enhanced decadal ACD recovery by more than 50%, from 2.9 to 4.4 megagrams per hectare per year. This magnitude of response, coupled with modal values of restoration costs globally, would require higher carbon prices to justify investment in restoration. However, carbon prices required to fulfill the 2016 Paris climate

agreement [\$40 to \$80 (USD) per tonne carbon dioxide equivalent] would provide an economic justification for tropical forest restoration.

## Genome Biology (2019)

doi: 10.1186/s13059-020-02068-2

**Cell type-specific genome scans of DNA methylation divergence indicate an important role for transposable elements**Kartal O; Schmid MW; Grossniklaus U

In population genomics, genetic diversity measures play an important role in genome scans for divergent sites. In population epigenomics, comparable tools are rare although the epigenome can vary at several levels of organization. We propose a model-free, information-theoretic approach, the Jensen-Shannon divergence (JSD), as a flexible diversity index for epigenomic diversity. Here, we demonstrate how JSD uncovers the relationship between genomic features and cell type-specific methylome diversity in *Arabidopsis thaliana*. However, JSD is applicable to any epigenetic mark and any collection of individuals, tissues, or cells, for example to assess the heterogeneity in healthy organs and tumors.

## Trends in Ecology &amp; Evolution (2020)

doi: 10.1016/j.tree.2020.02.002

**Measuring coevolutionary dynamics in species-rich communities**Hall AR; Ashby B; Bascompte J; King KC

Identifying different types of coevolutionary dynamics is important for understanding biodiversity and infectious disease. Past work has often focused on pairs of interacting species, but observations of extant communities suggest that coevolution in nature occurs in networks of antagonism and mutualism. We discuss challenges for measuring coevolutionary dynamics in species-rich communities, and we suggest ways that established approaches used for two-species interactions can be applied. We propose ways that such data can be complemented by genomic information and linked back to extant communities via network structure, and we suggest avenues for new theoretical work to strengthen these connections. Quantifying coevolution in species-rich communi-

ties has several potential benefits, such as identifying coevolutionary units within networks and uncovering coevolutionary interactions among pathogens of humans, livestock, and crops.

## Nature Plants (2020)

doi: 10.1038/s41477-020-0618-2

**Anthoceros genomes illuminate the origin of land plants and the unique biology of hornworts**Li FW, Nishiyama T, Waller M, Frangedakis E, Keller J, Li Z, Fernandez-Pozo N, Barker MS, Bennett T, Blázquez MA, Cheng S, Cuming AC, de Vries J, de Vries S, Delaux PM, Diop IS, Harrison CJ, Hauser D, Hernández-García J, Kirbis A, Meeks JC, Monte I, Mutte SK, Neubauer A, Quandt D, Robison T, Shimamura M, Rensing SA, Villarreal JC, Weijers D, Wicke S, Wong GKS, Sakakibara K; Szövényi P

Hornworts comprise a bryophyte lineage that diverged from other extant land plants >400 million years ago and bears unique biological features, including a distinct sporophyte architecture, cyanobacterial symbiosis and a pyrenoid-based carbon-concentrating mechanism (CCM). Here, we provide three high-quality genomes of *Anthoceros* hornworts. Phylogenomic analyses place hornworts as a sister clade to liverworts plus mosses with high support. The *Anthoceros* genomes lack repeat-dense centromeres as well as whole-genome duplication, and contain a limited transcription factor repertoire. Several genes involved in angiosperm meristem and stomatal function are conserved in *Anthoceros* and upregulated during sporophyte development, suggesting possible homologies at the genetic level. We identified candidate genes involved in cyanobacterial symbiosis and found that LCIB, a *Chlamydomonas* CCM gene, is present in hornworts but absent in other plant lineages, implying a possible conserved role in CCM function. We anticipate that these hornwort genomes will serve as essential references for future hornwort research and comparative studies across land plants.

## Nature Communications (2020)

doi: 10.1038/s41467-020-16679-7

**Adaptive reduction of male gamete number in the selfing plant *Arabidopsis thaliana***Tsuchimatsu, T; Kakui, H; Yamazaki, M; Marona, C; Tsutsui, H; Hedhly, A; Meng, D; Sato, Y; Stadler, T; Grossniklaus, U; Kanaoka, MM; Lenhard, M; Nordborg, M; Shimizu, KK

The number of male gametes is critical for reproductive success and varies between and within species. The evolutionary reduction of the number of pollen grains encompassing the male gametes is widespread in selfing plants. Here, we employ genome-wide association study (GWAS) to identify underlying loci and to assess the molecular signatures of selection on pollen number-associated loci in the predominantly selfing plant *Arabidopsis thaliana*. Regions of strong association with pollen number are enriched for signatures of selection, indicating polygenic selection. We isolate the gene REDUCED POLLEN NUMBER1 (RDP1) at the locus with the strongest association. We validate its effect using a quantitative complementation test with CRISPR/Cas9-generated null mutants in nonstandard wild accessions. In contrast to pleiotropic null mutants, only pollen numbers are significantly affected by natural allelic variants. These data support theoretical predictions that reduced investment in male gametes is advantageous in predominantly selfing species. Reduction of pollen grain number is widespread in selfing plants, but the determining gene is unknown. Here, the authors show that a ribosome-biogenesis factor encoding gene RDP1 is responsible for adaptive reduction of male gamete number in *Arabidopsis thaliana*.

## Nature Communications (2020)

doi: 10.1038/s41467-020-16620-y

**The effect of flow on swimming bacteria controls the initial colonization of curved surfaces**Secchi, E; Vitale, A; Mino, GL; Kantsler, V; Eberl, L; Rusconi, R; Stocker, R

The colonization of surfaces by bacteria is a widespread phenomenon with consequences on environmental processes and human health. While much is known about the molecular mechanisms of surface colonization, the

influence of the physical environment remains poorly understood. Here we show that the colonization of non-planar surfaces by motile bacteria is largely controlled by flow. Using microfluidic experiments with *Pseudomonas aeruginosa* and *Escherichia coli*, we demonstrate that the velocity gradients created by a curved surface drive preferential attachment to specific regions of the collecting surface, namely the leeward side of cylinders and immediately downstream of apexes on corrugated surfaces, in stark contrast to where nonmotile cells attach. Attachment location and rate depend on the local hydrodynamics and, as revealed by a mathematical model benchmarked on the observations, on cell morphology and swimming traits. These results highlight the importance of flow on the magnitude and location of bacterial colonization of surfaces. Bacterial colonization of surfaces has a profound environmental, technological and medical impact. Here, Secchi et al. show how fluid flow affects the magnitude and location of bacterial colonization on curved surfaces through its coupling with cell morphology and motility.

## Nature Communications (2020)

doi: 10.1038/s41467-020-14409-7

**Global determinants of freshwater and marine fish genetic diversity**Manel, S; Guerin, PE; Mouillot, D; Blanchet, S; Velez, L; Albouy, C; Pellissier, L

Genetic diversity is estimated to be declining faster than species diversity under escalating threats, but its spatial distribution remains poorly documented at the global scale. Theory predicts that similar processes should foster congruent spatial patterns of genetic and species diversity, but empirical studies are scarce. Using a mined database of 50,588 georeferenced mitochondrial DNA barcode sequences (COI) for 3,815 marine and 1,611 freshwater fish species respectively, we examined the correlation between genetic diversity and species diversity and their global distributions in relation to climate and geography. Genetic diversity showed a clear spatial organisation, but a weak association with species diversity for both marine and freshwater species. We found a predominantly positive relationship between genetic diversity and sea surface temperature for marine

species. Genetic diversity of freshwater species varied primarily across the regional basins and was negatively correlated with average river slope. The detection of genetic diversity patterns suggests that conservation measures should consider mismatching spatial signals across multiple facets of biodiversity.

## Nature Communications (2020)

doi: 10.1038/s41467-020-14541-4

**Plant diversity effects on forage quality, yield and revenues of semi-natural grasslands**Schaub, S; Finger, R; Leiber, F; Probst, S; Kreuzer, M; Weigelt, A; Buchmann, N; Scherer-Lorenzen, M

In agricultural settings, plant diversity is often associated with low biomass yield and forage quality, while biodiversity experiments typically find the opposite. We address this controversy by assessing, over 1 year, plant diversity effects on biomass yield, forage quality (i.e. nutritive values), quality-adjusted yield (biomass yield x forage quality), and revenues across different management intensities (extensive to intensive) on subplots of a large-scale grassland biodiversity experiment. Plant diversity substantially increased quality-adjusted yield and revenues. These findings hold for a wide range of management intensities, i.e., fertilization levels and cutting frequencies, in semi-natural grasslands. Plant diversity was an important production factor independent of management intensity, as it enhanced quality-adjusted yield and revenues similarly to increasing fertilization and cutting frequency. Consequently, maintaining and reestablishing plant diversity could be a way to sustainably manage temperate grasslands.

## Molecular Biology and Evolution (2020)

doi: 10.1093/molbev/msz272

**Domestication of high-copy transposons underlays the wheat Small RNA response to an obligate pathogen**Poretti, M; Praz, CR; Meile, L; Kalin, C; Schaefer, LK; Schlafli, M; Widrig, V; Sanchez-Vallet, A; Wicker, T; Bourras, S

## PhD Courses in Plant Sciences

### **Adaptomics – Population Genetics and Genomics of Adaptation**

22.–24.09.2020

Prof. Dr. Karl Schmid, University of Hohenheim  
Mireia Vidal-Villarejo, University of Hohenheim

The course introduces the study of plant genetic diversity and adaptation using population genomics approaches. Instructors will provide hands-on introduction to data handling, data exploration with summary statistics and data analysis with state-of-the-art methods for demographic analysis, population differentiation and selection detection of plant populations.

### **Get going with Statistics in Functional Genomics**

05.–07.10.2020

Prof. Dr. Anne Roulin, University of Zurich  
Dr. Jean-Claude Walsler, ETH Zurich, Genetic Diversity Center

In the field of genomics it is paramount to handle larger amounts of data efficiently, securely, and reproducibly. For this reason, the main objective of this course is to provide students the most basic and most crucial sets of skills to work with genomic datasets.

### **Filmmaking for Scientists**

21.–23.10.2020

Dr. Samer Angelone

We, scientists, have great stories, and we can learn to be 'scientists-as-filmmakers'! In this course participants will learn about camera, audio, lighting equipment, and how to use film editing software, together with how to write, design and carry out the basics of making a documentary.

### **Next-Generation Sequencing for Model and Non-Model Species (BI0610)**

11. & 12.11.2020

Prof. Kentaro Shimizu, University of Zurich  
Prof. Jun Sese, Artificial Intelligence Research Center, Japan  
Dr. Rie Inatsugi, University of Zurich  
Dr. Masaomi Hatakeyama, University of Zurich  
Dr. Jianqiang Sun, Research Center for Agricultural Information Technology, Japan  
Dr. Tatsuma Shoji, Artificial Intelligence Research Center, Japan

Handling of the huge data produced by next generation sequencers (NGS) requires experimental knowledge and computational skills. The aim of this course is to familiarize participants with experimental methods and data analysis about NGS. Topics will include: fundamental analysis of the sequence data, UNIX tools, and RNA-seq analysis.

### **Introduction to Genome-Wide Association Studies (GWAS)**

18.–20.11.2020

Prof. Matthew Horton, University of Zurich  
Dr. Ümit Seren, Gregor Mendel Institute, Austria

In this course, participants will discuss the pre-eminent tool for identifying genes that underlie natural phenotypic variation: genome-wide association studies (GWAS).

### **Next-generation Sequencing 2 – Continuation Course: Transcriptomes, Variant Calling and Biological Interpretation (BI0634)**

03.–04.12.2020

Dr. Carla Bello, Dr. Gregor Rot, University of Zurich

The aim of this course is to introduce students to the design and analysis principles of widely used NGS applications based on the course BIO 610. The focus of this follow-up course lies in SNP calling, transcriptome analysis and biological interpretation of gene lists. This course also provides hands-on computer training on the Linux/Unix command line and shell scripting.

### **PSC course registration**

[www.ethz.ch/services/en/service/courses-continuing-education.html](http://www.ethz.ch/services/en/service/courses-continuing-education.html)

Select: Plant Sciences

Contact: [psc\\_phdprogram@ethz.ch](mailto:psc_phdprogram@ethz.ch)

**Scientific Writing Practice 1 - General Principles**

16.9. &amp; 30.09.2020

**Writing a Post-Doctoral Grant**

28.– 29.09.2020

**Challenges in Plant Sciences – PSC Colloquium**

13.10. &amp; 10.11.2020

**Seminar Sustainable Plant Systems (ETHZ: 51-0209-00L) as part of Integrative Plant Sciences**

22.10. &amp; 03.12.2020

**Concepts in Evolutionary Biology (BIO395)**

26.–27.10.2020

**Scientific Presentation Practice**

03.11. &amp; 12.11.2020

**Genetic Diversity: Techniques**

04.11. &amp; 25.11.2020

**Current Challenges in Plant Breeding**

06.11.2020 &amp; 26.01.2021

**Introduction to UNIX/Linux and Bash Scripting (BIO609)**

09.11.2020

**Scientific Visualisations using R**

10.12. &amp; 17.12.2020

**Introduction to R**

21.01. &amp; 28.01.2021

## Science & Policy Courses

**Introduction to Political Sciences**

07.–09.09.2020

**Communicating Science**

12., 16., 19. &amp; 30.10.2020

**Building Political Support**

11.11. &amp; 07.12.2020

**Stakeholder Engagement**

26.–29.01.2021

Workbooks available at:

[www.plantsciences.uzh.ch/en/publications/sciencepolicyworkbooks.html](http://www.plantsciences.uzh.ch/en/publications/sciencepolicyworkbooks.html)

## Research with biological material from abroad – International regulations and due diligence in research

5 &amp; 6 November 2020

Do you work with biological material from abroad? Do you know, how to correctly proceed with access and benefit sharing, material transfer agreements and other procedures?

In this intensive 2-day training workshop with experts from the federal administration the focus is on your research examples and exemplified case studies to demonstrate how to correctly proceed. The course is open to PhD students, postdoc fellows and PIs. Register now!

The circulation of samples of plants, animals, microorganisms is not a new phenomenon. Passing them on as seeds, plants, germplasm, dried specimens etc. has a long tradition among scientists. It spurred innovation and knowledge production for the benefit of global health, agriculture, conservation and sectors such as pharmaceuticals and biotechnology.

It also generated questions and concerns about ownership (e.g. intellectual property, patents) and the fair share of the benefits that result from the use of biological material. This triggered a complex international regulatory landscape for the governance of genetic resources.

Now, existing regulations on access, import and exchange of biological material and samples strongly affect academic research, even for purely non-commercial purpose.

*The course will provide solid knowledge on*

- 1) correct and lawful access to genetic resources and benefit-sharing for academic research;
- 2) the multilateral system of the international plant treaty;
- 3) requirements for importing material under CITES;
- 4) Swiss regulations; and
- 5) available support and counseling services for scientists in Switzerland.

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# Nachtaktiv – Inspire the next generation

All over the world “Late Night” events in museums are emerging and are becoming extremely popular, providing a fresh approach to reach new audiences and a great way to engage with visitors.

In January 2021, the Zurich Basel Plant Science Center will put on its first such event aimed at teenagers and young adults in Zurich. It is a new format of science communication where entertainment, art and knowledge transfer are combined. *Nachtaktiv* is aimed for young people aged 16 and over. Once per month on a Friday evening, there will be a party-style evening event in various Zurich museums. Science activities will be led by students of ETH Zurich, University of Zurich and University of Basel in an entertaining way. ETH spin-offs enrich the program with their inventions and the museums will focus on certain exhibitions or offer guided tours.

The aim of *Nachtaktiv* is to bring a young audience onto a wide-ranging journey through cutting-edge science, technology, art and design that responds to some of the present challenges that society is facing. We want to enable young people to think critically, ask questions and participate in a social debate on future technologies. We also want to increase the interest in natural sciences and expand participants' career orientation. Each event focuses on a different theme: From future forecasting to designing nature, from big data to robotics.

*Nachtaktiv* starts late in the evening for a reason: 16-25's work or study during the day and cannot get to museums or attractions during regular opening hours. In addition, we want to offer young people a nice alternative to visiting a bar or to hanging out in the park. They are hungry for content and want to develop their own ideas and identity.

*Nachtaktiv* is more than just a place in which science and technology is presented. It's about becoming a center of activity, a place for social interaction – *Nachtaktiv* wants to lend to science personal touch, amazement, magic and mystery, in other words, an opportunity for people to have fun and find inspiration.

29.01.2021 WOW Museum  
 26.02.2021 Kulturama  
 26.03.2021 Museum für Gestaltung  
 29.04.2021 Kunsthaus  
 28.05.2021 FIFA World Football Museum  
 25.06.2021 Sukkulente Sammlung  
 24.09.2021 FocusTerra  
 29.10.2021 Mühlerama  
 19.11.2021 Six Finanzmuseum

Contact: Ulrike von Groll  
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[www.nachtaktiv.live](http://www.nachtaktiv.live)

This program receives funding from the Gebert RUF Foundation.

## Call for participation

### Climate Garden 2085

The greenhouses provide research material for numerous school projects from gas exchange to plant ecology. Two schools now have a *Climate Garden* as a semi permeant installation to do long-term experiments. We are looking for support from scientists to give workshops or short talks in the schools.

[www.klimagarten.ch](http://www.klimagarten.ch)

### CreativeLabZ for youth

This PSC outreach project for youth is running in the Student Project House of the ETH Zurich, the Startbahn 29 in Dübendorf and other venues. The workshops combine art and science for young people aged 12–16. Short talks from researchers are welcome (also in English). Or you can come and tinker and help make stuff with us in the makerspace.

[www.creativelabz.ch](http://www.creativelabz.ch)

### Nachtaktiv (Nocturnal)

A new monthly party event for youth (see left). The first event is in January 2021. We are looking for students, who can present their work in a humorous and entertaining way. Hands-on experiments and things to try out are welcome. Themes vary a lot, if you have a cool project, we will find the right *Nachtaktiv* for it.

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 GEBERT RUF STIFTUNG

# feminno – Career program for innovative women

Already 60 young women took part in the feminno career development program coordinated by the PSC. Thanks to a collaboration with the ETH Zurich School for Continuing Education we are taking the program to the next level. We will increase the diversity of our participants and can now include female professionals and alumnae holding a Master's degree in the program. The 4th program round has just started. Experienced career advisers, coaches, innovation experts and executives from successful life-science enterprises will share their work experience and inspire program participants to actively mature their ideas and their personal development.

Many participants found interesting and challenging jobs in industry or in consulting by the time they finished their assignments. The first promising ideas have become acknowledged projects, such as BABYLAT™ by Zina Yudina.

The feminno program will soon publish its guidelines to support successful innovation processes for female academics. This document aims to encourage both, female academics and academic institutions to establish a culture of open, unconditional mind-sets regarding alternative career paths and innovation.

The feminno program is supported by a multitude of university institutions (University of Zurich Career Services, and Gender Equality and Diversity Office; University of Zurich Graduate Campus, University of Zurich and ETH Zurich Life Sciences, University of Basel Diversity Management; University of Zurich Faculty of Medicine; and the ETH Zurich Department of Environmental System Sciences). The program is also supported by companies such as Roche, Lonza and Actelion. This broad support clearly demonstrates the need for and the acknowledgement of feminno, which is meanwhile known for its high quality and the opportunities it offers to its participants.

[www.feminno.com](http://www.feminno.com)

We warmly welcome our new feminno coordinator!

Dr. Ute Budliger who was coordinating the feminno program for the last 4 years is taking a new challenge at Syngenta Crop Protection in Stein. We deeply thank Ute for her passion and engagement building up this vibrant career program. From October 2020, Dr. Daniela Gunz will take over. Daniela Gunz holds a PhD in biochemistry from the ETH in Zurich. She has 15 years of experience in clinical research and drug development in big pharma with an extensive network in the Swiss clinical research environment. She has been working in a start-up in digital health for the last 6 years, with broad knowledge of the Swiss (health) start-up scene. She now works as student counselor and project manager at the Career Services and at the Student Advisory Services of University of Zurich. She co-founded hermelin gmbh in 2016 and consults in clinical research, digital health and organizational development. Additional assignments include board membership at Women in Digital Health Switzerland, advisory board membership of EUPATI Switzerland and co-lead at MyData Zurich hub.

Contact: [daniela.gunz@usys.ethz.ch](mailto:daniela.gunz@usys.ethz.ch)

ETH zürich University of Zurich University of Basel



feminno



Successful Innovation. A Guideline for Female Scientists in the Life Sciences at Swiss Universities. Ute Budliger and Melanie Paschke (eds.). With contributions by: Ute Budliger, Manuela Dahinden, Carl Emerson, Roger Gfroerer, Daniela Gunz, Christiane Löwe, Tanja Neve-Seyfarth, Melanie Paschke, Isabelle Siegrist, Carolin Strobl. Zurich-Basel Plant Science Center, 2020.

## Upcoming

### Feminno workshop

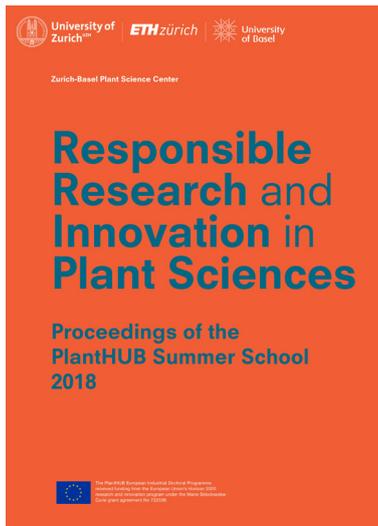
LS<sup>2</sup> Annual Meeting

18-19 Feb 2021

#### feminno – a stepping stone for careers in Life Sciences

This workshop offers an introduction to feminno with focus on its objectives and unique success factors, the benefits also for men, key insight into successful negotiation and some feedback from a former feminno participant. Main topics are innovation and entrepreneurship, career opportunities, gender equality and communication.

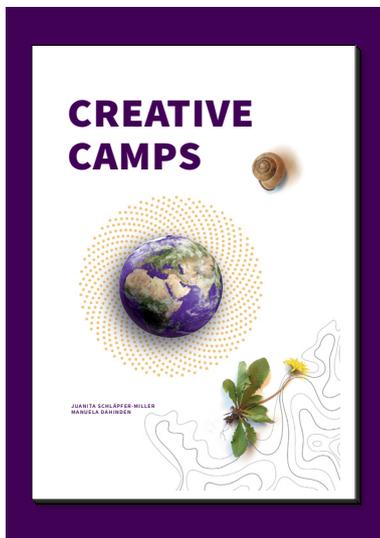
<https://annual-meeting.ls2.ch>



Proceedings of the PlantHUB Summer School 2018, **Responsible Research and Innovation (RRI) in Plant Sciences**.

Melanie Paschke (ed.). With contributions by: Manuela Dahinden, Gregory Grin, Melanie Paschke, Christine Rösch, Daan Schuurbiers, Foteini Zampati, Camilo Chiang, Franco Conci, Claudio Cropano, Florian Cueni, Seydina Issa Diop, Daniel Grogg, Manuel Nolte, Ina Schlathöfer, Giacomo Potente, Maximilian Vogt.

<https://doi.org/10.3929/ethz-b-000404539>



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 Flutsch, Joyce Kalumba, Mina Karrer, Renate Lerch, Alexandra Rosakis.

ISBN: 978-3-907234-04-4

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

## Responsible Research and Innovation (RRI) in Plant Sciences

Social transformation through innovation and research is a key element in the discussion as to how the global community can overcome its complex problems related to environmental and economic constraints in a resource-limited world. Innovation conflicts arise when transformation is mainly technology-driven and does not take up ethical, legal and social issues. In response, scientists are today being asked to play a role in the science-society dialogue.

In the PlantHUB Summer School (September 2018) we asked how Responsible Research and Innovation (RRI) could allow early-stage researchers to participate in the ongoing public debate on plant breeding and agricultural digitalization.

The Proceedings of the PlantHUB Summer School 2018 introduce the concept of RRI, highlight different stakeholder perspectives and related needs, values and concerns with three case studies from plant sciences. The Proceedings are completed with the abstracts of all keynote lectures and workshops.

The Summer School received funding from Swiss universities and the European Union's Horizon 2020 research and innovation program under the Marie Skłodowska-Curie grant agreement No 722338 – PlantHUB.

## Creative plant science experiments for youth

In collaboration with art educators from the Zurich University of the Arts (ZHdK), the PSC developed workshop activities for young people aged 8–14. The workshops are offered during holiday camps but also at Treffpunkt Science City, Scientifica, spring festival at the Botanical Garden of the University of Zurich and the Fascination of Plants Day.

The Creative Camp Agora project was designed together with different PSC research groups reflecting frontiers research on topics such as biocommunication, plant development and evolution, adaptation to climate change, modelling of future landscapes and ecosystem services. The project emphasizes our aim to enable more Plant Science Center's researchers to engage a broad cross-section of young people in Switzerland with hands-on learning experiences and open dialogue formats. The collaboration with bachelor students of Art Education at the ZHdK allowed us to combine creative and inquiry-based approaches to learning and teaching and thus, expand young people's capacity of understanding of science. We were able to foster children's own interests and explorations by encouraging their inquiry skills in particular observing and exploring, asking questions, reasoning and making interconnections.

The PSC Creative Camps for Youth are supported by the SNSF Agora, 2017–2020.

<http://p3.snf.ch/project-171682>

With contributions by research groups of Prof. Consuelo de Moraes (Chair of the Agora project), Prof. Loïc Pellisier (ETH Zurich), PD Dr. Diana Santelia (ETH Zurich), Prof. Antia Rodriguez-Villalon (ETH Zurich), Prof. Samuel Zeeman (ETH Zurich), Prof. Johan Six (ETH Zurich), Prof. Ueli Grossniklaus (University of Zurich), Prof. Joop Vermeer (University of Neuchatel), Prof. Kentaro Shimizu (University of Zurich).

Videos: [www.plantsciences.uzh.ch/de/outreach/ferienlager.html](http://www.plantsciences.uzh.ch/de/outreach/ferienlager.html)

# PSC Symposium 2020

## Connectivity: Plant interactions reloaded



**Specials:**  
Poster Awards  
Flash Talks

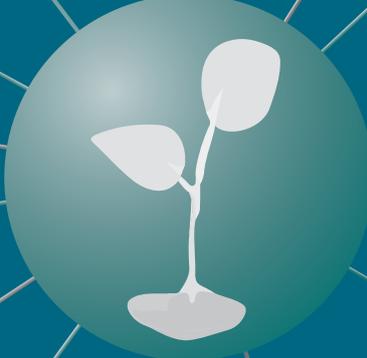
**2<sup>nd</sup> December, 9:00–17:00  
online**

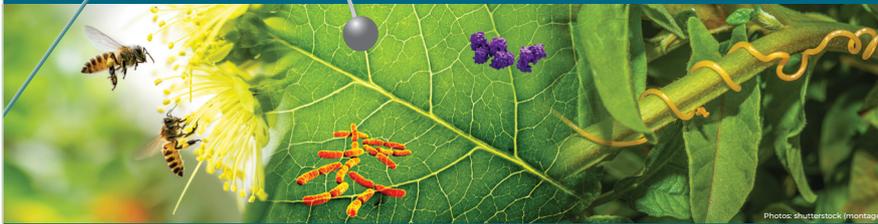
**Registration**  
[blogs.ethz.ch/psc2020](https://blogs.ethz.ch/psc2020)

9:30–11:15  
**Plant-plant interactions**  
Susann Wicke (HU Berlin)  
Christa Testerink (Wageningen)  
tbd

11:45–13:30  
**Plant-microbe interactions**  
Julia Vorholt (ETH Zurich)  
Heribert Hirt (KAUST)  
Anna-Liisa Laine (Uni Zurich)

15:00–16:45  
**Plant-animal interactions**  
Jordi Bascompte (Uni Zurich)  
Vivian Irish (Yale University)  
Rebecca E. Irwin (North Carolina State)





Photos: Shutterstock (montage)



@PlantSciCenter  
@PSCSymposium2020  
#PlantInteraction



**PhD students organizing the symposium**

Alicia Abarca, Laura Herold, Henning Muehlenbeck, Seydinaissa Diop, Zhenzhu Xiao & Giacomo Potente, University of Zurich; Santiago Perez Bernal, University of Basel; Yuanyuan Liang, ETH Zurich

**PSC Coordinators**

Luisa Last, Manuela Dahinden, Romy Kohlmann

**PSC Public Round Table**

**What will Swiss ski areas be like in 2050?**

3 Feb 2021, 17:15–19:00, online, in German



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In the absence of strict emission measures, Switzerland is expecting a temperature rise of over 2 to 3 °C by 2050. Changes in precipitation, decreasing snow security and retreating glaciers will continue to change the landscape. Small ski resorts at lower altitudes will hardly be able to operate profitably due to the rising snowfall line. Heavily affected areas will need adaptation strategies and measures to ensure their continuity. In the course of the discussion, experts from various fields of science, tourism, and politics will jointly develop visions on how to preserve the attractiveness of mountain regions and will clarify the potential for new approaches. A core point to discuss will be the fundamental role of plant science research, since plants and functioning ecosystems are indispensable in mountain regions.

**STIFTUNG  
MERCATOR  
SCHWEIZ**



[www.plantsciences.ch](http://www.plantsciences.ch)

The Zurich-Basel Plant Science Center is a competence center linking and supporting the plant science research community of the ETH Zurich, the University of Zurich and the University of Basel. The center promotes plant science research, education and outreach and 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

### 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

### University of Basel

Department of Environmental Sciences

## Zurich-Basel Plant Science Center, Managing Office

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### LINKEDIN

Plant Fellows  
PlantHUB  
Feminno

### BLOGS

[www.klimagarten.ch](http://www.klimagarten.ch)  
[www.creativelabz.ch](http://www.creativelabz.ch)  
[blogs.ethz.ch/Science\\_and\\_Policy](http://blogs.ethz.ch/Science_and_Policy)



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Manuela Dahinden

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