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PlantScienceNews

Newsletter of the Zurich-Basel Plant Science Center

No 37, Spring 2020

Editorial

Digital times

The theme of digital transformation in society is currently ubiquitous, and not least in plant sciences. This newsletter highlights ongoing and promising digital applications of herbaria. Herbaria have been a vital research infrastructure in plant taxonomy and systematics since the onset of botany in the 16th century. Thanks to large-scale digitization efforts they have recently gained the interest of plant science researchers. We explore how essential such collections are to answer fundamental questions in science, and how much benefit can be gained for human society. For example, herbarium specimens may provide clues to global challenges, such as the effects of land use change or the increase in atmospheric CO_2 on the evolution of plants and their co-evolved symbionts or pathogens. The analysis of samples from the early days of domestication represents an exciting and novel development for crop genomics with potential implications for breeding, microbial symbiosis and favorable agronomical traits.

In this context, we welcome Verena Schünemann, Professor of paleogenetics at University of Zurich as a new PSC member. Verena combines ancient DNA genomics, evolutionary genetics and phylogenomics to better understand the role of genomic changes that have accompanied processes of domestication and plant pathogen evolution.

Meanwhile, the *PSC PhD Program in Plant Sciences* offers more than 20 courses dedicated to skills and competences training in data analysis and management. The courses address all types of plant science-related data analysis such as genomics, transcriptomics, epigenomics, metagenomics, phenomics as well as environmental and spatial distributed data (satellite measurements, remote sensing).

And last not least, various outreach programs of the PSC combine plant sciences with technology, design and robotics. In our tinkering workshops we aim to promote curiosity about sensors and plant materials, engineer interesting objects, robots, measuring devices and other masterpieces of art-science design. The PSC is organizing the ETH exhibition at the OLMA again this year and the ETH digital platform will be the centerpiece, showcasing robotics research. The digital transformation in agriculture will of course be especially interesting for the OLMA visitors and we are counting on your support to create a great visitor experience.

Sincerly,
Manuela Dahinden & Melanie Paschke, PSC Managing Directors

Content

PSC Coordination office: Melanie Paschke, Managing Director Education, Science in Society and Fundraising; **Manuela Dahinden**, Managing Director Research, Communications and Fundraising; **Romy Kohlmann**, Finances and PlantHUB Coordinator; **Luisa Last**, Coordinator PSC PhD Programs & RESPONSE DP; **Juanita Schläpfer**, Outreach Manager; **Ulrike von Groll**, Outreach Program Assistant; **Ute Budlinger**, *fem*inno 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 each host 5 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.

Contact: Manuela Dahinden, mdahinden@ethz.ch

www.plantsciences.uzh.ch/en/research/fellowships/jrc

RESPONSE Doctoral Program (RESPONSE 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. Each PhD student will contribute to one stakeholder meeting and one citizen consensus conference. 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.

Eight PhD students have started or will start in the research groups of Ueli Grossniklaus (University of Zurich), Kentaro Shimizu (University of Zurich), Marco Mazzotti (ETH Zurich), Tobias Schmidt (ETH Zurich), Giovanni Sansavini (ETH Zurich), Célia Baroux (University of Zurich), Maria J. Santos (University of Zurich) and Bruno Studer (ETH Zurich).

3rd open call for research project submission from 1 April until 30 June 2020

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

2nd open call for PhD candidate applications from 1 April until 1 July 2020

Applications have to be submitted via the application platform of the Life Science Zurich Graduate School (Choose: PhD Program Science and Policy).

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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 can enroll in the *PSC PhD Program Plant Sciences.*

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www.plantsciences.ch/research/fellowships/syngenta

Awards

Prof. Consuelo De Moraes (ETH Zurich) received the 2019 Recognition Award in Insect Physiology, Biochemistry and Toxicology (PBT) of the Entomological Society of America (ESA) for innovative research in these fields.

www.entsoc.org/pbt/recognition-pbt-award-winners

Together with a group of colleagues from Côte d'Ivoire, Burkina Faso and Sri Lanka, **Prof. Emmanuel Frossard** (ETH Zurich) received the 10th CSRS-Eremitage Award for Scientific Research in Partnership.

Prof. Ueli Grossniklaus (University of Zurich) was elected «Foreign Visiting Professor of Nagoya University» in Japan from September to December 2019 and «Infosys Visiting Chair Professor» at the Indian Institute of Science in Bengaluru for the years 2020 to 2022.

PSC Symposium Poster Award: 1st prize to **Patrick Möhl,** for his poster Carbon limitation: facts or fiction? (Erika Hiltbrunner group, U Basel), 2nd prize to **Claudio Cropano,** for his poster: Natural variation for pseudo self-compatibility in perennial ryegrass (*Lolium perenne* L.) – an untapped resource for hybrid breeding (Bruno Studer group, ETH Zurich), 3rd prize to **Florian Cueni** for his poster: Predicting the geographic origin of berries using mechanistic oxygen and hydrogen stable isotope models (Ansgar Kahmen group, U Basel).

Janine Steinmann won the SFIAR Master Thesis Award for her thesis: Effect of Natural and *Mucuna pruriens* fallow on soil properties and crop performance in *Dioscorea alata* (water yam) based systems in Liliyo and Tieningboué (Côte d'Ivoire) and Léo (Burkina Faso), supervised by Prof. Emmanuel Frossard (ETH Zurich).

Herbarium genomics – Opportunities and challenges

Herbaria and natural history museums worldwide constitute an irreplaceable record of biodiversity in space and time. In Switzerland, about two dozen institutions hold some 12 Mio. specimens, of which about half were collected in this country during the past 450 years. The herbaria at the Universities of Basel and Zurich and the ETH Zurich together hold about 4.5 Mio. specimens of land plants, algae and fungi, including thousands from the beginnings of botany in the early 17th century.

Within the PSC, the curators Alessia Guggisberg, Reto Nyffeler and Jurriaan de Vos collaborate with the research groups of Simon Aeschbacher, Verena Schünemann, Alex Widmer, and PhD students Gülfirde Akgül and Thomas Grubinger, to jointly use these collections for genomic investigations. While herbaria and museums continue to be a unique source of information for comparative morphological and systematic studies, the advent of Next Generation Sequencing (NGS) and substantial advances in the extraction of DNA from ancient specimens (aDNA, ancient DNA) now provide the opportunity to value them as priceless windows into past genetic processes.

In one project, the scientists are tracing the genome-wide footprint of plant domestication by integrating whole-genome aDNA from up to 420-year old herbarium specimens with publicly available modern DNA from cultivars and wild relatives. Their aim is to establish the evolutionary relationships among historical and modern samples, and uncovering the genomic signature of evolutionary forces that acted during domestication, including introgression, admixture, and artificial selection. In another project, the PSC researchers are developing a pipeline to efficiently screen herbarium tissues for plant pathogen aDNA. Their goal is to enrich and sequence the pathogen aDNA using NGS technology to study the (co-)evolutionary dynamics of plant pathosystems. A third endeavor aims at monitoring putative genetic changes in alpine plant species to inform conservation management institutions on the potential threats posed by climate change. With many collections dating back to 1800, it is possible to reconstruct patterns of gene flow, population expansion/bottleneck and population differentiation at ecological timescales of tens of generations. In all projects, the scientists are initially restricting their efforts to a small set of focal species, hoping though that their work will inspire future herbarium genomic studies across a wider taxonomic range.

Despite the current hype in herbarium genomics, a number of technological and methodological challenges remain. Most importantly, due to physical and biochemical degradation, the quality of aDNA sequence data may vary tremendously across samples and genomic regions. Moreover, even though herbarium specimens in principle feed independent information about time and space into population genomic analyses, the sampling along these two axes often remains scattered. In practice, approaches to effectively integrate such sparse information to improve inference first need to be developed and validated. The PSC researchers aim at tackling both of these challenges through a combination of bioinformatic, population genetic, and statistical approaches. The historical perspectives also underline the importance of continued, targeted expansion of herbaria with contemporary accessions to enlarge their value for scientific ventures for centuries to come.

Project funded by individual research budgets, Evolution in Action University Research Priority Program, University of Zurich and Basler Stiftung für biologische Forschung.

Project leaders

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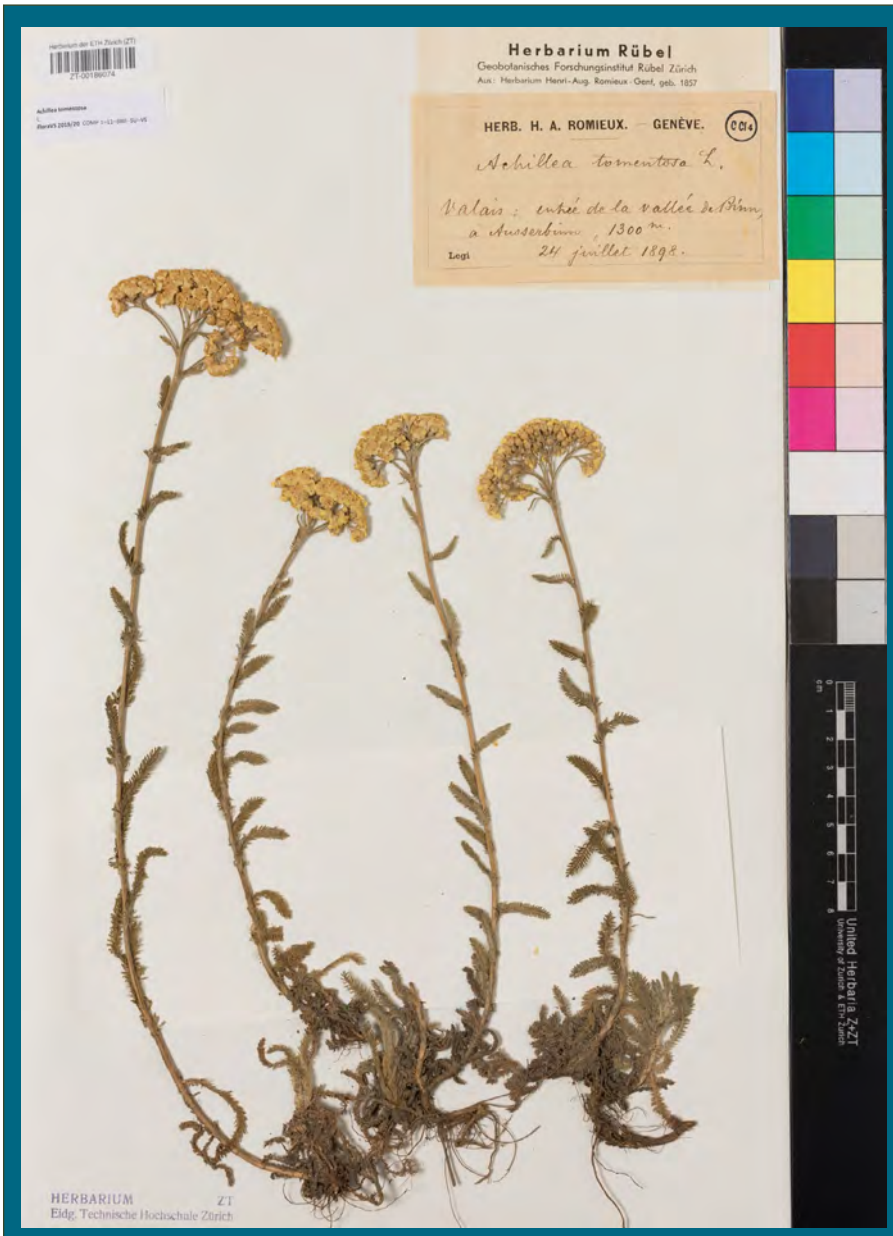


Herbarium specimens at the University of Basel. Herbaria are stored in protective boxes. The boxes (ca. 50) represent ca. 2% of the whole collection at the University of Basel. © Sylvia Martinez

Below left, examples of digitized vouchers from the United Herbaria Z+ZT of the University and ETH Zurich. Consult www.herbarien.uzh.ch/en/belegsuche

ZT-00186074, ZT-00172726 and ZT-00079281, CC-BY-SA 4.0

Below right, sampling a herbarium specimen for DNA from of a plant grown by Caspar Bauhin (1560–1624) at Herbaria Basel. © Jurriaan M. de Vos

Great potential for (Swiss) Herbaria

Herbaria store dry, pressed plants, along with ancillary sampling information, and thus document biodiversity in space and time. The oldest herbarium vouchers worldwide date back to the second half of the 16th century, such as the collections of Felix Platter (1536–1614) and Caspar Bauhin (1560–1624) stored at the Burgerbibliothek Bern and at the University of Basel, respectively. Since their inception, Swiss herbaria have amassed 12 Mio. specimens, of which half originate from Switzerland, thereby providing a time series of indigenous and non-native plant diversity of national and international importance. Until recently, these collections were only accessible physically, either by visiting the given institutions, or by requesting loans of the desired material. Thanks to augmented digitization efforts, they can now increasingly be consulted in digital showrooms on the Internet.

Herbarium vouchers provide two kinds of data that can be accessed from the organic material itself and the accompanying labels, respectively. The preserved specimens entail structural, phytochemical and genetic information, as well as eventual «by-catch» of epiphytic or parasitic organisms. Furthermore, the biological objects may yield environmental data from substances absorbed by the organisms during their lifetime. By contrast, labels provide information about the spatio-temporal presence of the organisms, as well as about its condition at the time of conservation.

In comparison to modern, single-use samples (e.g. silica gel or alcohol preserved tissues), most herbarium specimens were not initially meant to extract DNA or metadata for subsequent analyses. Luckily, technological advances, such as Next Generation Sequencing (NGS) and machine learning algorithms, make it continuously easier to exploit such information. In this context, digitization plays a central role in allowing interested parties from all over the world to assess the availability and quality of the material for specific research questions. Accordingly, large datasets containing detailed metadata are increasingly looked-for as they enable projects that address spatial and temporal dynamics of organisms and their interactions with the environment over multiple centuries.

Digital Herbarium

A digital herbarium is a database of plant specimens that includes high-resolution images of the objects, as well as important metadata about their identification, geographical origin, sampling date, and collectors. While conveyor belt systems may speed up the imaging process, revising the identification of specimens, transcribing (most often) handwritten labels, and georeferencing locality information with the help of digital online maps remain daunting tasks, which cannot be fully automated yet, despite rapid progress in machine learning algorithms. Not to mention, most herbaria lack a robust and flexible database system that can handle such diverse data types, as adequate off-the-shelf solutions do not readily exist.

Workflow for digitizing herbarium specimens as applied for all 81'000 Brassicaceae specimens at the United Herbaria of the University and ETH Zurich. © Alessia Guggisberg

1. **Inventory**

   Cardaminopsis arenosa (L.) Hayek
   414 Schweizer Belege
   318 ausländische Belege

2. **Rename, if necessary**

   Cardaminopsis arenosa (L.) Hayek
   ↓
   Arabidopsis arenosa (L.) Lawalrée

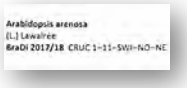
3. **Sort geographically**

   Kt. Neuenburg, Les Brenets, Saut du Doubs
   ↓
   CRUC–1–11–SWI–NO–NE

4. **Append barcode**

5. **Restore, if necessary**

6. **Label with a new tag**



7. **Photograph and record metadata**

8. **Release online**

https://www.herbarien.uzh.ch/en/belegsuche.html

Swiss Roadmap

Unlocking the full potential of Swiss herbaria comes with some challenges. Currently, an easily accessible digital register of the specimens is lacking. To date, only 10% of the vouchers have been recorded in locally maintained databases, and even fewer have been integrated in national or international portals such as the Global Biodiversity Information Facility, GBIF (www.gbif.org). Physical ordering systems are often incompletely implemented and specimens from the same collectors or localities are spread among herbaria, so that multiple institutions need to be searched for to reassemble a collection. Last but not least, backlogs of unprocessed material await mounting and identification for their integration into the main collection, thereby jeopardizing proper curation.

A concerted effort to digitize herbarium collections following standardized protocols would remedy this situation. A number of herbaria integrate the workforce of volunteers that contribute to the transcription and georeferencing of digitized (photographed) specimens through an online digital herbarium platform. A prime example for such a collaborative approach is the citizen science project of the Flora of the canton of Zurich (FloZ), for which about 34'000 historical records, about half of them based on herbarium specimens, were georeferenced to investigate the floristic changes in the canton over the past two hundred years.

We have proposed that the Swiss herbaria be recognized as a national research infrastructure, with the primary goal to unlock their potential for a diversity of projects in plant sciences that extend beyond taxonomy and systematics. An important first step would be to establish database systems that allow for collaboration among institutions, but also to appoint additional curators and technical assistants to revise the collections for upcoming digitization projects. In a second step, specimens should be digitally integrated among institutions, in order to unveil them and hence rendering new avenues for groundbreaking research studies for centuries to come.

Alessia Guggisberg, Reto Nyffeler, Jurriaan M. de Vos

Swiss Initiatives

SwissHerbaria, founded in 2015, is now under the patronage of the Swiss Botanical Society. In 2019, the board members of SwissHerbaria launched an initiative to be recognized as the competence center for herbarium collection management and digitization. Specific aims include the development of standard protocols for metadata recording and the establishment of a national data management platform together with SwissCollNet (see below) for the estimated 12 Mio. specimens held in Swiss herbaria.

SwissCollNet – The Swiss Natural History Collections Network aims to bring together and support collaboration among the Swiss natural history collections with the vision to promote the collections themselves and to harness the scientific and educational potential of these collections for science and society.

https://naturalsciences.ch/organisations/bio/scientific_collections

National significance of natural history collections in Switzerland: Archives and resources for modern science. Swiss Academies Report (2019) 14:2.

Biome mapping using large numbers of herbarium distribution records

Rapidly growing availability of species occurrence data from digitization of the world's herbarium collections is opening up tremendous opportunities to view, map and quantify biodiversity in novel ways. Using occurrence records from the world's central repository for species distribution data, the Global Biodiversity Information Facility, GBIF (www.gbif.org), plus other data portals such as DryFlor (www.dryflor.info) and SEINet (swbiodiversity.org/seinet), we are mapping key biome-related plant functional traits to refine our understanding of the world's major biomes. Using 47'575 quality-controlled occurrence points for c. 900 species from 102 genera and 22 plant families of stem succulents, that are a textbook example of evolutionary convergence, we have modelled the distribution of this key plant functional group. This provides a novel approach to produce the first quantitative global map of the little-known Succulent Biome, an assemblage of succulent-rich, drought-deciduous, fire-free forest, thicket and scrub vegetation disjunctly distributed across the Neotropics, Africa, Madagascar, and Arabia.

Project funded by the SNSF. Project leader is Dr. Colin Hughes (Oberassistent) with PhD student Jens Ringelberg, Department of Systematic and Evolutionary Botany, University of Zurich.

Map showing the modelled probability distribution of the world's stem succulent plants, a proxy for the distribution of the global Succulent Biome (Ringelberg et al. unpublished data). © Colin Hughes

Herbarium phylogenomics of tropical legumes

Vachellia nilotica, an important tropical arid zone mimosoid legume tree, here being used for animal fodder in Rajasthan, India. © Colin Hughes

Our research is tapping into the world's richest herbarium collections, including the United Herbaria of the University and ETH Zurich, to obtain DNA of species from across the tropics. Using c. 300 often highly fragmented DNA extracts from preserved herbarium plant specimens we can sample species on a global scale that would be unrealistic based on field collecting. We are using these DNAs to sequence 960 nuclear genes via Hybseq across the mimosoid legumes, an important pantropical clade of trees. Alongside geographical and macroecological data, robust phylogenies can provide insights into trajectories of evolutionary diversification and assembly of high species richness across the tropics. Initial results point to the importance of the rainforest, savanna and dry tropical forest biomes in structuring mimosoid phylogenetic diversity, reveal an episode of hyperfast species diversification that cannot be resolved even using sequences of 950 genes, and show that more than 20% of the genera are non-monophyletic prompting a major reclassification of mimosoid legumes.

Project funded by the SNSF. Project leader is Dr. Colin Hughes (Oberassistent) with PhD students Jens Ringelberg and postdoc Dr. Erik Koenen, Department of Systematic and Evolutionary Botany, University of Zurich.

Impressions of tropical mimosoid legume diversity. Above left: *Parkia bahiae*; above right: *Piptadenia flava*; below left: *Calliandra nebulosa*; below right: Fabaceae *(Parapiptadenia zehntneri)* seeds.
© Colin Hughes

Vegetation dynamics in the Central Swiss Alps

The canton of Valais, in the Central Swiss Alps, is renowned for its specialized cold alpine and dry steppe environments. In order to preserve such a hotspot of plant diversity, it is of utmost importance to assess the susceptibility of those fragile habitats to climate change. The United Herbaria of the University (Z) and ETH Zurich (ZT) possess some 150'000 specimens from this region, which date back to the very beginning of the 18th century, the oldest vouchers stemming from Johann Jakob Scheuchzer, Johannes Gessner and Albrecht von Haller. With the aim of modelling the vegetation dynamics through time of the unique Valais flora, the United Herbaria Z+ZT are currently digitizing the collections of this canton. Thanks to a new crowdsourcing platform, volunteers from botanical societies and research institutions can then help transcribing and geo-referencing specimens in order to compile standardized datasets for vegetation distribution modelling.

Project funded by the ETH Library, individual ETH and UZH research budgets. Project leaders are Dr. Alessia Guggisberg, Curator Vascular Plants United Herbaria of the University and ETH Zurich (Z+ZT) and PD Dr. Reto Nyffeler, Curator Vascular Plants United Herbaria of the University and ETH Zurich (Z+ZT).

Workflow of georeferencing digitized specimens with the support of volunteers and a web-based crowdsourcing platform to compile large datasets of past distribution records. © Alessia Guggisberg

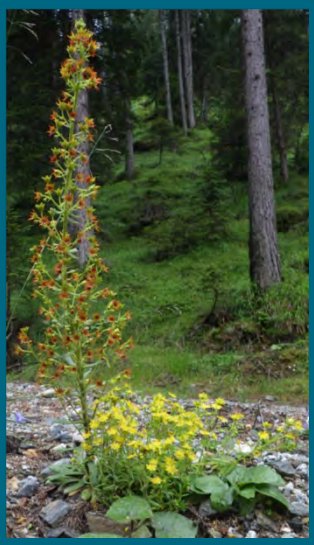
Evolution of plant reproduction in alpine areas

The contrasting environmental conditions along elevational gradients have massive effects on plant phenotypes, but there are important differences among species. In addition, responses of reproductive traits (flower number, morphology, inflorescence structure, etc.) are poorly understood. Overall, it is generally unclear what causes differences among species in elevational distributions, and if there are fundamental or lineage-specific constraints to evolving ecological niches. In a series of projects that leverage digitized herbarium specimens, we address different aspects of these general questions. In one project we use digitized herbarium specimens of Saxifraga species across the Alpine arc (high- and lowland) to quantify phenotypic trends in plant- and inflorescence structure along elevational gradients, for each species. Then, using a phylogenetic approach, we investigate how these phenotypic responses evolve. The results shine light on fundamental constraints to plant adaptation to the different environmental conditions and the nature of convergent evolution.

In a project funded by the SNSF (PRO-Alp), we address the question which environmental factors, among the many that change along elevational gradients, are the main drivers of the evolution of plant- and inflorescence structure. We first reconstruct phylogenies using genetic material obtained from herbarium specimens, for four genera that have lowland, alpine, and partly tropical alpine representatives. Then, we quantify phenotypic traits from herbarium specimens and fieldwork, and link these to modeled and measured environmental conditions at different latitudes and elevation, using our phylogenies. This approach then allows to quantify the extent to which different environmental drivers had similar or divergent effects across genera. It thus leverages convergent evolution as a means to infer plant functionality versus phylogenetic inertia. Both projects would not be possible without digitized herbarium specimens. They allow us to circumvent logistic challenges (e.g. sampling the whole alpine arc in a one-year project), enable access to genetic material for otherwise hard-to-obtain species, jointly allowing to address fundamental questions in evolution and ecology.

Project funded by the SNSF. Project leader is Dr. Jurriaan M. de Vos, Senior scientist and Curator of the Herbaria, with PhD student Livio Bätscher and MSc student Seraina Rodewald, Department Environmental Sciences, University of Basel.

The sister species *Saxifraga mutata* (left) and *S. aizoides* have contrasting elevational ranges, but co-occur in montane gravelly sites (here, in the Pfitschtal, South Tirol, *A.*). In alpine areas, only the compact, highly branching species *S. aizoides* occurs.
© Jurriaan M. de Vos



Herbarium specimens of *Saxifraga paniculat*a from 1800 m. (left) and 2490 m. (right). Label data such as elevation enables using herbarium specimens to study the relation between plant phenotype and environmental conditions.
© Herbaria Basel

Distribution dynamics of 1'100 bryophyte species in Switzerland

Switzerland comprises only 0.4% of the European land surface but hosts 55% of the bryophyte taxa present in Europe. This extraordinary biodiversity provides key ecosystem services and because of their high responsiveness, bryophytes serve as indicators for environmental changes. However, the identification of most bryophytes requires microscopic examination of collected material and documentation of their spatial and temporal distribution. This documentation is maintained and advanced by swissbryophytes, the national data and information center. The physical storage is essential because it allows the reexamination of specimens. Because of their high phenotypic plasticity, the identification of bryophytes is not straightforward and often needs to be reexamined by experts. Furthermore, taxonomic changes continuously require reevaluation to place the specimens in their current taxonomic units. The data forms the basis for national and international research and species conservation in Switzerland. They are also consulted extensively for the ongoing revision of the Swiss Red List of bryophytes and for various environmental impact assessments.

Project leaders are Dr. Heike Hofmann, Curator of Bryophytes and Coordinator swissbryophytes, United Herbaria of the University and ETH Zurich (Z+ZT), and Dr. Thomas Kiebacher and Markus M. Meier, Department of Systematic and Evolutionary Botany, University of Zurich.

Swissbryophytes

The national data and information center holds a database with currently approx. 338'000 records of digitized and georeferenced bryophyte specimens from Switzerland kept in more than 40 national and international herbaria. More than 70% (close to 239'000) of the digitized specimens are part of the collections at the United Herbaria of the University and ETH Zurich and associated with Department of Systematic and Evolutionary Botany at University of Zurich.

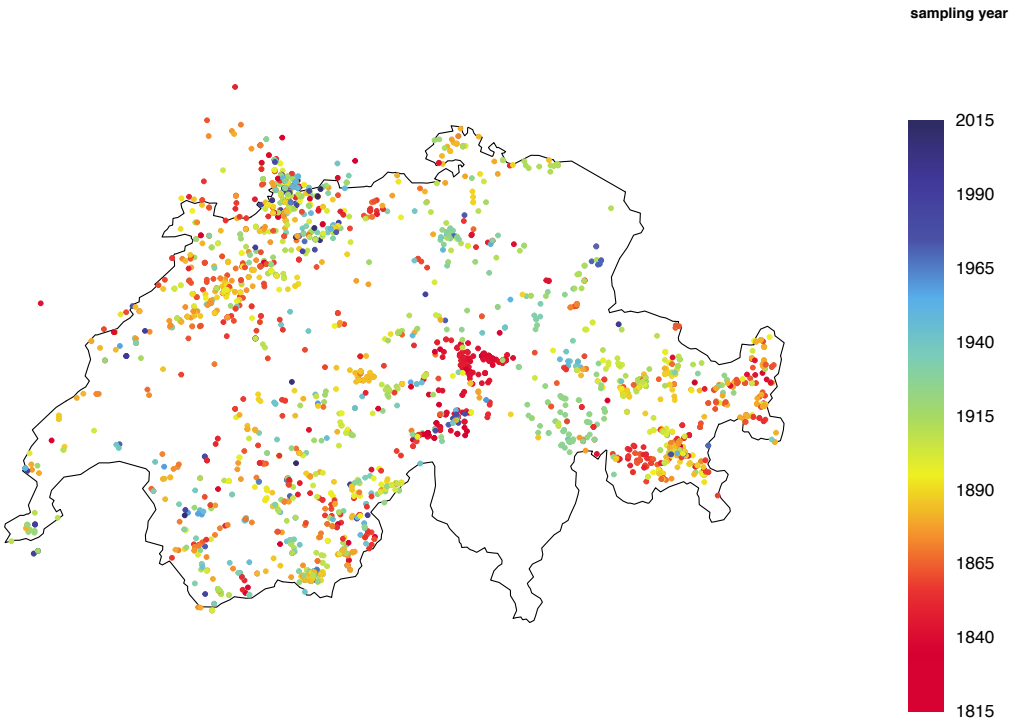
www.swissbryophytes.ch

Assessing long-term physiological responses of plants to global environmental change

Understanding plant physiological responses to environmental and climate change is a critical research task in ecology and earth system science. In particular, photosynthetic assimilation rates and stomatal conductance are key processes that shape the global carbon and water cycles. The response of these small-scale processes to environmental and climate change will determine biogeochemical processes at the ecosystem-level and global scale and alter ecosystem goods and services that societies depend on. A multitude of global change experiments – at the plant and ecosystem level – have already given insight into the mechanisms underlying plant physiological responses to environmental and climate change. Yet, most experimental global change studies are of relatively short duration, typically covering only a few growing seasons. The important long-term responses of plants and ecosystems to, e.g. elevated CO_2 or N deposition, and the physiological acclimation processes to these changes can thus not be assessed with experimental studies and therefore remain elusive.

The analysis of the stable carbon and oxygen isotope composition of archived plant material in herbaria offers new opportunities to obtain long-term retrospective records of the physiological activity of plants. This is, because the isotopic composition of plant tissues constitutes an integrated indicator of leaf-level physiological processes such as stomatal conductance and photosynthetic assimilation rates that occurred in a plant during the formation of plant tissue. Current research efforts at the University of Basel have the aim to exploit the physiological information that is recorded in the plant tissue of archived herbarium specimens via stable isotope carbon and oxygen isotope analysis. The wealth of herbarium vouchers available in Swiss herbaria provides the unique opportunity to not only deduct general long-term response (over centuries) and acclimation patterns of plant, but to carefully differentiate these responses among different plant functional groups and among plants that originate from contrasting environments. In the long-term, this research will unmask plant physiological information archived in Swiss herbaria providing critically needed data to refine global biogeochemical models for the prediction of future earth system processes such as carbon and water cycling.

Project funded by ERC Consolidator Grant HYDROCARB REP-724750-1. Project leader is Prof. Ansgar Kahmen with postdocs Dr. David Basler and Dr. Cristina Moreno-Gutierrez, Department of Environmental Sciences, University of Basel.



Plant origin and collection year for the herbarium specimens sampled for stable isotope analysis. © David Basler

Reviving plant genetic resources for our future crops

Today, the majority of agricultural land is used to grow a few highly productive crops that make up a large part of our diet. Plant genetic resources in general and germplasm from orphan crops in particular have the potential to contribute to a diversification – from landscape to the gene pool level of crop species. Since 1999, the Federal Office for Agriculture (FOAG) is supporting projects aiming to sustainably utilize plant genetic resources under the NAP-PGREL program, thereby bringing diversity back to our fields and plates. A recent beneficiary of this program is buckwheat (Fagopyrum esculentum Moench). Buckwheat is a highly nutritious and undemanding crop that originated in the southwestern part of China and reached Europe through the Silk Road. Historically, buckwheat was an important food crop in the southern part of Switzerland, but with the intensification of agriculture during the last century, it was largely neglected and replaced by more productive and higher yielding crop species. Consequently, very few original Swiss varieties are still preserved and accessible, mainly from genebanks or mainted by ProSpecieRara.

Starting with the available Swiss buckwheat accessions and a lifelong collection of more than 200 accessions of worldwide origin, the Molecular Plant Breeding group and its collaborators aim at reviving, characterizing and making these buckwheat genetic resources accessible for their future use. Seed multiplication of the collection is currently ongoing – a tedious task considering the outcrossing nature of buckwheat that requires accessions to be multiplied in isolation. As a next step, large field trials to characterize the material are planned and genetic studies based on a modified genotyping-by-sequencing protocol to resolve allele frequencies at thousands of genetic loci will be conducted. While genebanks often have limited information available about their accessions, we will support entries with a comprehensive, digitally-available description of their agronomic, phenotypic and genotypic diversity. These data will also be used to explore some of the dynamics that have shaped current and historical varieties of buckwheat and hopefully will allow to adapt it to thrive in our modern cropping landscape.

Project funded by «Nationale Aktionsplan zur Erhaltung und nachhaltigen Nutzung der pflanzengenetischen Ressourcen für Ernährung und Landwirtschaft (NAP-PGREL)». Project leader is Prof. Bruno Studer, with postdoc Dr. Michelle Nay, Department of Environmental Systems Science, ETH Zurich.

Buckwheat flowers opening in the morning dew. © Michelle Nay

Professor Verena Schünemann, University of Zurich

In December 2017 Verena Schünemann took up her position as Assistant Professor for Paleogenetics at the Institute of Evolutionary Medicine of the University of Zurich. She started her scientific career in Tübingen, where she obtained her two PhDs, the first (2007–2010) in biochemistry at the Max-Planck Institute for Developmental Biology under the supervision of Prof. Andrei Lupas and the second (2010–2014) in archaeological sciences at the University of Tübingen supervised by Prof. Johannes Krause. As a postdoctoral researcher Verena worked with Prof. Johannes Krause at the Institute of Archaeological Sciences at the University of Tübingen, where she then became a group leader for Archeo- and Paleogenetics in 2015.

Verena has been pioneering the field of ancient pathogen genomics in order to uncover the long-term evolution of various pathogens. She uses a combination of ancient DNA methods and Next Generation Sequencing (NGS) to identify unknown causative agents of past pandemics and to reconstruct their genomes. These molecular fossils can be used to trace pathogens through time and analyse their evolution from a broader perspective via understanding of their past. In addition, ancient strains can help to estimate how fast a pathogen changes over time, allowing for more accurate predictions of the pathogen's future such as the development of antibiotic resistance. Verena's previous research centered around several major human pathogens with a strong impact on humans' past: She was involved in the identification of the *Yersinia pestis* strain from the Black Death as well as in the retrieval of a historic strain of the plant pathogen *Phytophthora infestans* that could be linked to the Irish potato famine. She also established the first recovery of historic *Treponema pallidum* genomes from human remains. Subspecies of this bacterium causes amongst others syphilis and yaws in humans. One of her projects focused on *Mycobacterium leprae*, the causative agent of leprosy, of which she reconstructed several medieval genomes to better understand the long-term evolution of this bacterium and to find traces of its potential origins. Further directions of her work included research on ancient plant genomes such as 6000-years-old barley or pre-Columbian maize.

After her move to Zurich, Verena continued with her research on ancient pathogens with the support of the University Research Priority Program «Evolution in Action: From Genomes to Ecosystems» and the Mäxi Foundation Zurich. She also obtained a SNSF project grant in 2019 to continue working on different aspects of her research on *Treponema pallidum*. Furthermore, Verena and her team are part of the herbarium genomics network within the PSC together with the herbaria curators Alessia Guggisberg (ETH Zurich), Reto Nyffeler (University of Zurich) and Jurriaan de Vos (University Basel) and the research groups of Simon Aeschbacher (University of Zurich) and Alex Widmer (ETH Zurich) to study historic plant pathogens and the evolution of plant pathosystems.

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www.iem.uzh.ch/en/research/paleogenetics_group_schünemann.html

Solanum lycopersicum herbarium sample from the United Herbaria of the University and ETH Zurich. © Verena Schünemann

Nature (2019)
doi: 10.1038/s41586-019-1418-6

Soil nematode abundance and functional group composition at a global scale

Van den Hoogen, J.; Geisen, S.; …Pellissier, L.; … Crowther, T.W.

Soil organisms are a crucial part of the terrestrial biosphere. Despite their importance for ecosystem functioning, few quantitative, spatially explicit models of the active belowground community currently exist. In particular, nematodes are the most abundant animals on Earth, filling all trophic levels in the soil food web. Here we use 6'759 georeferenced samples to generate a mechanistic understanding of the patterns of the global abundance of nematodes in the soil and the composition of their functional groups. The resulting maps show that 4.4 ± 0.64 × 1020 nematodes (with a total biomass of approximately 0.3 gigatonnes) inhabit surface soils across the world, with higher abundances in sub-Arctic regions (38% of total) than in temperate (24%) or tropical (21%) regions. Regional variations in these global trends also provide insights into local patterns of soil fertility and functioning. These high-resolution models provide the first steps towards representing soil ecological processes in global biogeochemical models and will enable the prediction of elemental cycling under current and future climate scenarios.

Nature (2019)
doi: 10.1038/s41586-019-1693-2

One thousand plant transcriptomes and the phylogenomics of green plants

Leebens-Mack, J. H.; Barker, Michael S.; Carpenter, E.J.; Deyholos, Michael K.; Gitzendanner, Matthew A.;… Szövényi; P.; …

Green plants (Viridiplantae) include around 450'000-500'000 species of great diversity and have important roles in terrestrial and aquatic ecosystems. Here, as part of the One Thousand Plant Transcriptomes Initiative, we sequenced the vegetative transcriptomes of 1'124 species that span the diversity of plants in a broad sense (Archaeplastida), including green plants (Viridiplantae), glaucophytes (Glaucophyta) and red algae (Rhodophyta). Our analysis provides a robust phylogenomic framework for examining the evolution of green plants. Most inferred species relationships are well supported across multiple species tree and supermatrix analyses, but discordance among plastid and nuclear gene trees at a few important nodes highlights the complexity of plant genome evolution, including polyploidy, periods of rapid speciation, and extinction. Incomplete sorting of ancestral variation, polyploidization and massive expansions of gene families punctuate the evolutionary history of green plants. Notably, we find that large expansions of gene families preceded the origins of green plants, land plants and vascular plants, whereas whole-genome duplications are inferred to have occurred repeatedly throughout the evolution of flowering plants and ferns. The increasing availability of high-quality plant genome sequences and advances in functional genomics are enabling research on genome evolution across the green tree of life.

Science (2019)
doi: 10.1126/science.aax4737

Above- and belowground linkages shape responses of mountain vegetation to climate change

Hagedorn, F.; Gavazov, K.; Alexander, J.M.

Upward shifts of mountain vegetation lag behind rates of climate warming, partly related to interconnected changes belowground. Here, we unravel above- and belowground linkages by drawing insights from short-term experimental manipulations and elevation gradient studies. Soils will likely gain carbon in early successional ecosystems, while losing carbon as forest expands upward, and the slow, high-elevation soil development will constrain warming-induced vegetation shifts. Current approaches fail to predict the pace of these changes and how much they will be modified by interactions among plants and soil biota. Integrating mountain soils and their biota into monitoring programs, combined with innovative comparative and experimental approaches, will be crucial to overcome the paucity of belowground data and to better understand mountain ecosystem dynamics and their feedbacks to climate.

Trends in Ecology & Evolution (2019)
doi: 10.1016/j.tree.2019.03.003

The impact of mutualisms on species richness

Chomicki, G.; Weber, M.; Antonelli, A.; Bascompte, J.; Kiers, E.T.

Mutualisms – cooperative interactions among different species – are known to influence global biodiversity. Nevertheless, theoretical and empirical work has led to divergent hypotheses about how mutualisms modulate diversity. We ask here when and how mutualisms influence species richness. Our synthesis suggests that mutualisms can promote or restrict species richness depending on mutualist function, the level of partner dependence, and the specificity of the partnership. These characteristics, which themselves are influenced by environmental and geographic variables, regulate species richness at different scales by modulating speciation, extinction, and community coexistence. Understanding the relative impact of these mechanisms on species richness will require the integration of new phylogenetic comparative models as well as the manipulation and monitoring of experimental communities and their resulting interaction networks.

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 biodiver-

sity 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 × 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.

Genome Biology (2019)
doi: 10.1186/s13059-019-1767-3

Linker histones are fine-scale chromatin architects modulating developmental decisions in Arabidopsis

Rutowicz, K.; Lirski, M.; Mermaz, B.; Teano, G.; Schubert, J.; Mestiri, I.; Kroten, M.A.; Fabrice, T.N.; Fritz, S.; Grob, S.; Ringli, C.; Cherkezyan, L.; Barneche, F.; Jerzmanowski, A.; Baroux, C.

Chromatin provides a tunable platform for gene expression control. Besides the well-studied core nucleosome, H1 linker histones are abundant chromatin components with intrinsic potential to influence chromatin function. Well studied in animals, little is known about the evolution of H1 function in other eukaryotic lineages for instance plants. Notably, in the model plant Arabidopsis, while H1 is known to influence heterochromatin and DNA methylation, its contribution to transcription, molecular, and cytological chromatin organization remains elusive.

We provide a multi-scale functional study of Arabidopsis linker histones. We show that H1-deficient plants are viable yet show phenotypes in seed dormancy, flowering time, lateral root, and stomata formation—complemented by either or both of the major variants. H1 depletion also impairs pluripotent callus formation. Fine-scale chromatin analyses combined with transcriptome and nucleosome profiling reveal distinct roles of H1 on hetero- and euchromatin: H1 is necessary to form heterochromatic domains yet dispensable for silencing of most transposable elements; H1 depletion affects nucleosome density distribution and mobility in euchromatin, spatial arrangement of nanodomains, histone acetylation, and methylation. These drastic changes affect moderately the transcription but reveal a subset of H1-sensitive genes.

H1 variants have a profound impact on the molecular and spatial (nuclear) chromatin organization in Arabidopsis with distinct roles in euchromatin and heterochromatin and a dual causality on gene expression. Phenotypical analyses further suggest the novel possibility that H1-mediated chromatin organization may contribute to the epigenetic control of developmental and cellular transitions.

Nature Communications (2019)
doi: 10.1038/s41467-019-12798-y

Fungal-bacterial diversity and microbiome complexity predict ecosystem functioning

Wagg, C.; Schlaeppi, K. ; Banerjee, S.; Kuramae, Eiko E.; van der Heijden, M. G. A.

The soil microbiome is highly diverse and comprises up to one quarter of Earth's diversity. Yet, how such a diverse and functionally complex microbiome influences ecosystem functioning remains unclear. Here we manipulated the soil microbiome in experimental grassland ecosystems and observed that microbiome diversity and microbial network complexity positively influenced multiple ecosystem functions related to nutrient cycling (e.g. multifunctionality). Grassland microcosms with poorly developed microbial networks and reduced microbial richness had the lowest multifunctionality due to fewer taxa present that support the same function (redundancy) and lower diversity of taxa that support different functions (reduced functional uniqueness). Moreover, different microbial taxa explained different ecosystem functions pointing to the significance of functional diversity in microbial communities. These findings indicate the importance of microbial interactions within and among fungal and bacterial communities for enhancing ecosystem performance and demonstrate that the extinction of complex ecological associations belowground can impair ecosystem functioning.

Nature Communications (2020)
doi: 10.1038/s41467-019-14002-7

Terrestrial land-cover type richness is positively linked to landscape-level functioning

Oehri, J.; Schmid, B.; Schaepman-Strub, G.; Niklaus, P. A.

Biodiversity–ecosystem functioning (BEF) experiments have shown that local species richness promotes ecosystem functioning and stability. Whether this also applies under real-world conditions is still debated. Here, we focus on larger scales of space, time and ecological organization. We develop a quasi-experimental design in which we relate land-cover type richness as measure of landscape richness to 17-year time series of satellite-sensed functioning in 4974 landscape plots 6.25 or 25 ha in size. We choose plots so that landscape richness is orthogonal to land cover-type composition and environmental conditions across climatic gradients. Landscape-scale productivity and temporal stability increase with landscape richness, irrespective of landscape plot size. Peak season near-infrared surface albedo, which is relevant for surface energy budgets, is higher in mixed than in single land-cover type landscapes. Effect sizes are as large as those reported from BEF-experiments, suggesting that landscape richness promotes landscape functioning at spatial scales relevant for management.

Frontiers in Plant Sciences

Introduction to Genome-Wide Association Studies (GWAS)

Matt Horton (IPMB) and Ümit Seren (GMI, Vienna)
15–17 Apr 2020, 3 days

In this course, we will discuss one of the main tools for identifying genes that underlie natural phenotypic variation: Genome-Wide Association Studies (GWAS). The course provides an introduction to GWAS and python. Participants will discuss the history of gene mapping and the genetic and statistical background on which GWAS are based.

Get going with Statistics in Functional Genomics

Anne Roulin
22–24 Apr 2020, 3 days

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 the most basic and most crucial sets of skills to work with genomic datasets.

Taming the Beast

Alexei Drummond, Tanja Stadler, Remco Bouckaert, Denise Kühnert
31 May–5 Jun 2020, 6 days

Taming the Beast (Bayesian Evolutionary Analysis by Sampling Trees) is a one-week workshop organised in collaboration by several research groups from all around the world.

https://bsse.ethz.ch/cevo/taming-the-beast.html

Science & Policy Courses

Scenario-building and Participatory Modelling Approach

Véronique Lamblin (Futuribles), Claude Garcia
26–28 Feb 2020

Communicating Science

Jacopo Pasotti
16 Mar & 30 Apr, 2 days

Introduction to Political Sciences

Sarah Bütikofer
1 & 3 Apr, 2 days

Building Political Support

Sebastian Köhler, Sarah Bütikofer
13 May & 17 Jun, 2 days

Workbooks available at:

www.plantsciences.uzh.ch/en/publications/science-policyworkbooks.html

PSC course registration

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

Select: Plant Sciences

Contact

psc_phdprogram@ethz.ch

Plant Sciences Courses

The Microbiome of the Plant-Soil System: Part I – Theory, Methods and Case Studies
20 Feb–28 May, 8 events

How can you make Open Data work in your own research projects?
9–11 Mar, 3 days

Responsible Conduct in Research
3 Apr & 26 May, 2 days

Concepts in Evolutionary Biology (BIO395)
6–7 Apr, 2 days

Scientific Presentation Practice
21 & 30 Apr, 2 days

Introduction to UNIX/Linux and Bash Scripting (BIO609)
27 Apr, 1 day

Next-Generation Sequencing for Model and Non-Model Species (BIO610)
28–29 Apr, 2 days

Project Management for Research
4–5 Apr, 2 days

Next-Generation Sequencing 2: Transcriptomes, Variant Calling and Biological Interpretation (BIO634)
14–15 May, 2 days

Scientific Writing Practice II
5, 8 & 11 Jun, 3 days

Basic Plant Disease Diagnostics
9–11 Jun, 3 days

Dealing with the Publication Process
10–12 Jun, 3 days

Genetic Diversity: Analysis
15–19 Jun, 5 days

The Microbiome of the Plant-Soil System: Part II – Processing Next-Generation Sequencing data
22–25 Jun, 4 days

Advanced Data Management and Manipulation using R
2 & 9 Jul, 2 days

Upcoming

Being interdisciplinary

Date tbd, ETH Zurich

This retreat will invite all fellows, trainers, PIs and collaboration partners of the PSC-Mercator fellowship program. We will reflect on the outcomes of the program and discuss on how to develop boundary-crossing skills. Boundary-crossing skills are, for instance, the ability to change perspectives, to synthesize knowledge of different disciplines, and to cope with complexity.

Contact: Luisa Last, llast@ethz.ch

*fem*inno

The *fem*inno *Career Program for Innovative Women in Life Sciences* will start its 4th course series in autumn. Registration will open in May.

Upcoming: Accenture invites to a speed dating event at University of Zurich **on 25th of March 2020** (18:15–21:30) – open to all students. After a presentation of Accenture you will have the chance to get familiar with new technologies such as Blockchain and hear from experts how these are leveraged to bring organizations into the future. At the subsequent Apéro we will have time to answer your questions about life as a consultant and your career opportunities.

Send an email until **15th March** including your name, field of study and semster with the subject «Speed Dating to the NEW!» to: **recruiting.switzerland@accenture.com**

If you have been a participant of the feminno program, please indicate it in your email.

Nachtaktiv – a new PSC outreach project

Outreach activities which combine natural sciences, design and technology have enormous creative potential for engaging adolescents with complex topics. The new *Nachtaktiv (Nocturnal)* project is a series of evening events similar to a science slam or science fair, and will take place in various museums around Zurich. By creating a fun and relaxed atmosphere we aim to encourage young people to cultivate an interest in science.

Each evening is devoted to a different theme from digitalization, through sustainability to future technologies. We are choosing themes with a link to ongoing research and social issues that also include an element of humor. The subjects will be presented at activity tables or as short tours in the museum. We will offer hands-on activities and a topic related food or drink experience – e.g. insect tasting, glow-in-the-dark (non-alcoholic) cocktails, special and weird food combinations. The absence of children in a museum setting is unusual and allows adolescents to play in a group of their peers. *Nachtaktiv* takes place once a month, starting in autumn and we are partnering with Focus Terra, Kulturama and the Finance Museum among others.

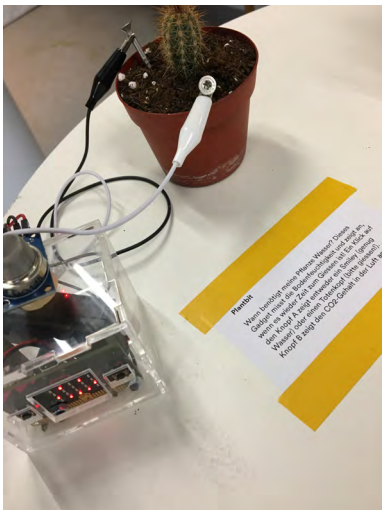
If you have ideas for themes or activities, they are most welcome and we are recruiting scientists to participate, so please contact us and get involved. As the target group is young adults there is no language barrier, English is fine.

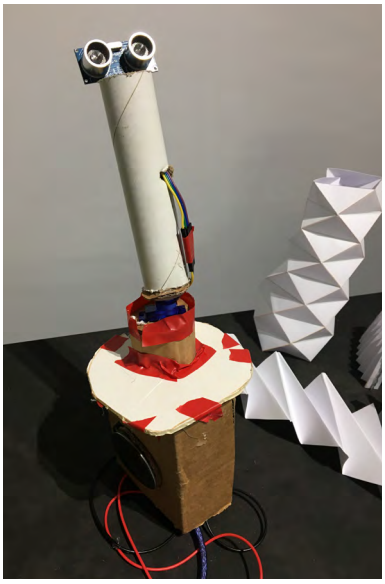
CreativeLabZ – combines art, science and engineering

On February 1 & 2, 2020, our partner, the Museum of Digital Art (MuDA) in Zurich, presented the first CreativeLabZ exhibition. Visitors played and tested astounding objects that were created by youngsters age 12 to 16 years during the workshops and holiday camps held since spring 2019. Inspired by current nature, science and engineering challenges, teenagers got up close with design thinking and plant ecology. Focusing on air and water quality, soil moisture, and even how to grow plants on Mars, workshop participants immediately became thinkers and innovators. They investigated sensors and materials at hand, to engineer interesting objects, robots, measuring devices and other masterpieces of art-science design.

www.creativelabz.ch

The project is supported by the Drosos Foundation.





CreativeLabZ exhibition. © PSC & MuDA

These images were created at the *Climate Garden 2085* in FHS Rapperswil, during a Botanical Monoprints workshop © PSC

Translating art-science collaboration into science communication

In collaboration with art educators from the Zurich University of the Arts (ZHdK), the PSC develops creative and inquiry-based 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 University of Zurich and the Fascination of Plants Day.

For example, inspired by the colour extraction work of James Simms (Consuelo de Moraes lab at ETH Zurich) we repurposed an old Japanese plant printing technique – the Hapazome. Grasses and flowers can be hammered onto cloth or heavy cardboard creating beautiful patterns and prints. This extracts the flower/plant colour one to one in a monoprint, without using any other extraction methods. In our art & science workshops we observe that art can better facilitate reflexive learning and in doing so can produce other types of knowledge, such as aesthetic or embodied knowledge. An aesthetic experience enables emotion and empathy and thereby inquiry-based learning. By communicating science from a position of building empathy with an audience — rather than simply telling an audience what it needs to know — we can create more compelling, memorable experiences that invite participants to arrive at their own understanding.

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

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

Call for participation

Climate Garden 2085

will be installed at four high schools this year. 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

Creative Camps for youth

In collaboration with art educators from the Zurich University of the Arts, PSC scientists develop creative and inquiry-based workshop activities for young people aged 8–14. The workshops are offered during holiday camps. Students can provide scientific input for the camps and activities and help to run the holiday camps. We welcome support this year from 13–15 July for a camp on the lake of Zug.

CreativeLabZ for youth

This PSC outreach project for youth is running in the Museum of Digital Art and the Student Project House of the ETH Zurich. Short talks from researchers are welcome (also in English). Or you can come and tinker and help make stuff with us in the makerspace. The camp in July is on Biomaterials.

www.creativelabz.ch

Nachtaktiv (Nocturnal)

A new monthly party event for youth. The first event is in September so we welcome help with planning starting soon.

OLMA

The 2020 theme is ETH wide robotics research, which of course includes digitalization in agriculture. If you want to pitch in and come and help at the OLMA it is on from 8–18 Oct 2020 (free lunch and travel. German speakers only).

Contact: Juanita Schläpfer

juanita.schlaepfer@usys.ethz.ch

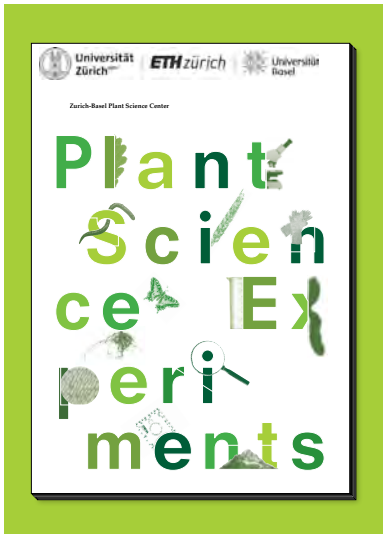
Paschke M. and Zurgilgen K. (2019)
Science-policy boundary work by early-stage researchers: Recommendations for teaching, internships and knowledge transfer.
GAIA - Ecological Perspectives for Science and Society, 28 (3), 310-315.

doi: 10.3929/ethz-b-000374028

Science-policy boundary work

Based on a Delphi study we summarized opportunities and challenges of our educational model: Real-world experience through secondments and co-creation of knowledge with policy organizations facilitates boundary crossing of research results to policymaking. Most important for the success of policy work are institutional incentives and resources to engage as academic supervisor and early-stage scientist in the process. **Incentives could include:** Establish career paths for scientists who engage in policymaking. Science-policy boundary work should become an appreciated part of scientific CVs for tenured positions for researchers responding to societal needs. Policy reports carefully reviewed in collaboration with policy partners should get the same recognition as peer-reviewed scientific publications. Selection committees for academic positions, or for grant applications, need to pay attention to science-policy qualifications. Establish financial incentives for scientists engaging in knowledge transfer activities as part of grant-awarding mechanisms. **Long-term institutional support:** Best-practice examples of regular exchange between scientists and policymakers are generally project-funded. But institutions should commit sustained financial support to this area. Programs should teach early-stage scientists to use widely accepted policy formats such as policy briefs, fact sheets, etc. early in the programme. Organizers of science-policy programs need to install policy mentors in the academic institution easily accessible to early-stage researchers. These mentors could offer guidance in distributing time between research and policy work, offer methodological support in policy work, and facilitate outreach, dialogue and information planning. Complementary to these, advisors at the policy organization need to reserve time for guidance on structures in the policy institution. Both parties can offer support with the project design at the science-policy interface. Make the collaborations and policy outcomes visible. Showcase successful projects and use them as examples to inspire others.

https://blogs.ethz.ch/Science_and_Policy



Pflanzenwissenschaftliche Experimente für Familien und Schulklasse.
Manuela Dahinden & Melanie Paschke (Hrsg.)
Zurich-Basel Plant Science Center, 2019.

ISBN: 978-3-906327-05-1
eISBN (ePUB): 978-3-906327-33-4
eISBN (mobi): 978-3-906327-35-8

Plant science experiments

The book contains a collection of experiments on plant science research topics that can be carried out by children and adolescents between 9 and 16 years of age together with accompanying adults. The experiments can be easily implemented in the classroom or in everyday family life. We believe teachers, science communicators and educators, parents, grandparents will have fun trying out these experiments with children and adolescents.
With contributions from: Melanie Paschke, Juanita Schläpfer (PSC), Carole Rapo & Harald Rauter (former PSC), Jake Alexander (ETH Zurich), Valeria Gagliardini (University of Zurich), Ueli Grossniklaus (University of Zurich), Erika Hiltbrunner (University of Basel), Nicole Inauen (Landwirtschaftliches Zentrum SG / Fachstelle Pflanzenbau und Umwelt), Beat Keller (University of Zurich), Norbert Kirchgessner (ETH Zurich), Christian Körner (University of Basel), Frank Liebisch (ETH Zurich and Agroscope), Reto Nyffeler (University of Zurich), Christophe Randin (University of Basel), Achim Walter (ETH Zurich).

www.plantsciences.uzh.ch/de/experimente.html

General Assembly & RESPONSE Kick off

18 Mar 2020, UniTurm of University of Zurich, Rämistrasse 71, 16:30–19:00

PSC invites its members to its annual general assembly that will be followed by the launch of the RESPONSE Doctoral Program. This program receives funding from the European Union's Horizon 2020 research and innovation program under the Marie Skłodowska-Curie Actions.
Invited guests are partner organizations such as the World Food System Center and Energy Science Center as well as MWSchmid GmbH (CH), CIMMYT (MX), German Research Centre for Geosciences GFZ (DE), Bellona Europe (BE), Swiss Energy Foundation (CH), Swiss Federal Office of Energy (CH), Bitplane (CH), Nitidae (FR), WWF (BE) and Barenbrug (FR).

Registration: https://doodle.com/poll/epu5wyh6mbzsqkpi

Save the date – PSC Symposium 2020

Connectivity – Plant interactions reloaded

2 Dec 2020, Audimax, ETH Zurich, 9:15–17:00

This year's PSC symposium will highlight the manifold interactions plants are engaged in. The interactions range from the molecular to the environmental level and are indispensable for development, reproduction, nutrient exploitation and disease resistance against pathogens. Currently, genome sequencing, computational advances, high resolution imaging, new modelling approaches and a whole range of high-throughput technologies bring us new paths to study plant networks. Interactions drive evolution and shape the natural communities. Studying plant connectivity at different levels, in a more contextual way and combining different disciplines is key to move forward in our understanding of the plant systems. This multidisciplinary research can be integrated in an ecological framework where optimal management of nature's ecological functions and biodiversity may improve agricultural system performance, efficiency and farmers' livelihoods.

PSC junior scientists are invited to present posters and flash talks. Three poster awards will reward the best presenters.

PhD students organizing the symposium
Alicia Abarca, Laura Herold & Henning Muehlenbeck, University of Zurich, Department of Plant and Microbial Biology; Seydinaissa Diop, Zhenzhu Xiao & Giacomo Potente, University of Zurich, Department of Systematic and Evolutionary Botany; Santiago Perez Bernal, University of Basel, Department of Environmental Sciences; Yuanyuan Liang, ETH Zurich, Institute of Molecular Plant Biology (D-BIOL)

PSC Coordinators
Luisa Last, Manuela Dahinden, Romy Kohlmann

www.plantsciences.uzh.ch/en/outreach/conferences

Plant Biology Europe 2020

The joint EPSO / FESPB conference, will be held at the Centro Congressi Lingotto in Turin, Italy from 29 June – 2 July 2020. The themes will be:
Abiotic stress, plant performance and productivity; Mobile signals;
Plant metabolism;
Plant and ecosystem adaptation to environmental change;
Plant development and flowering;
Protein modifications and trafficking;
Carbon fixation and plant productivity;
Regulation of plant immunity;
Belowground physiology and interactions; Genomics, epigenomics, and genome editing for crop design.

On 1st of July 2020, PlantHUB will highlight the outcomes of the European Industrial Doctoral Program with two dedicated sessions. PlantHUB funded by the H2020 PROGRAMME Marie Curie Actions – People, Initial Training Networks (H2020-MSCA-ITN-2016).

https://europlantbiology2020.org

Swiss-Taiwan Workshop

The Institute of Molecular Plant Biology at ETH Zurich invites to a workshop with colleagues from Academia Sinica and NCHU on June 8 and 9, 2020 at ETH Zurich. Please use the Doodle link to indicate your availability by March 16, 2020.

https://ethz.doodle.com/poll/5zgg-23h6c79nxwsu.

8th World Sustainability Forum (WSF2020)

The WSF2020 will be held from 15–17 September in Geneva, Switzerland. WSF2020 is coordinated by the MDPI Sustainability Foundation, under the patronage of the University of Basel, the University of Geneva and the UN Sustainable Development Solutions Network (UN SDSN).

https://wsf-8.sciforum.net/

www.plantsciences.ch

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Courtesy of PSC staff or indicated. Frontpicture: Collage of herbarium specimens of Caspar Bauhin (1560-1624) at the University of Basel. © J. M. de Vos

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