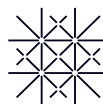




University of
Zurich^{UZH}

ETH zürich



University
of Basel

Zurich-Basel Plant Science Center

PlantScienceNews

No. 50, Fall 2026



Editorial

Welcome to the 50th issue of the Plant Science Newsletter

The Plant Science Newsletter offers a window into the vibrant plant science community across Zurich and Basel. Through 50 editions, we have brought together scientific discoveries, collaborations, people and ideas, reflecting the diversity and evolution of plant science across our institutions.

For this anniversary edition, we wanted to celebrate the people, research and relationships that make this community what it is. Our science highlights are organised around five CONNECT themes, revealing shared questions and complementary approaches across research groups.

Today, the Zurich-Basel Plant Science Center (PSC) connects around 50 research groups across ETH Zurich, the University of Zurich and the University of Basel. We have selected collaborative projects spanning topics from plant reproduction and crop improvement to biodiversity monitoring, ecological resilience and the development of bioinspired technologies. Together, they offer a glimpse of the curiosity, creativity and collective expertise that make our community so dynamic.

Our education section highlights opportunities for doctoral researchers to develop their skills and explore career pathways, while a new PSC survey offers insights into how PhD researchers are using generative AI and where further training is needed.

From 2027 onwards, the Newsletter will become fully digital and appear more regularly. While we are saying goodbye to the printed format, our commitment remains unchanged. It has been a pleasure and a privilege to share your stories, celebrate your achievements and give visibility to the research happening across our community.

Thank you for being part of these 50 editions. We look forward to the stories still to come.

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This anniversary issue was made possible by the time, expertise and commitment of everyone who contributed. Special thanks go to **Jelena Stepanovic-Mladenovic**, who wrote many of the articles, and to **Sabrina Stettler**, who created the layout and illustrations.



PSC Managing Office: **Manuela Dahinden**, Managing Director Research and Outreach | **Melanie Paschke**, Managing Director Education and Policy Dialogue | **Romy Kohlmann**, Finances, Events and EU-Programme Coordinator | **Luisa Last**, Coordinator PhD Programme Science and Policy | **Bojan Gujas**, Coordinator PhD Programme Plant Sciences | **Daniela Gunz**, *feminno* Programme Coordinator | **Juanita Schläpfer**, CreativeLabZ and NaturStudio | **Beatrice Kiser**, CreativeLabZ and NatureEcho | **Savannah Goetsch**, CreativeLabZ and NACHTAKTIV | **Aline Veillat**, Art & Science | **Dijana Vukovic**, Continued Education | **Valentina Huwiler**, Continued Education | **Jelena Rajkov**, Coordinator at University of Basel.

Save the Date – PSC General Assembly 2027

Wednesday, 3 March 2027 | 16:00–18:00 | NMZ, University of Zurich

Join us for the PSC General Assembly and Retreat 2027! We look forward to welcoming our new members and discussing future projects of the Plant Science Center. Alongside the presentation and approval of the Annual Report 2026 and the election of Sebastian Dötterl as ETH representative and PSC Co-Chair, we want to hear your ideas and perspectives. What does being part of the PSC mean to you? How can you benefit from the network, contribute to its activities and help shape its future? We kindly invite members to propose and host breakout sessions.

Apéro – From 18:00, we invite you to enjoy drinks and conversations with fellow PSC members. Afterwards, you are warmly invited to join a guided tour of the exhibition *Plants Talk* at the Natural History Museum of the University of Zurich.

We look forward to seeing you there!

STAY CONNECTED

From 2027, the PSC Newsletter will be digital only. PSC members receive it automatically; all other interested readers are invited to subscribe.

<https://www.plantsciences.uzh.ch/en/publications/newsletter/newslettersubscription.html>

Early career award

Katharina Jung is one of three recipients of the 2026 Jeanie Borlaug Laube Women in Triticum Early Career Award.



Presented by the Borlaug Global Rust Initiative, the distinction recognises early-career scientists contributing to wheat research and improvement while supporting leadership development, mentorship and participation in the international wheat research community. Katharina was recognised for her research on the genetic basis of yellow rust resistance and drought adaptation in bread wheat. Her work focuses on modern and traditional Asian wheat varieties whose genetic diversity remains underrepresented in contemporary breeding programmes. The research grew in part from her PSC RESPONSE doctoral project in the group of Kentaro K. Shimizu. Conducted from April 2020 to March

2024 in partnership with the International Maize and Wheat Improvement Center (CIMMYT), the project combined a nested association mapping population with large-scale field trials, controlled experiments and genomic analyses to identify genetic variation relevant to disease resistance and environmental stress. These genetic resources could broaden the variation available to wheat breeders and contribute to more durable resistance against yellow rust. Their value is likely to increase as pathogen distributions and disease pressure change under increasingly variable climatic conditions.

PUBLICATION

Jung, K. et al. (2025). Unveiling yellow rust resistance in the near-Himalayan region: insights from a nested association mapping study. *Theoretical and Applied Genetics*, 138, 135. <https://doi.org/10.1007/s00122-025-04886-z>

Prestigious international awards

Ueli Grossniklaus, Professor of Plant Developmental Genetics at the University of Zurich, has received the prestigious Plant Reproduction Medal from the International Association for Sexual Plant Reproduction Research (IASPRR).



Presented at the association's 28th Congress, the award recognises his outstanding scientific achievements and leadership in plant reproduction research over the past three decades. His pioneering contributions span epigenetic gene regulation, genomic imprinting, reproductive signalling, gametophyte development and apomixis. Ueli has also been appointed a Corresponding Member of the Australian Society of Plant Scientists, recognising his internationally established research and long-standing collaborations with Australian scientists. His research has advanced our understanding of the genetic and

epigenetic regulation of sexual reproduction and apomixis—the formation of seeds without fertilisation. Engineering apomixis in crops could enable favourable genetic combinations, including those of hybrids, to be maintained across generations through clonal seeds. Ueli contributes this expertise to ApoSoy, an international public-private collaboration supported by the Foundation for Food & Agriculture Research, which aims to develop apomixis-based breeding technologies. In earlier proof-of-concept research, his group demonstrated the feasibility of producing clonal seeds in maize.

KEY PUBLICATIONS

<https://orcid.org/0000-0002-0522-8974>

[Google scholar](#)

Official announcements

<https://www.mnf.uzh.ch/en/fakultaet/news/preise.html>

<https://www.mnf.uzh.ch/en/events/artikel#news561>

US National Academy of Sciences

Kirsten Bomblies, Professor of Plant Evolutionary Genetics at ETH Zurich has been elected to the US National Academy of Sciences.



The Academy elected 120 new members in 2026 in recognition of distinguished and sustained achievements in original research. Kirsten and her research group investigate how plants adapt to genome duplication. Newly formed polyploids inherit additional chromosome copies that can disrupt meiotic pairing, chromosome segregation and fertility. Using *Arabidopsis arenosa* as a model, the Bomblies group examines how evolved polyploid lineages modify

chromosome behaviour and restore stable reproduction. These mechanisms are relevant to both evolutionary biology and crop improvement. Polyploidy is widespread among cultivated plants and can generate increased genetic diversity and stress tolerance, but newly produced polyploids frequently suffer from reduced fertility. Understanding how natural lineages overcome these constraints could inform strategies for exploiting genome duplication in breeding.

KEY PUBLICATIONS

<https://orcid.org/0000-0002-2434-3863>

[Google scholar](#)

Official announcements

<https://www.nasonline.org/news/2026-nas-election/>

<https://ethz.ch/staffnet/en/news-and-events/internal-news/archive/2026/04/two-eth-researchers-elected-to-the-national-academy-of-sciences.html>

Academic promotion

Meredith Schuman, Professor of Spatial Genetics of Ecosystems and PSC chair, has been promoted to Associate Professor ad personam at the University of Zurich, effective 1 April 2026.



Merry joined UZH's Department of Geography as a visiting professor in 2018, following research in the Department of Molecular Ecology at the Max Planck Institute for Chemical Ecology and at the German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig. She was appointed Assistant Professor of Spatial Genetics the following year, building a research programme at the interface of chemical ecology, functional plant genetics and remote sensing. Her group investigates how genetic and functional diversity vary across space and time within ecosystems, and where these differences matter for ecology and for people.

Combining direct chemical analysis of plant tissue with remote sensing, the group develops approaches to assess genetic and chemotypic variation, plasticity, and adaptive potential within plant species and their interactions, in the context of global environmental change. This promotion recognises a research trajectory that bridges molecular-scale genetic analysis and landscape-scale ecosystem monitoring, reflecting the University's continued investment in interdisciplinary approaches to biodiversity and global change research.

KEY PUBLICATIONS

<https://orcid.org/0000-0003-3159-3534>

[Google scholar](#)

Official announcement

<https://www.uzh.ch/de/explore/management/professorships/calls/calls-2026/calls-260330.html>

Ig Nobel Prize

Marcel van der Heijden was promoted to Full Professor ad personam of Agroecology and Plant–Microbiome Interactions at the University of Zurich. In September, he and his colleagues received the 2026 Ig Nobel Prize in Soil Science for the citizen science project Proof by Underpants.

The project involved around 1,000 citizen scientists across Switzerland, who buried cotton underwear in gardens, fields and meadows to investigate soil biological activity. As soil organisms decompose the cotton, its degradation provides a simple indicator of biological activity. The unconventional approach generated valuable scientific data while engaging the public directly in soil research.

Marcel combines his position at UZH with his research at Agroscope, focusing on mycorrhizal fungi, soil microbial diversity and plant–soil interactions. His research contributes to understanding how belowground biodiversity supports plant productivity, ecosystem resilience and more sustainable agriculture.



PUBLICATION

Bender, S. F. & van der Heijden, M. G. A. (2025). Assessing soil health with underpants. *Science*, 387, 936. <https://doi.org/10.1126/science.adw0030>

Official announcements

https://www.news.uzh.ch/en/articles/news/2026/Ig-Nobel.html?utm_source=chatgpt.com

<https://www.nature.com/articles/d41586-026-02650-x>

Cozzarelli Prize

Jordi Bascompte, Professor of Ecology at the Department of Evolutionary Biology and Environmental Studies at the University of Zurich received the Cozzarelli Prize for Eukaryotic Origins.

Jordi has received one of the six 2025 PNAS Cozzarelli Prizes, awarded annually to six papers selected for scientific excellence and originality from among the more than 3,600 research articles the journal publishes each year. Jordi, with co-authors Enrique M. Muro, Fernando J. Ballesteros and Bartolo Luque, received the prize in the biological sciences category for their comparative genomic analysis of the prokaryote-to-eukaryote transition. The analysis spans 6,519 species and examines the scaling relationship between gene length and the length of the protein each gene encodes. Across prokaryotes, this relationship

is close to linear — longer genes produce proportionally longer proteins. The finding the prize recognises is a discontinuity at the emergence of eukaryotes: protein length plateaus at roughly 500 amino acids, while gene length continues to increase, driven not by additional coding sequence but by the expansion of non-coding regulatory regions. The authors frame this decoupling as an algorithmic phase transition — a shift in evolutionary strategy from information encoded directly in protein sequence to information encoded in regulatory control of gene expression, which scales combinatorially rather than linearly.



PUBLICATION

Muro, E. M., Ballesteros, F. J., Luque, B. & Bascompte, J. (2025). The emergence of eukaryotes as an evolutionary algorithmic phase transition. *Proceedings of the National Academy of Sciences*, 122(13), e2422968122. <https://doi.org/10.1073/pnas.2422968122>

Official announcement

<https://www.nasonline.org/news/pnas-2025-cozzarelli-recipients/>

<https://www.news.uzh.ch/en/articles/news/2026/cozzarelli-prize-bascompte.html>

<https://www.bascompte.net>

SCNAT Executive Board

The General Assembly of the Swiss Academy of Sciences (SCNAT) has elected Nina Buchmann Professor of Grassland Sciences and Head of the Institute of Agricultural Sciences at ETH Zurich to its Executive Board.



SCNAT brings together scientific societies, expert committees and research networks across Switzerland. Its activities connect disciplines, strengthen scientific exchange and provide knowledge for public debate and evidence-informed decision-making. Nina's election brings expertise spanning ecosystem biogeochemistry, environmental systems science, grassland management and sustainable food systems to the Academy's strategic leadership. As a member of the SCNAT Executive Board, she intends to contribute to dialogue between science, society and politics,

while helping to shape the conditions under which research is conducted in Switzerland. She has identified evidence-based decision-making, research culture and open science as particular priorities. The appointment creates a direct connection between contemporary plant and ecosystem research and national scientific coordination. It also recognises the importance of long-term environmental observations and interdisciplinary agricultural research when addressing climate change, biodiversity loss and the sustainable management of natural resources.

KEY PUBLICATIONS

<https://orcid.org/0000-0003-0826-2980>

Official announcements

<https://usys.ethz.ch/en/news-events/news/archive/2026/06/nina-buchmann-in-den-scnat-vorstand-gewaehlt.html>

https://scnat.ch/en/uuid/i/84447d1b-b203-52ce-85ba-adb3f39e24e6-Nina_Buchmann_in_den_Vorstand_gew%C3%A4hlt

2026 Prix Schläfli

Julian Rogger has been awarded the 2026 Prix Schläfli in Geosciences by the Swiss Academy of Sciences (SCNAT) for his doctoral thesis at ETH Zurich, co-supervised by Loïc Pellissier.



The Prix Schläfli is awarded annually to the best doctoral theses at Swiss universities across four disciplines. Rogger's work addresses a question that inverts the usual framing of climate research: rather than asking how climate change affects vegetation, it asks what role vegetation itself plays in regulating climate over geological time. A central result concerns the limits of vegetation's stabilising role. Plants do not merely respond to environmental change; they help regulate it, by fixing carbon and accelerating silicate weathering. But when climate shifts faster than vegetation can adapt through migration and evolution, this stabilising capacity

weakens — plants sequester less carbon, and warming can amplify further. By coupling this idea to the geological record, Rogger's thesis showed how such tipping points in the carbon-climate system may have unfolded during past hyperthermal events. Julian completed his PhD at the Department of Earth and Planetary Sciences at ETH Zurich and is currently a postdoctoral researcher at the University of Bristol, where he continues to study the interactions between climate, vegetation and geological processes.

PUBLICATIONS

Rogger, J., Mills, B. J. W., Gerya, T. V. & Pellissier, L. (2024). Speed of thermal adaptation of terrestrial vegetation alters Earth's long-term climate. *Science Advances*, 10, eadj4408. <https://doi.org/10.1126/sciadv.adj4408>

Rogger, J., Judd, E. J., Mills, B. J. W., Goddérís, Y., Gerya, T. V. & Pellissier, L. (2024). Biogeographic climate sensitivity controls Earth system response to large igneous province carbon degassing. *Science*, 385, 661–666. <https://doi.org/10.1126/science.adn3450>

Official announcement

SCNAT: Prix Schläfli 2026: <https://scnat.ch/en/awards/schlaefli>

10 years of Molecular Plant Breeding: celebrating innovation, impact and vision



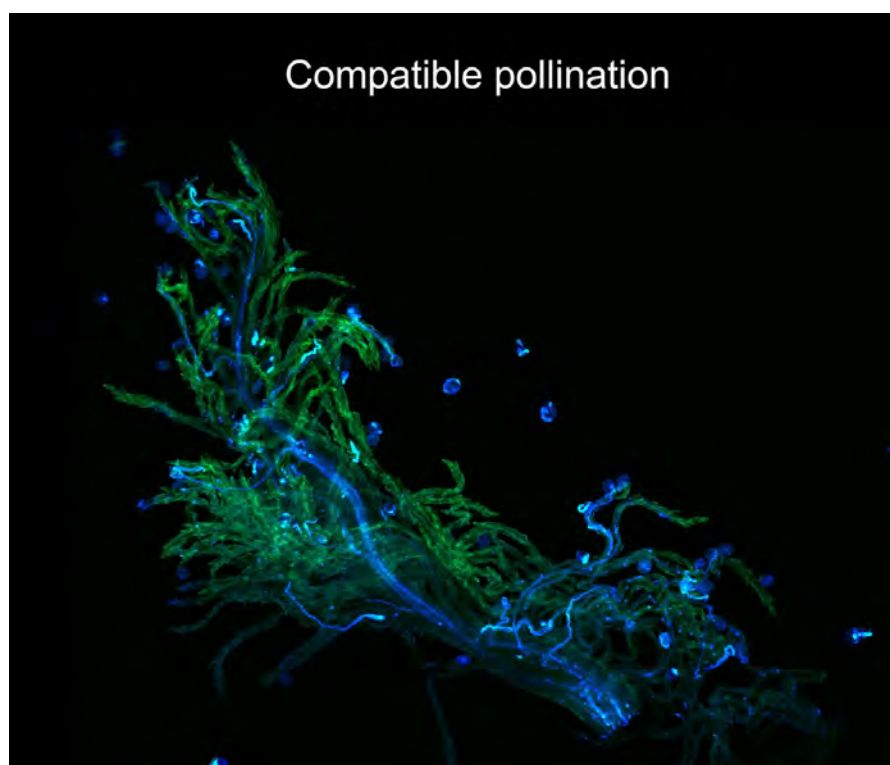
In 2026, the Molecular Plant Breeding (MPB) group at ETH Zurich celebrates its 10-year anniversary as a professorship under the leadership of Bruno Studer, former PSC chair. Over the past decade, the group has established itself as a leading force in plant breeding research, combining cutting-edge genomics, computational approaches, new genomic techniques and practical breeding to address some of agriculture's most pressing challenges, including food security, resource efficiency and climate resilience.

From the outset, MPB embraced a vision of bringing fundamental research and practical plant breeding closer together. A defining milestone has been the establishment of a unique research ecosystem together with Agroscope and the newly founded Swiss Plant Breeding Center. This highly successful model of collaboration has become a benchmark for translational plant breeding research in Switzerland, fostering strong partnerships between academia and plant breeding and generating substantial scientific and societal impact.

Scientific innovation has been at the heart of MPB's success. The group pioneered the development of chromosome-scale and haplotype-resolved genome assemblies for forage crops, contributed to international pangenome initiatives and advanced genomic prediction methods that integrate environmental data and machine learning. These contributions have strengthened the ability to understand, predict and efficiently utilise genetic variation for crop improvement. Among the most significant scientific achievements is the identification of the genes controlling

self-incompatibility in grasses, a discovery that solved a long-standing biological question and opened new opportunities for breeding innovations in one of the world's most important plant families. The impact of MPB extends well beyond research. The group has trained and mentored a new generation of plant scientists who contribute to academia, breeding and agriculture. Its members actively serve the scientific community, provide expertise to policymakers and regulatory bodies and foster an informed dialogue on new genomic techniques and the future of sustainable agriculture.

Looking ahead, the future of MPB will be shaped by genomic precision breeding, artificial intelligence, advanced phenotyping and the integration of large-scale genomic and transcriptomic data. By combining plant science, data science and breeding innovation, MPB is well positioned to contribute to the development of the next generation of sustainable and resilient crops needed for a rapidly changing world.



In vitro pollination assay to test for self-incompatibility in perennial ryegrass (*Lolium perenne* L.). In a compatible pollen-stigma interaction, the pollen tubes (blue) grow into the stigma (green) to reach the ovule and complete fertilisation. © B. Studer.

Selected Key Publications

[1] Chen, Y., Copetti, D., Kölliker, R., Mascher, M., Himmelbach, A., Stein, N., & Studer, B. (2025). Chromosome-level haplotype-resolved assembly of highly heterozygous grass genomes with PhaseGrass. *Nature Communications*, 17(1), 12. <https://doi.org/10.1038/s41467-025-66377-5>

[2] Watts, S., Yates, S., Vanderzande, S., Deng, C. H., Zúñiga, F., Chen, Y., Dow, G., Studer, B., & Broggini, G. A. L. (2026). Haplotype-resolved chromosome-level genome assemblies of nineteen apple (*Malus domestica* Borkh.) cultivars. *Scientific Data*, 13, 258. <https://doi.org/10.1038/s41597-026-06583-y>

[3] Avni, R., Kamal, N., Bitz, L., Jellen, E. N., Bekele, W. A., Angessa, T.T., et al. (2024). A pangenome and pantranscriptome of hexaploid oat. *Nature*, 649(8095), 131–139. <https://doi.org/10.1038/s41586-025-09676-7>

[4] Jung, M., Quesada-Traver, C., Roth, M., Aranzana, M. J., Muranty, H., et al. (2025). Integrative multi-environmental genomic prediction in apple. *Horticulture Research*, 12(2), <https://doi.org/10.1093/hr/uhae319>

[5] Younis, O. G., Turchetta, M., Ariza Suarez, D., Yates, S., Studer, B., et al. (2023). ChromaX: A fast and scalable breeding program simulator. *Bioinformatics*, 39(12), btad691. <https://doi.org/10.1093/bioinformatics/btad691>

[6] Käch, D., Loera-Sanchez, M., Reidy, B., Studer, B., & Kölliker, R. (2026). Genetic diversity unveiled: Cost-effective methods for grass-land species. *Molecular Ecology Resources*, 2: e70108. <https://doi.org/10.1111/1755-0998.70108>

[7] Schlathölter, I., Broggini, G. A. L., Streb, S., Studer, B., & Patocchi, A. (2023). Field study of the fire-blight-resistant cisgenic apple line C44.4.146. *The Plant Journal*, 113(6), 1160–1175. <https://doi.org/10.1111/tpj.16083>

[8] Grogg, D., Rohner, M., Yates, S., Manzanares, C., Bull, S. E., Dalton, S., et al. (2022). Callus induction from diverse explants and genotypes enables robust transformation of perennial ryegrass (*Lolium perenne* L.). *Plants*, 11(15), 2054. <https://doi.org/10.3390/plants11152054>

[9] Rohner, M., Manzanares, C., Yates, S. A., Thorogood, D., Copetti, D., Lübberstedt, T., Asp, T., & Studer, B. (2023). Fine-mapping and comparative genomic analysis reveal the gene composition at the S and Z self-incompatibility loci in grasses. *Molecular Biology and Evolution*, 40, msac259. <https://doi.org/10.1093/molbev/msac259>

[10] Cropano, C., Manzanares, C., Yates, S. A., Copetti, D., Do Canto, J., Lübberstedt, T., Koch, M., & Studer, B. (2021). Identification of candidate genes for self-compatibility in perennial ryegrass (*Lolium perenne* L.). *Frontiers in Plant Science*, 12, 707901. <https://doi.org/10.3389/fpls.2021.707901> <https://mpb.ethz.ch/>

New Phytologist
Tansley Medal
for excellence in plant science
Deadline: 1 November



Open call: apply for the 2027 New Phytologist Tansley Medal

Are you, or do you know, an early career scientist who has made an outstanding contribution to plant science? The New Phytologist Tansley Medal is a prestigious prize, awarded annually to early career scientists that have made an outstanding contribution to plant science. Winners receive £2000 (GBP) and their work is highlighted in *NewPhytologist*, a leading plant science journal.

How to apply:

- Applicants submit a completed pro forma, their CV, and a supporting reference.
- Shortlisted candidates will be invited to write a single-authored Tansley insight for submission to *New Phytologist*.
- All competition articles that pass successfully through peer review will be published in *New Phytologist*, and the winner selected from these final articles.

This is a global competition open to early career scientists with 3 to 5 years' experience since gaining their PhD. Career breaks do not count towards this time period.

Tonni Grube Andersen · University of Zurich



Tonni Grube Andersen joined the Department of Plant and Microbial Biology at the University of Zurich on 1 January 2026 as Associate Professor of Molecular Plant Biology. As a new member of the PSC, he brings expertise in the mechanisms that allow plant roots

to control their exchanges with the soil environment. Tonni's group investigates how plant roots perceive, organise and communicate with their immediate environment, with a particular focus on the spatial and physiological logic of belowground chemical signalling.

Tonni completed a BSc in Natural Resources and Forestry and an MSc in Biology-Biotechnology at the University of Copenhagen, where he also earned his PhD in 2012. He continued as a postdoctoral fellow at the Danish National Research Foundation Centre of Excellence for Dynamic Molecular Interactions in Copenhagen, followed by a Marie Curie Intra-European Fellowship and postdoctoral research at the University of Lausanne. Since 2020, he has led his own research group as a Research Group Leader at the Max Planck Institute for Plant Breeding Research in Cologne, within the Cluster of Excellence on Plant Sciences (CEPLAS).

His research combines high-resolution fluorescence microscopy, near-native physiological setups, microfluidics and transcript- and translationalomics with microbiome-based community studies. His group works primarily with *Arabidopsis thaliana*, exploiting its extensive genetic toolbox to resolve gene expression at single-cell resolution, and with *Lotus japonicus* to study the specialised root structures — nodules — that host nitrogen-fixing bacterial symbionts. Key research directions include:

Chemical landscapes in roots

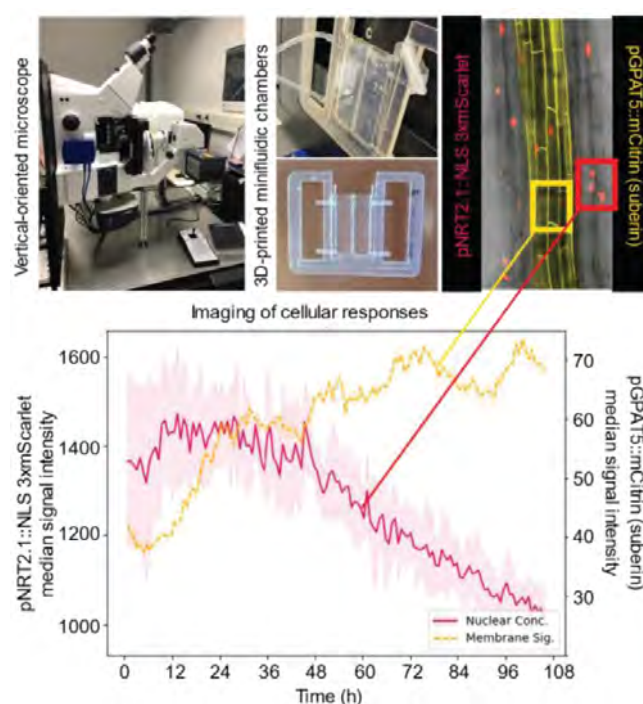
Tonni's group has shown that plants actively organise defence compounds such as glucosinolates along the root axis, creating spatial “chemical landscapes” that shape which microbes can colonise different root zones — a mechanism relevant to both *Arabidopsis* and the oilseed crop *Camelina sativa*.

Root-microbiome communication

By combining transporter mutants with spatial metabolite profiling and microbiome sequencing, the group is uncovering how plants use chemical gradients to structure their associated bacterial communities, rather than simply tolerating whichever microbes happen to be present in the soil.

Symbiotic root structures

Through work on *Lotus japonicus*, Tonni's team studies how nodule formation is coordinated with the plant's transport systems, shedding light on the developmental logic underlying beneficial plant-microbe partnerships. Tonni's arrival strengthens the PSC's growing cluster of expertise in plant-microbiome interactions, complementing ongoing work by other members on root exudates, microbiome feedbacks and beneficial microbial associations.



The group of TGA also specializes in long-term physiological imaging. They employ, and continuously develop, sophisticated 3D-printed microfluidic growth setups compatible with direct imaging. This allows the group to detect and quantify gene-expression signals in roots at the single-cell level in vivo and over time. In the example on this figure, the signal of a suberization (root barrier) marker is shown in yellow, together with signal associated to expression of a nitrate transporter (NRT2.1) in cortex/epidermal cells.

Publication

Shen, D. et al. (2025). Apoplastic barriers are essential for nodule formation and nitrogen fixation in *Lotus japonicus*. *Science*, 387. <https://doi.org/10.1126/science.ad08680>

Recent preprint

Roman, A. O. et al. (2026). Transport-driven spatial patterning of glucosinolates structures the root microbiome. *bioRxiv*. <https://www.biorxiv.org/content/10.64898/2026.02.23.707459>

Andersen Group, University of Zurich:

<https://www.botinst.uzh.ch/en/research/andersen.html>

<https://www.linkedin.com/in/tonni-andersen-43b9b64/>

Megan McDonald · ETH Zurich



Megan McDonald joined ETH Zurich in 2026 as Associate Professor of Plant Disease Dynamics at the Department of Environmental Systems Science. She studied Molecular and Cellular Biology at the University of Arizona before moving to Switzerland for her PhD in phytopathology at ETH Zurich. After completing her doctorate in 2012, she joined the Australian National University as an SNSF postdoctoral fellow and subsequently remained there as a research fellow until 2020. She then moved to the University of Birmingham as a Birmingham Fellow and Assistant Professor, and from 2024 to 2026 held a UKRI Future Leaders Fellowship. Her appointment at ETH therefore marks a return to the institution where her research career in plant pathology began.

Her research investigates how fungal plant pathogens adapt, from changes occurring within individual genomes to evolutionary processes acting across entire pathogen populations. By combining comparative genomics with experimental approaches, her group seeks to identify the mechanisms that generate genomic variation and ultimately influence pathogen virulence.

Plant disease dynamics

A central focus of Megan's research is how transposable elements contribute to the exceptional plasticity of fungal genomes and accelerate the evolution of pathogenicity. Her group combines comparative genomics with experimental approaches to investigate structural genome variation, horizontal gene transfer and the emergence of virulence traits.

A particularly striking example is the wheat virulence factor ToxA. In a 2025 mBio study, Megan and colleagues characterised Sanctuary, a giant "Starship" transposon implicated in the horizontal movement of ToxA between fungal wheat pathogens. Together with the related Starship Horizon, these mobile elements provide a mechanistic framework for understanding how virulence-associated DNA can move between species occupying the same host niche.

Recent work on ToxB extends this theme. In *Pyrenophora tritici-repentis*, Megan and colleagues showed that transposons can drive contrasting evolutionary outcomes: promoting amplification of ToxB, with consequences for virulence, while also inserting into and disrupting the gene. The findings illustrate how mobile elements can simultaneously generate gene dosage variation and loss-of-function alleles within pathogen populations.

At ETH Zurich, Megan plans to extend this work through experimental systems that make it possible to observe transposon-mediated genome evolution in real time and to compare experimentally evolved populations with diversity found in nature. Her programme also includes plant-health policy and biosecurity, with the longer-term goal of connecting fundamental pathogen genomics with improved diagnostics and plant-health surveillance in Switzerland.

Publications

Bucknell, A., Wilson, H. M., Gonçalves dos Santos, K. C., Simpfendorfer, S., Milgate, A., Germain, H., Solomon, P. S., Bentham, A. & McDonald, M. C. (2025). Sanctuary: a Starship transposon facilitating the movement of the virulence factor ToxA in fungal wheat pathogens. *mBio*, 16(10). <https://doi.org/10.1128/mbio.01371-25>

Gourlie, R., McDonald, M. C., Hafez, M. & Aboukhaddour, R. (2026). The virulence gene ToxB is both amplified and disrupted by transposons in the wheat pathogen *Pyrenophora tritici-repentis*. *Molecular Plant-Microbe Interactions*, 39:3, 474-488. <https://doi.org/10.1094/MPMI-01-26-0003-R>

Science Highlights

Across three partner universities, PSC members represent a wide range of disciplines. Together, they connect plant science from molecular mechanisms and genes to organisms, ecosystems, landscapes and decision-making. The five CONNECTs in this issue trace some of these shared research pathways through recent published work.

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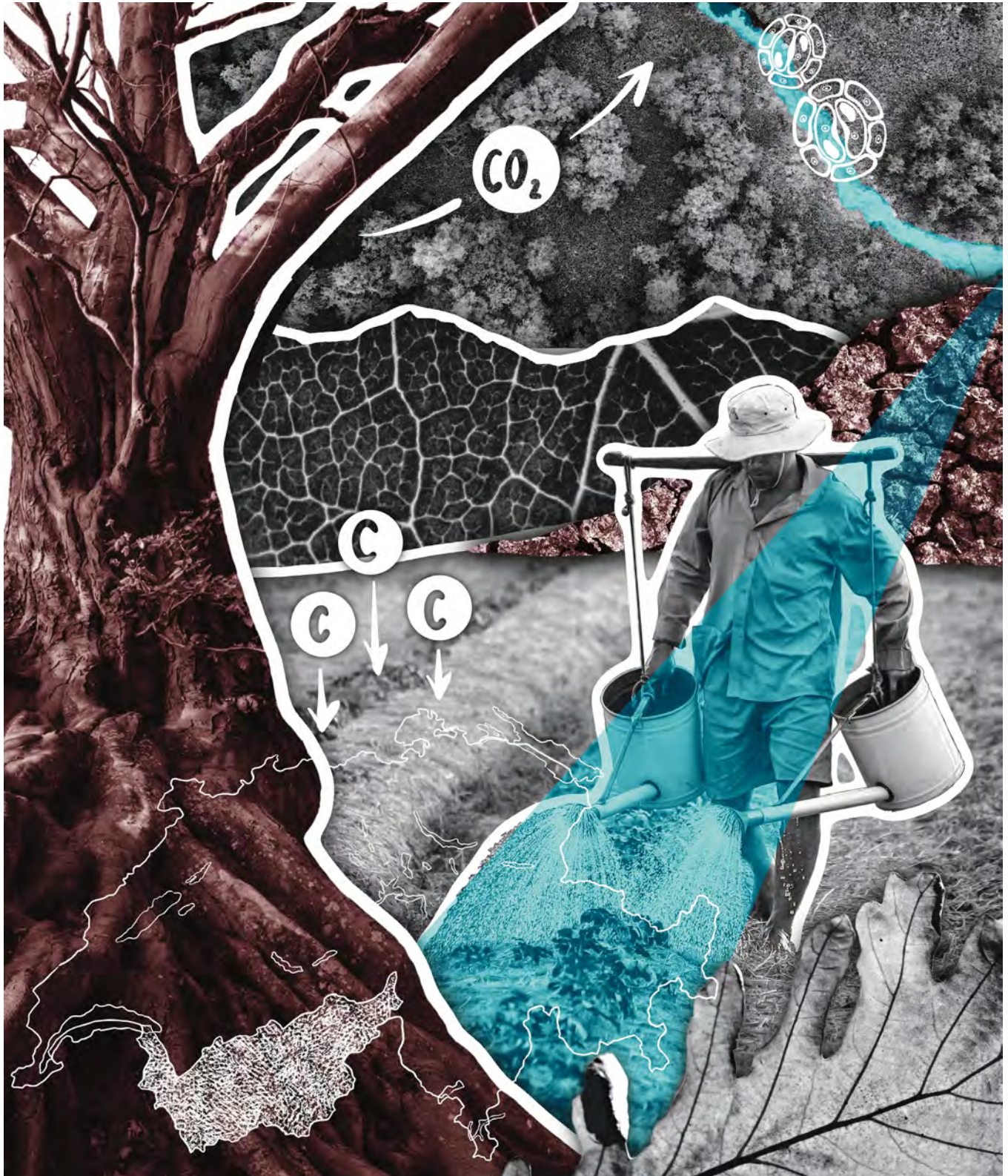
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CONNECT — Water across scales

Soil physics determines when plants experience water limitation—but how does this scale from individual roots to forests and ecosystem carbon cycling? Research across PSC groups approaches this question through plant hydraulics, isotope ecology, ecosystem fluxes and remote sensing.



Where drought begins: soil physics sets the hydraulic limits of plants



Andrea Carminati · ETH Zurich

When soils dry, plants close their stomata to limit water loss. When exactly this happens depends strongly on the soil itself. Research by Andrea Carminati shows that soil physics sets a common hydraulic threshold for stomatal regulation across very different vascular plant species.

Andrea and colleagues recently showed how soil texture governs ecosystem-scale water limitation (Wankmüller et al., Nature, 2024): sandy soils lose hydraulic conductivity faster as they dry, making vegetation more sensitive to soil drying, while clay-rich soils are more sensitive to atmospheric dryness. Does that constraint also shape how individual plants regulate their stomata, across species with very different hydraulic strategies?

The researchers combined a meta-analysis of 19 vascular plant species, from herbs to canopy trees, with a model predicting the point at which stomata should close based purely on the physical cost of extracting water from drying soil. Stomatal regulation began, on average, at a leaf water tension of 1.3 ± 0.6 MPa across all 19 species. The model, built without any species-specific biological parameter, independently predicted 1.4 ± 0.6 MPa. The close match indicates that soil physics, not the diversity of leaf or xylem traits, sets the operating range within which stomata function. Species-specific traits determine how each plant behaves within that range, not whether the range applies to it.

Two companion papers in *New Phytologist* localise and extend this mechanism. Using neutron radiography, the researchers tracked water movement around maize roots during drying. Once soil water potential crosses a texture-dependent threshold (around -5 kPa in sand, -200 kPa in loam), the root–soil interface itself becomes the first hydraulic bottleneck, before any leaf-level stress signal appears. A second study shows that internal water storage in trees, or hydraulic capacitance, is not universally beneficial: in spruce it extends transpiration under drought, but in beech, which regulates stomata more flexibly, the same trait can trigger earlier stomatal closure. A related *Geoderma* paper shows that simple,

sand-and-clay-based models transfer more reliably across regions than complex ones, which matters for scaling to global soil datasets.

Such results could improve predictions of drought responses and help identify which plant traits, species and management strategies suit which soils.

Publications

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Separating isotopic signal from artefact in tree water uptake



Ansgar Kahmen · University of Basel

Understanding where trees obtain their water is essential for predicting how they respond to drought and changing environmental conditions. Research by Ansgar Kahmen improves the reliability of stable-isotope methods used to trace water from the soil through trees.

Stable oxygen and hydrogen isotopes are widely used to determine where plants obtain their water, but these inferences depend on whether water recovered from soil and plant tissues retains its original isotopic composition. Cryogenic vacuum distillation is the standard extraction method, and recurring discrepancies, particularly in

hydrogen isotope values, have raised questions about whether they reflect physiological processes, distinct water pools or extraction artefacts.

Ansgar's research group investigated this in two controlled irrigation experiments with juvenile temperate trees. They compared water extracted by cryogenic vacuum distillation from soil, xylem and phloem with the known irrigation water, and with sap obtained by mild vacuum extraction as an independent reference for mobile water. This design separates methodological effects from possible isotope fractionation during uptake and stem transport.

The irrigation water and mildly extracted sap showed closely corresponding $\delta^{18}\text{O}$ and $\delta^2\text{H}$ values, indicating that uptake and transport largely preserved the isotopic signature of the source. Cryogenically extracted soil water displayed small but consistent offsets, suggesting that bulk extraction recovers both a mobile, plant-available pool and a more tightly retained pool unavailable to roots.

The largest discrepancies occurred in $\delta^2\text{H}$ values from cryogenically extracted xylem water, while differences in $\delta^{18}\text{O}$ were comparatively small. Comparisons with phloem water and mildly extracted sap indicated that these hydrogen-isotope offsets arose during extraction, not through physiological modification within the tree. Cryogenic vacuum distillation can therefore provide reliable $\delta^{18}\text{O}$ measurements for identifying plant source water, while $\delta^2\text{H}$ data require correction and cautious interpretation.

Publication

Steger, D. N., Amicabile, E., Nelson, D. B. & Kahmen, A. (2026). Artefacts associated with cryogenic vacuum distillation do not compromise plant source water extraction from soil and xylem for isotope analysis. *Ecohydrology*, 19(3), e70206. <https://doi.org/10.1002/eco.70206>

Trees remember water abundance seven years after irrigation ends



Janneke Hille Ris Lambers · ETH Zurich

Trees can carry the effects of past environmental conditions long after those conditions have changed. A long-term experiment in a Swiss forest shows that nearly two decades of increased water availability left lasting signatures in newly formed leaves and twigs years after

irrigation ended, revealing how ecological memory can shape trees' responses to future drought.

Forest growth models typically assume that current tree performance reflects current environmental conditions. That assumption breaks down if trees retain a physiological memory of past water availability. A new study from the long-running Pfywwald irrigation experiment in Valais tests this directly. After 18 years of continuous irrigation, watering was discontinued across part of the site, creating three comparable groups: never-irrigated trees, continuously irrigated trees, and formerly irrigated trees sampled seven years after their water supply ended.

The team led by Janneke Hille Ris Lambers used synchrotron X-ray microscopy to quantify 47 anatomical traits in leaves and twigs formed well after irrigation had stopped, tissue that developed entirely under the post-irrigation water regime. If current conditions alone determined anatomy, these tissues in the formerly irrigated group should have converged with the never-irrigated controls. They had not. Twig anatomy showed differences that appeared to be attenuating with time, consistent with a fading legacy signal. Leaf anatomy showed the opposite trajectory: traits continued to reflect the trees' prior high-water history and pointed toward a persistent shift in strategy associated with water-stress adaptation, one that emerged only after irrigation ceased.

The difference between twig and leaf trajectories indicates that ecological memory is not a uniform property of a tree. It is organ- and tissue-specific, with different decay dynamics depending on the anatomical structure involved. That has a direct consequence for how tree performance is modelled: relating current growth or drought vulnerability solely to current environmental variables risks misattributing a multi-year legacy effect to present-day stress. Such a legacy, spanning multiple cycles of tissue formation, is visible only in a long-term manipulative experiment, and remains rare in forest ecology at this timescale.

Publication

Chin, A. R. O., Gessler, A., Láin, O., Østerlund, I., Schaub, M., Thérout-Rancourt, G., Voggeneder, K. & Hille Ris Lambers, J. (2025). The memory of past water abundance shapes trees 7 years later. *American Journal of Botany*, 112(1), e16452. <https://doi.org/10.1002/ajb2.16452>

Two decades of grassland measurements reveal how management interacts with climate extremes



Nina Buchmann · ETH Zurich

Grasslands play an important role in the carbon cycle, but their carbon uptake is shaped by both climate and agricultural management. Twenty years of measurements from a Swiss grassland reveal how the two interact, and show with innovative machine learning approaches which drivers contribute when how much to grassland carbon dioxide fluxes.

Long-term carbon dioxide flux records of grasslands are rare, because most eddy-covariance sites are forests. However, to understand how human interventions change carbon fluxes, we need to separate management and climate as distinct drivers.

A new study from Nina Buchmann's group closes this gap using twenty years of continuous flux data from the Chamau grassland site (canton of Zug, 2005–2024), combined with a complete management log: every mowing date, grazing period, fertilisation event and sward renewal over the two decades.

The team trained XGBoost models on this dataset and used SHAP analysis to determine the contributions of individual drivers to gross primary production (GPP) and ecosystem respiration: light, temperature, soil water content, time since management and fertilisation status, separately for each regrowth period between interventions. The relative importance of each driver can therefore change over time. Two results stand out. First, despite twenty years of warming and declining soil water content at the site, neither GPP nor respiration during regrowth periods showed a significant long-term trend. Under typical conditions, light, temperature and management dominated productivity, while respiration was driven by temperature, productivity and management. Second, that hierarchy broke down during the four exceptionally dry and hot summers in the record (2018, 2019, 2022, 2023): soil water availability became the dominant driver of GPP, even more important than high vapor pressure deficits. The effect of nitrogen fertilisation was more differentiated, depending both on

water availability and on vegetation performance before or after sward renewal.

The absence of a long-term trend is not a sign of resilience but of climate-smart management adaptations. Within the observed 2005–2024 range, management has so far offset the climatic trend embedded in the flux record. If management is able to continue such compensation remains to be seen. The study clearly shows that management is not "noise", but a quantifiable variable with its own weight in the carbon budget.

Publication

Wang, Y., Feigenwinter, I., Hörtnagl, L., Gilgen, A. K. & Buchmann, N. (2026). Drivers of long-term grassland CO₂ fluxes: effects of management and meteorological conditions during regrowth periods. *Biogeosciences*, 23, 1625–1652.
<https://doi.org/10.5194/bg-23-1625-2026>

When satellites miss forest water stress below the canopy



Alexander Damm · University of Zurich

Reliable monitoring of forest water stress is becoming increasingly important as droughts intensify, but commonly used satellite indices may miss important changes within the canopy. A study shows that combining optical satellite data with signals that penetrate deeper into forests gives a more complete picture of how trees respond to drought.

Satellite-derived water indices are the default operational tool for monitoring forest canopy water status at scale, but their retrieval physics constrains what they can detect. A joint study by Alexander Damm and Nina Buchmann compares the Normalised Difference Water Index (NDWI) from Sentinel-2 against vegetation optical depth (VOD) retrieved in situ from GNSS receivers installed above and below the canopy, across four seasons in an evergreen coniferous stand and a deciduous broadleaved stand, alongside

eddy-covariance evapotranspiration, soil moisture and meteorological data.

The divergence is conditional, not uniform. In the deciduous stand, NDWI and VOD tracked each other across the seasonal cycle but decoupled during the 2022 summer drought: VOD and evapotranspiration both registered a clear stress response while NDWI showed little corresponding signal, a false negative for any drought-monitoring pipeline relying on optical indices alone. In the evergreen stand, the two indices diverged in pattern even outside drought conditions, pointing to a more structural mismatch than simple underestimation.

The explanation lies in retrieval depth. NDWI is sensitive mainly to the upper canopy and saturates at high water content, whereas VOD integrates signal across a greater vertical fraction of the canopy, including lower layers optical sensors cannot reach. The two indices sample different physical volumes, which is why they decouple under drought, when vertical heterogeneity in plant water status is highest. Apparent stability at the canopy surface does not mean the forest as a whole is unaffected.

Publication

Kesselring, J., Humphrey, V., Niederberger, M., Feigenwinter, I., Shekhar, A., Buchmann, N. & Damm, A. (2026). Divergence between in situ and satellite-based estimates of forest canopy water content. *Remote Sensing of Environment*, 332, 115097. <https://doi.org/10.1016/j.rse.2025.115097>

Conceptual pitfalls in the forest carbon debate



Christian Körner · University of Basel

Forests are central to discussions of climate-change mitigation, but interpreting their contribution requires a clear distinction between carbon uptake, growth and long-term carbon storage. Christian Körner, Professor emeritus at University of Basel, revisits several conceptual pitfalls that lead these processes to be conflated.

Tree growth represents a carbon flux into biomass, but a high rate of growth does not necessarily translate into a sustained increase in ecosystem carbon stocks. Long-term storage depends equally on how long carbon remains within the system, including the effects of tree longevity, mortality, disturbance and biomass turnover. Christian therefore cautions against reading increased growth or productivity alone as evidence for enhanced carbon sequestration.

The distinction matters particularly when assessing the effects of rising atmospheric CO₂, forest management or extended rotation periods. Evaluating the climate-mitigation potential of forests requires consideration of carbon uptake rates, but also of carbon residence times and changes in ecosystem carbon stocks over appropriate spatial and temporal scales. The article offers a concise conceptual framework for researchers across forest ecology, plant physiology and carbon-cycle science, clarifying terminology that is increasingly important in both scientific and policy discussions. By considering carbon uptake together with residence time, mortality and turnover, it provides a more robust basis for evaluating the long-term contribution of forests to climate mitigation.

Publication

Körner, C. (2026). Conceptual pitfalls in the forest carbon debate. *Carbon Balance and Management*, 21, 59. <https://doi.org/10.1186/s13021-026-00412-w>

CONNECT — The rhizosphere

Root anatomy, microbial ecology and crop management meet in the rhizosphere. Bringing these perspectives together could help reveal when root-microbiome relationships contribute to crop performance—and when environmental stress changes the rules.



Root–microbiome relationships in maize depend on water availability



Tania Galindo-Castañeda,
Johan Six &
Martin Hartmann · ETH Zurich

A field study in maize links variation in root anatomy and architecture to differences in rhizosphere microbial communities, and shows that these associations depend strongly on water availability.

Root traits define the physical and metabolic interface between plants and soil microorganisms. The relative contributions of root system architecture and cellular anatomy to rhizosphere community structure remain poorly resolved under field conditions. A field study involving Elena Giuliano, Johan Six, Martin Hartmann and Tania Galindo-Castañeda therefore tested whether naturally occurring variation in maize root traits significantly correlate with prokaryotic and fungal community composition, and whether these associations persist under drought.

The researchers grew 22 maize inbred lines in the field with either optimal water availability or drought imposed using rainout shelters. Grain yield was measured alongside root architectural traits quantified by shovelomics and anatomical traits resolved by laser ablation tomography of root cross-sections. Rhizosphere prokaryotic and fungal communities were characterised by DNA metabarcoding. Drought reduced grain yield by 42.6%, a strong environmental perturbation against which the stability of root phenotype–microbiome relationships could be assessed.

Several associations involved microbial groups with recognised roles in plant–soil interactions, including *Bradyrhizobium*, *Mesorhizobium*, *Massilia*, *Sphingomonas* and the arbuscular mycorrhizal genus *Rhizophagus*. Variation in cortical structure may therefore help define microbial niches, through changes in root metabolic costs, exudation or the physical environment available for colonisation. The study remains correlational and does not establish that individual anatomical traits directly recruit particular microorganisms.

The phenotype–microbiome relationship depended strongly on water availability. Under drought,

community-level associations between the measured root traits and microbial β -diversity were no longer detectable. Root phenotypes associated with rhizosphere composition under favourable conditions did not predict community structure under water limitation. Root–microbiome associations are thus not fixed properties of a genotype, and water availability is an important modifier of the relationship between root phenotype and rhizosphere assembly.

Publication

Giuliano, E., Sidhu, J. S., Lopez-Valdivia, I., Feola Conz, R., DePew, C. L., Lynch, J. P., Six, J., Hartmann, M. & Galindo-Castañeda, T. (2026). Digging for meaningful connections: associations between root phenotypes and rhizosphere microbial diversity in maize. *Plant and Soil*, 525, 1249–1272. <https://doi.org/10.1007/s11104-026-08822-y>

Beneficial soil microbiome feedbacks enhance both plant growth and defence



Klaus Schlaeppi · University of Basel

Plants do more than absorb nutrients from the soil. Through compounds released by their roots, they actively modify the microorganisms living around them. These changes can persist in the soil and influence the growth and health of the next generation of plants, a process known as plant–soil feedback.

Research from the group of Klaus Schlaeppi shows that soil microbiomes conditioned by maize benzoxazinoids improve plant growth and defence, and that plant-available soil iron controls where these benefits arise in crop rotations.

Maize roots release benzoxazinoids (BXs). BXs are specialised defence metabolites that restructure the surrounding soil microbiome and leave a lasting microbial legacy. In the first study, published in *New Phytologist*, *Arabidopsis thaliana* was grown in soils conditioned either by wild-type maize or by a *bx1* mutant unable to produce benzoxazinoids. On the BX-conditioned soil, plants developed larger rosettes, reached more advanced

developmental stages and activated more defence genes in their leaves. They were also better protected against the fungal pathogen *Botrytis cinerea*. Defence priming explains this: the microbiome places the immune system in a state of alert, ready to respond quickly and strongly when a pathogen attacks. The plants gained resistance without sacrificing growth.

The second study, published in *Microbiome*, examined these feedbacks in maize–wheat rotations and searched for the soil factors that control their strength and direction. Plots grown with wild-type maize or with a *bx1* mutant were compared in a two-season trial at Agroscope Reckenholz, and the results were confirmed in two further field experiments. The decisive factor was plant-available soil iron. Where iron was scarce, wheat following BX-producing maize grew taller than wheat following the mutant; as iron availability increased, this advantage faded and could even reverse. Controlled *Arabidopsis* experiments confirmed the pattern: adding iron to a low-iron soil was enough to abolish the positive microbiome effect. Beneficial feedbacks thus emerge where soils are suboptimal and disappear where plants are nutritionally well supported.

These studies provide an experimental model for understanding how plants perceive complex soil microbiomes and translate microbial signals into development and immunity. A new study, forthcoming in *Nature Genetics*, now offers a first insight into the genetic mechanisms behind this process. The researchers identified Mediator of Microbiome Feedback 1 (MMF1), an immune receptor gene in *A. thaliana* that enables plants to respond to beneficial soil microbiomes. Plants lacking this gene no longer showed the enhanced growth or defence-related responses triggered by the microbiome. This discovery provides a first molecular explanation of how plants sense and respond to complex microbial communities. Together, these findings support a longer-term goal: developing crops selected both for assembling beneficial microbiomes and for responding productively to them.

Publications

Stengele, K., Stauber, L., Thoenen, L., Janse van Rensburg, H., D'Adda, V. & Schlaeppi, K. (2026). Benzoxazinoid-mediated microbiome feedbacks enhance *Arabidopsis* growth and defence. *New Phytologist*, 250, 3334–3348. <https://doi.org/10.1111/nph.71098>

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Janse van Rensburg, H., Schandry, N., Waelchli, J., Civelek, H., Stengele, K., Cadot, S., Jandrasits, K., Crosbie, D., Adachi, H., Becker, C., Schlaeppi, K. (2026). A TNL receptor locus mediates microbiome feedbacks in *Arabidopsis*. *Nature Genetics* (in press)

When beneficial microbes and a virus send the same metabolic signal



Hannier Pulido & Consuelo De Moraes & Mark C. Mescher · ETH Zurich

Plants interact simultaneously with microbes, pathogens and insects, and these relationships can have unexpected effects on one another. A new study in soybean shows that beneficial root bacteria and viral infection alter plant metabolism in surprisingly similar ways, making plants more attractive to an insect that also transmits the virus.

Soybean plants routinely engage with more than one microbial partner at once: nitrogen-fixing rhizobia, growth-promoting rhizobacteria and, less welcome, insect-transmitted viruses. Mutualists and pathogens can tap into overlapping metabolic pathways despite opposing interests in how the plant behaves. What happens to plant chemistry, and to the insects reading it, when both act on the same host at once has been unclear. A new study by Hannier Pulido, Consuelo De Moraes and Mark C. Mescher addresses this in soybean colonised by two rhizobacteria, the nitrogen-fixing symbiont *Bradyrhizobium japonicum* and the plant growth-promoting *Delftia acidovorans*, together with Bean pod mottle virus (BPMV), a pathogen transmitted by the Mexican bean beetle, *Epilachna varivestis*.

Combining metabolomics, transcriptomics and behavioural choice assays, the researchers found that rhizobacterial colonisation and viral infection converge on the same metabolic direction. Both increased primary metabolites such as amino acids, organic acids and myo-inositol, while depleting defence-associated secondary metabolites, including the flavonoids kaempferol and rutin. A beneficial symbiont and a pathogen, with no shared evolutionary interest in the outcome, therefore reshape the host's biochemistry along a similar axis. Behavioural assays showed that beetle vectors preferentially fed on rhizobacteria-inoculated and virus-infected plants alike, linking this shared metabolic shift to feeding preference and, by extension, to the plant's exposure to viral transmission. A simple mutualist-versus-pathogen framing of

plant–microbe interactions does not hold: a plant's association with beneficial soil bacteria can leave it biochemically more attractive to a herbivore that also vectors disease, even though the bacteria and the virus have no direct relationship to one another.

Publication

Pulido, H., Mauck, K. E., De Moraes, C. M. & Mescher, M. G. (2026). Beneficial rhizobacteria and virus infection modulate the soybean metabolome and influence the feeding preferences of the virus vector *Epilachna varivestis*. *New Phytologist*, 250(4), 2599–2618. <https://doi.org/10.1111/nph.71104>

Making soil life visible – and putting it to work



Marcel van der Heijden ·
University of Zurich / Agroscope

Beneficial root-associated microbes can reshape interactions far beyond the rhizosphere, but turning that into agriculture requires tools that make soil life visible and manageable. Research by Marcel van der Heijden embeds microbial functions in regenerative agriculture.

A pair of cotton underpants is an improbable proxy for soil biology. Yet this was precisely the appeal of the Swiss citizen-science project 'Proof by Underpants', led by Franz Bender and Marcel van der Heijden. Cotton cellulose becomes a substrate for soil decomposers, and the degree of degradation offers a readily visible indication of biological activity. Combined with conventional soil measurements, the experiment brought a hidden process quite literally to the surface.

As Franz and Marcel discussed in *Science* in 2025, cotton decomposition is no comprehensive measure of soil health: moisture, temperature, organic matter, management and decomposer communities all influence the outcome. Its value lies in making soil biological activity tangible, and in opening a more consequential question: what functions do below-ground organisms perform in agricultural soils?

A 2026 Perspective in *Nature Communications* points out that arbuscular mycorrhizal fungi, nitrogen-fixing bacteria

and other beneficial microorganisms can influence nutrient acquisition, growth and stress tolerance, yet the capacity of crops to establish and exploit these associations has received little attention as a breeding objective.

The authors propose a framework spanning both partners. On the plant side, targets include root architecture, nutrient transport, exudates and the signalling pathways involved in microbial recruitment and symbiosis, with gene editing expanding the toolbox. On the microbial side, soil management and inoculation can maintain, restore or introduce beneficial communities. Their central recommendation is to match the strategy to the biological state of the soil: in degraded soils, inoculation and soil-improving management take priority, while in soils that already harbour active microbial communities, genotypes bred for stronger associations promise the greater gain. Native inoculants are considered more promising than foreign ones, and products are shifting from single strains towards consortia designed to perform more reliably across environments. What is still missing is field evidence, since research on breeding for microbial associations remains largely confined to the laboratory and greenhouse.

An evaluation by Marcel's group recently found that over 80% of commercial mycorrhizal inoculants failed to colonise plant roots, which strengthens the case for building on the communities already in the soil. Plant genetics, microbial ecology and management thus connect: crop traits determine the opportunities for microbial partnerships, soil communities provide the functional potential, and management shapes the environment in which both interact.

Publications

Bender, S. F. & van der Heijden, M. G. A. (2025). Assessing soil health with underpants. *Science*, 387, 936. <https://doi.org/10.1126/science.adw0030>

Rog, I., Lutz, S., Fesenfeld, L., Hiltbrunner, J., Bouwmeester, H. & van der Heijden, M. G. A. (2026). Breeding for beneficial microbial associations. *Nature Communications*, 17, 7695. <https://doi.org/10.1038/s41467-026-76260-6>

Bardgett, R. D. & van der Heijden, M. G. A. (2026). Soil microbiomes and regenerative agriculture. *Cell Host & Microbe*, 34(8), 1489–1493. <https://doi.org/10.1016/j.chom.2026.07.002>

Realistic pesticide mixtures reveal contrasting responses across Swiss soils



Pascal Niklaus · University of Zurich &
Marcel van der Heijden · University of Zurich /
Agroscope

Agricultural soils are exposed to mixtures of pesticides throughout the growing season, yet their combined effects on soil life remain poorly understood. A study shows that key nutrient-cycling functions remain largely stable, while pesticide mixtures can alter fungal communities and decomposition processes, with effects depending strongly on land-use history.

Ecotoxicological assessment of agricultural soils has relied on single-compound dose-response designs, which do not capture the sequential, multi-active-ingredient exposure that field soils experience across a growing season. A research collaboration between FHNW, Agroscope, Eawag and University of Zurich, involving Pascal Niklaus and Marcel van der Heijden, addresses this gap, applying realistic commercial spray-plan mixtures rather than isolated active ingredients to microcosms drawn from ten soils with contrasting management histories.

The design used five grassland and five arable soils from north-western Switzerland, exposed to pesticide mixtures replicating spray plans of differing intensity as used in current agricultural practice. At 14 and 56 days post-application, the team quantified net nitrogen mineralisation, potential nitrification and denitrifying enzyme activity, alongside decomposition rates of two litter substrates chosen for contrasting recalcitrance: labile green tea versus recalcitrant rooibos, following the standardised Tea Bag Index protocol. Microbial community structure was resolved via 16S rRNA and ITS amplicon sequencing to separate bacterial from fungal responses.

The functional and compositional results diverge. Nitrogen cycling proved comparatively robust: even under the high-intensity mixture, net mineralisation, nitrification potential and denitrification activity showed only weak treatment effects. Litter decomposition told a different

story, and not a uniform one. Green tea decomposition accelerated under pesticide exposure while rooibos decomposition slowed, so the effects fall differently on the labile and the recalcitrant decomposer guilds instead of suppressing decomposition across the board. Fungal diversity declined significantly in grassland soils under the high-intensity treatment but was buffered in arable soils, while bacterial diversity did not respond in either. Shifts in fungal community composition were detectable, but consistently smaller than the variance already explained by prior land-use history.

The asymmetry between arable and grassland soils fits a selection-history hypothesis: soils under long-term, recurrent agrochemical input may already have been filtered for pesticide-tolerant fungal taxa, leaving grassland communities, with a comparatively low baseline exposure history, more susceptible to an equivalent acute dose. Decomposition metrics may therefore register community-level perturbation before bulk nutrient-cycling functions do, making them candidate early-warning indicators in soil monitoring. Whether repeated field-realistic exposure over several growing seasons produces cumulative, non-additive effects is a question for longitudinal field validation.

Publication

Medici, L. Ä., Lüthi, A., Niklaus, P. A., van der Heijden, M. G. A., Walder, F. & Langer, M. (2026). Ten grassland and arable soils show variable microbial responses to realistic pesticide mixtures. *Applied Soil Ecology*, 223, 107035. <https://doi.org/10.1016/j.apsoil.2026.107035>

When beneficial bacteria become a biosafety question



Leo Eberl · University of Zurich

Microbial biocontrol could reduce agriculture's reliance on chemical pesticides, but its wider use depends on ensuring that beneficial bacteria do not pose unintended risks. A new strain-level framework helps distinguish promising biological control agents from closely related bacteria with pathogenic potential, supporting the safer development of microbial solutions for crop protection.

Microorganisms associated with plant roots can improve nutrient acquisition, suppress fungal pathogens and strengthen plant resilience, which makes them attractive candidates for biological pesticides and inoculants. Their use raises a biosafety question: how can beneficial strains be distinguished from closely related bacteria capable of causing opportunistic infections?

The problem is particularly acute within *Burkholderia sensu lato*. Members of this diverse group inhabit soils, plant tissues and rhizospheres, where they contribute to nitrogen fixation, phosphate solubilisation and antifungal compounds. Others include plant pathogens and opportunistic human pathogens. Recent taxonomic revisions have separated *Burkholderia sensu stricto* from predominantly environmental genera such as *Paraburkholderia*, but classification alone cannot establish the safety of an individual strain.

A study led by Leo Eberl combines phenotypic and genetic information. The authors analysed 76 *Burkholderia sensu lato* strains for pathogenic potential, antifungal activity and traits associated with environmental fitness, using *Galleria mellonella* larvae as an experimental infection model. Most strains with elevated pathogenic potential belonged to *Burkholderia sensu stricto*, but several *Paraburkholderia* isolates also produced comparatively strong effects. Genus-level classification was therefore insufficient for reliable risk assessment.

Proteolytic activity and siderophore production were associated with higher pathogenic potential, while oxalate utilisation and several environmental traits correlated with lower potential. The researchers also transferred an ornibactin biosynthesis gene cluster from a clinical *Burkholderia* isolate into the environmental strain *Paraburkholderia sacchari*. Acquisition of the cluster increased pathogenic potential in the insect model without reducing biocontrol capacity or environmental persistence, showing how a single genetic determinant can alter the balance between agricultural benefit and biosafety risk.

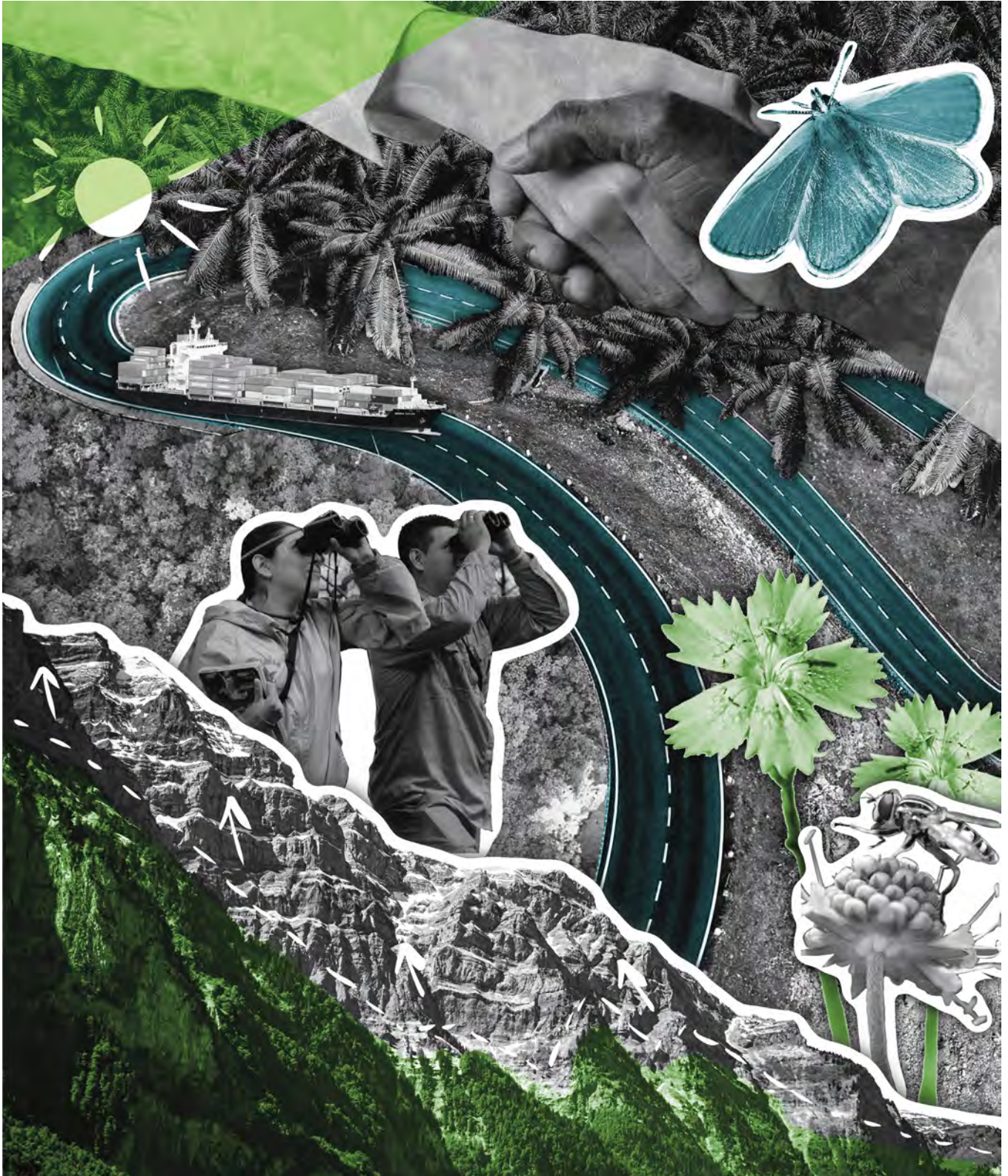
The study does not demonstrate that the strains identified through the insect model cause human disease. It proposes experimentally supported traits and genetic markers for preliminary strain-level assessment, a more precise basis for selecting microorganisms that protect crops while limiting risk.

Publication

Agnoli, K., Mathew, A., Gualdi, S., Paszti, S., Moulin, L., Vergunst, A., Mergaert, P. & Eberl, L. (2026). Identifying phenotypic and genetic traits for assessing pathogenic potential and biocontrol capacity in *Burkholderia sensu lato* strains. *The ISME Journal*, 20, wrag081. <https://doi.org/10.1093/ismejo/wrag081>

CONNECT — From biodiversity data to decisions

Documenting biodiversity is only one part of conservation. Linking ecological monitoring with governance and science–policy interfaces raises a broader question: what kinds of evidence are needed to turn knowledge into effective action?



Genomics reveals the hidden impact of direct seeding on Swiss dry meadows



Jasmin Tschan & Alex Widmer · ETH Zurich

Direct seeding is widely used to establish and promote species-rich meadows, but its long-term genetic effects are difficult to assess. A study demonstrates how population genomics can identify seeded populations, trace the geographical origins of seed material and distinguish human-mediated introductions from natural gene flow.

Research led by Jasmin Tschan, Alex Widmer and Martin Fischer used population genomics to reconstruct the origins and genetic effects of direct seeding in Switzerland, combining heterogeneous genomic datasets covering *Dianthus carthusianorum*, the Carthusian pink, across its European range. The analyses identified six strongly differentiated evolutionary lineages and produced a chromosome-scale reference genome for the species.

The team then examined 310 plants from 31 Swiss populations and found genomic evidence of direct seeding in 15 populations, 48.4% of those surveyed. Most seeded populations originated from Swiss material, but several showed evidence of human-mediated admixture or included evolutionary lineages from elsewhere in Europe. Within the same evolutionary lineage, the researchers found no systematic reduction in genetic diversity between natural and seeded populations.

Restoration measures can therefore leave detectable genomic signatures within a few decades, and seed provenance matters: genetically divergent material may alter the genetic composition of restored populations, even when the species itself is native to the area.

Genomic monitoring could complement conventional ecological assessments and support restoration strategies that preserve both species diversity and the genetic variation needed for future adaptation.

Publication

Tschan, J. N., Reutimann, O., Fior, S., Cornille, A., Roman, A., Ursu, T.-M., Widmer, A. & Fischer, M. C. (2026). Genomic identification of direct seeding and evolutionary lineages by combining heterogeneous genomic resources. *BMC Biology*, 24, 14. <https://doi.org/10.1186/s12915-025-02476-5>

When warming and pollinators interact, genomic adaptation becomes unpredictable



Florian P. Schiestl · University of Zurich

*Both rising temperatures and pollinators can influence the evolution of plant traits. A new study in *Brassica rapa* shows that their combined effects on the genome are complex, with pollinator-mediated selection and genetic drift shaping evolutionary responses under warming.*

Earlier research by Florian Schiestl and colleagues showed that temperature stress alters plant traits and plant–pollinator interactions in *Brassica rapa* through phenotypic plasticity. A new study takes this work to the genomic level: How do increased temperature and different pollinator communities jointly shape evolutionary change in the plant genome?

The researchers built on a six-generation evolution experiment combining two temperature regimes—ambient and hot—with bumblebee, butterfly, mixed bumblebee–butterfly, and hand-pollinated control treatments. They performed whole-genome pool sequencing of the ancestral population and 16 experimentally evolved populations, allowing them to track changes in allele frequencies across the genome.

The results reveal no simple genomic response. No genomic region responded consistently across all treatments, or even within a single pollinator type across both temperatures. Warming amplified genome-wide divergence most strongly in bumblebee-pollinated lines, yet few individual loci in these lines crossed the statistical threshold for selection. The restricted pollination window in the bumblebee treatment reduced effective population size, allowing genetic drift to obscure locus-specific selection signals. Butterfly-pollinated lines showed strong phenotypic selection in companion work but little detectable genomic response, suggesting that adaptation may involve many small-effect loci or regulatory mechanisms. The clearest genomic selection signal emerged in the hot mixed-pollinator treatment, where a larger effective population size reduced the influence of genetic drift, allowing pollinator-mediated selection to become more readily detectable.

The study therefore shows that the genomic signature of adaptation depends not only on the strength of selection itself, but also on the demographic consequences of plant–pollinator interactions. Under warming, changes in pollinator behaviour and effective population size can determine whether adaptive evolution leaves a detectable signature in the genome.

Publication

Ding, Y. & Schiestl, F. P. (2026). Genomic responses to increased temperature and pollinator selection in *Brassica rapa* L. *New Phytologist*, 250(2), 1231–1247. <https://doi.org/10.1111/nph.70977>

Can wild plants evolve quickly enough to keep pace with climate change?



Jake Alexander · ETH Zurich

A new study from Jake Alexander's research group at ETH Zurich provides direct evidence that flowering times can evolve over just a few decades. By comparing plants grown from seeds collected 44 years apart, the researchers found that wild lettuce now flowers more than a week earlier, potentially helping it cope with increasingly warm and dry conditions.

Understanding how plants adapt to climate change is essential for predicting their future survival and distribution. Yet direct evidence of evolutionary responses in wild plant populations remains scarce. The researchers investigated *Lactuca serriola* (prickly lettuce) in Israel and the Golan Heights, comparing plants grown from historical seeds collected in 1976 with contemporary populations. This so-called resurrection experiment allowed them to observe evolutionary changes over 44 years of climate change. The results revealed that contemporary plants flowered more than seven days earlier than their historical counterparts. Earlier flowering was also observed under experimentally imposed drought conditions, suggesting that changes in flowering time may help plants complete their reproductive cycle before conditions become too hot and dry. However, comparisons between populations from different climatic regions produced a surprising result:

plants originating from wetter environments flowered earlier than those from drier locations.

This discrepancy challenges a common approach to predicting climate change responses, in which differences between populations across geographical climate gradients are used to anticipate how species will change over time. The study demonstrates that evolutionary responses to climate change can occur within decades, but cannot necessarily be predicted from present-day geographical patterns. The findings highlight the importance of long-term biological collections and experiments for understanding how wild plants adapt to a rapidly changing climate.

Publication

S. Van Deurs, S. Fior, A. Singer, E. Mayzlish-Gati, & J.M. Alexander (2026). Evolution of flowering phenology over 44 years of climate change. *Proc. Natl. Acad. Sci. U.S.A.* 123 (37) e2613665123, <https://doi.org/10.1073/pnas.2613665123>

A global view reveals why treelines do not simply follow warming



Sabine B. Rumpf · University of Basel

Mountain treelines are expected to shift uphill as the climate warms, making them an important indicator of ecological responses to climate change. A global analysis shows that treeline shifts are far from uniform, and are shaped not only by climate but also by fire, land use and other human influences.

Earlier research by Christian Körner and Erika Hiltbrunner showed that treelines in the Eastern Alps are advancing uphill but lag substantially behind the shift expected from climate warming. A new study involving Sabine Rumpf at the University of Basel takes the question to the global scale, examining how climate, land use and disturbance jointly shape treeline dynamics worldwide.

The study combines 30-metre-resolution satellite-derived canopy-height data with modelled estimates of climatically potential treeline position, comparing observed conditions in 2000 against 2020. This yields both the direction of treeline movement and the magnitude of its lag behind the position climate alone would predict. The lag metric

separates the question of whether treelines are shifting from the question of whether they move as fast, and in the direction, that warming alone would generate.

The global pattern is heterogeneous: 42% of analysed treelines shifted uphill, 25% shifted downhill and 34% remained stable. Even the uphill-shifting generally lagged behind the climatically expected position, so upward shifts are occurring, but more slowly than a pure climate-tracking model predicts. Fire disturbance emerged as a significant driver of downhill retreat, counteracting the expected warming-driven advance. Human land-use pressure showed a clear gradient effect: treelines under lower anthropogenic pressure shifted upward faster and showed smaller discrepancies between observed and climate-predicted positions, while treelines in intensively used areas showed the largest lags.

Treeline advance is therefore no direct climate-tracking proxy. Treeline position is co-determined by climate, disturbance regime, land abandonment, grazing pressure and other management legacies acting at the same time. In intensively used systems such as the European Alps, these factors can slow, reverse or entirely mask the signal that warming alone would produce. Elevational shift is therefore a poor direct proxy for climate-change response wherever land-use and disturbance history are not explicitly controlled for.

Publications

Körner, C. & Hiltbrunner, E. (2024). Rapid advance of climatic tree limits in the Eastern Alps explained by on-site temperatures. *Regional Environmental Change*, 24, 98. <https://doi.org/10.1007/s10113-024-02259-8>

Liang, T., Tian, F., Zou, L., Gravey, M. & Rumpf, S. B. (2026). Global elevational shifts and drivers of alpine treelines. *International Journal of Applied Earth Observation and Geoinformation*, 146, 105088. <https://doi.org/10.1016/j.jag.2026.105088>

No one-size-fits-all: how flower-rich gardens support urban pollinators



Marco Moretti · WSL &
Jaboury Ghazoul · ETH Zurich

Flower-rich gardens can help sustain pollinators in increasingly dense cities, but not all pollinators benefit in the same way. A study across private gardens in Zurich shows that the effects of floral diversity depend on pollinator traits, and points to more targeted approaches for designing urban green spaces.

Urban densification is widely assumed to erode pollination services, and flower-rich planting is a standard mitigation recommendation. Whether floral enrichment actually compensates for densification, and for which pollinators and plants, is rarely tested with a design capable of separating the two gradients. A new field experiment across 24 private gardens in Zurich does exactly that, placing four sentinel plant species along independent, orthogonal gradients of urban densification and local floral richness. The surrounding landscape context can therefore be disentangled statistically from the resource environment of the individual garden.

The study led by Marco Moretti at the Swiss Federal Institute for Forest, Snow and Landscape Research (WSL) and Jaboury Ghazoul at ETH Zurich recorded flower visitation rates, pollinator taxonomic and functional diversity, and reproductive success in the sentinel species. As expected, both pollinator visitation and diversity declined with increasing urbanisation and decreasing local floral richness. The response to floral enrichment itself was not uniform across pollinator functional groups. Small solitary bees and large social bees responded positively to increased floral diversity, while hoverflies, beetles and small social bees showed weaker or qualitatively different responses. Floral enrichment therefore compensated for urbanisation-driven declines only for those sentinel plant species that depend on the pollinator groups responsive to floral diversity, not across all plant–pollinator combinations tested. That challenges the assumption behind uniform garden-based interventions: that more floral diversity benefits the pollinator community as an undifferentiated whole. Outcomes instead depend on functional traits, on body size, sociality and specialisation, which determine which groups can exploit a given increase in floral resources. A garden optimised for bee visitation will not deliver equivalent gains for hoverfly- or beetle-mediated pollination.

Publication

Reji Chacko, M., Frey, D. J., Albrecht, M., Ghazoul, J. & Moretti, M. (2026). No one-size-fits-all: Trait-dependent effects of local plant diversity on pollinators and pollination service in a densifying city. *Journal of Applied Ecology*, 63, e70384. <https://doi.org/10.1111/1365-2664.70384>

Legacy effects of land use on tropical soils: Constraints on forest restoration success in Uganda



Matthew Cooper &
Sebastian Doetterl · ETH Zurich

Planting trees does not necessarily restore the soils and ecosystem functions lost through previous land use. Research in tropical East Africa shows that soil carbon recovery can lag behind vegetation regrowth and that land-use patterns strongly influence erosion, which makes belowground processes central to forest restoration and land management.

Historical land use leaves measurable, long-lasting signatures in tropical soils, and these can constrain the outcome of reforestation long after tree planting begins. Matthew Cooper, former PSC RESPONSE fellow supervised by Sebastian Doetterl examined how past forest clearing and encroachment in Uganda altered soil carbon, nutrient status, fertility and water-holding capacity, and how these legacies shape carbon sequestration, structural recovery and arboreal biodiversity. Reforestation success cannot be predicted from tree cover alone: the condition of the soil beneath it is an independent constraint. The researchers reported that vegetation recovery and soil carbon recovery follow decoupled trajectories in reforested tropical montane ecosystems, with mineral-associated stabilisation processes governing the pace of belowground carbon accumulation independently of aboveground biomass gain. The result supports depth-resolved, process-oriented soil analysis as a standard component of restoration assessment.

A second study, published in *Scientific Reports*, extends the question to erosion. Using UAV monitoring across more than 800 smallholder fields in eastern DR Congo and western Uganda, the researchers found that rill erosion is frequent during the rainy season but spatially highly localised by the patchy field structure characteristic of smallholder landscapes. This patchiness limits hydrological and sediment connectivity, so land consolidation or agricultural intensification could raise erosion risk unless soil-conservation measures are built in from the outset.

Forest recovery, soil carbon stabilisation and erosion dynamics are coupled processes in the same landscapes, following different rates and drivers. Restoration planning therefore needs a landscape-scale view of soil alongside canopy recovery.

Publications

Cooper, M., Bauters, M., Riemer, K., van Goor, W., Mugenyi, K., Summerauer, L., Cook, J., Kigenyi, R. & Doetterl, S. (2026). Decoupled recovery of soil and vegetation carbon reveals mineral-driven stabilisation in reforested tropical montane ecosystems. *EGU General Assembly 2026*, Vienna, Austria, EGU26-20803. <https://doi.org/10.5194/egusphere-egu26-20803>

Wilken, F., Fiener, P., Batista, P. V. G., Cooper, M., Haist, J., Muhindo, D., van Oost, K., Rueegg, M. & Doetterl, S. (2026). Rill erosion dynamics in smallholder farming systems of wet tropical Africa. *Scientific Reports*, 16, 15863. <https://doi.org/10.1038/s41598-026-50821-7>

Why Europe's biodiversity monitoring falls short of policy needs



Alejandra Morán Ordóñez · University of Basel

Effective biodiversity policy depends not only on collecting more data, but on turning existing monitoring into reliable and comparable evidence. A study identifies the main gaps in Europe's biodiversity monitoring system and shows what would make it more useful for environmental policy and decision-making.

Environmental policy increasingly depends on standardised biodiversity indicators, yet Europe's monitoring infrastructure was largely built before such standardisation was a design requirement. A new study led by Alejandra Morán Ordóñez asks whether existing coordinated programmes can deliver what policy frameworks demand. The authors assessed 17 coordinated European monitoring programmes against the 84 Essential Biodiversity Variables (EBVs) defined by the EuropaBON initiative. The evaluation went beyond data availability. It examined whether programmes' variable definitions align with EBV specifications, whether taxonomic and spatial-temporal

coverage is adequate, whether raw and derived datasets are accessible, and whether analytical pipelines are automated enough to support repeated, reproducible indicator production.

The study identifies four major, interconnected barriers that limit the capacity of existing European monitoring programmes to generate Essential Biodiversity Variables (EBVs) suitable for environmental policy reporting. First, a mismatch between monitoring outputs and EBV specifications: although programmes already collect substantial biodiversity data, their outputs frequently fail to meet the required taxonomic scope, spatial resolution or temporal frequency. Second, gaps in monitoring coverage: several taxonomic groups, including freshwater zooplankton, lichens, terrestrial arthropods and crop pests, lack coordinated European-scale monitoring, while marine biodiversity data remain fragmented across regional programmes with inconsistent protocols. Third, restricted data accessibility: limited access to raw biodiversity observations, together with insufficiently shared analytical code and models, constrains data integration, reproducibility and reuse. Fourth, insufficient automation: many programmes still rely on partially manual workflows for data processing, harmonisation and analysis, limiting their capacity to produce regularly updated EBVs. Together, these findings demonstrate that the availability of biodiversity observations alone is insufficient; their effective use in policy reporting also depends on harmonised standards, accessible data and reproducible, automated analytical workflows.

Publication

Morán-Ordóñez, A., Blasi, M., Santana, J. et al. (2026). Europe's bottlenecks to the operationalisation of Essential Biodiversity Variables for Environmental Policy Support. *npj Biodiversity*. <https://doi.org/10.1038/s44185-026-00147-4>

Safeguarding Amazonia's biocultural heritage



Rodrigo Cámara-Leret &
Jordi Bascompte · University of Zurich

The Amazon is home not only to extraordinary biodiversity but also to generations of Indigenous knowledge about plants. Both are deeply interconnected and increasingly under threat. A new study reveals where climate change and the loss of Indigenous knowledge could jointly erode this biocultural heritage, and identifies priority areas for its conservation.

Amazonia harbours extraordinary biological diversity, and an equally remarkable diversity of Indigenous knowledge about plants. These two forms of diversity have evolved together over millennia, yet both are increasingly threatened by climate change and rapid cultural transformation. A new study led by Rodrigo Cámara-Leret and Jordi Bascompte provides the first basin-wide assessment of how global environmental change may erode Amazonian biodiversity and the traditional knowledge associated with it at the same time.

The researchers assembled a database integrating more than 700 ethnobotanical sources published over five centuries, documenting the uses of 5,796 native Amazonian plant species by more than 400 Indigenous groups. The dataset was combined with species distribution models and projections of future climate, to identify where biologically important species and the cultural knowledge linked to them are most at risk.

Indigenous peoples currently use almost one third of all known Amazonian plant species, an exceptional contribution of traditional knowledge to understanding and managing tropical biodiversity. Projected climate-driven shifts in species distributions, together with the continuing loss of Indigenous languages and knowledge systems, threaten to disrupt this long-standing relationship between people and plants. The study identifies geographic hotspots where biological and cultural losses are expected to overlap, an evidence-based framework for prioritising conservation efforts that protect both.

Combining ecology, ethnobotany and biogeography at this scale, the work shows that conserving Amazonian ecosystems cannot be separated from safeguarding the cultural traditions that sustain knowledge of their plant diversity. The publicly available database is also an important resource for future research. Turning such priorities into conservation action requires governance mechanisms that reach the people managing land and commodity production.

Publication

Cámara-Leret, R., Roehrdanz, P. R. & Bascompte, J. (2026). The forest of knowledge under global change. *Nature* 655, 1212–1216. <https://doi.org/10.1038/s41586-026-10741-y>

Why zero-deforestation commitments are missing many smallholder farmers



Janina Grabs · University of Basel &
Rachael D. Garrett · University of Cambridge

Over the past decade, voluntary zero-deforestation commitments have become a central component of corporate sustainability strategies in global agricultural supply chains. These initiatives have encouraged companies to reduce forest conversion, but their effectiveness depends on whether they reach the millions of smallholder farmers who supply international markets.

A new study led by ETH Zurich PhD Adelina Chandra and including Janina Grabs at the Faculty of Humanities and Social Sciences at the University of Basel and former PSC member Rachael D. Garrett examines how these commitments are implemented in Indonesia's oil palm sector, and identifies the gaps between corporate ambitions and conditions on the ground.

The researchers combined survey data from 1,541 smallholder oil palm farms, interviews with supply-chain actors and spatial analyses, to investigate how zero-deforestation commitments influence farmers' market access, production practices and participation in sustainable supply chains. The study assessed both independent and scheme

smallholders across different production regions, one of the most comprehensive evaluations of corporate sustainability commitments at farm level.

Zero-deforestation commitments currently reach only a limited proportion of Indonesian smallholders. "Participation in supply chains by committed actors depends largely on geographic location and existing supply-chain connections, not on farmers' willingness to adopt more sustainable practices. Independent producers in particular receive little technical support, few economic incentives and limited information about corporate sustainability requirements. While the study found little active exclusion of farmers from markets governed by voluntary zero-deforestation standards, the lack of outreach and ZDC implementation to date raises concerns regarding the ability of smallholder farmers to fulfill mandatory zero-deforestation requirements such as the EU Deforestation Regulation."

Voluntary corporate commitments alone are unlikely to achieve broad landscape-scale conservation unless accompanied by stronger public policies, improved traceability and targeted support for smallholder inclusion. In highlighting the social dimensions of environmental governance, the study provides evidence for designing sustainability initiatives that are both environmentally effective and socially equitable.

Publication

Chandra, A., Grabs, J., Meemken, E.-M., Hidayat, N. K., Dharmawan, A. H., Mardiyarningsih, D. I. & Garrett, R. D. (2026). Limited reach of zero-deforestation commitments to Indonesian oil palm smallholders. *Nature Sustainability* 9, 1338–1351. <https://doi.org/10.1038/s41893-026-01861-4>

Tracking the true cost of Brazil's soybean–chicken value chains



Johanna Jacobi · ETH Zurich

Brazil's soybean and poultry industries are deeply interconnected and supply both domestic and global food markets, which makes their combined environmental footprint an important sustainability challenge. A new study compares conventional and organic soybean–chicken systems across the entire value chain, revealing where environmental impacts arise.

Brazil's agro-industrial soybean and poultry sectors feed a global shift toward animal-rich diets. The environmental footprint of the full value chain, from soybean cultivation through feed, farming, slaughter and distribution to local and international markets, has rarely been assessed as a single connected system. A new study led by Johanna Jacobi's group compares conventional and organic soybean–chicken production systems across their entire life cycle.

Using a regionalised life cycle assessment, the authors traced the ecological footprint of soybean and poultry products from cultivation in Paraná and São Paulo states through four value-chain stages, feed production, chicken farming, slaughter, and supply to local versus global markets, for both eggs and meat. The analysis is deliberately end-to-end: it follows the product to the point of final supply, capturing costs that stop at the farm gate in most sustainability assessments. While the sustainability results were mixed, organic value chains showed the lowest impacts on climate change, ecotoxicity and biodiversity loss.

The result with the clearest practical implication concerns transport. Shipping chicken meat from western Paraná to global markets accounted for up to 30% of the product's total carbon footprint. A share large enough to rival production-stage impacts and one that is typically invisible in farm-level accounting. The researchers argue this points toward strengthening local supply chains as a concrete lever for reducing the sector's footprint, alongside its potential to close nutrient loops regionally. They also flag a gap for future work: standard life cycle assessment, including this one, still omits animal welfare, meat quality and social outcomes.

Publication

Malembaka, R. B., Pfister, S., Torres, B. F. & Jacobi, J. (2026). Environmental sustainability of soybean–chicken systems: productions, local and global value chains analysis from Paraná and São Paulo states, Brazil. *Environmental Research: Food Systems*, 3(1), 015007. <https://doi.org/10.1088/2976-601X/ae41c4>

Publication

Hofmann, B., Fischer, M., Ingold, K., Lieberherr, E. & Hoffmann, S. (2025). Knowledge cumulation at science-policy interfaces: opportunities for environmental governance research. *Environmental Policy and Governance*, 35(3), 538–546. <https://doi.org/10.1002/eet.2155>

Rethinking where knowledge accumulates in environmental governance



Eva Lieberherr · ETH Zurich

How scientific knowledge accumulates is usually assessed through publications and academic debate. A new perspective challenges this view, arguing that knowledge in environmental governance also advances at science–policy interfaces, where research is integrated, tested against real-world problems and synthesised for decision-making.

Environmental governance research is often criticised for growing without becoming more coherent: findings accumulate, but rarely build systematically on one another. A new perspective paper co-authored by Eva Lieberherr argues that this concern overlooks a critical site of knowledge cumulation, one that unfolds not within academia but at the interfaces where science, policy and practice meet. Drawing on the science–policy literature and on their own experience in Sinergia projects on pesticide governance and ecosystem resilience, the authors identify five opportunities for cumulating knowledge at science–policy interfaces (SPIs): 1) proximity to democratic discourse and decision-making, as illustrated by citizens' assemblies deliberating food policy; 2) suitability for inter- and transdisciplinary integration; 3) a combined focus on problems and solutions; 4) the potential to increase the generality of scientific findings by testing them against real governance contexts; and 5) the creation of targeted synthesis products aimed directly at decision-makers. Each is illustrated with empirical examples from governance debates on climate change, biodiversity, natural resources and food systems.

Science–policy interfaces should therefore be recognised as a legitimate and complementary locus of knowledge cumulation. By integrating research, testing it against real governance contexts and producing targeted syntheses, these interfaces help environmental evidence become usable knowledge for policy and practice.

CONNECT — From genes to plant architecture

How does genetic information become plant form and function? Across these studies, epigenomic states, protein interactions, genome architecture and imaging technologies provide complementary views of how plants organise, regulate and interpret their genomes.



Epigenomic profiling from minimal plant material



Sara Simonini · University of Zurich

Mapping chromatin states shows where epigenetic regulation is encoded. A new method gives plant developmental genetics a cost-effective approach for examining chromatin states in scarce tissues and at developmental stages that were previously difficult to analyse genome-wide.

Understanding how chromatin regulates gene expression requires methods capable of mapping histone modifications across the genome. Conventional chromatin immunoprecipitation followed by sequencing (ChIP-seq) generally requires substantial quantities of tissue and provides limited resolution in rare plant cell populations. Yixuan Fu, Marc W. Schmid and Sara Simonini have now adapted the high sensitive Cleavage Under Targets and Tagmentation (CUT&Tag) method for high-resolution epigenomic profiling in *Arabidopsis thaliana*.

CUT&Tag uses an antibody-targeted transposase to cleave DNA directly next to a selected chromatin feature and simultaneously introduce sequencing adapters. Unlike ChIP-seq, it generates a high signal-to-background ratio from substantially less starting material.

The researchers profiled three histone modifications, H3K27me₃, H3K4me₃ and H3K27ac, from approximately 0.01 grams of *Arabidopsis* seedlings. CUT&Tag reproduced the broad chromatin patterns detected by established approaches while resolving features at close to single-nucleosome scale. That resolution revealed genomic patterns less apparent with ChIP-seq, including enrichment of H3K27me₃ within exons and the epigenetic state of the first nucleosome downstream of transcription start sites. The protocol can be transferred to other model and non-model plant species. Its low tissue requirement is particularly relevant for reproductive structures such as ovules, gametes and developing seeds, where the limited number of cells has long constrained epigenomic analysis.

Publication

Fu, Y., Schmid, M. W. & Simonini, S. (2026). CUT&Tag for High-Resolution Epigenomic Profiling From a Low Amount of *Arabidopsis* Tissue. *Plant Direct*, 10, e70161. <https://doi.org/10.1002/pld3.70161>

A streamlined method for mapping plant chromatin interaction networks



Nicole Corina Härter &
Sylvain Bischof · University of Zurich

*Understanding how plants regulate gene activity requires knowing not only which proteins are involved, but how they interact on chromatin. A new optimised workflow makes it faster and more reliable to identify these protein complexes in *Arabidopsis thaliana*, a practical tool for research into epigenetic regulation, genome stability and plant development.*

Chromatin-associated proteins rarely act alone. By identifying the complexes they form is essential for understanding how epigenetic regulation controls gene activity, genome stability and plant development. A methodological publication from Alberto Linares, former RESPONSE fellow, supervised by Nicole Corina Härter and Sylvain Bischof, presents an optimised workflow for resolving such interaction networks in *Arabidopsis thaliana*.

The protocol combines immunoprecipitation of nuclear chromatin-linked proteins with mass spectrometry (IP-MS). Unlike conventional workflows, it does not require a separate, time-consuming isolation of nuclei: optimised extraction conditions give rapid access to chromatin-associated protein complexes. An enzymatic DNA-digestion step further reduces non-specific associations between proteins bound independently to the same DNA region, improving the specificity of the resulting interaction profiles. Candidate partners identified by mass spectrometry can then be validated by co-immunoprecipitation.

The approach produces high-quality eluates while simplifying sample preparation, and is particularly relevant for investigations of chromatin remodelling, histone-variant deposition and the molecular complexes governing transcriptional or transposable-element regulation. It makes a technically demanding component of plant chromatin biology more accessible and reproducible.

Publication

Linares, A., Härter, N. C., Rannou, E. & Bischof, S. (2025). Identification of plant chromatin interaction networks using IP-MS and co-IP. In C. Baroux & C. Tatout (eds), *Methods for Plant Nucleus and Chromatin Studies. Methods in Molecular Biology*, 2873, 129–143. https://doi.org/10.1007/978-1-0716-4228-3_8

How new polyploid plants build an evolutionary identity



Rie Shimizu-Inatsugi &
Kentaro K. Shimizu · University of Zurich

Understanding how new plant species emerge is fundamental to explaining the diversity and adaptability of plants. A new study closes an important knowledge gap about the earliest stages of polyploid evolution, showing how genetic inheritance and environmental conditions interact from the beginning of a new evolutionary lineage.

Whole-genome duplication has repeatedly shaped plant evolution. It can create polyploids, plants carrying more than two complete sets of chromosomes, and provide the genetic diversity from which new species may emerge. The changes occurring during the first generations after polyploidisation have remained difficult to observe. A research team led by Rie Shimizu-Inatsugi and Kentaro K. Shimizu investigated these early changes in *Arabidopsis kamchatica*, an allotetraploid species that originated from the combination of the genomes of *Arabidopsis halleri* and *Arabidopsis lyrata*. The researchers assembled genomes of the two progenitor species and compared artificially re-synthesised *A. kamchatica* plants with established natural tetraploids. They then examined changes in DNA methylation and gene expression across successive generations and under two environmental conditions.

The most extensive DNA methylation changes occurred immediately after allopolyploidisation, while subsequent generations showed smaller modifications. The newly formed polyploids also followed two contrasting trajectories. Across generations, their methylation patterns moved closer to those of natural *A. kamchatica*, showing evolutionary convergence. Descendants grown under different conditions, however, showed distinct patterns, revealing environmentally associated divergence.

Polyploidisation therefore does not lead to a single, fixed epigenetic outcome. The combination of two parental genomes initiates rapid regulatory reorganisation, while environmental conditions add further diversification.

Publication

Milosavljevic, S., Copetti, D., Yip Tong, K. et al. (2026). Convergence and divergence of DNA methylation and gene expression patterns in neopolyploid *Arabidopsis kamchatica*. *Nature Communications*, 17, 8419. <https://doi.org/10.1038/s41467-026-75042-4>

Liverwort genomes reveal an early stage of sex chromosome evolution



Péter Szövényi · University of Zurich

Sex chromosomes can evolve along very different trajectories, from nearly identical chromosome pairs to highly differentiated forms. A new chromosome-level genome study of a liverwort reveals how ancient non-recombining regions coexist with large recombining regions, providing new clues to the transition between homomorphic and heteromorphic sex chromosomes.

Sex chromosomes originate from autosomes, with recombination typically suppressed around the loci controlling sex. In diploid XY or ZW systems, asymmetric recombination can drive one chromosome towards degeneration and morphological difference. *Bryophytes* work differently: sex is expressed in the haploid gametophyte, females carrying a U chromosome and males a V chromosome. Because both are directly exposed to selection, theory predicts they may keep similar morphology for long evolutionary periods. Yet liverworts contain both strongly heteromorphic and apparently homomorphic UV systems, and how the two relate is unresolved.

A study led by Péter Szövényi now gives the first chromosome-level characterisation of homomorphic UV sex chromosomes in a liverwort. The team assembled male and female genomes of *Blasia pusilla* from PacBio and Oxford Nanopore long reads with Hi-C scaffolding, spanning approximately 377 Mb in the male and 390 Mb in the female. The male genome resolves into nine chromosome-scale scaffolds; the female assembly, scaffolded against the male, is less contiguous, with 14.

Chromosome nine has a sharp internal organisation. Approximately two-thirds of it, 21.4 Mb, forms a

pseudoautosomal region (PAR) in which the male and female chromosomes retain extensive synteny and low sequence divergence. The terminal 8.6 Mb forms a non-recombining sex-determining region (SDR), with lower gene density, increased structural divergence and strong accumulation of Copia and Gypsy retrotransposons. Male and female SDRs show much greater synonymous divergence than the PAR, independent evidence for long-term recombination suppression.

Comparison with *Marchantia polymorpha* adds a time dimension. The *B. pusilla* SDR contains homologues of the gametologs found on the highly heteromorphic U and V chromosomes of *M. polymorpha*, and several male–female gene pairs diverged before the two species separated, so part of the region is ancient. Other genes were incorporated more recently: the SDR is not static, but has gathered sex-linked content in several waves. Orthologues of the core regulators BPCU and BPCV are retained within the U and V SDRs respectively.

This architecture suggests a route from homomorphic to heteromorphic UV chromosomes: a large recombining PAR around a smaller ancestral SDR may be an early state within *Marchantiidae*, and losing the PAR would then generate the compact, strongly differentiated sex chromosomes seen in *Marchantia*. An alternative remains open, fusion between an ancestral micro-sex chromosome and an autosome, and further genomes will be needed to tell the two apart.

Publication

Yue, Y., Sablok, G., He, X., Hyvönen, J., Dong, S., Potente, G., Liu, Y. & Szövényi, P. (2026). Genome assemblies of the liverwort *Blasia pusilla* uncover a well-defined pseudoautosomal region on homomorphic UV sex chromosomes. *Genome Biology*, 27, 166. <https://doi.org/10.1186/s13059-026-04101-2>

How chloroplasts built a new RNA-splicing machinery



Samuel Zeeman &
Barbara Pfister · ETH Zurich

Chloroplasts depend on an RNA-splicing machinery inherited from a bacterium, but how it evolved to function in plants has remained unclear. A new study reveals that the chloroplast splicing factor MatK operates as part of a protein complex, and shows how an ancestral metabolic enzyme was repurposed to support this essential process.

Chloroplast genomes retain around 20 introns, most descended from mobile bacterial group II ribozymes. In bacteria these introns are largely self-catalytic, but depend on intron-encoded maturases that bind their own RNA with high specificity. Plant chloroplasts followed a different route: only the *trnK* intron retains a maturase gene, *matK*, yet its protein product MatK acts on seven distinct group IIA introns. How it became a broader plastidial splicing factor has remained unresolved. Yuanyuan Liang, former RESPONSE fellow, supervised by Barbara Pfister in the lab of Samuel Zeeman, now identifies and characterizes a hetero-multimeric complex centered on MatK.

Co-immunoprecipitation and mass spectrometry in *Arabidopsis thaliana* and transplastomic tobacco revealed three essential plastid-targeted partners: MKIP1, the putative valyl-tRNA synthetase ValRS2 and the plastid-development factor EMB3120. The strongest evidence concerns MKIP1, previously annotated as BRANCHING ENZYME1 for its homology to enzymes that introduce α -1,6 linkages during starch biosynthesis. Phylogenetic and biochemical analyses overturn that annotation. MKIP1's catalytic centre has extensively diverged, and orthologues from diverse land plants and a streptophyte alga all lacked glucan-branching activity, so the loss predates land plants. MKIP1 has instead acquired an approximately 150-amino-acid insertion, essential in planta, which together with a repurposed carbohydrate-binding module forms an interaction surface for the N-terminal region of MatK. RNA immunoprecipitation and sequencing showed that MKIP1 associates *in vivo* with all known MatK-targeted group IIA introns. Depleting MKIP1 in developing leaves, using

inducible artificial microRNAs, caused chlorosis and severe reductions in the splicing of multiple group II introns. MatK abundance was largely unchanged, so MKIP1 is directly required for MatK-dependent splicing. These findings raise the question of why MatK now operates within a complex rather than on its own, as its bacterial ancestors did. MatK has lost much of the N-terminal reverse transcriptase architecture that gives bacterial maturases their sequence-specific RNA binding properties. Instead, the N-terminus of MatK has become a hub for protein-protein interactions. Plastidial splicing may therefore have evolved through the assembly of new protein-assisted machinery around an ancestral maturase, and complex formation may now enable MatK to interact more diversely with different intron RNAs. Future work will address the roles of the other complex components, EMB3120 and ValRS2, and how the MatK complex recognises its intron targets and helps their splicing.

Publication

Liang, Y., Gao, Y., Fontana, A., Abt, M., Giegler, A., Gehring, M., Liu, C., Sharma, M., Zoschke, R., Zeeman, S. C. & Pfister, B. (2026). Maturase K forms a plastidial splicing complex with a neofunctionalized branching enzyme. *Nature Communications*, 17, 4341. <https://doi.org/10.1038/s41467-026-70734-3>

Sharper vision for cellular architecture: A new algorithm for cryo-electron tomography



Benjamin D. Engel · University of Basel

Cutting-edge microscopy increasingly depends on equally sophisticated computational methods to turn noisy measurements into high-resolution views of cellular structures. A new algorithm for cryo-electron tomography combines advances in imaging theory and self-supervised deep learning to produce faster, higher-fidelity 3D reconstructions of cells in their near-native state.

Cryo-electron tomography (cryo-ET) is the method of choice for visualising cellular architecture in its near-native state, but reconstructing usable 3D volumes from the raw data remains technically demanding. The signal-to-noise ratio is very low, and the geometry of data acquisition leaves a "missing wedge" of unsampled angles that systematically degrades reconstruction quality. Existing deep-learning approaches to denoising and artefact correction have improved on earlier iterative methods, but their performance still falls short of what the technique's native resolution should allow. A new collaboration between Benjamin Engel's group at Biozentrum Basel, Ivan Dokmanic at the Department of Mathematics and Computer Science at the University of Basel, and mathematicians at INSA Lyon working on imaging theory addresses this gap.

The resulting method, Icecream, builds on the self-supervised learning approach used by prior tools but changes how the algorithm handles symmetry in the data, drawing on the recently developed equivariant imaging framework. Combined with engineering refinements including mixed-precision arithmetic, this produces measurably better denoising and more reliable recovery of information in the missing-wedge region, while reducing both training and inference time relative to comparable methods such as CryoCARE, IsoNet and DeepDeWedge. Across a range of experimental datasets, the improvements were quantified using Fourier shell correlation, a standard metric for reconstruction fidelity in cryo-EM.

As cryo-ET moves toward routine use for resolving macromolecular architecture directly inside cells, computational reconstruction is becoming as central to what the technique can reveal as the microscopy itself.

Publications

Kishore, V., Debarnot, V., Righetto, R. D., Engel, B. D. & Dokmanić, I. (2026). ICECREAM: high-fidelity equivariant cryo-electron tomography. *Acta Crystallographica Section D: Structural Biology*, 82, 295–313. <https://doi.org/10.1107/S2059798326001622>

Lamm et al., 2026. MemBrain v2: an end-to-end tool for the analysis of membranes in cryo-electron tomography. *Nature Methods*. <https://doi.org/10.1038/s41592-026-03178-8>

More about MemBrain v2: The freely available software finds membranes, locates specific membrane proteins and analyzes how these are spatially arranged, showing how cellular processes are organized at the molecular level.

<https://www.biozentrum.unibas.ch/news/detail/weeks-of-work-in-a-few-hours-ai-tool-reads-cell-membranes>

Software: <https://github.com/CellArchLab/MemBrain-v2>

CONNECT — Resilience

Resilience takes different forms across biological scales. How do plants recognise pathogens and coordinate immunity and defence, how do metabolic exchanges determine whether plant-associated microbial communities coexist or oscillate, and how can crops limit yield losses after disturbance? Research across PSC groups connects molecular recognition, signalling, population dynamics and crop metabolism.



A molecular decoy reveals how WTK4 detects wheat powdery mildew



Javier Sánchez-Martín &
Beat Keller · University of Zurich

Plants rely on sophisticated immune mechanisms to recognise pathogens and defend themselves against disease. New research reveals how a poorly understood class of immune receptors detects fungal pathogens, with insights that could contribute to more durable disease resistance in crops.

Tandem kinase proteins (TKPs) are an important but still poorly understood class of immune receptors in cereal crops. Unlike the well-characterised nucleotide-binding leucine-rich repeat (NLR) family, the pathogen effectors recognised by TKPs remain largely unidentified, limiting our mechanistic understanding of TKP-mediated resistance and our ability to assess its potential durability. Research by Javier Sánchez-Martín and Beat Keller showed that the kinase-fusion resistance protein Pm4 recognises one powdery mildew effector, AvrPm4, while another fungal protein suppresses the resulting immune response. A new study extends these insights into kinase-mediated immunity to the tandem kinase *WTK4*, which confers resistance to wheat powdery mildew in the wild wheat relative *Aegilops tauschii*. Combining bi-parental genetic mapping with UV mutagenesis of *Blumeria graminis* f. sp. *tritici* isolates, the researchers identified *AvrWTK4*, an RNase-like effector gene, as the target of *WTK4*-mediated recognition. Loss-of-function mutations in *AvrWTK4*, or reduced expression of the gene, were sufficient to confer virulence: the fungus escapes detection not by evolving a structurally divergent effector, but by disabling or downregulating the one *WTK4* already recognises. Conversely, transient expression of the avirulent form of *AvrWTK4* in *Aegilops tauschii* protoplasts carrying *WTK4* specifically triggered a hypersensitive cell-death response, direct functional evidence that the receptor detects this fungal protein.

Biochemical assays clarified how recognition occurs. The avirulent *AvrWTK4* variant bound the N-terminal heavy metal-associated (HMA)-like domain of *WTK4* more

strongly than the virulent variant did, establishing an allele-specific correlation between binding affinity and recognition outcome. The integrated HMA-like domain therefore likely functions as an effector-binding decoy, mimicking the effector's genuine host target to bait direct binding and trigger immune activation. The same strategy has already been documented for the related TKP *RWT4*, which suggests that integrated domains may be a recurring solution among tandem kinase receptors rather than a mechanism specific to *WTK4*.

Integrated domains therefore become potential targets for receptor engineering, although their capacity to broaden or stabilise resistance in the field still requires validation in crop plants.

Publication

Bernasconi, Z., Stirnemann, U., Xu, Y., Herger, A. G., Chen, R., Widrig, V., Heuberger, M., Lettieri, M., Müller, M. C., Wulff, B. B. H., Wicker, T., Keller, B. & Sánchez-Martín, J. (2026). An HMA-like integrated domain in the wheat tandem kinase *WTK4* recognises an RNase-like pathogen effector. *Nature Communications*, 17, 8458. <https://doi.org/10.1038/s41467-026-74940-x>

New insights into plant immune recognition and signalling



Cyril Zipfel · University of Zurich

Plant immunity begins with the recognition of pathogens at the cell surface, but effective defence requires these signals to be amplified and coordinated across tissues. A series of studies reveals how plants can broaden pathogen recognition, and identifies changes in extracellular pH as a key mechanism linking immune perception to signalling and defence priming.

Recent research by former PSC fellow Songyuan Zhang and Cyril Zipfel showed how plant immune responses unfold from initial detection to coordinated defence. Focusing on the cell-surface receptor FLAGELLIN SENSING 2 (FLS2), which detects the bacterial peptide flg22. The team reverse-engineered natural FLS2 variants able to recognise flg22 sequences that evade other receptors. Two routes towards broader recognition emerged: strengthening direct interactions between FLS2 and

altered flg22 epitopes, and enhancing recruitment of the co-receptor BAK1 when pathogen-derived peptides act as weak or antagonistic ligands.

Two publications in 2026 move downstream of recognition, to a response that has accompanied studies of plant immunity for decades: the rapid alkalinisation of the extracellular space after receptor activation. In *Molecular Cell*, Keran Zhai and colleagues used several receptor–ligand systems, including FLS2–flg22, EFR–elf18 and MIK2–SCOOP18, to show that alkalinisation is no secondary consequence of immune signalling. It forms part of a conserved circuit linking activated receptor kinases to plasma-membrane H⁺-ATPases. The receptor-like cytoplasmic kinase BIK1 sits at the centre of that circuit. Downstream of activated receptors it phosphorylates GENERAL REGULATORY FACTOR proteins, disrupting their association with autoinhibited H⁺-ATPases. Reduced proton-pump activity limits H⁺ export and raises extracellular pH, and that shift feeds back on receptor signalling itself, contributing both to immune responses and to signalling initiated by cell-wall damage.

A study in *Cell* extends the mechanism to communication between tissues. Hongze Wang and colleagues found that infection with *Pseudomonas syringae* raises apoplastic pH not only at infected sites but in neighbouring, uninfected tissues of *Arabidopsis*, where calcium-dependent protein kinases phosphorylate two major H⁺-ATPases, reducing their activity and promoting the pH increase. Plant elicitor peptides (Peps), serine-rich endogenous peptides (SCOOPs) and their receptors are transcriptionally activated, while alkaline conditions make tissues more sensitive to these immune peptides, which in turn promote further alkalinisation and disease resistance, a mutually reinforcing network. The extracellular environment is therefore not simply transmitting an alarm: it is remodelled to prime surrounding tissues for stronger defence. With receptor engineering, that points towards crops which detect more pathogens and mount more durable responses.

Publications

Zhang, S., Liu, S., Lai, H.-F., Bender, K. W., Kim, G., Caflisch, A. & Zipfel, C. (2025). Reverse engineering of the pattern recognition receptor FLS2 reveals key design principles of broader recognition spectra against evading flg22 epitopes. *Nature Plants*, 11, 1642–1657. <https://doi.org/10.1038/s41477-025-02050-5>

Zhai, K., Derbyshire, P., Zhang, S., Choi, S., Wang, L., Song, B., Kinoshita, T., Zhou, J.-M., Menke, F. L. H., Bender, K. W. & Zipfel, C. (2026). A phosphorelay circuit drives extracellular alkalinization in receptor kinase-mediated immune and cell-wall damage signaling. *Molecular Cell*, 86, 1797–1814.e9. <https://doi.org/10.1016/j.molcel.2026.03.035>

Wang, H., Li, X., Zhai, K., Rhodes, J., Sang, T., Zhao, J., Gao, Y., Ma, S., Song, B., Pan, Q., Hu, M., Xin, P., Chu, J., Wang, P., Zipfel, C. & Zhou, J.-M. (2026). A regulatory network promotes apoplastic alkalinization to prime plant immunity in tissues distal to site of infection. *Cell*, 189, 1389–1406.e19. <https://doi.org/10.1016/j.cell.2026.01.027>

Metabolic feedbacks shape the hidden dynamics of leaf bacteria



Julia A. Vorholt &
Roman Stocker · ETH Zurich

Leaves host diverse bacterial communities whose members continually exchange nutrients and metabolic by-products. These interactions help determine which microorganisms persist, which disappear and how the community functions. Predicting how individual chemical exchanges translate into the behaviour of microbial population has remained a major challenge.

An interdisciplinary team led by the groups of Julia Vorholt at the Department of Biology and Roman Stocker at the Department of Civil, Environmental and Geomatic Engineering at ETH Zurich has now linked specific metabolic exchanges to distinct ecological outcomes among leaf-associated bacteria.

The researchers studied bacteria that degrade plant-derived oligosaccharides. To observe their interactions directly, they developed a microfluidic system containing microscopic channels in which individual bacterial cells could be monitored while the metabolites released into their environment were measured quantitatively. Different bacterial recipients depended on different combinations of shared resources. Some benefited from carbon compounds released by neighbouring bacteria, while others required vitamins. These exchanges created feedback loops in which the growth of one population changed the environment and altered the growth of its partner.

Depending on the metabolites involved and the quantities exchanged, the interactions produced different ecological outcomes. One bacterial strain could outcompete another, both populations could reach a stable coexistence, or their abundance could repeatedly rise and fall in oscillating cycles. The team combined these observations with computational metabolic modelling. The models reproduced the observed population dynamics and predicted how changes in individual metabolic mediators could shift a community from one outcome to another, predictions that were then tested experimentally.

The study connects molecular interaction mechanisms with the population-level behaviour of environmental

microorganisms, and could help design synthetic microbial communities with more stable and predictable properties, including communities intended to support plant health.

Publication

Pacheco, A. R., Ugolini, G. S., Rüdiger, S. H. et al. (2026). Metabolic feedbacks drive population dynamics and can lead to oscillations among leaf bacteria. *Nature Communications*, 17, 6983. <https://doi.org/10.1038/s41467-026-73686-w>

Cassava's hidden amylase: A target for reducing post-pruning starch loss



Samuel Zeeman · ETH Zurich

Cassava is a major staple crop in sub-Saharan Africa, but stress and common farming practices such as shoot pruning can trigger the breakdown of starch stored in its roots, reducing yield and quality. A new study identifies a key enzyme responsible for this starch loss and shows that suppressing it preserves root starch without impairing the plant's ability to regrow.

Cassava storage roots are among the most important carbohydrate sources for smallholder farmers across sub-Saharan Africa. They are also carbon reserves the plant will remobilise under stress, a source-sink reversal triggered by drought, stem propagation or shoot pruning, a practice farmers routinely use for leaf harvest, intercropping or pre-harvest management. Each pruning event can substantially deplete root starch content, reducing yield and crop value. A new study led by Samuel Zeeman's group identifies the enzyme principally responsible and shows that suppressing it limits starch remobilisation without compromising regrowth.

Using transcriptomic and proteomic profiling of cassava storage roots after shoot pruning, the authors found that starch biosynthesis genes were broadly repressed while

degradation genes were induced, most strikingly AMY3A, a plastid-targeted α -amylase orthologous to *Arabidopsis* AMY3. This was unexpected: in *Arabidopsis*, AMY3 is dispensable for everyday starch turnover, redundant with other degrading enzymes. In cassava roots, RNAi-mediated suppression of AMY3A reduced post-pruning starch mobilisation by up to 7.5-fold relative to controls under field conditions at the International Institute of Tropical Agriculture in Nigeria. AMY3A is therefore a non-redundant, rate-limiting factor in this tissue and context, distinct from its minor role in leaves.

AMY3A-suppressed lines showed no reduction in their capacity to resprout, whether from the rootstock or from stem cuttings used for propagation. The trait improves storage root quality without the agronomic trade-off that might otherwise make it unusable in the field, and opens a route to cassava varieties that retain more starch under stress or repeated pruning.

Publication

David, L. C., Deslandes-Hérol, G., Hostettler, C., Bischof, S., Fischer-Stettler, M., Carluccio, A. V., Pfister, B., George, G. M., Wang, W., Stabolone, L., Gisel, A., Bull, S. E., Abt, M. R. & Zeeman, S. C. (2026). Understanding and modifying starch metabolism to limit yield losses in field-grown cassava. *Plant Physiology*, 201(3), kiag341. <https://doi.org/10.1093/plphys/kiag341>

HybridCrop – process-oriented machine learning for climate-resilient crop modelling

Led by Florian Zabel at the University of Basel, a new SNF-funded international project integrates machine learning with biophysical modelling to improve agricultural risk assessment under climate extremes.

As droughts, heatwaves and compound weather events intensify, the accuracy of crop models — the scientific tools used to simulate plant growth and forecast agricultural production — has never been more consequential. Two approaches currently dominate the field, each with real strengths and real limitations. Mechanistic models offer biophysically grounded representations of plant growth — transparent, interpretable, and deeply rooted in plant science — but are computationally demanding, often rely on uncertain or poorly constrained parameterizations, and are prone to structural failures, particularly under extreme conditions where reliable predictions matter most. Machine learning models can match or exceed their predictive accuracy at a fraction of the computational cost, but learn from historical data and cannot reliably extrapolate to future climate conditions beyond their training range. They predict yields without explaining the biophysical processes that produce them.

The project HybridCrop proposes a genuinely new paradigm to overcome both sets of limitations simultaneously. Rather than treating the two approaches as alternatives, the project trains physics-informed machine learning modules to represent specific fundamental crop processes: leaf area development, phenological progression, evapotranspiration, and soil moisture dynamics. These

modules are integrated into two established crop models, EPIC and LPJmL, creating hybrid systems in which mechanistic interpretability and computational efficiency coexist — free from the opacity of black-box prediction. To analyse rare and compound extreme events with statistical robustness, HybridCrop uses Single-Model Initial-condition Large Ensembles — SMILEs — large sets of climate simulations that go well beyond what any individual model run can capture. Open-access benchmark datasets based on Earth observation and in-situ data will accompany the modelling work, enabling systematic and reproducible comparisons across the scientific community.

HybridCrop is funded by the Swiss National Science Foundation through its WEAVE programme, which supports international research collaborations. The project is led by the University of Basel and partners with three institutions: the International Institute for Applied Systems Analysis (IIASA) in Austria, the Potsdam Institute for Climate Impact Research (PIK) in Germany, and the University of Hamburg. Three doctoral researchers and two postdoctoral scientists will carry out the research over the project's three-year duration — a team whose training will span plant science, computational modelling, and climate data analysis, reflecting the hybrid ambition of the project itself.

The scope of HybridCrop reaches well beyond crop science. More reliable models of agricultural risk under climate extremes are urgently needed to support adaptation planning at regional and global scales. By establishing a framework in which process



understanding and data-driven methods are genuinely integrated, the project aims to set a new standard for crop modelling and climate impact assessment — more accurate, more transparent, and more computationally accessible than current approaches allow. The methodology itself is designed to travel: as Florian Zabel notes, the hybrid modelling approach can in principle advance modelling practices across many research domains where mechanistic and data-driven methods currently operate in parallel without fully speaking to each other.



HybridCrop

process-oriented machine learning for crop modeling

More Information

<https://duw.unibas.ch/en/research-groups/land-use-changes/projects/>

CLIMSUIT – an interdisciplinary project to enhance global crop modelling under climate change

Benjamin is a doctoral student in the PhD Programme in Plant Sciences at the University of Basel, where he is co-supervised by Ruth Delzeit, Head of the Land Use Change Research Group, and Sabine Rumpf, Head of the Ecology Research Group. His research combines quantitative modelling approaches from ecology and agricultural science to assess trade-offs between biodiversity conservation and agriculture under climate change. Together with his supervisors and the agricultural modeller Florian Zabel, Benjamin successfully applied for the Collaborative Research Data Science Projects scheme of the Swiss Data Science Center (SDSC). In their project CLIMSUIT, a senior data scientist from the SDSC will integrate ecological species distribution models (SDMs) into one of the leading global crop suitability frameworks, aiming to make agricultural projections under climate change more accurate, robust, and data-driven.

Interview with Benjamin

What is the project about?

CLIMSUIT tackles a problem that has bothered me for a while. Models used to predict where crops can be grown in the future often rely on expert-derived rules from field trials, rather than the data-driven, statistically robust methods ecologists use to predict where wild species can persist under changing environmental conditions. CLIMSUIT will change that by integrating this ecological approach into a practice-oriented globally applied crop suitability framework. Suitability models capture agronomic realities

that SDMs typically do not, e.g., a crop's full growing cycle, from sowing to harvest while SDMs bring the statistical rigour that such models typically lack. Combining the two is the novel step CLIMSUIT is taking. Over the course of the two-year project, we will develop, test, and ultimately apply the new framework globally to project suitable growing conditions for up to around 100 crops under a range of future climate scenarios.

What do you personally find most exciting about this project?

The interdisciplinary nature of the project itself. CLIMSUIT only works because it brings together people who seldom collaborate this closely: ecologists, land-use economists, agricultural modellers, and a data scientist, each with their own methods, assumptions, and even language. Making sure a concept from ecology actually makes sense to someone trained in agricultural modelling, and vice versa, is where I think the most interesting and most difficult work will happen.

What is your role in the project?

I'll be collaborating with the three PIs and the SDSC data scientist for the two-year duration. I'll meet regularly with the data scientist to help route ecological, agricultural, or technical questions to whoever on the team is best placed to answer them. Because my own PhD work already combines SDMs with agricultural suitability modelling, I'll also be contributing thematic and methodological expertise directly.



How did the idea for the project come about?

The idea took shape during one of our regular PhD update meetings, where we were discussing pathways to improve the current state of the art in crop suitability modelling. The most promising direction we identified was also the most technically demanding, and clearly beyond what we could build with our expertise alone. Around that time, the SDSC's Call for Collaborative Research Data Science Projects gave us the opening we needed: a data science professional who could bridge the technical gap and help us to build what we had in mind. We put together the CLIMSUIT proposal, and here we are.

How can you get involved in the project?

If your work touches on agricultural modelling, SDMs or agricultural systems more broadly, we'd welcome an exchange to help shape how we build and parameterise the model. Beyond that, once CLIMSUIT's model and underlying datasets are released as open source, they'll be freely available for everyone to use.

Engaging Plants: a new understanding of action, interaction and agency

Led by Meredith C. Schuman at University of Zurich and Chris Salter at the Zurich University of Arts the Engaging Plants project was launched in June 2026. With funding from the John Templeton Foundation, an interdisciplinary research team investigates plant agency from scientific, philosophical and artistic perspectives.

Agency – the capacity to act – fundamentally shapes how we understand and relate to other beings and the world around us. Over the next two years, this project will bring together perspectives from plant biology, ecology, Earth system science, social sciences, philosophy, arts and design. Rather than assuming a single definition of agency, the team will develop a comparative framework that examines characteristics associated with agency in plants, animals, humans and even machines. These may include perception, communication, decision-making, goal-directedness, learning, memory and social networking.

The aim is not to anthropomorphise plants, but to establish rigorous criteria for determining what forms of agency-related traits can actually be observed and measured.

Making plant agency tangible

A particularly innovative part of *Engaging Plants* connects fundamental research with art, experience design, and public engagement. The project team will create an immersive environment in which humans experience plant agency. In this way, participants would no longer be passive observers but become part of a dynamic plant-human system.

A genuinely interdisciplinary collaboration

Overall coordination is shared by Meredith C. Schuman and Manuela Dahinden (PSC). Meredith, together with Sofia van Moorsel, Camille Schneider and Bernhard Schmid, leads the development and experimental validation of the scientific framework. Christopher L. Salter (ZHdK), in collaboration with Rasa Smite, leads the design and implementation of the public experiment and its experiential components. Ghassem R. Asrar contributes to the conceptual development of the experimental framework, while Felix Morsdorf and Toja Guerra bring additional expertise to its pilot testing. This combination of expertise is central to the project: questions of agency cannot be answered by biology, philosophy or the arts alone. Instead, *Engaging Plants* creates a shared space in which conceptual thinking, empirical experimentation and embodied experience can inform one another.

The framework developed in this project may contribute to discussions in ecology and evolutionary biology, but also to debates about collective and network agency, environmental policy and even artificial intelligence. Most importantly, it invites us to reconsider a deceptively simple question: What does it actually mean to act – and how many different forms can agency take?



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More Information

<https://www.plantsciences.uzh.ch/en/research/research-projects.html>

Combining plant biology and blockchain technology

For Kentaro Shimizu the UZH–Kyoto University Symposium carries a particular resonance. A Kyoto University alumnus, Shimizu has maintained active research ties with two groups there since moving to Zurich.

The 2026 edition of the symposium — held under the theme "Improving Quality of Life" — brought scientists from both institutions together across disciplines. Shimizu co-led a workshop on plant science alongside Kyoto ecologist Hiroshi Kudoh, drawing in plant physiologists, theoretical ecologists, and computer scientists. The session explored an unexpected intersection: how blockchain technology might strengthen plant biology

research by improving data collection, traceability, and transparency across institutions. The collaboration involved UZH blockchain specialist Claudio Tessone alongside plant biologists from both universities, pointing towards practical tools for ensuring that field data and experimental results can be reliably shared and verified. "Plant science is essential for both food security and the conservation of biodiversity, which are key to environmental quality," Shimizu noted, framing the broader stakes of the work.

The symposium identified concrete next steps: mutual exchanges for early-career researchers, and longer-term ambitions to establish a joint



PhD degree programme and a joint research centre in biodiversity. The UZH–Kyoto partnership, now in its fourth edition, is taking on new depth — with plant science and digital innovation pointing towards shared research infrastructure that could benefit both institutions and the wider scientific community.

More Information

www.news.uzh.ch/en/articles/news/2026/kyoto-symposium.html

Can you hear biodiversity?

"We spent a few very pleasant minutes somewhere far from our usual urban soundscape. Rain falling through the canopy, soft bird calls emerging from the vegetation, insects layered over a dense background: choosing between them was not always easy."

The journey is prompted by *Voices of the Tropical Forest*, an online survey that takes listeners to the forests of Costa Rica. Anyone over 18 can compare pairs of five-second recordings and choose the one they prefer; it takes about five minutes, works best with headphones, and is anonymous. The survey is coordinated by doctoral researcher Giacomo Delgado and hosted on *Biodiful*, a platform run by CNRS researcher Nicolas Mouquet that gathers surveys on human

perceptions of nature. It runs until 30 October 2026 in English, French and Spanish. The recordings serve a scientific purpose beyond their sensory appeal. Ecoacoustic methods capture changes in biological communities and help researchers assess how forests recover after degradation. Delgado and his colleagues analysed 16,658 hours of audio from 119 sites across Costa Rica's Nicoya Peninsula to evaluate the country's Payment for Ecosystem Services programme, which pays landowners to protect and restore forest. Naturally regenerating sites proved 1.4 times more acoustically similar to mature reference forests than to pastures, while monoculture timber plantations reached only 1.24 times. Asking which of these soundscapes people find most appealing brings in a further



dimension. The survey is supervised by Millie Chapman at ETH Zurich. Her Environmental Policy Lab works at the intersection of ecology, data science and environmental decision-making, with a particular interest in who benefits from the information on which conservation decisions are based.

Take part:

https://www.biodiful.org/#/soundscapes_en

AGILE: resolving plant nuclear organisation across space and time

How does a plant cell know when and where to activate a gene? The answer lies not only in the molecular signals that regulate transcription, but increasingly in the three-dimensional organisation of the nucleus itself.

The organisation of DNA within the nucleus, the location of genes and where they are activated all influence how plants respond to environmental changes and develop. Yet our understanding of gene regulation has remained largely molecular and one-dimensional. Translating it into a spatial and temporal picture of the living nucleus — tracking where genes are activated, how that positioning shifts over time, and what

structural elements govern these dynamics — represents a defining challenge for the field.

This is the frontier that AGILE was built to push. Launched in March 2026 under the Marie Skłodowska-Curie Actions of the European Union's Horizon Europe programme AGILE — Advanced Training for Next Generation Scientists in Spatio-Temporal Imaging of Plant Cells — is a four-year Doctoral Network that unites fifteen academic partner institutions across eight European countries, alongside a range of non-academic partners including microscopy technology leaders ZEISS, Andor, and Abberior. Fifteen doctoral candidates are pursuing individual research projects that,

taken together, advance our understanding of chromatin dynamics, nuclear architecture, and the quantitative imaging approaches required to study them.

Célia Baroux at the University of Zurich is one of the co-founders of the network and today co-coordinates it alongside Frédéric Pontvianne of the CNRS, the official grant coordinator, and Christophe Tatout of the Université Clermont Auvergne.

More Information
www.msca-agile.eu



PhenoMix: Multidimensional field phenotyping of crop mixtures

An interdisciplinary team comprising Achim Walter and Nina Buchmann (ETH Zurich), Michele Volpi (Swiss Data Science Center) and Susanne Vogelgsang (Agroscope) is investigating the ecological processes and interactions that determine how crops perform when grown together.

Pure stands of our major agricultural crops account for the majority of calories consumed worldwide. The cultivation of mixed crops — such as legumes with cereals — has the potential to combine various benefits, including reduced use of fertilisers and pesticides, greater drought resilience and, above all, increased biodiversity in the field. However, our knowledge of the best mixtures

— whether in terms of species or varieties — is still very limited, making it difficult to fully realise these benefits.

In the PhenoMix project (funded by the SNF, 2026 to 2030), we aim to use modern methods from image processing, plant ecophysiology and data science to collaboratively investigate how these mixtures perform in the field. We will conduct field trials in Eschikon, Tänikon and on farms to compare pure stands of legumes (peas, lentils) and various varieties of several cereal crops (wheat, oats, barley) with their corresponding two-species mixtures. We will i) track plant development in 3D throughout the growing season using state-of-the-art optical methods, ii) develop

models that allow us to draw conclusions about optimal variety combinations based on these data, iii) characterise the corresponding use of light, carbon, nitrogen and water in the stands, and iv) analyse the agronomic quality and economic value of the mixed crops. This will enable us to develop recommendations for more sustainable cropping systems.

Interested in joining us?
Please get in touch!
nina.buchmann@usys.ethz.ch
<https://gl.ethz.ch/>



Looking beneath the canopy: HiBiDiS takes forest biodiversity into orbit

Led by Maria J. Santos at the University of Zurich, the European Space Agency's newly approved HiBiDiS mission will combine hyperspectral imaging with multi-angle observations to investigate forest vegetation across different canopy layers. By making the largely invisible understorey observable from space, the mission aims to advance biodiversity monitoring and our understanding of forest structure and ecosystem functioning.

The European Space Agency has approved HiBiDiS, the Hyperspectral Biodiversity Scout, a satellite mission designed to resolve a structural blind spot in conventional Earth observation: the vertical stratification of forest canopies. Standard optical remote sensing is dominated by return signal from the uppermost canopy layer, which means the understorey — despite holding a disproportionate share of forest plant diversity, hosting regeneration through juvenile trees, and contributing materially to carbon-cycling and resilience processes — is largely invisible to existing sensor architectures at landscape scale.

HiBiDiS addresses this through a combination of hyperspectral imaging, which resolves reflected radiance across finely partitioned spectral bands rather than the broad channels typical of multispectral sensors, and a multi-angle observing geometry that images the same forest target from three viewing angles. The angular diversity is the mission's key design innovation: by observing identical ground targets from geometrically distinct perspectives, the retrieval pipeline can in principle disentangle the spectral contribution of the upper canopy — which dominates

the nadir-equivalent signal — from that of lower vegetation strata that become preferentially visible at oblique angles. The mission's core scientific objective is to establish whether this angular-spectral separation can be converted into quantitative, spatially explicit estimates of Essential Biodiversity Variables and forest structural composition, rather than remaining a purely qualitative signal decomposition. Maria J. Santos is the mission's scientific lead, extending her existing research programme at the intersection of ecosystem science, biodiversity monitoring and hyperspectral remote sensing from airborne and field-based methods into a dedicated orbital platform. Her Earth System Science group at the University of Zurich is responsible for defining the mission's core scientific questions, simulating expected sensor output ahead of launch to guide instrument and orbit design, and validating retrieved products against ground reference data once operational. Industrial development and platform engineering are coordinated separately by the aerospace company SITAEL.

By targeting both canopy and understorey layers within a single retrieval framework, HiBiDiS is positioned to complement rather than replace existing forest-observation missions, which remain largely canopy-limited by design. Its ultimate scientific value will depend on the calibration and ground-validation campaigns still ahead — multi-angle hyperspectral retrieval of sub-canopy vegetation is methodologically unproven at operational scale — but the mission opens a concrete pathway toward measuring a dimension of forest biodiversity that has so far resisted systematic observation from space.



More Information

<https://www.geo.uzh.ch/en/news/2026/esa-mission-hibidis.html>

European Space Agency: Green light for the next two ESA Scout missions

https://www.esa.int/Applications/Observing_the_Earth/FutureEO/Greenlight_for_next_two_ESA_Scout_missions

Integrating tip growth in biology and robotics

A new interdisciplinary collaboration between Ueli Grossniklaus (University of Zurich), Bradley Nelson and Salvador Pané i Vidal (both ETH Zurich) combines plant reproductive biology, microrobotics and materials science. By investigating how pollen tubes regulate directional tip growth, the researchers aim to develop new tools for manipulating cellular processes and to engineer growing microrobots capable of targeted molecular delivery.

Pollen tubes are among the fastest-growing plant cells and provide a remarkable model for studying polarised cell expansion. During sexual reproduction, they grow through the female reproductive tissues towards the ovule, responding to biochemical gradients and mechanical cues that regulate their growth rate and direction. This highly coordinated process, known as tip growth, also occurs in fungal hyphae and neuronal axons. Although many molecular components involved in pollen tube growth have been identified, how extracellular signals are integrated with intracellular regulatory processes to control directional growth remains incompletely understood.

A particular challenge is the precise manipulation of local conditions at the pollen tube cell wall. While methods for monitoring and modifying intracellular processes are well established, tools for delivering biochemical stimuli to defined regions of the growing cell surface remain limited. The project will address this challenge by developing microrobotic systems based on metal-organic frameworks (MOFs). These microscopic carriers will be guided to specific locations on the pollen tube surface, where they will release

effector molecules to modify the local biochemical environment. Combined with live-cell imaging and genetically encoded biosensors. This approach will allow the researchers to investigate how spatially restricted external signals influence intracellular dynamics, growth rates and directional responses.

The project also aims to translate the biological principles of tip growth into engineered systems. Using reaction-diffusion-controlled self-assembly, the researchers will develop soft micro-assemblies that extend progressively at their tips, mimicking the growth behaviour of pollen tubes. Unlike conventional microrobots, these structures would generate their own extension through local material assembly, potentially enabling navigation through confined and complex environments.

As a proof of concept, the team will investigate whether these tip-growing micro-assemblies can deliver bioactive molecules to plant ovules in microfluidic devices. This experimental approach, described as robotic *in vitro* “fertilisation”, aims to reproduce selected functional aspects of pollen tube-mediated molecular delivery without relying on a living pollen tube. It will provide a test system for evaluating the precision, controllability and delivery capabilities of the engineered structures.

Beyond advancing our understanding of pollen tube growth and fertilisation, the research could establish new principles for the development of growing microrobots. In the longer term, such systems may contribute to technological applications requiring precise interventions in confined environments, including targeted drug delivery, diagnostics and minimally invasive microsurgery.



More Information

<https://data.snf.ch/grants/grant/10008915>

<https://www.botinst.uzh.ch/en/research/grossnik.html>

https://msrl.ethz.ch/the-lab/team/Brad_Nelson.html

From plant science to career opportunities

BAYER MENTORING PROGRAMME

1 ECTS, 6 monthly meetings with work in between, 01.09.2026
- 01.04.2027

Have you ever wondered what it is like to work as a scientist in industry, or how your expertise could translate beyond academia?

The Bayer University Mentoring Programme provides doctoral researchers with the opportunity to explore career pathways beyond academia through six months of individual mentoring with experienced Bayer scientists and professionals. Each participant is matched with a mentor based on their scientific background, professional interests, and development goals. Rather than following a fixed curriculum, the mentoring relationship is tailored to the participant's individual questions and aspirations. Through once-a-month one-to-one conversations, participants gain first-hand insights into working in an international life science company, reflect on their own career ambitions, and can develop transferable skills relevant to a wide range of professional contexts. The programme may also include webinars and a visit to a Bayer site, providing opportunities to deepen participants' understanding of industry relevant topics and expand their professional networks. The Bayer University Mentoring Programme is not a recruiting programme. Participation is not linked to employment opportunities at Bayer. Its purpose is to provide an open environment for career mentoring, professional growth and honest discussions about working in industry.

The programme is intended primarily for advanced PhD researchers working in crop sciences, particularly crop breeding and crop protection, however the applications from doctoral researchers in other areas of plant sciences and related disciplines are also encouraged.

Registration

<https://ethz.ch/staffnet/en/service/courses-continuing-education/details.15554o.html>

FEMINNO MENTORING AND CAREER DEVELOPMENT PROGRAMME

4 ECTS, fully accredited in PhD programmes; postdocs are credited 120 hours

Coordinated by PSC, feminno offers mentoring and career development for female scientists interested in innovation: participants develop their ideas and create a Business Model Canvas, train pitching and negotiation skills, explore start-up funding instruments, and meet role models during company visits, before presenting their projects at the closing event in early March 2027. It is open to female PhD students, postdocs and researchers from all faculties at Swiss universities, the ETH Domain and universities of applied sciences; up to 25 participants are admitted per round.

Further information

www.feminno.ch

<https://blogs.ethz.ch/feminno/files/2026/06/feminno-broschuere-A5-5-June-2026.pdf>

Science & Policy – Winter School: Decision making for applied ecology and conservation

Scientists and managers working to preserve biodiversity constantly need to make and advise management decisions, often with conflicting objectives, time pressure, limited resources and incomplete knowledge. Recognizing this complexity, conservation increasingly uses a range of principles and tools to make rational decisions in difficult situations.

This five-day course provides a primer in decision analysis for conservation. It is aimed at students of ecology and evolution who seek a career in making or advising conservation decisions, independently or interacting with management agencies and practitioners. Each day combines lectures, practical training, and small group activities to enable application to real-world conservation challenges. All speakers are leading experts in conservation decision making, with years of experience in delivering training to future and current scientists, managers and practitioners.

Lecturers: Prof. Dr. Alejandra Morán Ordóñez (University of Basel), Dr. Stefano Canessa (University of Bern / University of Milano), Dr. Benedikt Schmidt (University of Zurich), Prof. Dr. Sabine Rumpf (Unibas), Dr. Virgilio Hermoso (CSIC, Spain), Dr. John Ewen (Zoological Society London, UK)

Location: University of Basel, Klingelbergstrasse 27, Seminarraum EG 0-09

Dates: 25-29 January 2027

Time: 09:00-17:00

Credit Points: 2 ECTS



Species reintroduction. © Caitlin E. Andrews

Prior Knowledge and Registration

Registration is primarily open to doctoral students with an MSc in Biology, Ecology, Conservation, Environmental Sciences, or related disciplines who are affiliated with the University of Basel, ETH Zurich, or the University of Zurich. External participants may register if additional places are available. As part of the registration process, applicants who are not enrolled in a PSC PhD programme are required to submit a motivation letter.

Number of Participants

Participation is limited to 14, with priority given to PSC PhD students.

SCIENCE and POLICY Training

Science & Policy: Introduction to Political Sciences

Dr. Sarah Bütikofer (Department of Political Science, UZH and DeFacto), 1 ECTS, ETH Zurich, 20.-27.10.2026

Science & Policy Workshop B: Stakeholder Engagement

Dr. Anna-Kathrin Heydenreich (University St. Gallen) and Dr. Luisa Last (PSC), 2 ECTS, ETH Zurich, 09.11.-08.12.2026

Science & Policy Workshop D: Building Political Support

S. Bütikofer, Global Governance (ETH Zurich); S. Koehler (Queen Mary University of London, UK), and L. Mettler (effectiva, CH), 2 ECTS, ETH Zurich, 27.08.-29.09.2026

Science and & Policy Talk

Between Evidence and Controversy: How Can Researchers Navigate Policy Advice?

Tome Sandevski (Goethe-University Frankfurt), ETH Zurich, 22.10.2026

RESEARCH

Compulsory

Colloquium: Challenges in Plant Sciences

PSC lecturers, 2 ECTS, ETH Zurich, 26.10. & 23.11. 2026

Research & Seminars

Concepts of Evolutionary Biology (Seminar)

Prof. K. Shimizu, 1 ECTS, UZH, 05.-06.04. 2027

Crop Phenotyping

PD Dr. A. Hund, 1 ECTS, ETH Zurich, spring term 2027

Current Challenges in Plant Breeding

Prof. Dr. B. Studer, 1 ECTS, ETH Zurich, 13.11. 2026 - 13.01.2027

Sustainable Plant Systems

Dr. M. Paschke et al., 1 ECTS, ETH Zurich, 01.10.-01.12. 2026

Transdisciplinary Skills, System Thinking

Transdisciplinary Seminar on Research: Challenges of Interdisciplinarity and Stakeholder Engagement

PD Dr. B. V. Baptista, Prof. Dr. C. E. Pohl, 1 ECTS, ETH Zurich, 23.09.-25.11. 2026

TECHNIQUES

Techniques in Plant Biology

Genetic Diversity: Analysis

Dr. J-C Walser, 1 ECTS, ETH Zurich, spring term 2027

Genetic Diversity: Techniques

Dr. A. M. Minder Pfyl, 1 ECTS, ETH Zurich, 04.11.-25.11. 2026

Microbiomics 1: The Microbiome of the Plant-Soil-System

Dr. M. Hartmann, 1 ECTS, ETH Zurich, spring term 2027

Microbiomics 2: Metabarcoding - from Bioinformatics to Statistics

Dr. M. Hartmann, 1 ECTS, ETH Zurich, spring term 2027

TRANSFERABLE SKILLS

Project Management

Project Management for Research

Dr. C. Galli Marxer, 1 ECTS, ETH Zurich, spring term 2029

Research Integrity, Research Ethics

Ethics and Scientific Integrity for Doctoral Students

Prof. N. Buchmann, Dr. M. Paschke, 1 ECTS, ETH Zurich, spring term 2027

Research Funding

Writing a Postdoctoral Grant

Dr. Ingo Hebach (UZH), 1 ECTS, ETH Zurich, 15.-22.01. 2027

Science Communication and Teaching

Science Communication and Excursion Management in Botanical Gardens

Prof. Dr. A. Kahmen et al., 1 ECTS, UNIBAS, TBA

Teaching Science at University

Dr. S. Petchey, 1 ECTS, UZH, spring term 2027

Scientific Writing, Publishing and Information Management

Advanced Scientific Writing in Natural Sciences

Dr. P. Mayer, 1 ECTS, UNIBAS, 13.-26.11. 2026

Scientific Writing Practice 1

Dr. R. Mihalka, 1 ECTS, ETH Zurich, spring term 2028

Scientific Writing 2

Dr. R. Mihalka, 1 ECTS, ETH Zurich, spring term 2027

DIGITAL SKILLS and STATISTICS

Data Management

Advanced Data Management and Manipulation Using R

Dr. J. Wunder, 1 ECTS, ETH Zurich, spring term 2027

Reporting Using Quarto, R Markdown & Shiny

Dr. J. Wunder, 1 ECTS, ETH Zurich, spring term 2027

Statistics, Modelling

Applied Crop Modelling for Climate Risk Assessment

PD Dr. Florian Zabel, 1 ECTS, UNIBAS, 08.-10.09. 2026

Compositional Data Analysis

Dr. M. Templ, 1 ECTS, ETH Zurich, 11.-13.01. 2027

Data Analysis Clinic

Dr. Natacha Bodenhausen, 1 ECTS, UNIBAS, 23.09.-09.12. 2026

General Linear and Linear Mixed Models in R

Prof. Dr. P. Niklaus, 1 ECTS, UZH, spring term 2027

Introduction to R

Dr. J. Wunder, 1 ECTS, ETH Zurich, 29.01.-05.02. 2027

Introduction to Structural Equation Modelling

Dr. F. Pennekamp, 1 ECTS, UZH, 04.-06.11. 2026

Data Visualisation

Scientific Visualisation using R

Dr. J. Wunder, 1 ECTS, ETH Zurich, 27.11-11.12. 2026

Machine Learning

Introduction to ML for Genomics (UZH BIO610)

Prof. K. Shimizu, 1 ECTS, UZH, 28.10.-29.10. 2026

Introduction to ML for Plant Scientists 1

Prof. Dr. J. Wegner, 1 ECTS, UZH, 16.-18.11. 2026

Introduction to ML for Plant Scientists 2

Prof. Dr. J. Wegner, 2 ECTS, UZH, 19.11.-02.12. 2026

Image Analysis

Introduction to Plant Image Analysis

Prof. G. Lobet, Dr. A. Haghighattalab & Dr. N. Schandry, 1 ECTS, UNIBAS, 01.-05.10. 2026

Geospatial & Spatial Data Skills

PReSens: Proximal and Remote Sensing for Soil and Vegetation

Dr. F. Petibon, Dr. M. Beloiu Schwenke and Dr. P. Duddek, 2 ECTS, ETH Zurich, spring term 2027

Spatial Data: A GIS Introduction

Dr. R. Spirig, 1 ECTS, UNIBAS, 18.-25.09. 2026

Information events

Get to know the PhD programme in Science and Policy

Dr. Luisa Last, Online Event, 02.11. 2026

Registration: <https://doodle.com/group-poll/participate/bm0jg2ra/vote>

PSC survey: How PhD researchers are using generative AI in 2026

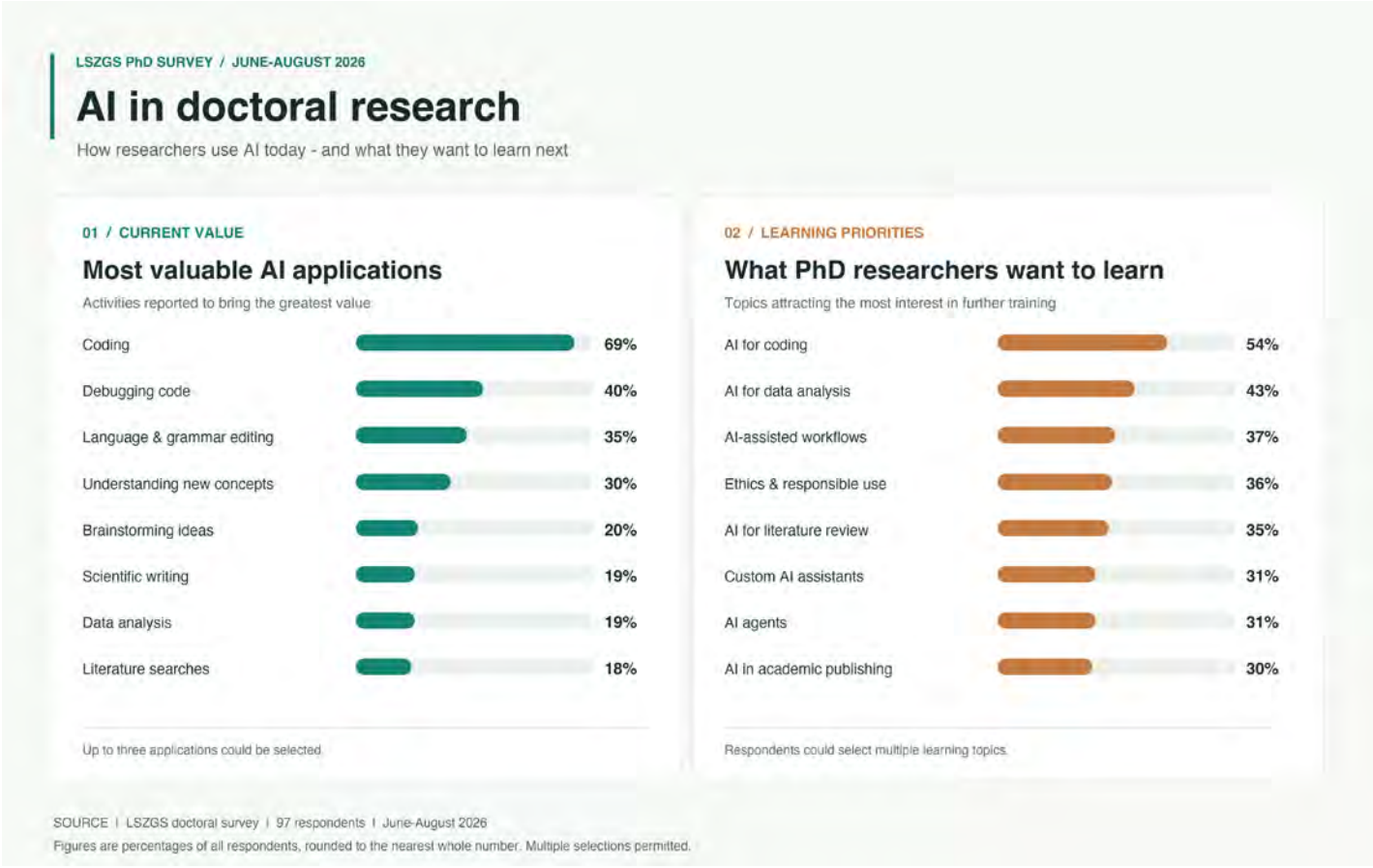
Generative AI is rapidly becoming part of everyday academic work. But how are PhD researchers actually using it, and where do they still need support?

PSC surveyed 96 PhD researchers enrolled in the Life Science Zurich Graduate School programmes, including the PhD Programme in Plant Sciences. In total, representing 16 PhD programmes. The largest groups came from Neuroscience (27%), Plant Sciences (15%) and Evolutionary Biology (14%), with respondents from a broad range of other life science programmes. The results suggest that generative AI is no longer an occasional experiment. Almost 69% of respondents use LLM-based generative AI at least daily, including 44% who use it several times per day. A further 20% use it several times per week.

AI is already part of the research workflow

PhD researchers use AI across a broad range of academic activities. Common applications include brainstorming and understanding new concepts, literature searches and summarising scientific papers, scientific writing and editing, as well as coding and debugging. Some respondents are also experimenting with AI for data visualisation, project planning and experimental design. Coding stands out in particular: 71% identified coding as one of the three AI applications currently providing the greatest value in their work, followed by debugging code (43%) and

language and grammar editing (35%). Researchers are also investing in these tools themselves. Around half of respondents reported using personal paid subscriptions. ChatGPT and Claude were among the most widely used tools, while university-provided services were used considerably less frequently. Notably, 36% of respondents did not know that their university might provide access to AI tools or related services. Yet the survey also reveals a group of researchers moving well beyond conventional chatbot use. Around 29% have already used AI agents, 14% have built a custom GPT or AI



assistant, 16% have worked with AI APIs, and 8% have fine-tuned an LLM. At the same time, 39% had done none of these things. This contrast points to an emerging training gap: while some PhD researchers are already developing sophisticated AI-assisted workflows, these approaches remain unfamiliar to many of their peers.

AI adoption outpaces awareness of guidelines

Supervisors appear largely open to this development: 57% of respondents described their supervisor as generally supportive of AI use. At the same time, 87% reported that their research group has no defined rules for using AI. While universities have introduced guidelines and recommendations for the use of generative AI, awareness of them remains uneven: only 39% of respondents said they were familiar with their institution's guidelines, while 28% knew they existed but had not read them, and 33% were either unsure or unaware of them. Importantly, guidance from the wider research community is not simply about restricting AI use, but about establishing conditions for its responsible use.

The European Commission's guidelines encourage the responsible adoption of generative AI in research, emphasising transparency, accountability and responsibility [1].

EU guidance also permits the use of generative AI in preparing research grant proposals, provided researchers remain responsible for the content, verify AI-generated information and disclose its use. Similarly, publishers such as *Nature Portfolio* [2] and *Elsevier* [3] allow AI tools to support aspects of manuscript preparation, while emphasising transparency, verification, human oversight and accountability.

This makes awareness and practical understanding of the rules increasingly important. Data privacy was the most frequently reported limitation to

Responsible AI: questions still unanswered

Respondents who said these topics were unclear

61%

Which AI tools meet university data-protection requirements?

59 of 97 respondents

55%

Copyright and ownership of AI-generated content

53 of 97 respondents

47%

How should AI tools be cited?

46 of 97 respondents

43%

Can unpublished research data be uploaded to AI systems?

42 of 97 respondents

Source: LSZGS PhD survey, June–August 2026 | n = 97 respondents
Multiple answers allowed; percentages do not add up to 100%.

effective AI use (51%), followed by verification of AI outputs (40%) and uncertainty about institutional policies (37%). Respondents also expressed concerns about hallucinations, copyright, scientific integrity, bias, overreliance on AI, reproducibility and the potential loss of critical thinking. At the same time, the survey suggests that PhD researchers approach AI-generated information with considerable caution. Almost 89% said they always or usually independently verify AI-generated information before incorporating it into their academic or scientific work. Yet confidence in recognising incorrect AI-generated information was more mixed. Learning how to document AI use, protect sensitive information, verify outputs and remain accountable for the resulting work is therefore becoming an important part of research practice.

From survey insights to hands-on training

The survey findings informed the design of the course **Explore the Responsible Use of Generative AI in Academic Work**, held on 23, 24 and 30 September 2026. Participants explored practical applications of

GenAI in scientific writing, literature research, coding, data visualisation and communication, as well as emerging AI agents and research workflows. Responsible use, including data privacy, scientific integrity, bias and reproducibility, was addressed throughout. Between sessions, participants tested GenAI tools in their own research and shared their experiences, challenges and lessons learned during the final session.

Link to the survey and detailed course programme:

https://www.plantsciences.uzh.ch/en/teaching/phdplantscience/program_ps/training/course_catalogue/digitalskills/genai.html

Contact: Bojan Gujas
bojan.gujas@usys.ethz.ch

References

- [1] https://research-and-innovation.ec.europa.eu/news/all-research-and-innovation-news/updated-era-living-guidelines-responsible-use-generative-ai-research-2026-05-08_en
- [2] <https://www.nature.com/articles/s41592-026-03020-1>
- [3] <https://www.elsevier.com/en-gb/about/policies-and-standards/publishing-ethics-books/generative-ai-policies>

StudioNatur – A makerspace for exploring natural history collections

How can natural history collections inspire curiosity, creativity and a deeper connection with nature?

StudioNatur is a new makerspace at the Natural History Museum of the University of Zurich, where visitors become active explorers of biodiversity. Through hands-on workshops, creative experimentation and scientific discovery, participants engage directly with museum collections – from examining plant structures and microorganisms under a microscope to exploring fossils and reconstructing prehistoric animals.

Developed in collaboration with CreativeLabZ at the Plant Science Center, StudioNatur brings together researchers from different disciplines to transform natural history collections into spaces for experimentation, dialogue and co-creation. Scientists contribute their expertise in ecology, evolutionary biology, plant sciences, palaeontology and anthropology, helping visitors discover not only what we know about nature, but also how scientific knowledge is created.

The project explores how creative making and direct engagement with scientists can strengthen biodiversity awareness, foster curiosity and encourage new relationships between people and the natural world.

Funded by the Swiss National Science Foundation (SNSF) through its Agora programme, the project **A makerspace for museums: Reconnecting nature and people through natural history collections** runs from August 2025 to July 2027.



Drop-in workshops are every Wednesday and Saturday afternoons from 14-16:30.

Light traces of plants

Create unique prints of plants using chlorophyll – the pigment that makes them green. Using herbarium specimens, participants discover just how varied plants can be – and what their shapes and structures reveal about how they live.

Seeds: the genetic data carriers

Seeds and fruit are the plant-world's carriers of genetic information. With the help of wind, birds, humans, and other mammals, they fly, float, and roll – spreading their genetic information. In this workshop we will take a closer look at seeds. What connections can you find in shape, size, and dispersal method?

4 hours workshops can be reserved for up to 12 people online under: <https://www.nmz.uzh.ch/de/fuehrungen/studionaturworkshop.html>

Secrets of the herbarium: build your own flower press

Sharks of the ancient desert: drawing the past

**naturhistorisches
museum**

der Universität Zürich

Research team: Jake Alexander (ETH Zurich), Manuela Dahinden (PSC), Christian Klug (University of Zurich), Kathelijne Koops (University of Zurich), Verena Schünemann (University of Basel) and Colin Shaw (University of Zurich).

Project partners: Alessia Guggisberg (ETH Zurich) and Isabel Kluseman (University of Zurich).

Project lead: Juanita Schlaepfer-Miller (PSC / CreativeLabZ).

<https://data.snf.ch/grants/grant/231116>

PSC Symposium 2026

From Genes to Landscapes – Understanding and Conserving Biodiversity



You want to present your research at the symposium? Get ready to submit your abstract with your registration!

Registration
<https://pscsymposium2026.com>



Organizing Committee

Janne van't Klooster – Plant Biochemistry, ETH Zurich
Helena Pfingst – Plant Evolutionary Genetics, ETH Zurich
Carlotta Marie Wehrkamp – Molecular Plant Biology and Phytopathology, University of Zurich
Leonardo Cruz de Souza – Ecology, University of Basel
Isabel Williams – Plant Biochemistry, ETH Zurich
Prasanth Bendalam – Crop Science, ETH Zurich

Scientific Committee

Alejandra Morán Ordóñez – University of Basel
Melissa Chapman – ETH Zurich
Meredith Schuman – University of Zurich
Janina Grabs – University of Basel
Manuela Dahinden – PSC

Symposium Coordination

Bojan Gujas – PSC

Addressing the challenges of biodiversity loss in a rapidly changing climate requires collaboration across scientific disciplines.

Researchers from diverse disciplines will share their latest findings and perspectives at the crossroads of ecosystem science, plant biology, biodiversity management and policy. Topics spanning ecosystem science include the reconstruction of past biodiversity, ecosystem modelling, and ecological interactions shaping species distributions. At the plant level, speakers will investigate the mechanisms that allow plants to survive and thrive, from epigenetic adaptation in alpine environments to defence against pathogens. Interdisciplinary researchers will present how to bridge the gap between scientific knowledge and conservation practice, in the light of biodiversity monitoring, adaptive forest management, and agricultural policy.

The PSC Symposium is biennial organised by PhD students together with a Scientific Committee. Each edition brings together more than 200 researchers for a day of scientific exchange and networking. We warmly invite researchers and anyone interested in learning more about plants, biodiversity, and their future in a changing world.



ETH zürich

Center for Climate Systems Modeling

ETH-Klimarunde

Wie hochauflösende Modelle helfen,
Wetterrisiken zu bewältigen

Dienstag, 10. November 2026, 16.30 - 20.00 Uhr
ETH Zürich, Hauptgebäude

The poster features a satellite image of Earth's clouds as a background. On the right side, there is a graphic of two human silhouettes standing on a dotted grid that represents a world map. Above the silhouettes are five circular icons: a sun, a cloud with rain, a mountain, a forest, and a sun with a cloud. In the bottom right corner, there is a small logo for the Center for Climate Systems Modeling (C2SM).



35 Jahre SKEK: für die Kulturpflanzenvielfalt

Eine Geschichte zum Feiern und
klimatische Herausforderungen
zum Erkunden

35 ans de la CPC : pour la diversité des plantes cultivées

Une histoire à célébrer et des
défis climatiques à explorer

19.11.2026 | 9:15 – 16:15
BILDUNGSZENTRUM WALD
CENTRE DE FORMATION FORESTIER
LYSS (BE)

PGREL-Fachtagung zur Erhaltung und nachhaltigen
Nutzung von Pflanzengenetischen Ressourcen für
Ernährung und Landwirtschaft

Congrès RPGAA pour la conservation et l'utilisation
durable des Ressources Phytogénétiques pour
l'Alimentation et l'Agriculture

The poster is split into two vertical panels. The left panel has a light green background with a faint image of pea plants. The right panel shows a close-up of a pea plant with pink and white flowers. In the top right corner of the right panel, there is a circular logo with a green pea inside and the text 'CPC-SKEK' around it.



12–13 JANUARY 2027
Early Career Meeting

13–15 JANUARY 2027
Symposium



SwissPLANT
2027

The SwissPLANT 2027 will bring together plant scientists from across Switzerland in Les Diablerets in January 2027 for two consecutive events dedicated to scientific exchange and networking.

The Swiss Plant Early Career Meeting (12–13 January 2027) invites senior PhD students and postdoctoral researchers to present and discuss their latest findings in a supportive atmosphere. Participants will present both a poster and a short talk, exchange ideas with peers, and connect with established researchers who will join the meeting as mentors.

The SwissPLANT 2027 Symposium (13–15 January 2027), bringing together the wider Swiss plant science community to discuss current research advances and foster new connections and collaborations.

Registration and abstract submissions

<https://sspb.ch/en/events>

Join us in Les Diablerets for the SwissPLANT 2027!

Organizers

Samuel C. Zeeman, Plant Biochemistry
Megan Mc Donald, Dynamic of Plant Diseases
Kirsten Bomblies, Plant Evolutionary Genetics
Diana Santelia, Plant Molecular Physiology
Elisabeth Truernit, Phloem Development and Function

ETH Zurich



Image: Christoph Biedermann

SWIFCOB 27 – Nature Conservation in Transition

Venue: Zentrum Paul Klee, 3006 Bern, Switzerland

How can different approaches to nature conservation work together to preserve and enhance biodiversity? What values and perceptions of the relationship between humans and nature shape our goals and actions?

At SWIFCOB 27, we will explore how approaches to nature conservation have evolved and how established practices can be complemented by new perspectives. We will discuss how biodiversity conservation and restoration goals can be put into practice, drawing on concrete examples from Switzerland. We will also examine how the projects presented can inspire change beyond their immediate areas of impact.

The conference is aimed at researchers, professionals working in public authorities, environmental consultancies, associations, politics and the private sector, as well as anyone interested in nature conservation and biodiversity.

Information on registration and the detailed programme will be available in mid-November:

https://scnat.ch/en/uuid/i/3c19834f-130d-5c3d-ac89-11203d283a97-SWIFCOB_27_-_Naturschutz_im_Wandel



Swiss Biodiversity Forum



European Plant Science Organisation
<https://epsoweb.org>

EPSO STATEMENT

Towards a Virtual Institute for AI in Plant Science



European Plant Science Organisation
<https://epsoweb.org>

Statement

Towards a Virtual Institute for AI in Plant Science

Brussels, 08.09.2026



EPSO welcomes the European Commission's thrust on artificial intelligence in science. In its response to the consultation on the European Research Area Act, EPSO proposed European virtual institutes dedicated to AI in specific research domains, identifying a **Virtual Institute for AI in Plant Science** as a concrete example.

A virtual 'AI in Plant Science' institute would strengthen Europe's technological sovereignty, economic security and research capacity in an area central to citizens' needs and wellbeing. Plant science and adjacent disciplines can establish an integrated AI and digital innovation chain extending from molecular discovery and breeding to field deployment. This will support the development of climate-resilient and climate-neutral crops and production systems, strengthening the competitiveness, sustainability, and resilience of Europe's agri-food, forestry, and bioeconomy sectors.

Therefore, EPSO has brought together experts from its member institutes, discussed the proposal at its General Assembly, exchanged views with DG RTD, and is now establishing a Working Group on AI and Plant Science.

<https://epsoweb.org/epso/epso-statement-towards-a-virtual-institute-for-ai-in-plant-science-epso-members-are-invited-to-join-the-new-ai-in-plant-science-working-group-and-confirm/2026/09/08/>

EPSO UPCOMING MEETINGS

WG Agricultural Technologies: Meeting, online, 12.11. 2026

57th PSS 'Plants as alternative sources of fossil fuel-based products', 19.11. 2026

58th PSS 'Coevolution with Endophytes', 17.12. 2026

WG Plants and Microbiomes 7th workshop: Cereals MiBi, Tulln / AT, 31.05. 2027

General Assembly, Geisenheim / DE, 14.-16.06. 2027



Confirmed speakers: Zürich, Switzerland | May 11-13th 2027

Ford Denison,
University of Minnesota

Feng-Min Li, Nanjing
Agricultural University

Jacob Weiner,
University of
Copenhagen

Hélène Fréville,
INRAE Montpellier

Registrations open
October 2026

[https://www.agroscope.
admin.ch/en/event-id-
3679](https://www.agroscope.admin.ch/en/event-id-3679)

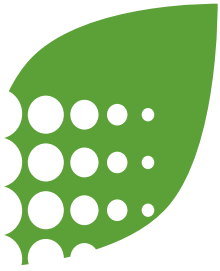
International Workshop on Crop Evolutionary Ecology

www.agroscope.ch

**Crop Evolutionary Ecology: Rethinking crop
improvement through ecology and evolution**

Crop Evolutionary Ecology (CEE), also known as *Darwinian Agriculture*, explores how ecological and evolutionary theory can help improve crop productivity, resilience, and resource-use efficiency. By putting theory at the centre of crop improvement, CEE offers a complementary perspective to AI- and big-data-driven approaches and may help identify more «radical» solutions for sustainable agriculture.

This workshop brings together researchers from ecology, evolutionary biology, plant science, agronomy, and breeding to discuss how CEE can move from conceptual insight to practical breeding and crop design.



www.plantsciences.ch

The Zurich-Basel Plant Science Center is a competence center linking and supporting the plant science research community at ETH Zurich, University of Zurich and University of Basel. The center promotes plant and environmental research, education and outreach. It provides platforms that enable interaction 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

Department of Social Science

Biozentrum

Zurich-Basel Plant Science Center, Managing Office

