

DUW Symposium 2026

Program & Abstracts

4th of November 2026



Symposium Program

Time	Program	Speaker/Topic
09:00 (15 min)	Welcome	Jelena Rajkov & Patrick Tschopp
09:15 (1 h 15 min)	Talks I	Life in and on the Substrate <ul style="list-style-type: none"> • <i>Alejandro Catalá Jimenez</i> • <i>Nathalie Amacker</i> • <i>Mikiko Karasawa</i> • <i>Katja Springer</i> • <i>Jasmin Lepper</i>
10:30 (30 min)	Coffee Break	
11:00 (45 min)	Poster Session I	
11:45 (45 min)	Talks II	Past & Present City Life <ul style="list-style-type: none"> • <i>Ismeni Lypiridou</i> • <i>Marguerita Schäfer, Kirsten Scheinberger, Benjamin Sichert</i> • <i>Guido de Bonfioli Cavalcabo</i>
12:30 (1 h)	Lunch break	
13:30 (10 min)	Welcome Back	Michael Vanek, <i>Sustainability Office</i>
13:40 (1 h)	Talks III	Animals: Micro to Macro <ul style="list-style-type: none"> • <i>Luca Pecalli</i> • <i>Carlos Manuel Herrera Castillo</i> • <i>Anne-Cathérine Gutzwiller</i> • <i>Marina Garrido Priego</i>
14:40 (35 min)	Coffee Break	
15:15 (45 min)	Poster Session II	
16:00 (1 h)	Talks IV	Changing Landscapes in a changing World <ul style="list-style-type: none"> • <i>Paul Southard</i> • <i>Leonardo Cruz de Souza</i> • <i>Benjamin Walter</i> • <i>Chun-Yu Chen</i>
17:00	Closing remarks & Aperio	Alessandro Rosa & Jelena Rajkov

Talks Program

Time	Speaker	Title of Abstract
Life in and on the Substrate		
09:15	Alejandro Catalá Jimenez	Measuring $\delta^{15}\text{N}$ in Low-Biomass Flatworms: A Denitrifier Method Approach
09:30	Nathalie Amacker	Hydrogen isotopes of fatty acids as a proxy for carbon use efficiency in soil microbes
09:45	Mikiko Karasawa	Bacterial metabolization of host-specific secondary metabolites
10:00	Katja Springer	Climate adaptation in alpine and lowland Brassicaceae
10:15	Jasmin Lepper	Cold stratification affects the composition of germinating grassland species
Past & Present City Life		
11:45	Ismini Lypiridou	Hydroclimate reconstruction from Uzuntarla Cave (Thrace, Türkiye) and the connection to the water supply of Constantinople
12:00	Marguerita Schäfer Kirsten Scheinberger Benjamin Sichert	Devilish Goat Feet in the Parish House? Mummified Archaeozoological Finds from the 17th–19th Century in Lantsch/Lenz (Graubünden, Switzerland)
12:15	Guido de Bonfili Cavalcabo'	A voxel-based approach for radiation modelling in urban environments with trees
Animals: Micro to Macro		
13:40	Luca Pecalli	Time series RNA-seq shows temporal expression of host resistance related genes
13:55	Carlos Manuel Herrera Castillo	Evolution of threespine stickleback dorsal spines via <i>hoxdb</i> gene regulation
14:10	Anne-Cathérine Gutzwiller	Influence of weather conditions on social associations in wintering White-winged Snowfinches
14:25	Marina Garrido Priego	The wandering years: Movement strategies of a raptor across the juvenile stage
Changing Landscapes in a changing World		
16:00	Paul Southard	Remotely-sensed impacts of NSWRM implementations in Switzerland during the summer 2026 drought of record
16:15	Leonardo Cruz de Souza	Glacier retreat drives species turnover and functional convergence across spatial scales and trophic levels
16:30	Benjamin Walter	Climate change reshapes the agricultural potential of Europe: a data-driven assessment of crop suitability to 2100
16:45	Chun-Yu Chen	Global Economic Impacts of Solar PV-Induced Land-use Change

Poster Session I

Time: 11:00 – 11:45

Number	Presenter	Title of Abstract
A01	Pascal Angst	A pangenome for <i>Daphnia magna</i>
A02	Martino Balestra	Cold microhabitats as refugia for alpine specialists above the treeline
A03	Amélie Marie Beauregard	Habitat selection of a rare bird species (<i>carduelis citrinella</i>) and suggestions for its conservation in the UNESCO Biosphere Entlebuch
A04	Eva Anna Burgunder	Future climate conditions increase severity of soilborne diseases in table beets
A05	Cristina Cipriano	Whose knowledge shapes the landscape? Towards transformative and just biodiversity planning
A06	Hilal Civelek	Soil Microbiome-induced DNA Methylation Mediating Feedbacks on Plant Growth
A07	Marco Túlio Pacheco Coelho	The global geography of non-native mountain floras
A08	Lorenzo Cresi	Planning the future of barely studied glacier forelands: filling the gaps before the ice cracks
A09	Thomas Dorey	What sets the warm edge? The role of biotic constraints on an alpine plant's range limit
A10	Fiona Fitchett	Harnessing compost microbes for new crop protection products against foliar diseases
A11	Jianrong Fu	Contrasting organic carbon burial and nitrogen cycling across muddy and sandy sediments of the East China Sea shelf
A12	Sophie Grotloh	Impacts of non-native plant species along an elevational gradient in mountain ecosystems
A13	Anja Haefeli	The evolution of the extracellular matrix

Poster Session II

Time: 15:15 – 16:00

Number	Presenter	Title of Abstract
B01	Andrea Karen	ECO-ICE: Reconstruction of the Climate in Potential Temperate Tree Microrefugia during the Last Glacial Maximum using Biomarkers
B02	Tim Kurth	Anaerobic methane oxidation in sediments of the High-Arctic Lake Isdammen, Svalbard
B03	Karolína Masárová	Key evolutionary innovations in the rapid diversification of Diploneis from Lake Tanganyika
B04	Yugandhar Nighojkar	Can Stalagmites Record Regional Floods? Evidence from Rayan Cave, Southern Zagros, Iran
B05	Peyman Parvizi	Holocene hydroclimate variability from a composite speleothem record of Kuna Ba Cave, northern Iraq
B06	Loïs Petitjean	Recent Dynamics of Chironomid and Invertebrate Assemblages in a Swiss Mountain Lake : Biotic and Geochronological Analyses
B07	Francesca Quitadamo	A reference-free approach to characterize Large Structural Polymorphisms in <i>D. magna</i>
B08	Loïc Thurre	Quantifying load and taxonomy of arbuscular mycorrhizal fungi in plant roots by long-read sequencing
B09	Kelly Tragash	The impact of a long-term drought manipulation on microbial metabolism and soil carbon cycling
B10	Jonathan von Oppen	Reconstructing snow time-series for modelling alpine microclimate
B11	Heleen Vos	Remote sensing of vegetation degradation during dust-inducing drought in South Africa
B12	Anlun Wei	Identification of genes required for growth on MBOA in the maize root bacterium <i>Sphingobium</i> LSP13
B13	Annalena Zengerle	Effects of Solar Photovoltaic Installations on Red Kite (<i>Milvus milvus</i>) Flight Behaviour in Spain and Portugal

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Measuring $\delta^{15}\text{N}$ in Low-Biomass Flatworms: A Denitrifier Method Approach

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Despite the ubiquity, high abundance, and likely importance of microturbellarians in benthic food webs, their trophic ecology remains poorly characterized. Stable isotope analysis, an analytic technique that quantifies the ratios of heavy to light stable isotopes, is a commonly used tool for investigating food-web structure. Particularly, the proportion of the rare ^{15}N and the more common ^{14}N , denoted as $\delta^{15}\text{N}$, is widely used as an indicator of trophic position due the characteristic enrichment of ^{15}N between trophic levels. However, conventional isotope ratio mass spectrometry typically requires milligrams of biomass, limiting the study of meiofaunal taxa. Here, we evaluate the nitrogen denitrifier method as an alternative approach for determining $\delta^{15}\text{N}$ values from few specimens of low-biomass flatworms. We estimated the amount of Nitrogen per worms constructing calibrations curves and evaluated the effect of different preservation techniques. Method performance was assessed using laboratory cultures of *Macrostomum* species as well as field-collected specimens. In addition, controlled trophic chains involving 3 *Stenostomum* species were established to test whether expected isotopic enrichment across trophic levels can be reliably detected using this approach. Our results show that the denitrifier method allows accurate $\delta^{15}\text{N}$ measurements from as little as six pooled *Macrostomum* specimens enabling trophic analyses of organisms that are typically difficult to access in conventional isotope techniques. This methodological approach provides a practical framework for incorporating microturbellarians into stable-isotope-based food-web studies and contributes to a better understanding of the ecological roles of meiofaunal flatworms in aquatic ecosystems.

Hydrogen isotopes of fatty acids as a proxy for carbon use efficiency in soil microbes

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The hydrogen isotope composition of fatty acids (d^2H FA) is strongly associated with central metabolism in microbes. In single species cultures of diverse bacteria, d^2H FA values increase with higher tricarboxylic acid cycle (TCA) activity. If this signal is conserved in complex communities, d^2H FA values can serve as an in situ proxy for group-specific microbial metabolism, with potential applications for reconstructing past community metabolism and modern CUE. Here, we used single- and two-species cultures of the Gram-positive *Bacillus aerius* and the Gram-negative *Pseudomonas* sp. grown on glucose or succinate, to test whether species interactions impact the metabolic signals encoded in d^2H FA values. Consistent with previous investigations, we found that d^2H FA values from single-species cultures grown on succinate, the TCA-cycle intermediate, were as much as 210 ‰ higher as compared to cultures from the same species when grown on glucose. These differences were generally maintained in two-species cultures. However, glucose-cultured *Pseudomonas* d^2H FA values were approximately 78 ‰ higher in two-species culture than in single-species culture due to the uptake of acetate released by *Bacillus*. These results demonstrate that high d^2H FA values reflect high TCA-cycle activity in two-species cultures, providing a foundation for applications in more complex systems.

Bacterial metabolization of host-specific secondary metabolites

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Plant roots are colonized by a diverse array of microbes, collectively known as the root microbiota. Plants shape the microbiota by secreting root exudates into the rhizosphere. Root exudates contain secondary metabolites that affect microbiota by semiochemical or toxic properties. *Arabidopsis thaliana* (*Arabidopsis*) and *Zea mays* (maize) exude secondary metabolites called coumarins and benzoxazinoids, respectively, and both alter their root microbiota composition and affect plant growth and health. Recently, our lab showed that various maize root bacteria could degrade the maize secondary metabolite MBOA, while selected non-host *Arabidopsis* bacteria did not. This finding suggests microbial adaptation to host-specific metabolites. To test whether adaptation to host-specific metabolites is common, we investigated the bacterial tolerance and metabolic capacity of host-specific metabolites using maize root bacteria and *Arabidopsis* bacteria. We monitored the growth of individual strains in the presence of *Arabidopsis*-derived coumarin scopoletin and followed compound degradation indirectly by scopoletin fluorescence. While most of the *Arabidopsis* bacteria and maize root bacteria did not metabolise scopoletin, a subset of *Arabidopsis* bacteria degraded scopoletin, which was confirmed by HPLC-MS analysis. For mechanistic understanding of this degradation, we are identifying degradation genes and degradation products. Additionally, we are testing how these degraders interact with the host plant.

Climate adaptation in alpine and lowland Brassicaceae

Katja Springer¹, Thomas Dorey¹, Yvonne Willi¹

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Climate can impose strong selection on natural populations, yet the capacity of alpine plants to respond to ongoing climate change through adaptation remains poorly understood. In this study, we tested for evidence of climate adaptation in six native Brassicaceae species along an elevational gradient in the Swiss Alps, including three alpine species (*Arabis caerulea*, *Cardamine resedifolia*, *Noccaea corymbosa*) and three low- to mid-elevation species (*A. ciliata*, *C. hirsuta*, *N. caerulescens*). Seeds were collected from low, mid, and high elevations within their distributions along two mountain transects. The lab-propagated plants were reciprocally transplanted across six field sites ranging from 489 to 2816 m a.s.l., encompassing their home ranges as well as beyond their lower and upper elevation limits. We monitored survival, growth, flowering phenology, and reproduction across all sites. Our approach allows us to assess whether populations are adapted to their home climate, whether adaptation is associated with life-history trade-offs across elevational gradients, and to identify the critical life stages during which climate adaptation affects performance. This work provides insight into the role of adaptation through natural selection in shaping population persistence under accelerating climate change, with implications for conservation and management.

Cold stratification affects the composition of germinating grassland species

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The persistence of local plant populations of grassland communities strongly and thus the resilience of grassland ecosystems depends on a viable soil seed bank. In line, soil seed banks are important for long-term conservation of declining grassland species as well as for restoration ecology, in particular under changing climate. However, the contribution of soil seed banks to the maintenance of communities is driven by environmental filtering. Climatic cues like temperature, moisture and duration of frost days determine the germination niche of plant species. In Switzerland the amount of frost days has decreased by 80 % since the 1960s. We therefore studied the impact of the cold stratification duration on the restoration potential of soil seed banks of calcareous grasslands and the ecological memory they harbor.

Soil samples were collected within 100 m² plots in each of 54 grassland remnants in the northwestern Jura mountains of Switzerland. Samples were subjected to three cold stratification treatments to simulate changing winter duration. 16 weeks of cold stratification at 4°C to simulate past winter duration, 8 weeks of stratification at 4°C, representing current winter duration in Central Europe, and no cold stratification to simulate an extreme future scenario.

Emerging seedlings were identified to species level and compared with the aboveground vegetation data from a long-term survey (1986, 1996, 2016, and 2024). Specifically, we tested for the effect of the stratification treatments and compared similarity of the emerged communities with those aboveground reported in the surveys, with the added goal of finding optimal restoration contexts of habitat specialists. Preliminary results show that the 8-week cold stratification treatment led to the highest species richness and number of emerging seedlings. The lack of cold stratification led to a lower species richness and lower similarity in the emerged species composition among remnants. The results provide important insights into the conservation and restoration of calcareous grasslands. To infer which species show sufficient recruitment from the soil seed bank, as well as the species that fail to do so and the respective role of cold stratification. The results on ecological memory show that under changing climate species composition might drastically be altered and could lead to reduced grassland resilience.

Hydroclimate reconstruction from Uzuntarla Cave (Thrace, Türkiye) and the connection to the water supply of Constantinople

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Hydroclimatic variability in the eastern Mediterranean during the last two millennia remains difficult to characterize because of strong spatial precipitation gradients and limited high-resolution terrestrial proxy records. These uncertainties also constrain our understanding of the climatic conditions under which major urban water-supply systems developed and operated. Constantinople (modern Istanbul), one of the largest cities of Late Antiquity and the medieval world, relied partly on an extensive aqueduct network transporting water from the Thracian mountains (Crow, 2019). Investigating the hydroclimatic background can provide valuable insights into the relationship between climate variability and societal responses to population growth and increasing water demand. Speleothems are mineral deposits that form within caves from water percolating through the soil and epikarst and serve as natural archives of past environmental conditions. They can reveal information about changes in local conditions (soil, vegetation and climate variations) and regional or global climate patterns (Fairchild and Baker, 2012). Because speleothems grow in layers, they can preserve long and continuous records of hydroclimate variability. In addition, precise uranium-thorium (U-Th) dating can provide robust chronological control. Here we present a speleothem stable isotope record from Uzuntarla Cave in Thrace, Türkiye, located near the aqueduct network, at semi-annual resolution. Building on the previously published record of Morgan et al. (2025), this study focuses on the last two millennia using a revised chronology integrating Uranium-Thorium dating, radiocarbon measurements, and indicators associated with historically documented earthquakes. By comparing the most recent part of the speleothem isotopic record ($\delta^{15}\text{C}$ and $\delta^{18}\text{O}$) with ERA5 climate reanalysis data, we explore potential relationships between precipitation, seasonality, and groundwater recharge, that ultimately affects the water-supply of Constantinople.

References:

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Devilish Goat Feet in the Parish House? Mummified Archaeozoological Finds from the 17th–19th Century in Lantsch/Lenz (Graubünden, Switzerland)

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During renovation work on the parish house in Lantsch/Lenz, in the canton of Graubünden, unusual archaeobiological finds dating from the 17th to 19th centuries were recovered from floor cavities. The bulk of the material consists of nearly 100 mummified feet from small ruminants. As part of a collaborative project involving, among others, the Archaeological Service of Graubünden and Integrative Prehistory and the Archaeological Science (IPNA) at the Department of Environmental Sciences, these finds were investigated by students during a one-week intensive course. The results suggest evidence of apotropaic/superstitious practices.

A voxel-based approach for radiation modelling in urban environments with trees

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Cities are major contributors to global greenhouse gas emissions, while also being highly exposed to the consequences of climate change, such as extreme weather events. Climate change mitigation and adaptation strategies urgently need to focus on cities and their shift towards sustainability.

This is why we are developing a 3D eco-physiological model that will simulate CO₂, water, and energy exchanges between vegetation and the urban atmosphere for neighbourhood scale areas. Here, we present the final version of the first module of the model, which describes the complete radiation component. The model represents the urban environment using a 3D isometric voxel structure generated from geospatial data, including detailed tree canopy geometry. This representation is analysed through a ray tracing algorithm to derive key radiative parameters such as sky view factor, shading, and light transmissivity. Shortwave and longwave radiation fluxes are subsequently calculated for any selected volume within the domain using measured incoming shortwave radiation, longwave radiation, and air temperature from a meteorological tower as forcing data.

To validate the model, we compared its outputs against field measurements collected from street level microclimate stations at three locations (two in Basel and one in Zurich) and benchmarked it against the TUF-3D pedestrian model. The results show that our simple and fast approach accurately predicts both shortwave and longwave irradiance, with errors primarily attributed to discretisation and physical simplifications. The error magnitudes remain comparable to other low-resolution models used in urban environment. By providing high spatial resolution in both the horizontal and vertical dimensions, the model is intended to improve the representation of interactions between trees and the urban environment, as well as their influence on urban microclimates. In this way, it may contribute to more detailed assessments of vegetation effects and support the planning of more climate resilient cities.

Time series RNA-seq shows temporal expression of host resistance related genes

Luca Pecalli¹, Dieter Ebert¹

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Coevolution has been suggested to be a major driver of biodiversity, shaping genetic and phenotypic evolution in natural populations. The crustacean *Daphnia magna* and the bacteria *Pasteuria ramosa* have been coevolving for at least 15 million years. *D. magna* genotypes differ strongly in their susceptibility to given isolates of *P. ramosa*. Genomic studies have identified genomic regions enriched for glycosyl transferases, but strong linkage prevented to pinpoint the genes that are responsible for these resistance polymorphisms. Parasite attachment is believed to be driven by the interaction between the proteins present on the surface of the parasite and the sugars attached to the glycoproteins on the cuticle of the host. To better characterize the molecular actors underlying this interaction, we conducted a time series transcriptomic study in *D. magna* across the entire moulting cycle. This approach allowed us to resolve the temporal expression of resistance-associated genes and to link them to genes involved in cuticle synthesis. We identified key glycosyltransferases are expressed during the building of the new cuticle and determined their co-expression with specific cuticular proteins. Moreover, we pinpointed three strong candidate genes for functional validation via knock-out or knock-down approaches in future work. Our works complements previous studies in creating a holistic picture of the evolution and maintenance of genetic diversity at resistance loci.

Evolution of threespine stickleback dorsal spines via *hoxdb* gene regulation

Carlos Manuel Herrera-Castillo, Tanja Brechbühl, Antoine Fages, Andrew MacColl, Laura Louise Dean, Patrick Tschopp, Daniel Berner

The repeated emergence of similar phenotypes in independent populations is a widespread feature of evolution, yet the extent to which repeated evolution reflects shared molecular mechanisms, and the factors that determine this similarity, remain unclear. Here, we investigate the genetic basis of dorsal spine reduction in threespine stickleback fish, an adaptive trait that has evolved repeatedly in freshwater populations. Phenotypic analyses of crosses between a spine-reduced population from Scotland and the ancestral marine form reveal a major-effect locus, with the spine-reducing allele acting dominantly and influencing body patterning. Bulk segregant analysis maps this effect to a single region on chromosome VI that overlaps the *hoxdb* gene cluster. Transcriptomic analyses of larval stages show a gain of *hoxdb* expression in the developing spine region of spine-reduced fish, consistent with the dominance of the derived allele. Together, these results indicate dorsal spine reduction in threespine stickleback through cis-regulatory changes at *hoxdb*, a mechanism found to mediate dorsal spine evolution in a different species of stickleback fish too. These findings show the role of *hox* genes in adaptive divergence between natural populations within a species and provide a clear example of parallel evolution at the molecular level between species.

Influence of weather conditions on social associations in wintering White-winged Snowfinches

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Short-term weather events that modify resource distribution can influence animals' decisions to join or leave a group. While connections to conspecifics may usually provide benefits, such as increased information transfer, they can become irrelevant or even costly when competition increases. Flexibility in social behaviour enables animals to cope with variation in social costs and benefits resulting from changing ecological conditions. We investigated this social flexibility in snowfinches (*Montifringilla nivalis*), a bird species adapted to alpine habitats where weather can change rapidly. In winter, snowfall and temperature strongly affect food availability and foraging needs. We observed colour-ringed snowfinches at two study sites in the Swiss Alps to understand how individuals adjust their sociality to weather changes and how weather conditions shape their group structures. We assessed social associations by recording which individuals foraged together in groups. Preliminary results show that snowfinches exhibit uniformly weak associations under harsher conditions, whereas milder conditions reveal a mix of strong and weak ties, indicating more pronounced social preferences. These findings suggest that in adaptation to alpine environments, social behaviour in snowfinches is context-dependent and variable.

The wandering years: Movement strategies of a raptor across the juvenile stage

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Movement strategies are shaped by age, experience, and access to resources, resulting in changes in space use throughout an individual's life. In long-lived raptors, juveniles disperse after fledging and may range for months or years before reaching maturity, often using temporary settlement areas. Early-life movements are expected to reflect exploratory behaviour and low foraging efficiency, whereas older juveniles should show residency and resource selectivity. However, juvenile movement and habitat use remain poorly known compared to adult breeding and migration. We tested these ideas in the Egyptian vulture (*Neophron percnopterus*), a long-lived scavenger that reaches maturity after four years of age. We tracked 17 GPS-tagged juveniles from their natal nests in the Iberian Peninsula across successive years. We quantified age-related changes in dispersal behaviour using movement metrics, including distance to the nest, travelled distances, and the use of temporary settlement areas. We then analysed space use and resource selection during the spring–summer period using movement-based home ranges and resource selection functions, and classified behaviour into resting, foraging, and soaring. Preliminary results show that in the first year, juveniles exhibit exploratory dispersal with no residency, whereas from the second year onwards, they move directly to the same summer and winter areas and exhibit prolonged residency, indicating emerging site fidelity. Behavioural time budgets also changed with age, with younger juveniles spending more time in foraging. Together, these results indicate that juvenile dispersal is a dynamic behavioural phase in which movement strategies shift from exploration to directed space use as experience accumulates.

Remotely-sensed impacts of NSWRM implementations in Switzerland during the summer 2026 drought of record

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Summer 2026 was the most severe drought Switzerland has experienced since systematic climate records began and caused significant financial losses for the Swiss agricultural sector via declines in yields of crops and products like maize, potatoes, hay and milk. To mitigate the negative impacts of increasingly common droughts like this one, there has been a surge in interest from the federal government, cantonal governments and individual farms in implementing natural small water retention measures (NSWRM, sometimes called Schwammland approaches) such as infiltration swales, retention ponds, reduced tillage, soil organic matter amendments, agroforestry systems and beaver-dam analogues, many of which have already been implemented at pioneering farms in different parts of Switzerland. The weather conditions during summer 2026, particularly the long summer period with little to no rainfall, provide stress-test conditions to assess whether these implementations provided measurable drought-mitigation services during the drought of record. To that end, we developed a high-throughput data analysis pipeline for high temporal and spatial resolution remotely sensed datasets to search for clear areal signals of beneficial impacts to vegetation, land-surface temperature and soil moisture from NSWRM at 15+ farms during the period of May 1st to September 15th, 2026. Initial results suggest that evidence of areally distributed impacts of the NSWRM is difficult to detect by a before-after-control-impact comparison with adjacent no-implementation fields in 2026 and with the same field's before-implementation response to historic droughts. Ongoing work seeks to compare remotely sensed results to field results and examine whether 1) NSWRM impacts only occur in a limited footprint, 2) remotely sensed indicators are ill-suited or too low-resolution to capture NSWRM impacts, or 3) that the exceptional weather conditions limited NSWRM's ability to provide drought mitigation services during this period. The analysis provides complementary findings to many ongoing field projects in Switzerland that seek to quantify the impacts of NSWRM with the goal of identifying the strengths and limitations of such approaches as climate-change adaptations.

Glacier retreat drives species turnover and functional convergence across spatial scales and trophic levels

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Glaciers around the globe are retreating at an accelerated rate due to climate change, leading to the emergence and development of new ecosystems in previously ice-covered areas. However, we still lack a systematic understanding of how biodiversity responds to glacier retreat across different spatiotemporal scales and biodiversity dimensions. Here, by assembling species community data from the literature spanning 52 glacier forelands worldwide, we assess how taxonomic, functional, and phylogenetic diversity of plants, carabid beetles, and spiders respond to glacier retreat and climatic variables. We found that local (alpha) and regional (gamma) diversity increase over time in postglacial ecosystems. This pattern is most pronounced for plant taxonomic diversity, but less evident for carabid beetles and spiders. Despite local increases in plant diversity, at the regional level, richness per square meter decreased on average by 1.4% per year. Taxonomic beta diversity within and between glacier forelands was very high, averaging $93 \pm 0.6\%$ dissimilarity across organisms, whereas functional and phylogenetic beta diversity averaged at $40 \pm 13\%$ and $70 \pm 15\%$, respectively. Temperature was a strong predictor of beta diversity, with warmer glaciers showing higher species turnover along their successional gradients. Together, glacier forelands harbor unique species assemblages, resulting in strong taxonomic spatial turnover, while species share similar traits that enable them to colonize and establish in these extreme and dynamic environments. Our findings highlight that biodiversity responses to glacier retreat cannot be fully captured by taxonomic or local-scale patterns alone, and emphasize the high conservation value of glacier forelands given the uncertain consequences of increasing global temperatures for poorly protected glacial biodiversity.

Climate change reshapes the agricultural potential of Europe: a data-driven assessment of crop suitability to 2100

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Agricultural land already occupies approximately one third of the global ice-free land surface. However, the global population continues to increase, and dietary changes towards more animal-based nutrition entail a growing demand for agricultural land. Europe represents an important pillar of the global food system, however, it is home to some of the world's most degraded soils and is warming faster than any other continent on the planet, threatening agricultural productivity and altering the spatio-temporal distribution of suitable agricultural land. Determining where agricultural production can be sustainably maintained under climate change in the future has ecological, economic, and social conflict potential. Conflicts are particularly evident when considering conservation efforts to protect 30% of terrestrial surfaces by 2030, as agreed in the Kunming-Montreal agreement. Resolving this conflict of interest between the stability of the food system and conservation requires, as a first step, robust spatial modelling of suitable agricultural areas.

Agricultural Land Suitability Analysis (ALSA) models allow the identification of suitable agricultural land at large spatial scales and are therefore pivotal for guiding the transformation of the European food system under climate change. Yet, current ALSA applications remain often limited to a few major crops, are mostly confined to Asia and Africa with only a small number of continental or global assessments, and rarely incorporate climate change projections. Furthermore, widely adopted ALSA models still rely on outdated and opaque crop-environment relationships, which are often transferred beyond the regions or crop varieties for which they were originally derived, and sometimes combined through subjective expert-assigned weights. More recent machine-learning approaches and species distribution models (SDMs) address some of those limitations by deriving crop-environment relationships directly from observed data. However, they introduce their own weaknesses, including sensitivity to sampling biases, over-reliance on single algorithms, or extrapolations into climates beyond environmental conditions represented in their training data, all of which can result in inaccurate and biased predictions.

The primary objective of this project is to couple the data-driven crop niche parametrization used in SDMs with the practice-oriented approach of a modern suitability model to overcome the existing limitations and assess the agricultural potential of Europe under climate change. For 40 European crops, models were fitted using ensembles of machine learning and advanced statistical algorithms to project their agricultural suitability at a spatial resolution of 1 km² under SSP1-2.6, SSP3-7.0,

and SSP5-8.5 climate scenarios from 1990 through to 2100. We find (i) an overall decline in suitable agricultural land for most crops, including widely cultivated staples such as maize, grapes, and olives; (ii) a pronounced north–south gradient, with climate change creating newly suitable areas in northern Europe while increasing drought constraints intensify losses in the Mediterranean region; (iii) substantial delays in optimal sowing dates for annual crops; and (iv) marked contrasts between perennial and annual crops, with annual crops being able to exploit changing intra-annual climatic conditions and partly buffer climate-driven losses. These results lay the foundation for a larger research effort that will identify future spatial conflicts between food security and biodiversity conservation.

Global Economic Impacts of Solar PV-Induced Land-use Change

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The growing demand for solar energy may bring about considerable land-use implications. Studies have shown that a large proportion of solar photovoltaic (PV) installations have been sited on previously cultivated agricultural land. Multiple studies have also highlighted a substantially increasing need for land to meet the future solar electricity demand, and the potential solar-driven land change. However, they have mostly focused on projecting the potential land area of solar expansion and it remains unknown how the global increase in solar land use would interact with both the electricity and agricultural markets. This study aims to explore the implications and dynamics between solar PV and agriculture on a global scale through land competition by explicitly taking land as a factor in solar power production into account. We first examine the relationship between existing solar farms and agricultural suitability. The results suggest that most of the current PVs are deployed on moderately or highly agriculturally suitable land, which could result in land competition with agricultural activities. We then employ a recursive dynamic global Computable General Equilibrium (CGE) framework with disaggregated solar power sectors. A solar-land-expansion (SLE) scenario with a large solar land demand is simulated to compare with a business-as-usual scenario with negligible solar land demand. The results show that under the SLE scenario, around 0.04% of global managed agricultural land area occupied by solar PV in 2040 is simulated, and half of the occupied area is pastureland. In addition, we also find a global drop in solar power share in the electricity mix when taking solar land value and competition into account, implying an overestimation of the solar PV growth. For agricultural market, on the other hand, our results suggest that large-scale solar PV expansion is unlikely to cause a substantial impact on both crop and livestock markets, despite an increasing demand for land associated with solar deployment. This is due to a relatively small land area of solar PV compared to the total agricultural land, which generated a limited response in agricultural prices and production.

A01: A pangenome for *Daphnia magna*

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Almost everything we know about genome-wide variation within species comes from comparing short sequencing reads against a single reference genome. This works well for relatively conserved regions, but structural variation, such as duplicated or rearranged sequence, and sequence missing from the reference are largely invisible to this approach. Even worse, reads from regions the reference does not represent are often mismapped, which adds noise and bias to genetic analyses. As a result, variation associated with phenotypes of interest can remain undetected, or false positive associations can arise.

Pangenomes address this by combining the genomes of many individuals of a species, or of closely related species, into a graph that holds alternative versions of each genetic region side by side. This separates the core genome, shared by all individuals, from the variable genome, which differs among them. The variable fraction can hold genes involved in immunity, stress response and environmental sensing. However, most evidence comes from humans and domesticated species, so we know little about how much structural variation wild populations, especially of invertebrates, carry, and what it does.

We are building the first pangenome for a crustacean, the water flea *Daphnia magna*, one of the best-studied ecological model organisms. The planktonic filter feeder inhabits ponds and is a long-established system for ecotoxicology, host–parasite interactions and adaptation to the environment. So far, we have assembled 33 *D. magna* genomes, including a new chromosome-scale assembly of the most widely used genotype, which anchors the pangenome. We combine it with the *D. magna* Diversity Panel, which spans the species' geographic range and offers more than 200 re-sequenced genotypes, extensive phenotypic, and ecological as well as climatic data. This allows us to quantify how much of the genome is core versus variable, and to test which structural variants are associated with traits and environments, with far less reference bias than single-reference approaches allow.

The best-known hotspots of variation associated with parasite-resistance in *D. magna* are structurally complex, with haplotypes carrying entirely different sets of genes. If such variation is widespread across the genome, the prevailing SNP-centric view of adaptation in natural populations misses a substantial part of the picture. By making this hidden variation accessible, our pangenome will help to pinpoint genomic regions under selection and offers a template for studying adaptation in other wild species.

A02: Cold microhabitats as refugia for alpine specialists above the treeline

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High-mountain ecosystems are among those most exposed to climate warming, yet their topographic complexity creates a mosaic of thermal microhabitats that can decouple local conditions from regional climate. Cold microhabitats, such as snowbeds and cold-air hollows, may therefore act as microrefugia, allowing alpine specialists to persist as surrounding environments warm. However, whether cold microhabitats measurably enhance the retention of alpine species across broad spatial extents remains poorly understood: most microrefugia studies operate at fine scales, whereas work conducted over biogeographically relevant extents rarely resolves the microhabitats at which refugial processes occur.

Here, we assess the contribution of thermal microhabitats to alpine plant diversity and specialist retention across the alpine zone of Switzerland. We combine a large, multi-source compilation of vascular-plant occurrences with targeted field inventories, thereby achieving broad spatial coverage while addressing the incompleteness and spatial bias of existing occurrence data in complex mountain terrain. Because apparent species absence may reflect insufficient sampling rather than ecological processes, we explicitly quantify inventory completeness using multiple estimators and compare their performance to assess the robustness of subsequent inference. Field surveys specifically target under-sampled grid cells to improve the reliability of local inventories.

Thermal microhabitat conditions are characterised using the high-resolution soil-temperature basemap for the European Alps developed within the MAPLe project and aggregated across multiple spatial grains. We then test how thermal heterogeneity relates to taxonomic, phylogenetic, and functional plant diversity, with particular emphasis on the retention of alpine specialists.

We hypothesise that the association between cold microhabitats and alpine-specialist retention strengthens towards finer spatial grains, where thermally distinct patches can be resolved explicitly, whereas at coarser grains their effects become diluted or confounded by broader environmental and habitat gradients. By jointly accounting for sampling completeness and spatial grain, this study aims to identify the conditions under which cold microhabitats function as realised refugia for alpine flora. Establishing the scales at which these refugia operate is essential for evaluating their relevance to biodiversity conservation under ongoing climate warming.

A03: Habitat selection of a rare bird species (*carduelis citrinella*) and suggestions for its conservation in the UNESCO Biosphere Entlebuch**Amélie Marie Beauregard¹, Alejandra Morán Ordóñez¹, Franziska Korner-Nievergelt¹**¹ Department of Environmental Sciences, University of Basel, Basel, Switzerland.

Habitat structures and conservation of the Citril Finch (*Carduelis citrinella*) in the UNESCO Biosphere Entlebuch The Citril Finch (*Carduelis citrinella*) is a mountain bird species whose population in Switzerland has been on the decline. Although general habitat requirements have been described for populations in other regions, detailed knowledge of habitat use during the breeding season in the UNESCO Biosphere Entlebuch is currently lacking. This is particularly relevant because the species occupies only parts of otherwise suitable habitats and shows high fidelity to its breeding grounds. Understanding which specific habitat structures are associated with its occurrence is therefore essential for developing effective and locally adapted conservation measures.

This study investigates which habitat structures are associated with Citril Finch occurrence during the breeding season in the Schrattenfluh area of the UNESCO Biosphere Entlebuch. Here, habitat structures encompass diverse features of the landscape, such as vegetation characteristics, rocks, water sources, and other landscape elements. The study further examines qualitatively how local agricultural practices influence habitat suitability.

A mixed-methods approach combines a systematic in-field examination of presence and absence points, focal individual observations, vegetation assessments, and semi-structured interviews with local farmers. Field data is combined with publicly available GIS data. A binomial generalised linear model (GLM) is used to identify habitat and landscape variables associated with Citril Finch occurrence. Qualitative analysis of the interviews complements the ecological modelling by providing insights into land-use practices, habitat management, and local knowledge. Documented plant species and behavioural observations provide additional information on the characteristics and use of occupied habitats.

This study aims to identify habitat structures that are particularly relevant to the Citril Finch during the breeding season in the Entlebuch area. The results will provide a basis for defining targeted habitat enhancement measures in the UNESCO Biosphere Entlebuch that will hopefully benefit the citril finch. More broadly, the study contributes to improving the evidence base for the conservation of a declining species for which Switzerland has a high national responsibility.

A04: Future climate conditions increase severity of soilborne diseases in table beets

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With climate change, the nature and intensity of crop diseases are likely to change (1). In Switzerland, wetter springs and hotter and drier summers are suspected to have led to a higher incidence of soilborne diseases in table beets (*Beta vulgaris*)(2). However, knowledge of how different soilborne pathogens respond to climate change is scarce. To investigate climatic effects on fungal community dynamics and plant health, beets were grown in six naturally disease-infested agricultural soils in phytotrons under end-of-century climate projections (RCP 4.5 and RCP 8.5) compared with a past control climate. Beet disease development was monitored over an entire growing season and during six months of storage. Climate effects on disease outcome were especially severe in the first half of the growing period, represented by increased post-emergence damping-off in the majority of soils under future climatic conditions. Fungal community profiling of beet seedling roots showed that while overall community composition changed minimally under future climate treatments (~5% of variation explained), the increase in post-emergence damping-off was associated with an increased abundance of a *Fusarium* spp. At harvest, a yield reduction of 25-60% was observed under future climate conditions. Abiotic stressors, including heat and drought, were the main drivers of biomass reduction under future climate conditions, while pathogens played a secondary role in further reducing beetroot weight. Future work will focus on assessing the role of oomycetes in climate-driven disease development and disentangling whether warming-associated increases in post-emergence damping-off reflect enhanced pathogen virulence and growth or reduced plant immunity.

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A05: Whose knowledge shapes the landscape? Towards transformative and just biodiversity planning

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Biodiversity conservation increasingly recognises the importance of Indigenous and local knowledge, yet recognition does not necessarily mean influence. Knowledge may be incorporated into conservation planning while the authority to define priorities, evaluate evidence, and make decisions remains elsewhere. My PhD examines this gap between knowledge and authority, asking how plural knowledge systems and justice-oriented arrangements might transform landscape planning towards biocultural resilience and ecosystem connectivity. The first stage of my research examines the structures that shape this evidence-to-governance process. In Chapter 1A, a critical review of environmental justice and landscape governance identifies scalar separation and epistemic extraction as important barriers to transformative environmental governance. I use epistemic extraction to describe situations in which knowledge is incorporated into governance without a corresponding transfer of decision-making authority. This raises a broader empirical question: when Indigenous and local knowledge enters landscape-scale conservation planning, does authority move with it? Chapter 1B, currently underway, addresses this question through a systematic review of tropical landscape-scale conservation and land-use planning. Rather than asking only whether Indigenous and local knowledge is included, I examine how it enters planning and what happens to it once it does. The review focuses on three linked dimensions: (1) whether Indigenous and local knowledge is considered; (2) the mechanisms through which it enters planning, such as participatory mapping, consultation, knowledge co-production, or governance arrangements; and (3) the degree of decision-making authority associated with that knowledge, ranging from data provision and consultation to co-decision or binding authority. I also examine which forms of knowledge and indicators are prioritised, how evidence is produced and attributed, and whether its uptake in planning is reported. The broader PhD moves from diagnosis towards empirical investigation in tropical forest landscapes. Subsequent case studies will explore how plural knowledge systems, scale, and authority interact in landscape planning, including where different forms of knowledge converge, conflict, or are rendered invisible. Rather than treating knowledge integration as an end point, this research asks what institutional arrangements are required for knowledge to shape decisions, and for authority to be shared alongside it. Ultimately, the aim is to understand how landscape planning can move beyond the inclusion of knowledge towards more just forms of biodiversity governance that support both biocultural resilience and ecosystem connectivity.

A06: Soil Microbiome-induced DNA Methylation Mediating Feedbacks on Plant Growth

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Soil microbiomes modulate plant performance through plant-soil feedbacks (PSFs) (1), but how plants perceive and respond to these feedbacks is still unclear. To differentially condition soils, we use maize lines that differ in the exudation of benzoxazinoids (BXs), multifunctional secondary metabolites that also structure soil microbiomes (2). The reference genotype of *Arabidopsis thaliana*, Columbia-0, grows better and is more resistant to pathogens on BX-conditioned soil microbiomes (3). However, natural *Arabidopsis* accessions showed high variation in this growth response (4). Through genome-wide association analysis, we identified several candidate genes associated with growth feedback. Among these was Mediator of Microbiome Feedback 2 (MMF2), which encodes a Tudor-like domain-containing protein, pointing to a possible involvement of epigenetics in PSFs. The *mmf2* mutant lost the beneficial growth response to BX-conditioned soil microbiomes. In roots, the *mmf2* mutant showed an altered transcriptional response to BX-conditioning compared with the wild type. Whole-genome bisulfite sequencing further revealed reduced genome-wide CHH methylation in the *mmf2* mutant. Loss of MMF2 reversed the direction of BX-induced DNA methylation in roots, from predominantly hypermethylation in the wild type to hypomethylation in the *mmf2* mutant. Taken together, our study shows that MMF2 is required for the beneficial microbiome feedback and suggests that soil microbiome-induced DNA methylation contributes to plant growth feedbacks.

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A07: The global geography of non-native mountain floras**Marco Túlio Pacheco Coelho¹, Jonathan von Oppen¹ and Sabine Rumpf¹**¹ Department of Environmental Sciences, University of Basel, Basel, Switzerland.

Mountain ranges harbor exceptional biodiversity and are often regarded as relatively sheltered from non-native plants because of their harsh climates and limited accessibility. However, how far non-native plant redistribution has progressed globally, and why some mountain ranges accumulate far more non-native species than others, remain poorly understood. Here we integrate nearly 16 million plant records across 4,953 named mountain ranges to examine the global distribution of non-native floras and the environmental and human conditions associated with their accumulation. Non-native plants occur in all but two of the 2,145 sufficiently sampled mountain ranges, revealing widespread occurrence despite pronounced differences in non-native plant richness. Larger, more productive mountain ranges with diverse habitats, denser human populations and larger surrounding pools of non-native species harbor more non-native plant species. Non-native plant richness also increases with annual precipitation and decreases with temperature seasonality. A spatial model integrating these conditions with mountain-range area and sampling differences explains 77.4% of deviance in observed non-native plant richness. Accounting for these differences reveals that high non-native plant richness does not necessarily indicate unusual accumulation: only 33 of the 214 mountain ranges with the richest non-native floras also contain unexpectedly many non-native species for their environmental and human setting. Conversely, other sufficiently sampled mountain ranges harbor substantially fewer non-native species than expected, identifying coldspots that cannot simply be equated with gaps in botanical knowledge. This distinction also identifies unexpectedly rich non-native floras within protected areas, extending its relevance to landscapes explicitly designated for conservation within mountain ranges. Despite their widespread occurrence, non-native floras retain strong regional signatures: across most continents, their largest documented native-range contribution comes from other regions within the same continent. Comparisons within individual mountain ranges show lower non-native plant richness in higher terrain, colder climatic belts and above treeline, after accounting for habitable area and inventory completeness. Together, these findings show that non-native plants are already widespread across sufficiently sampled mountain ranges, but their accumulation remains closely associated with environmental conditions, human activity and regional species availability. Strong regional signatures and lower non-native plant richness in colder, higher environments suggest that geographical and environmental constraints continue to structure this redistribution, while unexpectedly rich non-native floras also occur within protected areas. Our assessment thus reveals that the relative shelter offered by mountain

ranges is neither uniform nor absolute: understanding their non-native floras requires considering environmental constraints alongside human access and the regional availability of non-native species.

A08:Planning the future of barely studied glacier forelands: filling the gaps before the ice cracks

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Glacier forelands are often described as valuable future ecosystems, emerging progressively as glaciers retreat. Society's concern is mostly directed at managing these areas over the coming decades, while the past conditions and present mechanisms that explain how biological communities develop there remain largely unknown at the local scale. For instance, a single field campaign in four glacier forelands in 2024 revealed a remarkably rich and poorly documented arthropod fauna, including 76 spider species and strong compositional differences among neighbouring forelands. Today, while the number of vanished glaciers increases and most Alpine glacier systems are approaching the point at which almost no ice remains, forelands are reaching their maximum spatial extent: the production of newly deglaciated habitat declines, succession advances, and established alpine communities progressively colonise them. We are planning the future of these habitats while missing the chance to understand their present.

In my doctoral project, I investigate how biodiversity emerges, becomes locally realised and can be conserved across this transition in High-Alpine Alluvial Habitats. First, I use nested species-distribution models, combining continental occurrence data with high-resolution Swiss records, field observations and environmental predictors, to identify species associated with these habitats and estimate how environmental opportunities may shift. Second, I test whether this regional potential becomes realised biodiversity locally. Field campaigns began in 2024 in the western Valais forelands of Arolla, Zinal, Mont Miné and Moiry, continued in 2025 at Arolla and Moiry, and expanded to Rhône, Mutt, Siedelen and Tiefen in the Furka region, where sampling was repeated in 2026. Using this multi-year dataset on spiders and carabids, together with vegetation, substrate, disturbance and microclimatic measurements, I ask when communities become predictable from habitat condition, whether unexpected biodiversity persists in unlikely habitat states, and where regional suitability fails to translate into realised communities.

Finally, I integrate these relationships with projections of glacier retreat, future ice-free terrain, hydrology, climate change and socio-economic interests. The aim is a spatially and temporally explicit conservation model that identifies which land units should be protected, and when, as habitats emerge, develop, shift or disappear.

A09: What sets the warm edge? The role of biotic constraints on an alpine plant's range limit**Thomas Dorey¹, Katja Springer¹, Yvonne Willi¹**¹ Department of Environmental Sciences, University of Basel, Basel, Switzerland.

Understanding what limits species' distributions is central in predicting how plants respond to a changing environment. While cold range limits are often primarily associated with abiotic constraints, the relative contribution of climatic conditions and biotic interactions in setting warm-edge limits remains poorly understood. Here, we investigated whether biotic interactions limit the performance of the alpine plant *Noccaea corymbosa* near its warm-edge limit. In a reciprocal transplant experiment, we transplanted warm-, core-, and cold-origin populations to sites representing the species' core elevation, warm edge, and elevations beyond the warm edge. Across this gradient, we manipulated pollination and quantified leaf herbivory and florivory to assess their effects on performance. We found no evidence for pollen limitation across elevations, indicating that pollination does not contribute to species' range limits. In contrast, herbivory increased drastically towards the warm edge and beyond. Although leaf herbivory was similar across populations, florivory varied with population origin, with warm-edge populations experiencing lower florivory than other populations. Despite these differences in herbivory pressure, cold populations were more constrained by temperature, whereas warm-edge populations benefited from warmer temperature but were highly constrained by both leaf herbivory and florivory. Overall, our results suggest that pollination is a relatively weak driver of range limitation in *N. corymbosa*, whereas herbivory play a major role in constraining plant fitness near and beyond its warm edge. Our results demonstrate that warm-edge populations may already be adapted to warmer conditions but are instead constrained by biotic interactions near and beyond their warm edge.

A10: Harnessing compost microbes for new crop protection products against foliar diseases

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Plant diseases threaten sustainable crop production, highlighting the need for effective, environmentally friendly crop protection solutions. Composts and compost-derived extracts have been shown to suppress plant diseases, yet the microbial determinants underlying this activity remain poorly understood. Given that composts are largely produced from decomposed plant material, including leaves, we hypothesized that they may contain microorganisms originating from the phyllosphere and thus represent an underexplored source of potential biocontrol agents against foliar diseases. We focus on two major foliar diseases: tomato early blight, caused by *Alternaria solani*, and grapevine downy mildew, caused by *Plasmopara viticola*. To identify microorganisms associated with disease suppression, compost extracts are prepared and applied as foliar sprays to tomato and grapevine plants in bioassays. Microorganisms that successfully establish on leaf surfaces are recovered and characterized using comparative metabarcoding to identify taxa associated with disease suppression. In parallel, microbial isolates obtained from suppressive composts are screened for antagonistic activity through in vitro assays evaluating *A. solani* spore germination and *P. viticola* zoospore motility. Preliminary results show that a selection of compost-derived microbial extracts can suppress *A. solani* infection in tomato. In addition, several microbial isolates recovered from suppressive composts showed inhibitory activity against *P. viticola* in vitro. These findings support compost-derived microorganisms as a promising source of novel biocontrol agents against foliar diseases. Ongoing work focuses on identifying the microorganisms and mechanisms responsible for disease suppression, including antimicrobial metabolite production and induction of plant defenses, to support the development of sustainable crop protection strategies.

A11: Contrasting organic carbon burial and nitrogen cycling across muddy and sandy sediments of the East China Sea shelf

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Carbon and nitrogen cycling in continental shelf sediments regulates the burial of organic carbon and the removal of fixed nitrogen, yet the factors controlling their spatial variability remain poorly constrained. Here we investigated carbon and nitrogen dynamics in muddy and sandy sediments from 13 sites across the East China Sea (ECS) shelf by combining porewater geochemistry, metagenomics, and reaction-transport modeling. Model results showed that total particulate organic carbon (POC) degradation rates decreased across the shelf from approximately 3 to 0.5 mmol C m⁻² d⁻¹, primarily owing to decreasing sediment accumulation rates and organic carbon supply. In both sediments, POC degradation was dominated by aerobic respiration and sulfate reduction. Compared to sandy sediments, muddy sediments exhibited proportionally greater contributions from canonical denitrification, manganese reduction, and iron reduction. Oxidized N (NO₃⁻ and NO₂⁻) reduction pathways also differed markedly between muddy and sandy sediments. Higher denitrification in muddy compared to sandy sediments were primarily driven by faster POC degradation. The relative contribution of denitrification to oxidized N reduction decreased with increasing water depth, whereas the anaerobic oxidation of ammonium (anammox) became increasingly important as the sediments became more oligotrophic and less degradability. By integrating our results with data from an additional 139 sites, we estimate ECS shelf regional POC degradation and burial rates of 2 Mt C yr⁻¹ and 10 Mt C yr⁻¹, respectively. Although muddy sediments occupy less than 30% of the ECS shelf, they account for over 50% of total organic carbon burial. The exceptionally high organic carbon burial efficiency of the ECS shelf, particularly in muddy sediments, is attributed to high sediment accumulation rates. Overall, our results demonstrate that sediment accumulation and organic matter degradability are key controls on coupled carbon and nitrogen cycling, thereby regulating both carbon sequestration and fixed nitrogen removal across the ECS shelf.

A12: Impacts of non-native plant species along an elevational gradient in mountain ecosystems

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Invasive species are a major cause of biodiversity loss. Mountains have historically been less affected by non-native plant species than lowlands, but an increasing number of non-native species are being recorded in mountain ecosystems. Non-native species spread upslope along roads and trails and some even establish in undisturbed habitats. The current and especially future impacts they can have in mountain ecosystems are still less well understood. We present a field removal experiment investigating the impacts of non-native plants along an elevational gradient in the canton of Grison, Switzerland. During summer 2026, we established 224 sites covering an elevation gradient between 531-2639m a.s.l. At each site, two 1 m² plots were selected, one containing a focal non-native species (removal plot) and one containing only native species. Complete vegetation relevés were conducted in both plots, including species composition and abundance. Vegetation height, distance to nearest road and environmental characteristics, including elevation, slope, aspect and land use were also recorded. In the removal plots, all individuals of the target species were subsequently removed, dried and weighed to determine biomass. All sites will be revisited after two years to assess vegetation change over time and the potential re-establishment of neophytes. The nine focal species (*Bunias orientalis*, *Conyza canadensis*, *Erigeron annuus*, *Lupinus polyphyllus*, *Matricaria discoidea*, *Papaver croceum*, *Sedum spurium*, *Solidago canadensis*, *Trifolium hybridum*) were selected to encompass a broad range of life-history and ecological strategies and included both species currently classified as invasive and not. Seven of the nine focal species were recorded at least once above 2000 m a.s.l., demonstrating that several non-native species already occur at relatively high elevations in the study region. This study will allow us to investigate how non-native species influence vegetation composition, whether this varies with elevation and which non-native species have the potential to may become invasive.

A13: The evolution of the extracellular matrix**Anja Haefeli¹, Maxime Policarpo², Walter Salzburger¹, Patrick Tschopp¹**¹ Department of Environmental Sciences, University of Basel, Basel, Switzerland² Max-Planck-Institut für biologische Intelligenz

Every organism that consists of multiple cells possesses a material substance that keeps its cells together. Depending on the different kingdoms of life, the name of this substance changes but the main functions stay the same: connection and communication between cells. In animals this substance is called the extracellular matrix (ECM). Communication between cells can have different effects. Signals from the ECM to the cells can make them proliferate, differentiate and migrate. Cells secrete gene products into the ECM that in turn shape it and eventually influence other cells. Each organ or tissue has a unique ECM to fulfill its specific needs. This goes so far that a cell's identity can be determined solely based on its expressed ECM genes. Not only are there differences in the ECM within an organism, but most likely between different taxa as well. Considering vertebrate animals that are fundamentally different, such as a bird and a whale, it is not hard to imagine that the same tissue encounters different challenges that called for specific adaptations that can't be found in the other animal. To unravel evolutionary changes in the vertebrate ECM, we are using a combination of gene expression and genomic data across different organs and taxa. Comparing how strongly genes are expressed, how often they were duplicated or lost, and how fast their sequences evolved will help us understand which ECM genes are fundamentally important and unchanged in vertebrate evolution as well as which genes were subject to remodeling in individual lineages.

B01: ECO-ICE: Reconstruction of the Climate in Potential Temperate Tree Microrefugia during the Last Glacial Maximum using Biomarkers

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How and where did temperate trees survive during the Last Glacial Maximum (LGM)? Whether temperate trees survived only in the glacial refugia of Southern Europe or also in isolated pockets of refugia (i.e., microrefugia) north of 45°N in Western Europe has long been debated in ecology and conservation biology [1]. In an attempt to answer this question, the ECO-ICE project will combine multiple proxies to study LGM vegetation dynamics using sedimentary DNA and pollen and the climate dynamics using lipid biomarkers and chironomids.

We will use lipids, often called ‘molecular fossils’, preserved in lake sediments to reconstruct the climatic landscape of known refugia and potential microrefugia in Western and Southern Europe. To quantify mean annual air temperatures during the LGM, branched glycerol dialkyl glycerol tetraethers (brGDGTs), membrane-spanning lipids produced by bacteria, will be used. The structural variability of brGDGTs strongly depends on temperature and hence, the relative abundance of different brGDGTs in the sediments can be used to reconstruct temperature [2]. Furthermore, the hydrogen isotopic ratio of precipitation, $\delta^2\text{H}_{\text{pre}}$, will be isolated from the $\delta^2\text{H}$ values of plant wax n-alkanes and fatty acids, to give us insights into the variability in temperature, amount and sources of precipitation and vegetation changes during the LGM. Multiple fieldwork campaigns to selected lakes will yield sediment cores spanning the LGM and combining information from the aforementioned proxies will help us determine whether these supposed temperate tree microrefugia, particularly north of 45°N, existed during the LGM, and the climatic conditions that supported them.

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B02: Anaerobic methane oxidation in sediments of the High-Arctic Lake Isdammen, Svalbard**Tim Kurth¹, Geert Hensgens², Moritz F. Lehmann¹, Jakob Zopfi¹**¹ Department of Environmental Sciences, University of Basel, Basel, Switzerland² Arctic Geology, The University Centre in Svalbard, P.O. Box 156, N-9171 Longyearbyen

Freshwater ecosystems are important contributors to atmospheric methane, with lakes accounting for over two-thirds of these emissions. With climate warming, methane production in lacustrine sediments is expected to increase, especially in Arctic environments. Methane emissions are controlled by aerobic methane-oxidizing bacteria in the water column of lakes and in oxic sediments. In deeper, anoxic sediment layers, anaerobic methane oxidation (AOM) by archaea may also contribute to mitigating methane emissions. However, the quantitative importance of AOM in freshwater ecosystems and the environmental factors controlling AOM activity remain poorly constrained. In order to improve our understanding of methane cycling in High-Arctic lakes, particularly with regard to AOM, we conducted a study of Lake Isdammen (Svalbard). This glacier-fed lake was formed on a former wetland following the construction of a dam. We investigated the spatial and temporal variability of methane concentrations in the water column together with detailed geochemical sediment analyses. We measured porewater concentration profiles of methane and major ions, and quantified AOM rates using a ^{14}C -CH₄ radiotracer approach. The results indicate that AOM could be an effective benthic methane filter along the northern shoreline, preventing almost all sedimentary methane from diffusing into the water column. However, this contrasts with the elevated water-column methane concentrations observed at southern sampling sites, suggesting additional non-diffusive methane input through subaquatic groundwater discharge.

B03: Key evolutionary innovations in the rapid diversification of *Diploneis* from Lake Tanganyika

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Colonizing new habitats can drive evolutionary change by promoting the emergence of traits that facilitate adaptation and diversification. This process may give rise to evolutionary innovations that enable organisms to exploit newly available ecological niches. Such evolutionary dynamics are especially evident in diatoms, which have colonized virtually all aquatic habitats and exhibit remarkable trait diversity. However, it remains largely unknown which of these traits represent key evolutionary innovations underlying their ecological and evolutionary success. Here, we investigate a recently discovered morphological trait, a fin-like structure associated with rapid diversification in the diatom genus *Diploneis* from Lake Tanganyika, to assess its potential role as a key evolutionary innovation, alongside other morphological and physiological candidates such as structural lipids (sterols). To this end, we constructed a time-calibrated molecular phylogeny based on 11 genes to determine whether Tanganyikan *Diploneis* species diversified in situ. We then tested for associations between environmental variables and the fin structure as well as other morphological traits to assess their adaptive significance and potential contribution to in situ diversification. Our results indicate that *Diploneis* species evolved in situ during the early stages of Lake Tanganyika and subsequently underwent rapid diversification, enabling them to occupy newly emerging ecological niches. Associations between morphological traits and environmental conditions suggest potential adaptive significance, with higher density of striae (rows of pores on the cell wall) associated with greater water depth and lower pH. The same trait–environment correlation framework will be applied to sterols, while further genomic and transcriptomic analyses will investigate the genetic basis and functional responses of candidate traits under different environmental conditions, providing insight into their potential role as key evolutionary innovations and their contribution to the diversity and evolutionary success of freshwater diatoms.

B04: Can Stalagmites Record Regional Floods? Evidence from Rayan Cave, Southern Zagros, Iran

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The Southern Zagros Mountains of Iran are in a climatically vulnerable region where societies have historically been exposed to both prolonged droughts and high-intensity flood events (Nazaripour et al., 2024). Droughts are slow-onset events that can affect large areas over extended periods, potentially allowing time for mitigation measures to be implemented. In contrast, floods and heavy rainfall events are rapid-onset hazards with more concentrated impacts and can cause substantial damage to life and property (Nazaripour et al., 2024; Pizzorni et al., 2024).

Recent observations indicate that Iran's precipitation regime has shifted towards more concentrated and intense rainfall events (Nazaripour et al., 2024). Paleo flood reconstruction and magnitude estimation are therefore important for placing recent extreme events within a longer-term context and for improving future estimates of flood frequency, particularly in regions where instrumental records are limited. Existing paleoclimate archives in the region, including lake sediments, have demonstrated the potential to reconstruct past hydroclimatic variability and extreme events. However, these records may also be influenced by anthropogenic signals, as documented for Lake Parishan and Lake Maharlou (Brisset et al., 2018; Jones et al., 2015).

We present an ongoing paleo flood investigation from Rayan Cave in the Southern Zagros near Shiraz, Iran. Stalagmites collected from the cave contain well-defined sandy and silty layers within the carbonate fabric, suggesting episodes of enhanced sediment transport and high-energy hydrological conditions. The stratigraphic occurrence of these detrital layers provides a potential archive of past cave-flooding events. Our ongoing investigation aims to determine whether these marker horizons primarily reflect localized karst hydrological responses within the cave or whether they correspond to flooding events representative of the wider Southern Zagros region. We further assess the potential of Rayan Cave stalagmites to reconstruct the frequency and timing of extreme floods and to determine whether this archive can provide a reliable record of regional flood activity in a region where both instrumental observations and paleo flood records remain limited.

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B:05 Holocene hydroclimate variability from a composite speleothem record of Kuna Ba Cave, northern Iraq

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Southwest Asia lies in a climatic transition zone influenced by mid-latitude westerly circulation, and monsoon-related subsidence (Tyrllis et al., 2013). Along the Zagros mountain range within this region, moisture transport from the west and south, coupled with flow guidance along the range, mountain ascent, and leeward drying, creates significant precipitation gradients over short spatial distances (Evans & Smith, 2006). Understanding the hydroclimate dynamics of this water-stressed region is important for: (1) placing modern droughts, such as those of 1998-2000 and 2007-2010, in a meaningful historical context, (2) better anticipating future droughts, and (3) exploring hydroclimatic conditions associated with the emergence of agriculture, and the rise of cities and empires.

The Sinergia project 'MITRA', funded by the Swiss National Science Foundation, will reconstruct Holocene hydroclimate and environmental change along a transect extending from eastern Türkiye through the Zagros Mountains to the Persian Gulf. It combines a network of well-dated records from speleothems, lake/wetland, and marine sediments with regional climate model simulations to improve our understanding of drought dynamics across southwest Asia. Here, we present a composite record of Holocene hydroclimate variability from Kuna Ba Cave in northern Iraq, spanning approximately the past 10,500 years. We integrate stable isotope records from four stalagmites, KBC-3, KBC-6, KBC-7, and KBC-26, with previously published late-Holocene data (Sinha et al., 2019). High uranium and negligible initial thorium concentrations allow precise ²³⁰Th dating, of these records, which are aligned within their associated uncertainties using Intra-Site Correlation Age Modelling (ISCAM) (Fohlmeister, 2012). The composite reveals a long-term shift towards higher $\delta^{18}\text{O}$ values, with shorter-term fluctuations superimposed. The overlapping KBC-3

and KBC-6 records show contrasting isotope trends between 7.3 and 5.3 ka BP, when $\delta^{18}\text{O}$ increases while $\delta^{13}\text{C}$ becomes slightly more negative. Trace element analysis of KBC-6 reveals positive Mg- $\delta^{13}\text{C}$ and Sr-Ba correlations and negative U-Ba correlations across three selected intervals, 10.5-8.2, 8.2-7.3, and 7.3-5.3 ka BP, although their strengths vary through time. Together, our data suggests that centennial-scale trace element variations in the Kuna Ba stalagmites may reflect groundwater residence time, and water-rock interaction effects. Furthermore, a pronounced shift towards higher $\delta^{18}\text{O}$ and $\delta^{13}\text{C}$ values in our composite record is associated with the Neo-Assyrian “megadrought” previously identified by Sinha et al. 2019. Over this interval (2.65–2.50 ka BP), time-weighted mean $\delta^{18}\text{O}$ and $\delta^{13}\text{C}$ values are approximately 1.15‰ and 1.21‰ higher, respectively, than those of the remainder of the approximately 10,500-year record. Given that comparisons with other regional cave and lake records show broadly similar long-term trends, we propose that our composite record documents a regional climate signal (Fleitmann et al., 2025), and so could provide crucial information on the drivers, and consequences, of hydroclimate changes in southwest Asia during the Holocene. Further comparison with terrestrial sediment records and climate simulations will also help assess the roles of precipitation amount, moisture source, and seasonality.

B06: Recent Dynamics of Chironomid and Invertebrate Assemblages in a Swiss Mountain Lake : Biotic and Geochronological Analyses**Petitjean Loïs¹, Damber Maja¹, Jiménez-Liébanas Laura¹, Heiri Oliver¹**¹ Department of Environmental Sciences, University of Basel, Basel, Switzerland.

Two short sediment cores (SUVA and SUVU) were collected from Lej da Suvretta, a high-altitude lake (2601 m a.s.l.) in the Swiss Alps (Canton of Grisons), to study the responses of benthic communities - particularly chironomids - to recent environmental changes. Chironomid head capsules were extracted from 25 samples of the SUVA core and identified to morphotype level, revealing 20 taxa. A cluster analysis (CONISS) was performed to distinguish faunal zones. The SUVU core was analyzed using loss-on-ignition (LOI) to estimate organic matter and carbonate contents. A chronology based on ¹³⁷Cs was established for SUVA and transferred to SUVU by correlating water content. The chironomid assemblages reveal a dominance of four cold stenothermic and oligosaprobic taxa: Tanytarsus lugens-type, Paracladius, Micropsectra radialis-type, and Procladius (likely P. tatrensis). Despite indicating cool, oligotrophic conditions typical of high-altitude lakes, the assemblages showed abrupt shifts in composition across four distinct faunal zones. Some changes may reflect a reduction in ice cover associated with post-industrial warming in the early 20th century. Other taxonomic shifts may result from non-climatic factors, such as fish introductions. These results highlight the importance of considering both climatic and non-climatic drivers when interpreting subfossil chironomid records.

B07: A reference-free approach to characterize Large Structural Polymorphisms in *D. magna***Francesca Quitadamo¹, Dieter Ebert¹**¹ Department of Environmental Sciences, University of Basel, Basel, Switzerland.

The growing availability of de novo genome assemblies and long-read sequencing is revealing genomic regions with exceptionally high diversity, where alternative haplotypes can appear non-homologous. In the waterflea *Daphnia magna*, multiple pairwise alignments of de novo assemblies revealed several regions of this type, named large structural polymorphisms (LSPs). Two of them, the E-locus and the Pasteuria Resistance Complex (PRC), overlap with previously described regions associated with resistance to the endoparasite *Pasteuria ramosa*, and span genomic intervals from about 50 kilobases up to 5 Mb. Balancing selection has been suggested as a force maintaining these extreme polymorphisms; however, understanding their evolutionary history requires accurate characterization and comparison of highly divergent haplotypes. Traditional population genomics methods are poorly suited for this purpose due to limited sequence homology.

We present a reference-independent strategy to compare haplotypes within LSPs. Using 33 long-read genome assemblies of *D. magna*, we mapped the PRC region for each individual and extracted the gene content for all of the haplotypes. A coalescent-based approach was then used to combine the information from the single gene trees and infer clusters of haplotypes.

Our goal is to extend this approach to all known LSPs in the *D. magna* genome, using it to characterize the distribution of haplotype clusters across populations of *D. magna* and related species, providing a framework applicable to other organisms for elucidating the evolution of complex genomic regions.

B08: Quantifying load and taxonomy of arbuscular mycorrhizal fungi in plant roots by long-read sequencing**Loïc Thurre¹, Jan Waelchli¹, Klaus Schlaeppi¹**¹ Department of Environmental Sciences, University of Basel, Basel, Switzerland.

Root colonization by arbuscular mycorrhizal fungi is commonly assessed in studies investigating the relationships between mycorrhizae and root exudates of colonized plants. This assessment is generally time-consuming, as it involves a staining protocol followed by manual counting under a microscope. Although inexpensive, this method requires the trained eye of an expert and is therefore subject to observer bias. Moreover, in the absence of automation and standardization, it remains difficult to conduct large-scale experiments within a reasonable timeframe. More limitingly, microscopy lacks taxonomic resolution, constraining our ability to link variation in root exudates with changes in mycorrhizal community composition. To overcome these limitations, we are developing host-associated microbial PCR (hamPCR [1]) with long-read sequencing to study arbuscular mycorrhizal fungi. hamPCR is based on the co-amplification of a single-copy host gene and the SSU–LSU region of the ribosomal DNA for the fungi in complex DNA samples of colonized plant roots. This co-amplification enables estimation of fungal load relative to host DNA abundance. Further, the sequence of the fungal amplicon is then used for the taxonomic identification of mycorrhizal fungi within the host. The principle of the method, its main challenges, and its potential applications will be presented in the context of studying mycorrhizal colonization across different maize genotypes.

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B09: The impact of a long-term drought manipulation on microbial metabolism and soil carbon cycling

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Forest soils play a key role in climate change mitigation by storing large stocks of carbon, a process largely driven by microbial communities. However, our understanding of how these microbial communities will respond to environmental changes is still limited, especially as droughts become increasingly frequent. Drought conditions may impact microbial activity, substrate use, carbon use efficiency (CUE), and soil respiration as water becomes scarcer. However, the effect of long-term drought, our understanding of the impacts on microbial metabolism, and the way these factors interact are still not well understood. To address this knowledge gap, this project seeks to evaluate the effects of long-term drought on forest soil chemical characteristics, soil respiration, and microbial activity using the Swiss Canopy Crane II site in Hölstein, Switzerland. Rainfall exclusion shelters were installed at the site in 2022 after initial chemical characterization of the soil which were conducted on samples from each 10x10m square of a grid overlaying the site. The samples were used to test pH, total organic carbon, C/N ratios, bulk $\delta^{13}\text{C}$, and bulk $\delta^{15}\text{N}$ in 2018. Replicate samples for these analyses were collected in November 2025 following 3 summers of artificial drought stress. Continuous soil CO_2 fluxes were also measured from 2021 to 2023, and again since June 2026 to evaluate changes over time. An ongoing sampling campaign seeks to evaluate seasonal variability from four timepoints from April - October 2026, focusing on microbial CUE, metatranscriptomics, and metabolomic analyses as well as testing a novel proxy using hydrogen isotopes of phospholipid fatty acids (PLFA) which are compounds found in the cellular membrane, to evaluate metabolic pathways employed by soil microbes. Overall, the work will help inform how soil carbon cycling including the chemical makeup of the soil, microbial carbon metabolism, and soil carbon sequestration will be affected under changing rainfall patterns in central European forests.

B10: Reconstructing snow time-series for modelling alpine microclimate**Jonathan von Oppen¹, Sabine Rumpf¹**¹ Department of Environmental Sciences, University of Basel, Basel, Switzerland.

Temperatures in high-mountain areas have increased rapidly during recent decades. However, how this overall warming trend has translated into microclimatic conditions that the specialised alpine organisms experience remains largely unknown due to the lack of microclimatic data across large spatial and temporal scales. A central component of alpine microclimates is the presence of snow cover at least during parts of the winter season, but its accurate representation in microclimate models is only gradually emerging. We applied a dedicated snow model to reconstruct fine-scale time-series of snowpack properties for the alpine zone of the European Alps. First results show meaningful spatiotemporal patterns of snow, and detailed verification is currently ongoing. These snow models might valuably improve microclimate models, which are in turn necessary to understand current and forecast future distributions of cold-adapted alpine biodiversity in the course of ongoing climate change.

B11: Remote sensing of vegetation degradation during dust-inducing drought in South Africa

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The Northern Cape Province of South Africa is an arid region that showed a large increase in dust emissions in proximity to the coast following a multi-year drought from 2015 to 2022, with a peak in emissions occurring in 2021 (Vos et al. 2025a). A decline in vegetation cover was observed by long-term vegetation monitoring studies (e.g. Jürgens et al. 2025; Schmiedel et al. 2023) and has been identified as the main driver of this increase in emissions. This increase in wind erosion and dust emission could influence human health, local infrastructure, and ocean biogeochemical cycles. The vegetation and landform states associated with the emission of dust, and drivers behind the transition between these states, have been summarised in a State-and-Transition Model (STM, Vos et al. 2025b), which demonstrated the cascading effects of wind erosion and dust emission on vegetation decline and land degradation. With climate change projected to increase the frequency and severity of such droughts, being able to monitor the degradation at desert margins on a large scale becomes increasingly important for anticipating how these landscapes, their productivity, and their erodibility are changing.

In this study, remote sensing data were utilised to understand the spatial extent of this vegetation decline and dust emission increase beyond the in situ vegetation monitoring. Long-term vegetation monitoring data from Jürgens et al. (2025) and dust source point data from Vos et al. (2025a) were combined with common remote sensing indices and land cover classifications derived from both MODIS and Sentinel-2. These data include the Modified Soil Adjusted Vegetation Index (MSAVI), albedo-based roughness index (ω_{ns}), the percentage of bare land, and land cover classification based on the annual International Geosphere-Biosphere Program (IGBP). Furthermore, we extended the dust source point dataset until 2025 to show the recovery of the landscape following the drought from 2023 onwards. The dataset was divided into different emissive areas and compared to the observed degradation state and the emissivity of areas using a random forest model.

In contrast to common assumptions, our results show that MSAVI does not necessarily indicate a healthy or recovering landscape. Areas with high MSAVI values likely reflect annual vegetation growth instead of the regrowth of soil-stabilising shrubs, and therefore do not represent recovery of a degraded landscape or a long-term reduction in emissivity. The data analyses indicated that rather than the absolute values of the vegetation indices, the change in these indices and therefore the response to the drought indicate a degraded area. Furthermore, the degradation state and

the emissivity of a region are characterised by different remote sensing signatures, demonstrating the complexity of what might seem a straightforward detection problem. The results emphasise the importance of understanding the vegetation, ecology, landform states, and the long-term characteristics when assessing the erodibility of an area using remote sensing.

B12: Identification of genes required for growth on MBOA in the maize root bacterium *Sphingobium* LSP13**Anlun Wei¹, Christine Pestalozzi¹, Klaus Schläppi¹**¹ Department of Environmental Sciences, University of Basel, Basel, Switzerland.

Maize root exudates contain secondary metabolites (benzoxazinoids, BXs) that shape the root microbiota. Previous research has demonstrated that many maize rhizosphere bacteria are tolerant to BXs and some are capable of metabolising the major BX compound MBOA (6-methoxy-benzoxazolin-2-one). *Sphingobium* are abundant members of the maize rhizosphere that are further enriched on plants producing BXs. Furthermore, maize isolates belonging to the genus *Sphingobium* are able to metabolize MBOA and utilise it as sole carbon source. The lactonase BxdA was previously shown to be sufficient for MBOA degradation in vitro and we identified three bxdA homologs in *Sphingobium* LSP13. We produced a recombinant knock-out mutant that lacks all copies and analysed the growth with MBOA as sole carbon source. The wild type strain showed growth within 1-2 days, while the triple-gene mutant $\Delta 3\text{bxdA}$ showed no growth over a 4-day-period indicating that at least one of the bxdA homologs is required for growth with MBOA as sole carbon source. To identify other genes required for growth with MBOA, we performed Tn5 transposon mutagenesis and screened for loss of growth on plates containing MBOA as sole carbon source. Out of 11,000 mutants, we identified 9 mutants that were able to grow with glucose but not MBOA as sole carbon source. Transposon insertions in these mutants were mapped to 6 genes. Ongoing characterization of the mutants with candidate genes knocked-out aims to resolve the complexity of MBOA metabolism in *Sphingobium* and its broader implications for plant-microbe interactions in the maize rhizosphere.

B13: Effects of Solar Photovoltaic Installations on Red Kite (*Milvus milvus*) Flight Behaviour in Spain and Portugal

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The rapid expansion of photovoltaic (PV) energy is changing landscapes worldwide and may have consequences for wildlife. Beyond their direct impact on the ground, PV installations can modify local environmental conditions: for example, recent studies suggest PV plants foster a heat island effect, which may alter local thermal currents. Such changes could affect species that rely on thermals for soaring flight, such as the red kite (*Milvus milvus*), a raptor listed as endangered in Spain. This study asks whether the flight behaviour of red kites changes around PV plants once they are built.

Two opposing but biologically plausible responses were expected. Birds could circle more near PV plants, for example if local thermal conditions change, which would increase the share of Foraging. Alternatively, the fences and structures of a plant could offer perches and shelter, so that birds stop and rest there instead of passing through. This would increase Resting and reduce Directed Movement.

GPS tracking data from 274 red kites recorded in Spain and Portugal between 2015 and 2025 were combined with the locations and completion years of 2,471 PV plants. A hidden Markov model classified 1.4 million GPS locations into three behavioural states: Resting, Foraging and Directed Movement. To understand whether PV plants change how often each behaviour occurs, we estimated the change in its frequency before and after construction within 1 km of a plant and compared it with the change in the surrounding landscape 1 to 5 km away. Beta-binomial mixed models were used, with time of day, season and weather (thermal uplift, wind speed and cloud cover) as predictors, accounting for differences between individual birds and between plants.

Comparing different widths for the zone around each PV plant is under consideration. Preliminary results suggest that near PV plants red kites spent less time in Directed Movement after construction and slightly more time Resting, while Foraging showed no clear change. This pattern fits the second expectation better than the first. Understanding how soaring birds respond to PV plants may help inform the planning of future installations, ensuring that endangered species are taken into account to meet biodiversity targets while delivering energy goals.