



University of
Zurich ^{UZH}

ETH zürich



"Ecology Mini-Symposium" Program

12 October 2022

RAA-G-01, Aula. Rämistrasse 59

Zurich, Switzerland

***Hosted by Life Science Zurich Graduate School
PhD Program in Ecology***





12 October 2022

12:00 – 12:15 **Prof Dr. Anna-Liisa Laine**

Welcome

Director, PhD Program in Ecology; University of Zurich, Switzerland

12:15 – 13:00 **Student elevator pitch presentations**

13:00 – 13:10 **Dr. Debra Zuppinger-Dingley**

'Closing'

Program Manager, PhD Program in Ecology; University of Zurich, Switzerland

13:10 – 14:30 **Light lunch and Poster Session**

How to get there

Tram line number 10, stop ETH/Universitätsspital, walk downhill to the venue (Rämistrasse 59).

Tram Line number 9, stop Kantonsschule which is just in front of the venue (Rämistrasse 59).



Abstracts

Posters

Large regional differences in industrial development across the Arctic (Poster 10)

Cengiz Akandil

PhD Program in Ecology; University of Zurich, Switzerland

Increasing temperatures enable easier access to the Arctic where the anthropogenic effects on ecosystems might locally exceed the effects of climate change. Recent studies have documented the current state of infrastructure development in the Arctic or historical development of human activities in selected regions such as the Bovanenkovo oil fields. However, there is no comprehensive pan-arctic overview of industrial development and urbanization trends in the Arctic, which is crucial for the sustainable development of the region. In our study, we utilized artificial light at night (ALAN) to quantify the development of human activity across the Arctic from 1992 to 2013. We created a trend map and a cumulative map of ALAN to assess hotspots of development and the total area affected by human activity from 1992-2013. We analyzed 19.6 million km² and demonstrate that an area of 716'708 km² in the Arctic is affected by ALAN and corresponding human activity. The European Arctic and the oil and gas extraction regions are the hotspots of human activity, while the Canadian Arctic is least affected by ALAN. On average, the global human settlement data explains only 5.65% of the variation in ALAN in the Arctic in 2015, with large regional differences. We conclude that in most regions ALAN relate to industrial activity. The Arctic ALAN trend map shows that oil extracting regions, such as Khanty Mansi, have spatially dynamic ALAN trends, which indicates that some oil wells are depleted and abandoned while new wells are developed. With this study, we provide a new, standardized pan-arctic perspective on human industrial development and its use of the Arctic landscape that is crucial as a baseline for a sustainable development and conservation planning of this highly vulnerable region.

Why are ferns more desperate for water than angiosperms (Poster 11)

Daniela Aros

PhD Program in Ecology; University of Zurich, Switzerland

Ferns are worldwide more restricted to humid places than other vascular plants. Currently, the justification in literature has been over the necessity of water for fertilization to occur and the passive stomatal response to changes in the environment. Although true, this is not enough to explain the low diversity and abundance of ferns in dryer places. In this study, we evaluated if ferns lose more water to the environment than angiosperms. To achieve this, we measured gas exchange in the long- and short-term, in addition to the stomatal and cuticle permeability. We found that ferns have higher transpiration rates, permeability, and no circadian rhythms linked to gas exchange. Our study provides important novel insight into the ecophysiology of early divergent plants and the need to diversify the study models beyond plants of agricultural importance for a better understanding of ecosystem functioning.

Mechanisms Determining Ecological Forecast Skill in the Context of Environmental Change (Poster 1)

Uriah Dagaard

PhD Program in Ecology; University of Zurich, Switzerland

"Due to its broad field of application, forecasting in ecology and related fields is used to answer a variety of different research questions. Prediction is often considered the best or even the only metric with which the scientific understanding of nature can be measured. It has been pointed out that ecology lags other scientific fields, such as economics and climatology, in which prediction is routinely used to test models and understanding. Calls have been made for increased efforts in ecological forecasting.

One of the possible approaches that aim at reaching greater realized predictabilities in ecology is to investigate what makes certain ecological systems and measures more forecastable than others. This approach, with further focus on the biological mechanisms that lead to these differences in observed

forecast skill and their dependence on environmental change, will be a general aim of my PhD studies.

Here I present the results of my first chapter 1: Forecasting in the face of ecological complexity: number and strength of species interactions determine forecast skill in ecological communities. To investigate forecast skill within and across system complexity, we monitored a microbial system exposed to either constant or fluctuating temperatures in a five-month long laboratory experiment. We tested how forecasting of species abundances depends on number and strength of interactions and on model size (number of predictors). We also tested how greater system complexity (i.e. the fluctuating temperatures) impacted these relations. We found that the more a species interacted, the weaker these interactions were and the better its abundance was predicted. Forecast skill increased with model size. Greater system complexity decreased forecast skill for three out of eight species. These insights into how abundance prediction depends on the embedding of the species within the system and on overall system complexity could improve species forecasting and monitoring."

The effects of climate change and forest management on aquatic-terrestrial links in Swiss forests (Poster 12)

Bastiaan Drost

PhD Program in Ecology; WSL, Switzerland

Climate change and land management do not only influence species composition, but also species interactions, e.g. via consumption. Food webs are crucial for ecosystem functioning and can be linked between different ecosystems, such as streams in forests. However terrestrial and aquatic systems are often studied in isolation from each other. The main basal resource in streams is terrestrial leaf litter, while emerging aquatic insects provide a major input of polyunsaturated fatty acids (PUFAs) into terrestrial systems. In the present study, we test the effects of climate change and forest management on the poorly studied links between aquatic and terrestrial food webs.

Promoting pollinator diversity and sustainable pollination services in agroecosystems (Poster 15)

Chiara Durrer

PhD Program in Ecology; ETHZ, Switzerland

Human wellbeing is directly linked to agricultural systems yielding enough and stable amounts of food every year. To ensure this, ecosystem services providing a diversity of animals such as bees pollinating wild plants and crops are needed (Oerke 2005; Gallai et al. 2009; Garibaldi et al. 2013). Many different insect taxa such as butterflies, beetles and flies, and in particular bees, are important pollinators of entomophilous plants. However, a wide range of anthropogenic drivers such as habitat and floral resource loss caused by land-use change and agricultural intensification threaten pollinators. A decline of pollinator diversity and abundance has been observed in different regions of the world during the last 50 years (Potts et al. 2010; Goulson et al. 2015). In my PhD project I aim to evaluate how the pollinator diversity enables stable crop pollination services (especially concerning future climate change), determine resource-pollinator networks, towards a better understanding of the role of conservation measures and evaluate competition between honeybees and bumblebees.

Evaluating two amplicon-based protocols to analyze root-associated fungal communities in ferns and lycophytes (Poster 22)

Thais Guillen

PhD Program in Ecology; University of Zurich, Switzerland

Premise of the study: Paleontological and molecular evidence suggests that early-diverging plant lineages depended on ancestral fungi for the successful colonization of land. However, little is known about the co-evolution of ferns and lycophytes with fungi. Most studies so far have assessed fern-fungus interactions based uniquely on visual root inspection. In the present research, we establish and evaluate two metagenomic protocols to analyze the fungal communities associated to fern and lycophyte roots.

Methods: We adapted and compared two amplicon-based protocols using Illumina MiSeq sequencing to identify the root-associated fungi. The first approach utilizes the ITS rRNA region to screen the general fungal communities, whereas the second one uses the 18S rRNA as a

marker targeting Glomeromycotan fungi. To test these protocols, we collected and processed silica-dried roots from 12 phylogenetically distant fern and lycophyte species, with three replicates per species.

Results: The protocols yielded a total of 477182 and 1694828 quality reads corresponding to 4906 and 2169 ASVs, respectively. Per fern species, we obtained 28-292 ASVs with a relative abundance greater than 1%. The ITS approach allowed us to identify 138 fungus species belonging to 115 genera, 68 families, 24 orders, and 4 phyla, but the 18S-based protocol detected a greater diversity in Glomeromycota than the ITS protocol. Similarity analyses revealed that fungal communities were more similar between individuals of a single fern species than among different species.

Discussion: The ITS-based protocol is a consistent, replicable, and relatively simple tool to analyze the full fungal communities associated with fern and lycophyte roots. The 18S-based protocol is more appropriate for studies focused on the detailed screening of arbuscular mycorrhizal fungi.

Food intake drives skill development and carries over to affect timing of emigration in a large raptor species (Poster 18)

Julia Hatzl

PhD Program in Ecology; Vogelwarte, Switzerland

Conditions experienced in early life can have severe impacts on behavioral responses in later life-history stages with ultimate consequences for individual fitness. Differential post-fledging ontogeny of behaviors might be a key translator of these carry-over effects. However, little is known about the environmental drivers of behavioral development and how these impact individuals later in life. Here, we investigated early post-fledging behavioral development in tagged golden eagles (*Aquila chrysaetos*), with a focus on two flight behaviors differing in energy expenditure (flapping flight and soaring flight). We studied the relationships of these behaviors with feeding rates and timing of emigration from the parental territory. Based on classified accelerometer data we showed that while birds remained largely stationary after fledging, flapping flight occurred early in development and increased steadily thereafter. The less energetically costly soaring flight started with delay, but quickly became more dominant over flapping flight. High food intake behavior resulted in a steeper flapping flight increase than low food intake behavior, and a steep increase in flapping flight resulted in an early start of soaring flight. Birds that showed soaring flight earlier also emigrated earlier from the parental territory. Our results suggest that soaring flight skills drive the timing of emigration from the parental territory. Our study supports the use of accelerometer data to investigate the ontogeny of post-fledging behavior. The results show that post-fledging environmental conditions affect behavioral development and carry-over to affect early stages of dispersal behavior which, in turn, might have important consequences for survival and settlement decisions.

*Quaternary plant speciation in central Europe: evolution and conservation of the *Potentilla collina* aggregate (Poster 24)*

Gregory Jaeggli

PhD Program in Ecology; University of Zurich, Switzerland

The *Potentilla collina* aggregate is a group of poorly studied plants, thought to be allopolyploid hybrids of sympatrically growing *Potentilla* species that evolved in the last 1000 years, forming many locally endemic and endangered or even already extinct species. There are still major gaps of knowledge about different aspects of the evolution and biology of the species. Since genetic studies are scarce, most assumptions about the group's evolution are only based on morphology. We will combine molecular with morphological evidence to clarify the patterns of the evolution of species within the *P. collina* group.

*Infection sequence shapes virus community assembly during natural epidemics
(Poster 13)*

Maija Jokinen

PhD Program in Ecology; University of Zurich, Switzerland

Metagenomic studies have enabled the discovery of viral diversity and revealed that viruses are ubiquitous across ecosystems. When virus diversity across scales from single host individual to multiple populations has been uncovered, highly complex communities have been found. Coinfections of viruses are shown to be common and often resulting from sequential infections with varying arrival timing and order of the viruses. Priority effects describe the timing and order in which species arrive to an environment, and how the first arriving species may impact community assembly. However, the role of priority effects in virus community assembly is currently unknown. To investigate whether virus infection early in the season affects virus community assembly late in the season, we placed naïve *Plantago lanceolata* plants into natural *P. lanceolata* populations. The naïve plants were then repeatedly sampled during seasonal virus epidemics. We analyzed the samples by using PCR with specific primers to detect five focal *P. lanceolata* infecting viruses. Using the joint species distribution modelling framework, we explored the effects of early season virus colonization and plant characteristics on late season virus occurrences in host plants. We find both positive and negative effects of early infection on late season virus colonization patterns. The effects depend both on host genotype and the virus species colonizing the host early in the season. Jointly, our results suggest that arrival order is important for determining virus community complexity, and that host immune responses contribute to the assembly process.

Distribution and diversity of groundwater amphipods in Switzerland

Mara Knüsel (Poster 19)

PhD Program in Ecology; University of Zurich, Switzerland

A large part of freshwater is hidden beneath the earth's surface as groundwater. It represents a main drinking water resource in many regions across the globe. But groundwater is also an ecosystem that harbors a broad and highly adapted biodiversity. This biodiversity has long been neglected in research, mainly due to difficulties in groundwater accessibility. In the light of human-caused environmental changes, for example through pollution, the incomplete knowledge on groundwater fauna is alarming. To overcome the challenges of accessibility, we established a citizen science method with the aim of integrating water providers into the process of data collection. Hundreds of participants sampled their drinking water wells (springs) for macroinvertebrates all across Switzerland. By implementing such a standardized, systematic, and countrywide approach, we built one of the most extensive datasets on groundwater macroinvertebrates in Central Europe including over 1500 samples. Focusing on the order Amphipoda, we shed light on the diversity, distribution, and endemism in Switzerland. We found groundwater amphipods (genus *Niphargus*) in 25% of the springs sampled, belonging to 12 different species; several of these species are new to science or newly reported for this region. Overall, we conclude that the use of citizen science approaches can be helpful and efficient for hitherto largely underexplored aquatic ecosystems such as groundwater.

Can genotypic variation of social behaviors in soybean be quantified, and cooperative behaviors be associated to specific genes?

Emanuel Kopp (Poster 20)

PhD Program in Ecology; University of Zurich, Switzerland

One key hypothesis of evolutionary agroecology is the existence of a trade-off between a plant genotype's individual fitness and its performance as a (monoculture) group. While traits that increase individual fitness have been optimized by natural selection and are unlikely to offer much potential for breeding, there might be traits that increase group performance while decreasing individual fitness. Such "cooperative" traits are assumed to be evolutionary unstable, and thus rare and unlikely to be found by chance. Here, we want to exploit this trade-off to quantify genotypic variation in social behaviors and identify cooperative soybean genotypes, and the underlying traits and genes.

For this, we performed a factorial experiment where we grew 90 different soybean varieties in different social environments. According to game theoretical considerations, more cooperative genotypes will exhibit relatively high monoculture yields but low fitness in competition with more competitive neighbors, and vice versa.

This experiment should therefore allow us to rank the varieties from ""selfish"" to ""cooperative"", and we will use this ranking to associate traits or genes to such variation in social behavior.

The identification of genes for cooperation in crop species would be of high interest as it would allow for seamless integration of breeding for more cooperative genotypes into modern breeding schedules.

Climatic conditions influence the breeding phenology of an alpine population of the common toad (Bufo bufo) (Poster 8)

Omar Lenzi

PhD Program in Ecology; University of Zurich, Switzerland

Strong phenological shifts in response to changes in environmental conditions have been reported for many species. With increased global warming, amphibians are generally expected to breed earlier. Phenological shifts in breeding are observed in a wide number of amphibian populations, but less is known about populations living at high elevations, which are predicted to be more sensitive to climate change than lowland populations.

The goal of this study is to assess the main factors determining the timing of breeding in a specific alpine population of the common toad (*Bufo bufo*) and explain the observed shifts in its breeding phenology.

We modelled the effect of environmental variables on the start and peak dates of the breeding season using 39 years of individual-based data on an alpine population of common toads. We also investigated the effect of the lunar cycle, as well as the individual variation in breeding phenology. Finally, to estimate the genetic component of the breeding phenology we calculated the repeatability of the arrival timing at the breeding site.

Breeding advanced to earlier dates in the first years of the study but the trend continued only until mid-1990s. After the mid-1990s, there was no longer a trend in breeding phenology. Overall, toads are now breeding on average around 30 days earlier than at the start of the study period. We performed a linear regression of the breeding dates using environmental variables. High temperatures and low snow cover in winter and spring, as well as reduced spring precipitation were all associated with earlier breeding. Additionally, we found evidence in this population too of males arriving on average before females at the breeding site. On the other hand, we only found weak evidence of among-individual variation in shifts in the breeding phenology, as well as a low repeatability of arrival timing. We did not find a clear and strong effect of the lunar cycle.

Our findings show that the observed changes in breeding phenology are strongly associated with the environmental conditions. These results contribute to filling a knowledge gap on the effects of climate change on alpine amphibian populations. Moreover, we show that changes in phenology, especially in the mountains, can be hard to predict as local microclimatic conditions do not necessarily reflect the observed global climatic trends.

Where to bee? Different types of semi-natural habitat are required to sustain diverse wild bee communities in agricultural landscapes (Poster 2)

Corina Maurer

PhD Program in Ecology; Agroscope, Switzerland

Semi-natural habitats (SNHs) provide important resources for wild bees in agricultural landscapes. As floral resources fluctuate in space and time, different semi-natural habitat types within landscapes could have different effects supporting diverse bee meta-communities throughout the season. Such knowledge is of critical importance for pollinator conservation. Here, we integrate analyses of alpha- and beta-diversity, as well as species-habitat networks, to examine the relative contribution of major SNH types (extensively managed meadows, conventionally managed meadows, flower strips, hedgerows and forest edges) to wild bee meta-communities in agricultural landscapes in different seasonal periods. Results highlight the importance of extensively managed meadows supporting more rare species, habitat specialists and overall bee diversity during the entire season; yet flower strips were similarly important in late summer. Nevertheless, each of the

five investigated SNH harbored relatively unique sets of bee species, with different habitats generally acting as distinct modules in the bee-habitat network. Local floral richness explained alpha- and beta-diversity within and across habitats, while landscape composition and configuration also interactively influenced species turnover between habitats. Our findings underpin the critical importance of maintaining different types of SNH offering complementary resources throughout the season to sustain diverse meta-communities of bee pollinators in agricultural landscapes.

Species interactions in beaver engineered habitats link land-water ecosystem processes (Poster 9)

Valentin Moser

PhD Program in Ecology; WSL, EAWAG, Switzerland

Conservation action for freshwater biodiversity is needed due to losses in habitat area and quality. Restoration of freshwater habitat is challenging because it is difficult and resource intensive to recreate natural dynamics. Ecosystem engineering by beavers could support these restoration efforts. Construction and feeding activities of beavers create mosaic-like habitats which increase local species richness and abundance. However, while knowledge on some community aspects related to beaver activities are well known, knowledge about links between different species communities and the land-water boundary are limited. With this PhD, I will explore the potential of beavers as conservation agents. It is expected that beaver activities strengthen links between aquatic and terrestrial habitats and increase overall landscape diversity while providing resource hotspots for other organisms. Thus, beaver activities could be an important tool to restore biodiversity and strengthen ecosystem services and functions. The results of this theses could therefore provide a baseline for future evidence-based aquatic ecosystem conservation and appropriate beaver management policies.

Group-level specialization in space uses within a multilevel society (Poster 21)

Mina Ogino

PhD Program in Ecology, University of Zurich, Switzerland

Social groups can exhibit striking differences in behavior. However, while these differences can arise from the within-group social environment, they are often also shaped by the behavior of other groups. For example, territoriality limits where groups can move. But how do groups navigate space when they are not bounded by social boundaries? Here, we integrate long-term census data with fine-scale GPS tracking from a population of vulturine guineafowl (*Acryllium vulturinum*) in Kenya to study the partitioning of space among groups. Vulturine guineafowls live in a multilevel society, where groups interact regularly with other groups, and are not territorial. Our data allow us to capture changes in group membership over time and group history shaping space use. We show that group home ranges are consistent across years under similar ecological conditions, despite groups ranging in different areas under different conditions. However, group-level fidelity in space use varies between groups, and we relate these changes to changes in group dynamics, such as group splits and joins. Our study therefore provides insights into how group-level behavioral traits are maintained in wild populations, and the factors that affect their stability.

The role of indirect effects in coevolution as mutualism transitions into antagonism (Poster 14)

Fernando Pedraza

PhD Program in Ecology; University of Zurich, Switzerland

Species interactions have evolved from antagonistic to mutualistic and back several times throughout life's history. Yet, it is unclear how changes in the type of interaction between species alter the coevolutionary dynamics of entire communities. This is a pressing matter, as transitions from mutualisms to antagonisms may be becoming more common with human-induced global change. Here, we combine network and evolutionary theory to simulate how shifts in interaction types alter the coevolution of empirical communities. We show that as mutualistic networks shift to antagonistic, selection imposed by direct partners begins to outweigh that imposed by indirect partners. This weakening of indirect effects is associated with communities losing their tight integration of traits and increasing their rate of adaptation. The above changes are more pronounced when specialist consumers are the first species to switch to antagonism. A shift in

the outcome of species' interactions may therefore reverberate across communities and alter the direction and speed of coevolution.

Using eDNA to reveal aquatic and terrestrial community dynamics in the urban matrix (Poster 3)

Kilian Perrelet

PhD Program in Ecology; EAWAG, Switzerland

Blue-Green Infrastructure (BGI), which are a network of interconnected “blue” or “green” elements such as urban parks, green roofs, streams or urban ponds, can be used to help mitigate the biodiversity crisis in cities. However, BGI are typically designed for stormwater management purposes, and as a result, there is a lack of coordination between engineers and ecologists. In addition, our ecological understanding is highly fragmented throughout the literature, especially between biodiversity enhancements of “green” versus “blue” infrastructure. This lack of coordination and fragmented knowledge could result in sub-optimal conservation efforts and a disregard for interactions between aquatic and terrestrial communities that inhabit BGI. The goal of this PhD is to better characterize the ecological processes driving urban biodiversity, with the overarching goal to better design BGI for biodiversity enhancement. We will be building an integrated framework for better ecological understanding and further collaboration with engineers. Through this holistic approach, we will investigate how terrestrial and aquatic arthropod communities interact within and among infrastructure types, as well as their simultaneous response to urbanization using environmental DNA metabarcoding. Species distribution models and connectivity modeling will also be used to predict the distribution of species among these infrastructure and identify the green- or blueways used by arthropods to enter and cross the city of Zürich.

Catchment-based sampling of river eDNA integrates terrestrial and aquatic biodiversity of alpine landscapes (Poster 6)

Merin Reji Chacko

PhD Program in Ecology; ETHZ, Switzerland

Monitoring of terrestrial and aquatic species assemblages at large spatial scales based on environmental DNA (eDNA) has the potential to enable evidence-based environmental policymaking. The spatial coverage of eDNA-based studies varies substantially, and the ability of eDNA metabarcoding to capture regional biodiversity remains to be assessed; thus, questions about best practices in the sampling design of entire landscapes remain open. We tested the extent to which eDNA sampling can capture the diversity of a region with highly heterogeneous habitat patches across a wide elevation gradient for five days through multiple hydrological catchments of the Swiss Alps. Using an eDNA metabarcoding approach with relatively generic vertebrate and plant primers, we detected 101 vertebrate taxa spanning 41 families and 263 plant taxa spanning 79 families across ten catchments. The number of detected taxa was comparable to the species richness of mammals, amphibians, and plants found in that region in long-term records. Moreover, the dissimilarity of species compositions between elevational classes was more strongly related to the turnover component of beta-diversity than to nestedness, indicating that the biological signal in alpine rivers remains relatively localised and is not aggregated downstream. Accordingly, species compositions differed between catchments and correlated with catchment-level forest and grassland cover. Biomonitoring schemes based on capturing eDNA across rivers within biologically integrated catchments may pave the way toward a spatially comprehensive estimation of biodiversity.

Effects of the human menstrual cycle on female body odors and mosquito attraction (Poster 23)

Marion Risse

PhD Program in Ecology; ETHZ, Switzerland

Females have historically been underrepresented in biological and medical research, with adverse implications for women's health. Indeed, women are often consciously excluded from such studies to avoid temporal variation associated with the female reproductive cycle. In the case of studies addressing the role of human odors in the attraction of disease vectors, the

resulting knowledge gaps can have enormous implications for human health and wellbeing. For example, there is substantial evidence that pregnant women experience higher rates of infection by malaria and other mosquito-borne pathogens, with serious health consequences including reduced birth weight and higher rates of infant mortality. There is also evidence for more general differences between men and women in mosquito attraction. Yet, we currently know almost nothing about sex-specific differences in the odor cues that mediate mosquito attraction. To begin to address this gap in our current knowledge, the current project explores variation in female body odors over the course of the menstrual cycle and its implications for mosquito attraction. To track changes in skin volatile emissions, we will collect volatile samples from female subjects during the menstrual, fertile, and luteal phases of the menstrual cycle, as well as from with male controls, and analyze them via gas-chromatography and mass spectrometry. We will then test the attractiveness of volatile samples for the primary malaria vector, *Anopheles gambiae*, via a uniport olfactometer bioassay. The findings generated by this work will provide insight into potential sex differences in mosquito attraction and disease transmission and inform the development of strategies to mitigate adverse health outcomes.

Beyond structural stability: how coevolution controls resilience. (Poster 16)

Miguel Roman

PhD Program in Ecology, University of Zurich, Switzerland

In this proposal, I present my aim to assess several particular questions concerning the influence of complex coevolutionary dynamics and indirect effects in the persistence of ecosystems and how, conversely, ecosystem structure shapes and constrains the coevolution of the species that compose it. The importance of these questions stems from the growing concern about how underlying evolutionary phenomena can affect the fragility of communities, and how the proximity to extinction is reflected in more subtle predictors than simple declines in population sizes.

Towards taxon-specific growth prediction in microbial communities by metatranscriptomics (Poster 4)

Melanie Stäubli

PhD Program in Ecology, ETHZ, Switzerland

In natural environments, diverse microorganisms form complex communities and provide ecosystem functions. To better understand structural changes and their impact on such functions, it is important to assess the growth rates of individual members. Because most microorganisms cannot be cultivated, growth rates have typically been estimated using time-course incubations of mixed communities and isotopic tracers of DNA or protein synthesis. However, these methods lack information about individual taxa or may contain biases towards certain taxa. More recently, tools to estimate in situ growth rates of individual taxa have been developed based on the distribution of DNA sequencing reads along genomic locations. However, they are limited by the necessity of a reference genome, the assumption of bi-directional replication from one origin and the low accuracy for slow-growing bacteria.

To overcome some of these limitations, we aim to investigate novel methods to predict growth rates of microbial taxa in isolation and community from (meta)transcriptomic data. To this end, we conducted cultivation experiments of isolate strains using different carbon sources, pH and temperatures to achieve a wide range of growth rates. We used growth rate estimates from optical density and transcriptomic data to test prediction metrics. For benchmarking, we cross-validated our method with existing tools and datasets. Among the tested parameters, we found temperature to have a considerable impact on the predictions of existing tools and our methods. With this work, we hope to identify more universal and robust signatures to improve growth rate predictions of diverse microbial community members across various environments.

Conservation pest control in sugar beets (Poster 17)

Angela Studer

PhD Program in Ecology, Agroscope, Switzerland

Biodiversity loss is a major problem all over the world and particularly in high-input agricultural landscapes. This loss of species brings high costs because biodiversity-based ecosystem services can no longer be provided. Due to that, but also to protect human health and the environment, sustainable agriculture has become an increasingly important topic. Consequently, particular synthetic chemical pesticides have been prohibited such as neonicotinoids for seed coating since 2019 in Switzerland. In sugar beet cultivation, this ban caused yield losses up to 50 % due to yellows viruses which are transmitted by aphids. The aim of this PhD is to improve measures to promote biodiversity and derived ecosystem services such as pest control in sugar beet fields. In this context, the effectiveness of wild flower strips (WFS) as a conservation pest control measure against virus transmitting aphids will be investigated. In previous studies, WFS have been shown to be effective in regulating aphid density in potato fields through predation and parasitism of invertebrates. However, to effectively limit virus transmission in sugar beets, the period with the highest virus load of aphids during the season must be determined in order to synchronise the resource supply for the predators. Another fundamental aspect is to check whether the sown WFS plant species can act as overwintering refuges for aphids or whether they serve as virus reservoirs. Since the tested measures are intended to find solutions for practical application, the experiments are carried out directly on commercial fields.

Nesting of ground-nesting bees in arable fields is not driven by tillage system per se, but by other habitat features (Poster 7)

Philippe Tschanz

PhD Program in Ecology, Agroscope, Switzerland

Ground-nesting wild bees are crucial for the pollination of wild plants and agricultural crops and thus human wellbeing. Arable land currently covers 14 million km² globally, but little is known about the role of arable fields as potential nesting habitats and how agricultural management, such as tillage systems, affect nesting. We quantified nesting incidence and nest density of ground-nesting bees in 12 conventionally tilled and 13 no-till winter cereal fields in southwestern Switzerland. In each field, nests were quantified in eight belt transects at increasing distances from field edges within an area of 400 m², and vegetation cover and soil properties were measured at nest sites and sites without nests. Nest density ranged from 0 (32% of fields) to 16 nests (mean: 4.0 nests) per 400 m² sampling area, corresponding to 0 to 400 nests ha⁻¹ (mean: 101 nests ha⁻¹). Fifteen species of ground-nesting bees were captured. Tillage system had no significant effect on nest density. Nesting declined exponentially with distance from the field edge. Nesting was strongly positively related to proportion of bare ground. Nests occurred across a wide range of soil textural classes, and tended to increase with relative soil bulk density and sand content. Moreover, nesting tended to increase with the proportion of and proximity to areas under agri-environment scheme in the surrounding landscape. Our study shows that arable fields, irrespective of tillage system, are used as nesting sites by various ground-nesting bee species, including important crop pollinators. The concentration of nesting along field edges suggests that incentives to maintain small field sizes and to increase edge density have a great potential to support nesting of ground-nesting bees in agricultural landscapes. Moreover, measures to reduce crop cover, e.g., through increased row spacing, offer a promising way to promote nesting opportunities in arable fields, in particular if floral-rich agri-environment scheme areas are locally available. Further studies are needed to better understand to what extent tilled arable fields are suitable nesting habitats for ground-nesting bees or whether they act as ecological traps due to adverse effects of tillage on bee offspring.

Microbe-mediated interactions between coral reef-inhabiting organisms (Poster 5)

Fabienne Wiederkehr

PhD Program in Ecology, ETHZ, Switzerland

Coral reefs harbor a biodiversity unrivalled by any other ecosystem. The biological foundation of these productive and diverse ecosystems are reef-building corals. Yet, to generate and maintain both diversity and productivity, corals depend on interactions not only with other reef macroorganisms, but also with their associated microbial communities. To effectively conserve



reef ecosystems and counteract their unprecedented decline, we need to identify the mechanisms underlying such interactions at multiple scales—from key groups of macroorganisms (stony corals, soft corals, macroalgae, and sponges) down to their microbiome. By collecting both experimental and field data, we might eventually be able to resolve how these microbe-mediated interactions between hosts affect overall reef productivity and diversity. As a first step, we followed the changes in (1) the host-associated microbial community (stony- and soft-coral mucus, macroalgae biofilm, and sponge tissue) and (2) the microbial community exuded by the hosts into the surrounding filter-sterilized seawater over time and from poly- to monoculture and vice versa in a controlled experimental setting. With a combination of marker-gene analyses and genome-resolved metagenomics, we aim to uncover taxonomic and functional links between reef organisms at the microbiome level to contribute towards a more holistic understanding of reef-ecosystem functioning, which may guide conservation and coral-reef restoration efforts to preserve the key functions reef holobionts provide.