



**3rd Global Soil Biodiversity Conference
2023
Book of Abstracts**

Oral Presentations

Climate warming reduces microbial biodiversity in a temperate grasslandJizhong Zhou¹¹*University Of Oklahoma, Norman, United States*

The rapid loss of biodiversity due to human alteration of the global environment is threatening ecosystem functioning. Despite the critical importance of belowground soil biodiversity in maintaining ecosystem functions, whether and how climate change affects the richness and abundance distribution of soil microbial (e.g., bacterial, archaeal, fungal, and protistan) communities remains unresolved. Here, we examined the effects of warming, altered precipitation and clipping (annual biomass removal) on grassland soil bacterial and fungal biodiversity in a long-term multifactorial global change experiment. Our results based on long-term time-series observations revealed that experimental warming played a predominant role in shaping microbial biodiversity by decreasing the richness of soil bacteria (9.6%), archaea (1.4%), fungi (14.5%), and protists (7.5%). The warming effects varied greatly among different microbial lineages, with strong negative effects on slow-growing bacteria and arbuscular mycorrhiza fungi, but positive on fast-growing bacteria. Also, warming significantly decreased soil moisture, which was the major driver of microbial biodiversity reduction. Further analysis revealed significant positive linkages between microbial biodiversity and associated ecosystem functional processes. These results imply that the detrimental effects of biodiversity loss could be more severe in a warmer world, making future ecosystems more vulnerable.

Soil invertebrates in an evolutionary transition zoneNico M. van Straalen¹¹*Vrije Universiteit Amsterdam, Amsterdam, Netherlands*

Soil is an environment promoting the evolution of trait combinations that are uncommon in above-ground terrestrial ecosystems. This is due to soil-specific characteristics, such as spatial restriction, heterogeneity, resource limitation, abundant microbial life, stable abiotic conditions, and sharp transitions in the profile. In a recent book on soil invertebrates, I review the unique evolutionary aspects of soil biodiversity. First of all, soil invertebrates have population densities that are much higher than is expected for terrestrial animals of similar body size. However, effective population sizes are still small due to low dispersal rates, making genetic drift an important evolutionary phenomenon. Genetic population structure on a larger scale is characterized by strong founder effects and isolation. Passive long-range dispersal causes erratic patterns of genetic differentiation. Biomass turnover of soil invertebrate populations depends only little on body size, not matching allometric regressions established for above-ground communities. Uncommon trait combinations are also apparent in life-histories. Almost all soil-living invertebrates are iteroparous and relatively long-lived compared to their body size. The soil favours a K-selected life history, but this is combined with small body size. The widespread occurrence of parthenogenesis in soil invertebrates can be explained by constant resource availability, in line with Bell's tangled bank hypothesis, not by resource abundance like in above-ground parthenogens. In summary, the traits of soil invertebrates are shaped by various evolutionary histories involving terrestrialization, phylogenetic constraint and adaptation to soil conditions. This evolutionary history has made soil invertebrates unique and often quite different from fauna in above-ground communities.

The long-term impact of urease and nitrification inhibitor use on microbial communities in grassland soil

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Aim: Urease and nitrification inhibitors (UI and NI) applied in association with fertiliser have been demonstrated to slow microbial N transformation rates, with resulting decreases in environmental N losses. The specific objectives of this study were to assess whether there is an impact of 1) individual or combined inhibitor use on non-target microbial community composition and abundance; 2) the use of N inhibitors on the N functional community; and 3) applied N fertiliser type (i.e. CAN or Urea) on microbial community composition and function. A 5 year inhibitor trial on grassland was sampled in the southeast of Ireland.

Method: Treatments included a control (no N); CAN (Calcium ammonium nitrate); Urea; Urea & UI; Urea & NI; and Urea & NI & UI. A combination of phenotypic assays; gene abundances of total, nitrifiers and denitrifiers and 16S *rRNA* and ITS sequencing data were used to assess the objectives.

Results: The results indicated there was no impact of either UI or NI use on non-target microbial community composition or abundance; there was a significant impact by the use of NI to the nitrogen cycling functional community compared to standard urea; and finally there was a significant impact of fertiliser type (i.e. CAN or Urea) on the fungal community composition but no impact for the bacterial community composition.

Conclusions: Overall, the results demonstrate the effect of fertilisation on the microbial community is greater than the impact of inhibitor use.

Soil saprophages as an emerging global source for micronutrients

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Aim: "Hidden hunger" is the alarming phenomenon among both humans and livestock. It is triggered by the lack of sufficient volume of micronutrients (microelements, irreplaceable aminoacids and vitamins) in food and feed respectively and may cause serious diseases and pathological conditions. Finding enough micronutrients is often problematic: they are either obtained from limited external natural sources, or synthesised within organisms. Soil-dwelling saprophages bear one of the largest shares of zoomass on Earth but remain surprisingly neglected as potential sources of micronutrients. We analyzed soil saprophages as a potential source of micronutrients with respect to their ability to concentrate vitamins, microelements and amino acids.

Method: We assessed the nutritional value with respect to micronutrients in 30 model invertebrate species belonging to the major soil saprophage taxa. We used biochemical methods to assess proteinogenic amino acids, microelements and vitamins.

Results: Taxonomic differences in the composition and ratio of micronutrients were determined. We identified taxa enriched with micronutrients what makes them potentially interesting for further testing as resources for producing food and feed supplements.

Conclusions: We found that several taxa of soil saprophages (especially insect larvae, millipedes, and earthworms) are quite rich in micronutrients (amino acids, vitamins, and microelements), yet staying, with the few exceptions, ignored as a valuable food and feed supplement raw material. Our comparison in the micronutrient composition of the major soil saprophage taxa has demonstrated that many of them are similar with this respect to conventional meat products.

Restructuring of soil food webs reduces carbon storage potential in boreal peatlandsZoë Lindo¹¹*University Of Western Ontario, London, Ontario, Canada*

Aim: Warming is anticipated to accelerate soil carbon release to the atmosphere, especially in systems where aboveground productivity is low, such as boreal peatlands. Modeling how changes in belowground biodiversity under climate warming affect soil carbon dynamics is an important first step in predicting carbon storage potential in boreal peatlands under future climate scenarios.

Method: Using data from two large-scale field experiments (a sphagnum peatland vs a sedge peatland) exposed to passive (+2 °C) and active (+4 °C) warming, we estimate carbon flux and mineralization among trophic groups and the entire soil food web using the energetic food web package {soilfoodwebs}.

Results: Warming decreased the overall biomass of living organisms at both fen sites with losses largely due to declines in fungal biomass while bacterial biomass increased slightly. Carbon flux and mineralization were strongly correlated with the dominant microbial group at each site. Warming decreased carbon flux and mineralization by ~10% and 15% under passive and active warming at the sphagnum site, but both increased at the sedge site.

Conclusions: Carbon loss is apparent under warming at the sedge site over the short-term because of increases in bacterial biomass and turnover. At the sphagnum site, decreases in fungal biomass reduce their contribution to carbon release, reducing carbon loss in the short-term. But in both systems decreased metabolic efficiency reduces the long-term carbon storage potential.

Climate change impact on Collembola and their responses to predation: a synthesis of 6 experiments

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Aim: Collembola is an abundant group of soil organisms playing a major role on litter decomposition and nutrient cycling in forest ecosystems. Habitat structure and climatic conditions control their demographic parameters and their interactions with predators. Thus, the ongoing climate change, with decreasing precipitation, increasing temperature and altering tree species assemblages, may strongly impact Collembola and their responses to predation.

Method: We therefore examined within 6 complementary experiments how decreasing soil moisture, increasing air temperature and altering litter properties combined to the presence of distinct predators affect Collembola communities.

Results: Generally, increasing temperature or decreasing soil moisture negatively affected Collembola demographic parameters and the intensity of these effects were dependent on litter properties. In addition, we evidenced that altered climatic conditions amplify the negative effect of predation on Collembola whatever the predator considered.

Conclusions: These results point out that studying more complex systems appears essential to predict Collembola responses to climate change.

Comparison of Soil Fauna (Earthworms, Nematodes, Beetles) Community and Diversity under Perennial and Annual Wheat

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Aim:

Perennial cropping systems are known to highly support soil fauna and its diversity. This has been investigated for grassland and bioenergy systems before. Upon recent development, perennial wheat (Kernza®) is increasingly recognised throughout European agriculture. However, the impacts on soil, soil processes governed by soil microbes as well as on soil faunal assemblages are not well studied yet.

Method:

Within the EU-Biodiversa project NAPERDIV earthworm, nematode and beetle communities, among other research areas, were investigated in a Pan-European transect from Sweden to Belgium to South France representing a climatic gradient from south to north and variations in soil conditions.

Results:

Perennial wheat is characterised by a higher number of individuals and biomass for earthworms, resulting in a higher species diversity, with France having greater values than Belgium and Sweden. The beetle data followed the same trend, with diversity indexes being greater for the Kernza sites. Nematode data shows a distribution of lower c-p values (bacterivore) in annual (disturbed) soils, while the higher c-p value individuals (predatory, fungivore) are found in the perennial soil. The higher maturity index for perennial in comparison to annual soils further displays the greater biodiversity under perennial wheat.

Conclusion:

The differences in earthworm data is caused by the no-till management of perennial cropping sites and better food resources. Same goes for the beetle data. The earthworm distribution confirms the biogeographic gradient within Mid-Europe. Nematode communities mainly reflect the impact of land-use, tillage, fertilisation, and soil organic matter on their feeding behaviour.

The Global Distribution of Mycorrhizal Biodiversity

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Aim:

Mycorrhizal fungi form symbioses with plant roots and build extensive underground networks. These fungi support the health of plant and soil systems globally, provide critical ecosystem services, and help regulate the Earth's climate. Past work has focused on the biogeography of mycorrhizal associations within plant communities, identifying important environmental gradients that structure these symbioses and highlighting their connection to biogeochemical cycles. However, these efforts use aboveground vegetation surveys to assign plants a mycorrhizal category which is treated as a constant. While this provides a picture of where certain mycorrhizal symbioses are most dominant on the landscape, it does not necessarily show where fungal communities are the most diverse. Documenting the spatial distribution of mycorrhizal diversity is urgently needed because different mycorrhizal fungi are associated with different ecosystem functions, like enhanced carbon storage, improved plant stress tolerance, and efficient nutrient cycling.

Method:

Here, we present our efforts to map the diversity of mycorrhizal fungi at the global scale. In collaboration with the Crowther Lab (ETH Zurich) and GlobalFungi, we developed machine learning algorithms trained on a large fungal sequencing database encompassing nearly 10,000 soil and root samples.

Results:

These models were used to predict underground biodiversity hotspots for arbuscular and ectomycorrhizal fungi across the planet, revealing certain regions with extraordinarily diverse fungal communities.

Conclusions:

We discuss how such diversity hotspots mark high priority areas to explore, especially in the context of conservation and restoration of critical fungal interactions in underground ecosystems that face intensifying threats from climate and land use change.

Global hotspots for soil nature conservation

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Abstract

Soils are the foundation of all terrestrial ecosystems. However, unlike for plants and animals, a global assessment of the hotspots for soil nature conservation is still lacking. This hampers our ability to establish nature conservation priorities for the multiple dimensions supporting the soil system: from soil biodiversity to ecosystem services. Here, we conducted a global field survey including biodiversity (archaea, bacteria, fungi, protists, and invertebrates) and function (critical for six ecosystem services) observations within 615 composite topsoil samples from a standardized survey in all continents, to identify global hotspots for soil nature conservation. We found that each of the different soil ecological dimensions (i.e., soil species richness [alpha diversity, measured as ASVs], community dissimilarity, and ecosystem services) peaked in contrasting regions of the planet, and were associated with different environmental factors. Temperate ecosystems showed the highest species richness, while community dissimilarity peaked in the tropics, and colder high-latitude ecosystems were identified as hotspots of ecosystem services. These findings highlight the complexities of simultaneously protecting multiple soil ecological dimensions. We further show that most of these hotspots are not properly covered by protected areas (over 70%), and are vulnerable in the context of multiple global change scenarios. This first global estimation of soil nature conservation priorities, highlights the fundamental importance of accounting for the multidimensionality of soil biodiversity and ecosystem services to conserve soils for future generations.

Soil Microbiological Quality: State Of The Art And Importance Of Microbial Communities For Agricultural Soils.

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Aim:

Soils are one of the major reservoirs of biological diversity on our planet, hosting a huge diversity of microorganisms. Given the key role of soil microorganisms in the regulation of soil ecosystem functions, the environmental factors driving soil microbial diversity need to be understood. In France, we have the opportunity to benefit from a national soil survey (the French Soil Quality Monitoring Network), which represents one of the most extensive and without *a priori* soil sampling survey available to date, to decipher the spatial distribution of microbial diversity at the scale of France.

Method:

We applied various analytical and geostatistical approaches combining the data on soil microorganisms after amplicon sequencing targeting both 16S and 18S rRNA gene sequences, and large-scale environmental description in order to conduct a comprehensive analysis of soil microbial communities.

Results:

These analyses provided extensive maps of bacterial and fungal diversity, structure and composition and reveals the heterogeneous and spatially structured distribution of microbial communities at the nationwide scale. We also identified the ecological processes involved in the biogeographical patterns of microbial communities, and developed co-occurring networks identified within the relative abundance of bacterial taxa dataset to the scale of France.

Conclusions:

In a context of global change, first our results emphasize that the policies for biodiversity and habitat conservation should now integrate soil microorganisms conceptually and technically. To help them taking into account the microbiological part of soils, we also developed innovative tools allowing a robust diagnosis of soil biological quality.

Temporal Dynamics of Soil Animal Abundance and Diversity as Influenced by Forest Management

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Aim:

Land-use intensification is one of the main causes of biodiversity decline. The abundance and diversity of aboveground arthropods has declined significantly over the past 10-15 years. However, belowground species diversity, particularly in forests, appears to be buffered against changes in land-use intensity. As part of the open research platform 'biodiversity exploratories', we evaluated a comprehensive long-term dataset of soil-dwelling meso- and macrofauna species in forests of different management intensities. Our goal was to identify patterns and drivers of soil faunal biodiversity over time as influenced by forest management.

Method:

We sampled soil fauna from four forest types representing different forest management intensities in three regions in Germany. The abundance of soil-living meso- and macrofauna species was recorded in three-year intervals, covering 12 years from 2008 to 2020. Changes in abundance and species richness were analysed using linear mixed effects models with soil moisture, winter temperature, microbial biomass and C-to-N ratio of leaf litter as well as forest management intensity and the year as predictors.

Results:

While abundance and diversity of soil fauna in part differed between land-use types, we found no generally declining trend, but mainly temporal variations related to soil moisture and to soil temperature of the preceding winter months. Interestingly, this pattern was largely coherent among different taxa and even between meso- and macrofauna.

Conclusions:

Our results contrast above-ground biodiversity declines and suggest different above- and below-ground biodiversity dynamics. They may help to better understand the consequences of land-use change and the corresponding driving factors for changes in soil biodiversity.

Diversity and Functions of Microorganisms in the Hyphosphere of a Grassland Soil

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Aim:

The hyphosphere is defined as a sphere where fungi release exudates and stimulate the growth of specific bacterial communities. Consequently, the hyphosphere might bridge different microhabitats and might contribute to the trilateral interaction between plants, roots, and soil microorganisms. The aim of the study is to investigate the role of the hyphosphere for microbial colonization as well as C and N transport between different organic substrates and the rhizosphere.

Method:

We used newly developed HYPHOBOXES consisting of different compartments (filled with sterile soil) to separate the rhizosphere from the hyphosphere and a nutrient patch (¹³C and ¹⁵N labelled arginine or litter), only available for fungi and bacteria.

Results:

Roots of the grassland community colonized the rhizosphere compartment and took up ¹⁵N transported through hyphae from the N source. The carbon in saprotrophic fungi was up to 75% litter derived but they transported this carbon only partly to other compartments. Temporal as well as spatial pattern of carbon incorporated into bacterial PLFAs suggested that bacteria mainly used fungal exudates as secondary users of litter derived C. The bulk soil was dominated by oligotrophic bacterial groups (like acidobacteria and actinobacteria), whereas the newly established microhabitats of the HYPHOBOXES were characterised by a succession of different copiotrophic bacteria (like alpha- and betaproteobacteria). Sequencing of fungal ITS will clarify which fungal guilds are dominant colonizers of the different microhabitats.

Conclusions:

The experiment set up will allow to disentangle bacterial colonization, fungal exudation, and microbial nutrient transport in the hyphosphere under field conditions.

Temperature and Precipitation Jointly Shape the Plant Rhizosphere and Root Microbiome

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Aim: The ongoing change in climate extensively alters belowground interactions between plants and soil microbiota. Plant-microbial interactions drive a large array of plant community processes and changes in these interactions will therefore cascade into affecting whole ecosystem dynamics. To be able to predict ecosystem change, we need to understand how plant-microbial interactions are shaped by climatic factors.

Method: We tested how natural temperature and precipitation gradients shaped prokaryote and fungal rhizosphere and root associated communities of *Festuca rubra*. To achieve this, we sampled rhizosphere and root microbial communities as well as soil abiotic properties in the SEEDCLIM grid in the fjords of Southern Norway and combined this data with data on temperature, precipitation, soil moisture and whole plant community composition.

Results: We found that fungal and prokaryote rhizosphere communities were strongly shaped by temperature and to a lesser extent by precipitation. These changes were largely related to changes in soil resource cycling and overall plant community composition. Fungal and prokaryote root associated communities were less strongly shaped by climate.

Conclusions: We conclude that climate change will profoundly impact rhizosphere processes, but that root microbial interactions may remain relatively unaffected.

The soil microbiome governs the response of microbial respiration to warming across the globe

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Aim:

The temperature sensitivity of soil heterotrophic respiration (i.e., the factor by which soil microbial respiration increases with a 10°C rise in temperature; Q_{10}) is a major source of uncertainty in projecting the magnitude of the land C-climate feedback, as the factors driving Q_{10} patterns across ecosystems have been assessed in isolation from each other.

Method:

Here, we report a warming experiment using soils from 332 sites across all continents and major biomes to conduct the first simultaneous evaluation of the main drivers (i.e., substrate quantity, mineral protection, biochemical recalcitrance, and soil microbiome) of Q_{10} patterns across the globe.

Results:

Our analyses revealed that the soil microbiome (i.e., microbial biomass, richness, and microbial community composition) accounted for 49% of the explained variation in Q_{10} values ($R^2=0.54$), being the factor that explained the largest portion of its variation. We also noted that an important portion of Q_{10} variation is shared by the interactions between multiple factors (30%), suggesting that Q_{10} has highly multifactorial drivers. Moreover, Random Forest analyses showed that soil microbial biomass and soil community composition were the most important predictors determining the global patterns of Q_{10} .

Conclusions:

Our work provides a novel and important perspective on how soil C losses to the atmosphere in response to warming are governed by soil microbiome across biomes. These findings provide solid evidence that we need to monitor and conserve the diversity of soil microbiomes globally, as they are critical drivers of essential ecosystem services.

Trait-mediated responses to aridity and experimental drought by springtail communities across Europe

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Abstract

1. The capacity to forecast the effects of climate change on biodiversity largely rely on identifying traits capturing mechanistic relationships with the environment through standardized field experiments distributed across relevant spatial scales. The effects of short-term experimental manipulations on local communities, may overlap with regional climate gradients that have been operating during longer time periods. However, to the best of our knowledge, there are no studies simultaneously assessing such long-term macroecological drivers with local climate manipulations.
2. We analyzed this issue with springtails (Class Collembola), one of the dominant soil fauna groups, in a standardized climate manipulation experiment conducted across six European countries encompassing broad climate gradients. We combined community data (near 20K specimens classified into 102 species) with 22 eco-morphological traits and reconstructed their phylogenetic relationships to track the evolution of adaptations to live at different soil depths, which is key to cope with desiccation. We then applied joint species distribution models to investigate the combined effect of the regional aridity gradient with the local experimental treatment (drought and warming) over the assembly of springtail communities and tested for significant trait-environment relationships mediating their community-level responses.
3. Our results show: (1) a convergent evolution in all three major collembolan lineages of species adapted to inhabit at different soil strata; (2) a clear signature of aridity selecting traits of more epigeic species at a biogeographic scale, and (3) the association of short-term experimental drought with traits related to more euedaphic life-forms.
4. The hemiedaphic condition would be the plesiomorphic state for Collembola while the adaptations for an epigeic life would have been secondarily gained. Epigeic springtails are more resistant to drought but also have a higher dispersal capacity that allows them to seek more favourable micro-habitats after experiencing drier conditions. The observed relative edaphization of the springtail communities after short-term experimental drought may thus be a transient community response.
5. The disparity between macroecological trends and fast community-level responses after climate manipulations highlights the need of simultaneously assessing long-term and short-term drivers at broad spatial scales to adequately interpret trait-environment relationships and better forecast biodiversity responses to climate change.

Invasive Plant Control with Herbicide does not Impact Soil Microbial Biodiversity and Activity

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Aim:

Invasive plant species are a major concern for terrestrial ecosystems around the world, causing potential declines in biodiversity above- and belowground and shifts in nutrient and carbon cycling. Herbicide application can be effective at killing undesired plants, but questions remain on possible negative impacts to non-target species, including soil dwelling organisms.

Method:

In this study, we examined triclopyr oil-based herbicide control of invasive Amur honeysuckle bush (*Lonicera maackii*) in a degraded savanna in Illinois, USA. During winter, eight replicate plants were subjected to each treatment: control (no herbicide), oil (solvent, no active herbicide), and oil + herbicide. We used next-generation sequencing techniques to examine soil fungal, prokaryotic, and oomycotan diversity and community structure within 15cm of the treated plant. We microscopically examined target plant roots for arbuscular mycorrhizal fungal colonization rates. We also examined potential soil enzyme activity from a suite of carbon and nitrogen cycling enzymes.

Results:

Herbicide treatment killed 100% of plants to which it was applied. Soil microbial diversity and community structure were not impacted by herbicide application. Furthermore, soil enzyme activity and profiles did not differ among the treatments. Arbuscular mycorrhizal colonization rates on target plants declined with herbicide treatment, likely due to host death.

Conclusions:

Together, these data suggest that dormant season triclopyr application does not impact soil communities. Such an approach can be highly effective at removing Amur honeysuckle in highly invaded systems with little to no negative impact to soil microbial taxa and their functioning.

Biogeographical survey of soil microbiomes across sub-Saharan Africa: structure, drivers, and predicted climate-driven changes

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Aim:

Top-soil microbiomes make a vital contribution to the Earth's ecology and harbour an extraordinarily high biodiversity. While several recent studies have documented patterns in global soil microbial ecology, these are biased towards widely studied regions and rely on models to interpolate the microbial diversity of regions with a low data coverage. This is the case for sub-Saharan Africa, where the number of regional microbial studies is very low in comparison to other continents.

The aim of this study was to conduct an extensive biogeographical survey of sub-Saharan Africa's top-soil microbiomes, with a specific focus on investigating the environmental drivers of microbial ecology across the region.

Method:

In this study, we sampled 810 sample sites across 9 sub-Saharan African countries and used taxonomic barcoding to profile the microbial ecology of these regions.

Results:

Our results show that sub-Saharan top-soil microbiomes are shaped by a broad range of environmental factors including pH, precipitation, and temperature. We also developed a structure equation model to predict how soil microbial biodiversity in sub-Saharan Africa might be affected by future climate change scenarios.

Conclusions:

This study represents the most extensive biogeographical survey of sub-Saharan top-soil microbiomes to date. Importantly, this study allowed us to identify countries in sub-Saharan Africa that might be particularly vulnerable to losses in soil microbial ecology and productivity due to climate change. Considering the reliance of many economies in the region on rain-fed agriculture, this study provides crucial information to support conservation efforts in the countries that will be most heavily impacted by climate change.

Jardibiodiv: a digital community science tool on urban soil-surface dwelling invertebratesApolline Auclerc¹¹*University of Lorraine, France, France*

Aim: In a context of biodiversity erosion, a number of questions are currently being asked about soil biodiversity in urban areas. While the urban ecosystem integrates humans and all the disturbances they can induce, it is important to carry out a work of soil organism quantification and knowledge transfer to citizens in order to increase their awareness and make them more responsible by allowing them to better observe and understand the ecosystem around them. Developing a digital community science tool on urban soil biodiversity seemed to be an ideal solution to connect researchers and urban soil users. Jardibiodiv tool was born in France in 2017, with the objective of quantifying the soil surface-dwellers invertebrates following a fun activity and with the participation of as many people as possible.

Method: Several elements are available in this tool: simple protocols, a taxonomic identification assistance tool, several organism description forms, and forms to fill online or on the smartphone application to directly send observation to the scientist <http://ephytia.inra.fr/en/P/165/JardiBiodiv>. Each user has the choice to observe the organisms hidden under small habitats (stones, wood residues), or to install a cup buried into the soil to catch the organisms.

Results: Thanks to 830 smartphone application downloads and with online participation, 1214 forms were filled.

Conclusions: Thanks to the user observation, scientists can start to quantify the impact of pressures on soil biodiversity in urban areas. This tool is constantly evolving through new collaboration development and depending of the user needs following a process of co-construction.

Utilizing Different eDNA Fractions for Enhanced Insights into Soil Biodiversity

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Aim:

Environmental DNA (eDNA) can be split into an extracellular and intracellular fraction (exDNA vs. iDNA), each bearing different characteristics regarding its inherent information but also persistence in a given environment, such as the soil ecosystem. In our research, we aim to investigate how these fractions can provide quantitative, qualitative, physiological, temporal and spatial information on macro- and micro-organisms, and how they might contribute to define present, active, past or allochthonous species.

Method:

Environmental samples (e.g., soil, water, biogas slurry) are subject to sequential washings with buffers of increasing stringency, successively yielding free and surface-bound exDNA. Those obtained fractions, and ultimately the fraction of iDNA, are used to perform classical DNA-extraction, purification and respective downstream analyses.

Results:

Overall, we gained evidence that this fine-tuning eDNA approach (I) increases the sampling depth of a single eDNA sample, (II) decreases the probability of false-positive detections in eDNA monitoring by using the most appropriate fraction for the respective environment, (III) might be suited to specifically tackle autochthonous or allochthonous species, and (IV) provides insights into microbial activity, turn-over rate, and physiological state.

Conclusions:

Fine-tuning the extraction approach for eDNA by splitting it into exDNA and iDNA is an easy-to-implement method with great potential to augment spatial, temporal, quantitative and qualitative information retrievable from eDNA-studies. Past results were promising, and further research is ongoing to define general requirements for differing environments.

Human drivers of soil microbial responses to drought

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Aim:

The frequency and intensity of drought events is expected to increase, threatening agricultural systems where biodiversity is heavily managed. The soil microbiota play a central role in maintaining the health and productivity these ecosystems in the face of environmental change, but they are affected by agricultural management practices as well as the droughts themselves. Understanding the interactive effects of these perturbations on the microbiome is essential to the long-term maintenance of soil microbial communities, their functions, and agricultural fertility.

Method:

I will present a set of experiments where we manipulated agricultural management, aboveground, and belowground (mycorrhizal) diversity in mesocosms exposed to simulated drought events.

Results:

Across experiments, we have found consistent responses in soil microbiomes exposed to drought, as well as interactive effects of drought and aboveground diversity. In the above and belowground diversity manipulation experiments, community responses were dependent on both above and belowground diversity, as well as the identity of the plants aboveground and mycorrhizae belowground. Importantly, mycorrhizal diversity and composition was a stronger driver of the soil microbiome than aboveground diversity.

Conclusions:

Our findings suggest an additive effect of aboveground—and more importantly, mycorrhizal—diversity on soil microbial resilience, and highlight the potential of mycorrhizal management to bolster soil microbiomes in the face of climate change.

Nature restoration via bottom-up and top-down steering of soil organismsElly Morriën¹, Casper Quist², Emilia Hannula³*¹University of Amsterdam, Amsterdam, Netherlands, ²Wageningen University, Wageningen, Netherlands, ³Leiden University, Leiden, Netherlands*

Restoring natural plant communities on abandoned agricultural fields can be challenging due to a degraded soil community and a fertilizer legacy. We discovered that fungi are the initiators of a tighter connected soil food web which restores the closed carbon and nutrients cycles in soils, thereby accommodating species-rich plant communities in grasslands. Boosting the fungal channel as a bottom-up approach could thus be used as a next-generation restoration measure. We show data of soil inoculation experiments and trace the progression of change in the fungal community via sequencing and functioning via community response profiles. We assessed the top-down foraging of predators and consumers on the microbiome by analysing gut contents of consumers and predators from different restoration stages. We also assessed the bottom-up steering of microbial inocula from restored sites into agricultural soils and scored plant performance. In general we found stronger evidence for bottom-up regulation than for top-down regulation in the soil food chain. We will be able to show data on the effect of fungi and their higher trophic levels in stimulating species-rich plant communities as well as give a prospect on the wider applications for microbiome engineering.

Connecting above and below ground diversity in the Brazilian Atlantic Forest restoration

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Aim: The Brazilian Atlantic rainforest is considered an endangered biome and has only 12-16% of its original cover vegetation. Most of his original areas were predominantly converted to different land-use systems, such as pastures and sugarcane plantations. However, large-scale ecological restoration programs in Brazil have begun to transform degraded lands into young native ecosystems using different restoration strategies. However, there is little known about forest restoration's impact on the soil microbiome and its functional role in this environment.

Method: Thus, we investigated the effect of Active and Assisted Forest restoration methodologies with different time scales (Early-, Intermediate- and Late-stages) on soil microbial communities (Fungi, Bacteria-Archaea, and Protist-Nematode) in the Atlantic Forest region in São Paulo state, Brazil.)

Results: We found that the structure of the soil microbial communities still has not recovered by resembling any of the reference forests chosen in this study. However, when the potential functions displayed by these communities were accessed, it was found that Late-Assisted forests were similar to the Native forest. Generally, the diversity below- and above-ground was much more similar to degraded forests (like a Secondary Degraded and a Native Degraded). In addition, strong correlations between the above-ground diversity and the soil characteristics and between and between soil communities and soil characteristics.

Conclusions: Together, our results provide information to outline better methodologies to recover the above and below-ground communities of tropical forests by unraveling the “soil black box” in forest restoration.

Intensive grassland management disrupts below-ground multi-trophic resource transfers in response to drought

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Aim:

Understanding how soil food webs and their functioning are impacted by global change is of critical importance. Modification of soil food webs by historical land management may alter the response of ecosystem processes to climate extremes, but empirical support for this is limited and the mechanisms involved remain unclear. We hypothesized that land management alters the structure of soil food webs, and this in turn influences the response of soil functions to drought.

Method:

Drought shelters were installed in paired intensively and extensively managed grasslands. After removal of shelters, plants were pulse labelled with ¹³CO₂ and ¹⁵N and the fate of ¹³C and ¹⁵N was assessed by sequential sampling of plant tissue, soil organisms and greenhouse gas effluxes over 20 days. We quantified how historical grassland management modifies the transfer of recent photosynthates and soil nitrogen through plants and soil food webs during a post-drought period.

Results:

We show that intensive management decreased plant carbon (C) capture, its transfer through key components of food webs and soil respiration compared to extensive management. We observed a legacy effect of drought on C transfer pathways mainly in intensively managed grasslands, by increasing plant C assimilation but decreasing its transfer to plant roots, bacteria and Collembola.

Conclusions:

Our work provides insight into the interactive effects of land management and drought on C transfer pathways, highlights that capture and rapid transfer of photosynthates through multi-trophic networks is key for maintaining grassland resistance to drought and its legacy.

Niche breadth specialisation is a critical driver of microbial biodiversity and adaptation in changing environments

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Aim: Ecological theory predicts that the distribution and abundance of organisms depend on their abilities to adapt to environmental change. Attempts to increase understanding of organismal distribution have led to their classification as specialists (narrow niche breadth) and generalists (broad niche breadth). Studies in eukaryotes showed that generalists dominate specialists following environmental change, but this remains understudied in environmental prokaryotes. Here, we aimed to determine if pH niche breadth specialisation drives microbial biodiversity and adaptation.

Method: These concepts were investigated in Thaumarchaeota using pH niche breadth as specialisation factor, using empirical approaches (stable-isotope-probing and sequencing), and reconstruction of state-dependent diversification by integrating phenotypic traits into molecular phylogenies. We assessed microbial growth and activity following experimental soil pH perturbation using short-term soil microcosms and long-term pH-maintained plots.

Results: Following determination of a microbial specialist and generalist database, we demonstrated that generalists have greater environmental adaptation potential than specialists, due to higher metabolic versatility, except for environmental changes leading to more extreme conditions under which specialists are favoured. Environmental perturbations strongly influenced the community composition of both resident and active microbes and induced increased dormancy in perturbed ecosystems compared to native ones, influencing soil biodiversity. Finally, evolutionary ancestral state reconstruction analysis revealed a similar speciation rate for both states but a higher transition rate toward specialists.

Conclusions: Altogether, this study demonstrated a crucial ecological concept in prokaryotes and improved our knowledge of archaeal adaptation to environmental change. We showed that microbial niche breadth specialisation is essential in driving soil biodiversity.

Drought Increases Root-exudate-induced Soil Respiration Rate Across 17 Common Grassland Species

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Aim:

Root exudates, highly dynamic mixtures of carbon (C) compounds that are continuously exuded by roots, play an important role in ecosystem C cycling. Drought can alter the quality and quantity of root exudation, which can potentially alter soil C cycling. Here, we tested how drought affects root exudation across a range of temperate grassland species, and assessed their effects on soil respiration.

Method:

Seventeen common grassland species across three functional groups (7 grasses, 6 forbs and 4 legumes) were grown for 2 months and subjected to a 2-week drought followed by one week of recovery, after which root exudates of each individual plant were collected and analysed for their total organic C content. We analysed root traits and assessed root-exudate-induced respiration.

Results:

We found that root exudation on a per plant basis was reduced by drought. Droughted root exudates triggered the same amount of respiration as exudates from well-watered plants, but specific respiration rate (respiration per ug root exudate C per hour) was higher in root exudates from droughted plants, especially in forbs and legumes.

Conclusions:

Our findings suggest that drought might potentially reduce the soil C sink in temperate grasslands.

Soil bacterial communities and soil chemistry vary with plant species diversity in tallgrass prairies

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Aim: We investigated the impacts of planted tallgrass prairie monocultures and polycultures on soil chemistry and bacterial structure as well as soil nutrient pools and fluxes.

Method: Each of 127 plant species were planted in monocultures as well as 15 species polycultures with varying levels of phylogenetic and trait diversity. To assess the bacterial community, we sequenced the 16S rRNA gene from 2016, 2018, and 2021. We measured soil function using a combination of extracellular enzyme assays and nitrogen mineralization and nitrification assays. Soil chemistry was characterized using pH, organic matter content, organic carbon and nitrogen (TOC and TN), inorganic N, as well as total carbon and nitrogen measurements.

Results: Bacterial communities varied between polycultures and monocultures ($p = 0.03$) Within monocultures, the bacterial community differed by plant species and year ($p < 0.01$). Within polycultures, bacterial communities did not vary by phylogenetic diversity or trait diversity ($p \geq 0.05$) but did vary by year ($p = 0.001$). TOC was higher in polycultures than in monocultures ($p < 0.05$). In contrast, monocultures had larger total and inorganic N pools, as well as faster N mineralization and nitrification rates than polycultures ($p > 0.05$). Soil function and chemistry did not differ in polycultures by phylogenetic or trait diversity ($p \geq 0.05$).

Conclusions: Species diversity influenced both bacterial community structure as well as soil chemistry and function. This suggests that when planting tallgrass prairie restorations, including more species diversity will alter bacterial communities and increase soil carbon more quickly.

The effect of earthworm ecological group on plant-plant interaction

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Aim: Earthworms are keystone organisms in soil ecosystem, playing an important role in nutrient cycling and plant growth. Despite the effect of earthworms on plant growth is well recognized, little is known about how different earthworm ecological groups modulate interactions between different plant species.

Method: We conducted a mesocosm experiment with three earthworm ecological groups (epigeic, anecic and endogeic) and three plant communities of different plant functional groups, including legume, grass and their mixtures, to investigate the role of earthworm ecological groups in legume-grass interactions.

Results: Compared to plant monocultures, a plant mixture increased the productivity of both legumes and grasses, likely due to niche partitioning, with grass taking up nitrogen from the legume, and the legume benefitting from reduced intraspecific competition. Despite earthworms had no significant effect on plant growth, the presence of most earthworm species increased the plant quality of grass, and, in case of *A. chlorotica*, also of legumes. In addition, endogeic earthworms altered plant $\delta^{13}\text{C}$ values, with *A. caliginosa* increasing the $\delta^{13}\text{C}$ values of both legumes and grasses and *A. chlorotica* decreasing the $\delta^{13}\text{C}$ values of grasses, suggesting that endogeic earthworms play a greater role than epigeic and anecic ones in mediating plant resource acquisition.

Conclusions: The mixture of legume and grass facilitates the growth of both plant functional groups. Although they did not directly affect the interspecific interactions of plants, earthworms, in particular endogeic species, altered the resource acquisition of plants as indicated by shifts in plant quality and carbon isotopic signatures.

Soil Biodiversity in Solar Photovoltaic Parks: the Important Role of Inter-row AreaCristina Menta¹, Fabio Gatti¹, Sara Remelli¹¹*University of Parma, Parma, Italy***Aim:**

Ground-mounted solar panels are a strategic form of renewable energy production whose effects are still largely unknown on soil health and biodiversity. This study aimed to evaluate the effects of two photovoltaic plants (Northern Italy), characterised by partially different technical features and soil managements, on soil arthropod biodiversity.

Method:

Three conditions were identified in each plant: under photovoltaic panel (R), in the area comprised between the panel rows (IR) and around the photovoltaic plant (C), in spring and autumn 2021. Soil pH and organic matter (SOM), soil arthropod community, biodiversity and quality indices (e.g. QBS-ar index) were studied to evaluate the impact of photovoltaic panels, also depending on the management of the plant to which they belong.

Results:

SOM and pH showed higher values in C, compared to R and IR. Soil fauna (both in terms of density and diversity) and QBS-ar showed lower values in R compared to IR and C. Soil fauna assemblages, were also affected by seasonality and the plant of origin. These differences are determined mainly by: Acarina, Collembola, Hymenoptera and Hemiptera. These groups showed lowest density in R and, especially for Acarina and Collembola, this result was more marked depending on the photovoltaic plant.

Conclusions:

The results obtained for IR are more comparable to C than R, suggesting that the area between panel rows can be considered a good hotspot of soil biodiversity. The adoption of tracking panels could be a valid solution to reduce the negative effect of the panel on soil living community.

Deadwood mitigates the negative effect of forest gap formation on soil arthropodsAndré Junggebauer¹, Melanie Pollierer¹, Stefan Scheu¹¹*University Of Göttingen, Göttingen, Germany***Aim:**

Extensive forest management practices lead to severe declines in arthropod diversity. Especially, tree harvesting affects soil microclimate by forest gap formation. It also minimizes the supply of deadwood, an important resource for above- and belowground taxa in forests. Here, we use the “FOrest gap eXperiment (FOX)” as part of the research platform “Biodiversity Exploratories” to investigate consequences of forest gap formation and deadwood on soil fauna in beech and spruce forests in three regions of Germany.

Method:

To analyze effects of forest gaps and the presence of deadwood, a multi-site full-factorial study design was established in three regions in Germany in 2020. Plots with forest gaps were established with and without removal of deadwood, unlogged plots were enriched with deadwood or left unaltered for control. After one year, we sampled macrofauna (Chilopoda, Diplopoda, Isopoda, Lumbricidae) and mesofauna (Oribatida) and determined them to species. We used linear mixed effect models to analyze treatment effects on the abundance and diversity of soil animals and latent variable modelling to visualize changes in soil fauna communities.

Results:

Soil macrofauna differed significantly in abundance and community composition between regions. Forest gaps caused declines in the abundance of earthworms, isopods and Oribatida. By contrast, presence of deadwood positively affected the abundance of centipedes and isopods and mitigated negative effects of gap formation for earthworms and Oribatida.

Conclusion:

We show that forest gaps from extensive forest management have immediate negative effects on soil arthropods. We also highlight the value of deadwood enrichment as an important option for future management practices.

Temperature and rainfall patterns constrain the multidimensional rewilding of global forestsGuiyao Zhou^{1,2}, Manuel Delgado-Baquerizo²¹*German Centre For Integrative Biodiversity Research (div) Halle-jena-leipzig, Leipzig, Germany,*²*Laboratorio de Biodiversidad y Funcionamiento Ecosistémico. Instituto de Recursos Naturales y Agrobiología de Sevilla (IRNAS), CSIC, Sevilla, Spain*

The long-term contribution of global forest restoration to support multiple dimensions of biodiversity and ecosystem function remains largely illusive across contrasting climates and forest types. This hampers our capacity to predict the future of forest rewilding under changing global climates. Here, we synthesized 120 studies across five continents, and found that forest restoration promoted multiple dimensions of biodiversity and ecosystem function such as soil fertility, plant biomass, microbial habitat, and carbon sequestration across contrasting climates and forest types. Based on global relationship between stand age and SOC stock, planting 350 million hectares of forest under the UN Bonn Challenge could sequester >30 Gt soil C in the surface 20 cm over the next century. However, our findings also indicate that predicted increases in temperature and reductions in precipitation will constrain the positive effects of forest rewilding on biodiversity and ecosystem function. Further, we found important tradeoffs in very old forests, with considerable disconnection between biodiversity and ecosystem function. Together, our findings provide evidence of the importance of the multidimensional rewilding of forests, suggesting that on-going climatic changes may dampen our expectations of the positive effects of forest restoration on biodiversity and ecosystem function.

Keywords: forest restoration, tradeoffs, carbon sequestration, climate change, biodiversity-ecosystem function

Functional trait space of European earthworms: a trait database and definition of functional groups

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Aim:

Based on earthworm morphological and ecological characteristics, ecological categories were defined and represent the major lifestyles observed among earthworm species. These categories were latter use to predict earthworm response to environmental drivers and their effect of ecosystem functioning. However, this use goes beyond the initial goal of such categories. Using traits of French earthworm species, recent work revisited these categories and stressed that every earthworm species can be attributed a percentage of belonging to each category. The use of continuous trait rather than discrete categories allows a more precise and mechanistic description of earthworm diversity patterns and role in soil processes. To do so, harmonized trait data for a large number of earthworm species is still lacking.

Method:

To address this issue, we gathered traits with a link to soil functions (i.e., functional traits) for a large number of European earthworm species (~400 species), and performed multivariate analyses to determine objective and trait-based functional groups.

Results:

This allowed us to identify taxonomic groups of particular functional interest (uniqueness) and others with redundant traits. Using the most recent earthworm distribution dataset, we mapped earthworm functional diversity at the European scale and identified hotspots of functional diversity. We also explored how invasive vs native and peregrine vs endemic species are situated in the functional trait space to identify traits potentially linked to earthworm colonization capacities.

Conclusions:

We provide an open source database and code to facilitate its standardized use to explore earthworm functional diversity patterns and relationships between traits and functions.

Soil microbiome informs soil carbon storage and vulnerability in urban greenspaces worldwide

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Aim:

Urban greenspaces support multiple nature-based services, including soil carbon (C) storage. Yet, when compared with their natural analogues, little is known about the magnitude, environmental drivers and microbial sensitivity of soil C pools in urban greenspaces worldwide.

Method:

Here, we combine measures of soil C concentration and size fractionation with metagenomics and warming incubations across a global network of 56 paired urban greenspaces and natural ecosystems from six continents.

Results:

We show that surface soils in urban greenspaces support similar soil carbon concentrations to those in adjacent natural ecosystems. Moreover, soil C concentrations in natural and urban ecosystems follow similar negative correlations with temperature. However, we also showed that plant productivity and soil microbes contribute differently to explaining the global distribution of surface soil C in natural and urban ecosystems, with soil microbes appearing central to soil C storage and supporting greater sensitivity to warming in urban greenspaces worldwide.

Conclusions:

We show that urban greenspaces are important global reservoirs of surface soil C, supporting similar concentrations to those in adjacent natural ecosystems. Common temperature but distinct plant and microbial associations explain soil carbon in urban versus natural ecosystems globally. Given the important role of soil microbes in controlling C fluxes under climate warming, our findings suggest that urban soil C stocks might be particularly sensitive to climate warming.

Four Decades of Organic and Conventional Agriculture Promote Distinct Soil Microbiomes with Contrasting Metabolic Potentials

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Aim: Soil microorganisms deliver numerous ecosystem functions essential for crop production. Changes in agricultural practices can alter soil microbial diversity and the underlying metabolic potential encoded in their genomes. This offers opportunities to harness microbial resources for developing sustainable cropping systems. Here, we explored how different organic and conventional farming systems shape diversity and metabolic potential of the soil microbiome.

Method: Soils were collected from the DOK long-term field trial comparing five different farming systems since 1978. The soil microbiome was characterized by DNA metabarcoding and shotgun metagenomics. Extensive auxiliary data on soil properties, greenhouse gas emissions, and crop performance from decades of research were integrated into a comprehensive system comparison.

Results: Organic fertilization as an integral part of organic farming increased diversity and altered the taxonomic and functional structure of the soil microbiome compared to stockless systems. The plant protection regime was of subordinate importance. Organic fertilization promoted microbial guilds involved in degradation of complex organic compounds, whereas minerally fertilized systems were characterized by oligotrophic communities adapted to carbon-limited environments. Functional gene composition showed a gradual change based on the type of fertilizer inputs from organic to conventional and unfertilized systems. Organically fertilized soils were characterized by genes related to heterotrophic metabolism (e.g., tricarboxylic acid cycle), whereas minerally fertilized soils showed enhanced potential for protein synthesis.

Conclusions: These results add to the emerging evidence that long-term organic and conventional management can promote soil microbiomes with unique genetic capacities that might ultimately alter key biogeochemical processes in agriculturally managed soils.

Arbuscular Mycorrhizal Fungal Communities Vary by Year and Soil Properties in an Experimental Tallgrass Prairie

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Aim: In order to characterize the effects of restored plant communities on soil biodiversity, we investigated the relationship between both phylogenetic and trait diversity of plant communities and arbuscular mycorrhizal fungal (AMF) communities.

Method: We sampled soils prior to planting (year 0) and 2 and 5 years after establishing an experimental tallgrass prairie composed of 127 prairie plant species. These species were established by seed into 36 communities of 15 species each which vary in levels of both phylogenetic and trait diversity in a full factorial block design. To assess AMF communities, WANDA and AML2 primers were used to amplify the 18S region and sequenced on an Illumina MiSeq. Reads were processed into 97% similarity OTUs using QIIME2 and the maarjAM database.

Results: AMF community composition did not vary with plant phylogenetic or trait diversity. However, composition significantly differed by block in year 5 ($p = 0.03$). Both Shannon's and Simpson's diversity varied among years ($p < 0.001$) with diversity being highest in year 2 and slightly lower in year 5 while year 0 had the lowest diversity of the three years.

Conclusions: These results suggest that plant phylogenetic and trait diversity do not inform AMF diversity. Rather, AMF communities were determined by and responsive to underlying soil properties and time since plant establishment. That said, the increase in AMF diversity in year 2 followed by slight decreases over time mirror plant species diversity trends across the experiment suggesting that AMF are responsive to other metrics of plant diversity.

Effects of Exposure to Non-exhaust Particulate in Soil-dwelling Collembola Species

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Aim:

Road traffic is an important contributor of pollution in soils, and especially urban soils, due to both exhaust (fossil fuel combustion) and non-exhaust (abrasion of vehicle components, e.g., braking system, tires, and friction with road surfaces) emissions. Non-exhaust particulate emissions from road transport, which are the main sources of heavy metal pollution in soils, are of much concern due to the lack of regulations to mitigate them. In this study, we tested effects of long-term exposure to metal-based particulate matter from brake pads of two species of Collembola, living in different soil microhabitats and having different morphological and ethological characters.

Method:

The selected collembola species were *Sinella curviseta* (Entomobryidae), a surface-dwelling springtail characterised by high mobility, well developed furca and appendages, scales, ocelli and light brown pigmentation; and *Onychiurus sinensis* (Onychiuridae), a typical euedaphic species living inside soil pores, with reduced mobility due to absence of furca and reduced appendages, and no pigmentation.

Wear debris from brake pads were characterised chemically, morphologically and by size through a scanning electron microscope provided with X-ray spectroscopy (SEM/EDX). Specimens were subject to chronic exposure to high levels of heavy metal pollution and levels below the legal limit set by Italian regulations for metals of toxicological relevance such as Cr, Ni, Cu, Sn, and Zn (Decree Law 3/4/2006, n. 152 "Norme in materia ambientale", Gazzetta Ufficiale n. 88, 14/4/2006 - Supplement n. 96).

SEM/EDX analysis was carried out on faeces to demonstrate ingestion of the PM pollutants. Data on mortality and reproduction of treated specimens were collected and histopathological techniques were also applied to highlight possible sub-lethal effects.

Results:

SEM/EDX analysis on wear debris from braking systems confirmed the presence of heavy metals of toxicological relevance. Particle material including sub-micrometer PM from the braking systems was found inside the gut and faeces of treated Collembola which displayed histopathological abnormalities in specific tissues and organs, namely midgut, ovaries and fat bodies. Significant differences in the survival of adults and reproduction were also found.

Conclusions:

Our data provide a framework for more complex field studies aimed at addressing potential threats of non-exhaust emission sources from road traffic to soil biodiversity.

Global distribution of mycorrhizae is tightly linked to Earth microbial communitiesNadia Soudzilovskaia^{1,2}, Peter van Bodegom², Milagros Barcelo², Riccardo Mancinelli²¹*Hasselt University, Hasselt, Belgium*, ²*Leiden university, Leiden, The Netherlands***Aim:**

Mycorrhiza, a symbiotic relationship between plants and fungi, possessed by nearly all terrestrial plant species, represents an important, yet poorly understood dimension of plant functional diversity. Especially our understanding of spatial dynamics of mycorrhizal vegetation and associated microbial communities and a joint response of those to environmental change, is still in its infancy. The aim of this work is to advance our understating of global distribution of mycorrhizas and their impacts on soil microbial communities

Methods:

We have assembled global maps of distribution of aboveground and root biomass of mycorrhizal plants and intensity of root colonization by mycorrhizal fungi. Using these datasets, we assessed impacts of mycorrhizal distributions on microbial communities through a set of linear models.

Results: The new, yet unpublished (in-press) global dataset and maps of spatial distribution of plant mycorrhizal types and mycorrhizal fungal root colonization intensity reveal consistent relationships between distribution of mycorrhizal types and fungal and bacterial biomass.

Conclusions: Our results indicate that globally spatial dynamics mycorrhizal types of vegetation constitute a strong, yet poorly understood, driver of microbial biomass distributions. Altogether our new data and the analyses outcomes suggest that that environmental change is likely to affect distribution of soil biodiversity patterns, not only directly but also indirectly, via alteration of distribution of mycorrhizal symbiosis.

Earthworms and soil mesofauna as early bioindicators for landfill restoration

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Aim: Our aims were to identify the influence of reclamation practices on earthworm and mesofauna communities, and evaluate their role as bioindicators of early landfill restoration success.

Method: We investigated soil physico-chemical parameters, and earthworm and soil mesofauna communities at two newly restored landfill sites and the surrounding land uses. Alongside traditional soil fauna community analyses, we applied the QBS-collembola (QBS-c) and QBS-earthworm (QBS-e) index techniques for the first time in a reclaimed landfill setting.

Results: Natural colonisation of reclaimed landfill by earthworms occurred rapidly where original site topsoil was stockpiled, reapplied, and revegetated. Soil compaction and absence of ground vegetation cover were associated with extremely low earthworm populations. Both QBS-e and QBS-c index indicated that the most disturbed sites generally had the lowest soil biological quality. Mesofauna richness and abundance were generally high in the low-disturbance sites; overall, reclaimed soils possessed lower springtail total abundance and species richness, and a mite community dominated by disturbance-specialist groups in relation to the surrounding land.

Conclusions: Our findings demonstrate the value of recording a range of soil invertebrates during the investigation of land reclamation, since different soil bioindicator groups respond to soil disturbance in unique ways. The application of the QBS-c and QBS-e index techniques alongside traditional soil macro- and mesofauna assessments reinforced our observed soil fauna responses to reclamation practices. We encourage multitaxon soil monitoring, however where landfill restoration was carried out to a poor standard, mesofauna are potentially better indicators of soil status than earthworms.

Imaging the dynamics of symbiotic network architecture reveals a traveling-wave foraging strategy for tradeCorentin Bisot¹, Toby Kiers², Tom Shimizu¹, Loreto Oyarte Galvez^{1,2}¹*Amolf, Amsterdam, Netherlands, ²Vrije Universiteit, Amsterdam, Netherlands*

Aim: Arbuscular Mycorrhizal Fungi (AMF) are widespread symbiotic fungi colonizing the roots of the vast majority of plant species. While the importance of mycorrhizal fungi for global soils is largely recognized, the physical topology of these network has never been quantified across space or time. This is surprising because the architecture of a mycorrhizal network is hypothesized to influence both the diversity and functioning of soil ecosystems.

Method: We developed the first remotely controlled imaging robot to generate robust time-resolved datasets of fungal topologies, including the tracking of tens of thousands of hyphal tips simultaneously. In parallel, we can acquire videos of the transport of lipids within the network using fluorescent microscopy.

Results: We find that the growth of hyphal network follows a consistent, morphogenetic program that balances complex interdependencies of nutrient trade and resource foraging. This program requires a constant supply of lipids that is enabled by high-speed, two-directional cytoplasmic flow.

Conclusions: We found that the morphology of a fungal trade network reflects a complex interplay between exploitation, exploration, and resource transport strategies to meet demands, and potentially align the interests, of both plant and fungal partners

Soil Mixing Disturbance Decreases Soil Bacterial Diversity

Jaimie West¹, Thea Whitman¹

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Aim:

The patchy, disconnected web of soil microhabitats warrants ecological study in the context of community coalescence—the combining and restructuring of the soil environment and its microbial inhabitants. We hypothesized that frequent mixing disturbances would result in less diverse bacterial communities, while demonstrating homogenizing community assembly processes.

Method:

By mixing soil at various frequencies over a 16-week incubation, we explored the effects of community coalescence on soil's vast bacterial diversity by characterizing mixing-driven changes to community composition and ecological assembly processes using 16S rRNA gene sequencing. We then inferred community assembly processes using phylogenetic distance and community dissimilarity metrics in a null-modelling approach. We also tested our lab findings using real-world soil mixing modalities (e.g., agricultural tillage and earthworm bioturbation).

Results:

Frequently mixed soil harbored less rich bacterial communities (>20% decrease) while exhibiting community assembly patterns consistent with homogeneous selection and homogenizing dispersal. Further, communities within mixed soil became increasingly similar to each other, yet maintained dissimilarity from other soil communities subjected to similar treatment. These lab findings resonated in agricultural tillage comparisons, though earthworm bioturbation comparisons demonstrated more nuance.

Conclusions:

Our results imply that soil's vast bacterial diversity is supported by the unmixed and spatially heterogeneous nature of soil. This work also provides insight into the effects of physical disturbances, such as tillage or bioturbation, on soil communities. Better understanding relationships between spatial dysconnectivity, soil community composition, and ecological assembly processes will improve prediction of changes to broad soil functions due to the impacts of anthropogenic soil disturbances, such as land use or climate change.

What Are The Most Biodiversity-friendly Agricultural Practices?

Beillouin Damien¹

¹*Cirad, Le Lamentin, France*

Aim:

Agricultural activities are one of the main drivers of ongoing biodiversity loss. Numerous agricultural management practices impact plants, animals and micro-organisms abundance, richness or evenness. These effects are now compiled in a growing number of meta-analyses, yet, identifying the best agricultural options to preserve biodiversity remains a challenge.

Method:

We compiled the results of 191 meta-analyses integrating more than 58 000 paired-experiments. We extracted the effect (negative/neutral/positive) of each agricultural practices on each biodiversity indices and each taxa. We then used a cumulative link multilevel models to synthesize the ordinal vote count findings, using a hierarchical model and a variance-covariance matrix to consider possible common primary studies between meta-analyses.

Results:

Organic farming is 5 and 11 times more likely to benefit soil micro-organisms and vertebrates and invertebrates animals than to detrimentally affect it. Conservation farming also results in a 8 times more probable increase of animal biodiversity. Crop diversification could also play an important role to protect cropland biodiversity (estimated effect of 5.5X and 8.8X on animals and microorganisms). Drivers at the landscape scale also promote animal biodiversity (e.g. landscape complexification: Estimated effect of 7X). We then details our results for abundance, richness and evenness biodiversity indices.

Conclusions:

Alternative systems to conventional agriculture had large and positive effect on biodiversity. Our study rank best promising options to preserve cropland biodiversity, and are useful to guide future evidence based policy.

Ecological niche modeling predicts that soil fungi occupy a precarious climate space in boreal forests

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Aim

We model the climate niches of soil fungi and predict the sensitivity of North American soil fungal communities to climate change.

Method

We combine internal transcribed spacer (ITS) sequences from two continental-scale sampling networks spanning 113 sites in the USA and Canada. Using ecological niche models (ENMs), we estimate the climate niches of species-level operational taxonomic units (OTUs, 97% similarity) present in at least ten sites ($n = 8,597$). To describe the compositional turnover of soil fungal assemblages with respect to climatic gradients, we construct a novel niche-based metric of climate sensitivity, the Sørensen sensitivity index. We map climate sensitivity across major biomes in North America.

Results

ENMs have a mean out-of-sample predictive accuracy of 75.5%, demonstrating good alignment between fungal species distributions and climate, especially temperature. Niche edges display clustering across temperature and precipitation gradients, which suggests common physiological limits and predicts abrupt changes in composition. In general, soil fungi in North American climates are more likely to be limited by cold and dry conditions than by warm and wet conditions, though ectomycorrhizal fungi are limited to lower temperatures than saprotrophic fungi. Climate sensitivity peaks in climates that correspond to boreal forests and northern temperate grasslands.

Conclusions

The boreal forest occupies an especially precarious region of climate space for fungal assemblages across North America. The northward migration of boreal climates under climate change is therefore projected to bring sweeping changes to the composition of soil fungal communities in subarctic latitudes, characterized largely by the influx of warm-adapted species.

Soil biota of the temperate food forest – geographical location mattersIsabelle van der Zanden¹¹*Netherlands Institute of Ecology (NIOO-KNAW), Wageningen, Netherlands***Aim:**

Food forests are an alternative agricultural system using a polyculture of perennial plants to produce food. The system uses minimal management and little to no external inputs, potentially resulting in the development of a diverse and complex belowground biota. As a novel agricultural system in the temperate climate, little is nevertheless known about the belowground development of food forests established on former agricultural fields. This study therefore aims at understanding belowground biodiversity and species composition in temperate food forests.

Method:

We study soil biodiversity and community composition in 14 Dutch and Belgium food forests in comparison to local reference sites (cropland, grassland and natural forests). We focus on bacteria, fungi, protists, nematodes, and microarthropods using Phospholipid Fatty Acid (PLFA) analysis for bacterial and fungal biomass and Next-Generation Sequencing for more information on bacterial, fungal, protist, nematode and microarthropod species composition. Information on soil biodiversity and composition are supplemented with data on soil properties (e.g. nutrient concentrations, soil organic matter, pH) and field site information (e.g. management, external inputs, age).

Results:

PLFA results indicate that soil microbial community composition and biomass differs between food forest and local reference sites, but the direction and magnitude of the difference is often determined by geographical location. Multivariate analysis will unravel patterns of soil biodiversity and species composition by various soil and field site properties.

Conclusions:

Results indicate that food forests show potential for restoring soil biodiversity, but soil type, management and former land use are important characteristics determining final outcome.

Terrestrial isopods as model organisms to understand soil fauna distribution

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Aim: Species distribution is shaped by (a)biotic factors, currently subject to rapid global environmental changes inducing range shifts. Soil fauna is a crucial component of every terrestrial ecosystem, thus changes in species distribution can affect functions such as litter decomposition and nutrient cycling. Hence, understanding soil organisms' responses to global change helps predicting ecosystem functioning. Models of soil fauna distribution based on field data are generally of limited spatial extent or of low spatial granularity due to challenges in consistent sampling and species identification. Well-studied taxa can serve as model organisms to predict distribution of other taxa.

Method: We use data on terrestrial isopods surveyed in every 10x10 km-square in Belgium to model species ranges and to identify key climatic, soil and land use drivers. To validate the model outcome, we extend our predictions to another region, the State of Maryland, USA. Maryland is geographically independent but similar in size and its isopod fauna largely overlaps with Belgium's fauna, i.e., most species are of European origin. Based on their known ranges in Belgium, we generated predictions for these non-native species in Maryland, and compare predicted with actual distribution data based on a field sampling campaign in over 300 locations within the State.

Results: We found similar climatic and land use variables to be key drivers of species distribution both in their native and introduced ranges.

Conclusions: This indicates the potential of expanding the model to other geographical regions and other soil fauna taxa, however, predictability of species patterns proved to be very species specific.

Over 30 years of soil biodiversity monitoring in Germany – trends and drivers

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Aim: The decline in biodiversity in conjunction with global and climate change poses a threat to mankind and human well-being. Soil biodiversity represents a third of terrestrial biodiversity but our knowledge of soil biodiversity change and their drivers is limited. Long-term monitoring data are needed but are scarce or have not yet been analyzed. Here, we present time-series analyses of over 30 years of soil biodiversity monitoring in Germany.

Method: In roughly 800 plots, distributed throughout Germany, physico-chemical and biological parameters of soils have been monitored, partly since 1985. These plots were established in three major land-use types, i.e., agriculture, forest, and grassland. All plots are monitored in set intervals every few years. We have aggregated and harmonized all data and used time-series and meta-analytical tools to statistically analyze the data.

Results: We show how earthworm diversity and abundance, soil microbial biomass, and organic carbon changed over time. In addition, we link changes in these soil biodiversity variables to important drivers, such as soil pH, nutrient concentrations, and eco-toxin concentrations. We are able to show how these drivers interact with land-use type. Lastly, we present a statistical approach to deal with heterogeneous monitoring data.

Conclusions: Taken together, we present the first time-series of soil biodiversity change for Germany and make a case for the importance of soil monitoring. Furthermore, we show how our results can inform assessments on the state and change of biodiversity, potentially resulting in policies to protect and restore soil biodiversity.

Low Penetration of Edge Effects on Soil-Feeding Termites in a Neotropical RainforestYves Roisin¹, Pavel Babczenko¹, Antoine Dumortier¹, Édouard Duquesne¹¹*Université Libre de Bruxelles, Brussels, Belgium***Aim:**

Habitat fragmentation may affect rainforest soil fauna through two processes, which are difficult to disentangle: fragment size and edge effects. Here, we took advantage of a powerline clearing in an otherwise continuous neotropical rainforest to assess the effects of an artificial edge on the termite fauna, without fragment size constraints.

Method:

Sampling took place along the powerline clearing in the rainforest extending from Petit Saut dam, French Guiana, to the coastal area. Standard rapid assessment transects for termites, each comprising 25 quadrats of 5m², 10m distant from each other, were positioned in the forest parallel to the edge at distances of 10m, 30m, 60m, 100m, 250m and 500m from it.

Results:

The termite assemblage composition 10m from the edge demarcated itself from other distances. Species richness was lowest at 10m, especially for soil feeders. Wood feeders were more frequent at 10m, in particular *Heterotermes tenuis*, a widespread, sometimes invasive species. There was no detectable differences between transects 30m–500m from the edge.

Conclusions:

In a French Guiana rainforest, edge effects on the termite assemblage appear limited to a narrow fringe of <30m when evaluated independently of fragment area constraints. As expected, proximity to the edge favours widespread wood-feeding species but is detrimental to the frequency and species richness of soil feeders.

The impact of global change on soil fauna communities - a meta-analytical approach

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Aim:

Human-induced changes to the environment have affected biodiversity. Previous meta-analyses that investigate the patterns and magnitude of the impacts of different global changes on biodiversity have often been focused on aboveground biodiversity and omitted soil biodiversity. Not only is soil biodiversity incredibly important to many ecosystem functions and services, but by using soil biodiversity data we are able to look at effects of additional global changes that are understudied in other realms (e.g., pollution impacts).

Method:

We conducted a meta-analysis focused on the impact of six global changes (land-use intensification, habitat fragmentation, climate change, nutrient enrichment, invasive species and pollution), as well as some of their interactions, on soil fauna.

Results:

Land-use intensification and pollution had the largest negative impact on soil fauna communities. Land use intensity impacts were expected based on previous work, however the extremely negative impact of pollution is particularly worrying due to continually increasing levels of pollution, and the fact that pollution is understudied relative to other drivers. Unfortunately, there is a lack of data to investigate the interactive effects but preliminary analysis indicates that soil fauna is further decreased with multiple global changes.

Conclusions:

Overall, this work shows the importance of including soil biodiversity in large-scale analyses as soil organisms often do not show the same responses as organisms above-ground. It is important that we understand how soil organisms may respond to continuing human pressures, due to their importance in many of the services and functions that we rely on for our survival.

How Invasive Earthworms Alter Aboveground Arthropod Communities In A Northern North American Forest

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Aim: Assessing aboveground impacts of a belowground invader.

Declining arthropod communities have recently gained a lot of attention with land use and habitat loss among the most-commonly discussed drivers. Here, we focus on an underrepresented driver of arthropod community decline: biological invasions. For ~12,000 years, earthworms have been absent from most of northern North America, but they have been re-introduced. Most studies investigating the impacts of this invasion focus on the belowground world. We present observational data from a Canadian forest sampled in 2019 to assess the response of aboveground (vegetation- and ground-associated) invertebrate communities to earthworm invasion.

Method: Suction sampling of aboveground forest arthropods.

We sampled earthworm and aboveground arthropod communities in 60 plots, split into three areas with increasing invasion status (low, medium, high). We focused our analysis on arthropod macrofauna, which resulted in a total count of ~13,000 individuals, dominated by Hemiptera, Diptera, Araneae, Thysanoptera, and Hymenoptera.

Results: Earthworm invasion heavily reduced aboveground arthropods.

Total arthropod abundance, biomass, and species richness declined significantly from low to high invasion-status areas with reductions of 61, 27, and 18 %, respectively. While predator abundance (dominated by Linyphiid spiders) did not change, herbivore abundance (dominated by Cicadellidae, Hemiptera) declined by 71% from low to high invasion-status areas.

Conclusions: Belowground invasions might be an underappreciated driver of aboveground arthropod decline.

Our results illustrate how earthworm invasion alters aboveground arthropod communities in northern North American forests and show that belowground invasions might be an underappreciated driver of aboveground arthropod decline.

Food availability is the biggest driver of earthworm abundance not just habitat stabilityFelicity Crotty¹¹*Royal Agricultural University, Cirencester, United Kingdom***Aim:**

Understanding how agricultural management effects earthworms and how they differ spatially within fields and across farms is key to enhancing earthworm population and thus soil health. Earthworms are often used as the emblem of soil health, having a large effect on the physical soil environment – through burrowing, bioturbation mixing litter and soil, as well as being referred to as ecosystem engineers.

Method:

Two experiments measuring earthworm abundance and how they vary in relation to food availability were set up covering different agricultural systems. Within a grassland experiment earthworm abundance was monitored over time in relation to the proximity to cow slurry “pats”, do these act as an attractant or repugnant? Within an arable cover crop experiment, assessment of earthworm abundance occurred in relation to different cover crop species at the field scale.

Results:

Within both experiments, earthworm abundance was found to significantly vary with food source availability. Earthworm abundance varied with distance and time from the cow slurry “pats” and showed movement of earthworms towards this food source over a short time period. Monitoring over a longer timescale, a one year growing season, earthworm abundance changed and again showed movement towards different cover crop food sources.

Conclusions:

The main agricultural management trade-offs relate to food source/availability and habitat disturbance for earthworm abundance. Utilising both grassland and arable experiments, food source/availability was monitored and the results suggest a lack of food rather than earthworm feeding preferences are driving the changes in earthworm populations found.

A Global Perspective on Archaeal Diversity in Soils

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Aim:

High-throughput studies of soil microbiota reveal that the domain of archaea is a small, yet constant member of the prokaryotic community in soil ecosystems. Metabarcoding is the most widely used identification method in microbial ecology that has led to the discovery of an enormous prokaryotic diversity. Still, archaeal diversity has been largely neglected in cross-biome investigations, possibly due to limitations of available archaea specific primers.

Method:

A laboratory and analytical workflow to assess archaeal diversity in soils comprehensively was optimised using diverse soils (grasslands, forests, mountain soils, wetlands) and different primer pairs covering various variable regions of the 16S rRNA gene. Finally, a primer pair was selected and used to characterize the community structure of archaea from approximately 100 soil samples across contrasting terrestrial ecosystems including temperate forests, shrublands, grasslands, cold forests, forblands, moss heaths, dry forests, and tropical forests.

Results:

Irrespective of soil type, two of four primers tested failed to detect archaea at all or reflected the archaeal diversity poorly. Two primers shared many archaeal taxa found in all soil sites but still soil specific differences were detected in terms of richness and taxon diversity. First results of the global soil archaea assessment give novel insights into the community structure of soil archaea across geographic and climatic zones and reveal key drivers of archaeal diversity.

Conclusions:

The results allow a more precise estimate of the diversity of soil archaea and enable to evaluate how environmental parameters affect species richness and diversity across various biomes.

Functional Traits Inform Ecological Processes Underlying Global Collembola Diversity

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Aim:

Niche differentiation is one mechanism allowing multiple soil invertebrate species to co-occur locally. While ecological niches are represented by species traits, multidimensionality of functional traits has yet been revealed in soil invertebrates. We used two unique global datasets, #GlobalCollembola (43,601 communities) and trait data (1,384 taxa) to reveal assembly processes – filtering and niche partitioning – in Collembola communities across different habitats at both global and European scales.

Method:

We quantified trait responses using community weighted mean and mean pairwise distance among coexisting species with seven traits: antenna-to-body ratio, body length, pigmentation, coloration pattern, eye number, furca development and reproductive mode.

Results:

All these traits showed responses. At European scale woodland Collembola were smaller, possessing fewer ommatidia but longer furca and antenna and more parthenogenetic individuals than random expectations. In shrub habitats Collembola were less patterned and their antenna were shorter. Furca development and eye number represented the traits filtered by habitats, while reproductive mode revealed partitioning processes. Body length revealed filtering in shrubs but partitioning in agricultural fields. Antenna-to-body ratio, by contrast, revealed filtering in shrubs but partitioning in woodlands. Coloration pattern contributed to partitioning in agricultural fields but filtering in grasslands, shrubs and woodlands. Body pigmentation, as a filtering trait, however, could only be validated in shrubs. Putting all traits together, local Collembola communities were driven by partitioning in agricultural fields but filtering in shrub habitats.

Conclusions:

Our study demonstrates multidimensional functional traits underlying community assembly of Collembola. Applying trait-based methods improves our understanding of mechanisms regulating soil biodiversity.

Denitrification dynamics of N₂O emissions after re-flooding on dry paddy soilsYijia Tang^{1,2}, Budiman Minasny^{1,2}, Alex McBratney^{1,2}¹*School of Life and Environmental Sciences, The University of Sydney, Sydney, Australia 2015,*²*Sydney Institute of Agriculture, Sydney, Australia 2006*

In flooded paddies, peak greenhouse gas nitrous oxide (N₂O) emission after rewetting the dry soils is well known, but the relative contribution of biotic and abiotic factors to the emission is still unclear. In this study, we used the isotope technique ($\delta^{18}\text{O}$ and $\delta^{15}\text{N}^{\text{SP}}$) and molecular-based microbial analysis in an anoxic incubation experiment to evaluate the contributions of bacterial, fungal, and chemical denitrification to N₂O emissions. We collected eight representative paddy soils across China for an incubation experiment. Results show that total N₂O accumulations during the 10-day incubation period were mainly produced by fungal denitrification (58-77%) in six out of the eight investigated flooded paddy soils. The contribution of fungal denitrification was equal to or less than those of bacterial and chemical denitrification in the other two soil types. Moreover, around 11-35% of the total N₂O emissions were derived from chemical denitrification in all soil types, suggesting its important role in N₂O production. We further found that the initial soil organic carbon was the main regulator for the pattern of N₂O sources. Microbial interactions and gene expressions could also be the potential explanation rather than denitrifier community composition. Overall, these findings highlight the dominance of the fungal denitrification pathway for N₂O production in flooded paddy soils. This suggests that fungal contribution should be considered when optimising agricultural management system timing to control N₂O emissions in flooded paddy soil ecosystems, and for the relevant establishment of predictive numerical models in the future.

Liquid Soil Models for Risk Assessment of Engineered Organisms in Soil

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Aim:

Many engineered organisms have been developed for soil applications including biosensing and bioremediation. However, it is difficult to predict the behaviour of a genetically engineered microbe (GEM) in a given soil environment. Our goal is to create a rapid, scalable, and high-throughput model system to predict GEM survival, and the effects of GEMs on the existing microbiome, in target soils.

Method:

We developed an automatable and scalable liquid soil model for monitoring survival of the genetically tractable soil bacterium *Pseudomonas putida* in the context of an existing soil microbiome, using flow cytometry. We applied deep sequencing analysis (16S and ITS for bacteria and fungi, respectively) to understand how the microbiome changes in response to the introduction of the GEM. The results are compared to GEM survival in a solid soil sample, using both traditional colony forming unit assays and flow cytometry.

Results:

Engineered *P. putida* survival was similar in both the solid soil and liquid soil models we measured. Sequencing results showed that liquid soil models maintain a stable representation of the soil microbial community over a 14-day culture period. These results indicate that our liquid soil extract model is a flexible and scalable representation of the soil that enables prediction of GEM survival and performance.

Conclusions:

Our novel liquid soil models offer a new approach to risk assessment for GEM use in soils. Our results reveal important insights about the relationships between GEMs and native soil species, and open the possibility of manipulating native microbiomes for GEM control.

Global knowledge and use of soil biodiversity: Lessons from a worldwide survey

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Aim:

Present the results of the Global Soil Biodiversity Survey, undertaken by the FAO/GSP in March 2022.

Method:

The online survey was created using Survey Monkey v. 11 and was sent out by e-mail with a link to complete the survey to over 70 thousand persons. It included 122 questions in 11 sections including parts related to public policies, monitoring, inventories, sampling methods for various taxa and functions in soils, educational and communication activities, ecosystem services and economic valuation.

Results:

The survey had 2696 respondents (4% response rate) from >1350 institutions and 139 countries, mainly from Europe and Eurasia (39%), Asia (22%) and Latin American and the Caribbean (17%). Most (75%) respondents worked on issues relating soil biodiversity to agriculture, forestry and pastoral activities, and 75% worked with soil microbes, mostly bacteria (85%) and fungi (79%). Much fewer respondents worked with microfauna (19%), mesofauna (22%), macrofauna (28%) or megafauna (5%). The main purposes were to evaluate impacts of management practices/land use systems, of organisms on soil properties/ecosystem services, taxonomy/biodiversity surveys, and role as bioindicators, among others. Over 50% worked with ecosystem services related to soil biodiversity, mainly nutrient cycling and biodiversity conservation. However, many respondents (42%) had little knowledge of legal frameworks related to soil biodiversity and few countries had monitoring programs or inventories.

Conclusions:

Increased support and recognition of soil biodiversity is needed, particularly of its value and the need for its sustainable management and conservation, through appropriate policy and legal measures at both national and international levels.

Continental-scale mapping of soil bacteria and fungi compositional heterogeneity

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Soil microorganisms mediate a wide range of key processes and ecosystem services on which humans depend. In this study, we report on the biogeography and spatial pattern of soil biota for the Australian continent. We used as basis the DNA sequences from the Biome of Australia Soil Environments (BASE) which were collected over a range of different sites across Australia. We calculated the beta diversity of abundant taxa of soil bacteria and fungi, treating representative sequence data (OTUs) as individual taxa. Two ordination methods were applied to investigate the dissimilarities in microbial community composition, non-metric multidimensional scaling (NMDS) and Uniform Manifold Approximation and Projection (UMAP) for dimension reduction. The NMDS and UMAP used the weighted UniFrac distance for bacteria and Bray-Curtis dissimilarity for fungi on taxa relative abundance. The results of the NMDS for bacteria indicated that the structure of the data was captured fairly well, with a stress of 0.09. However, the stress of the fungi NMDS was 0.16, indicating that the fungi community composition was moderately well explained. We further collected a large set of environmental covariates that control the biogeography of soil biota, such as soil properties terrain attributes of vegetation indices, and of which maps are available. We fitted a quantile regression forest machine learning model to exploit the quantitative relationship between point-estimated values of beta diversity and environmental covariates, and used to model to predict beta diversity across Australia along with an estimate of uncertainty. We show that soil property and vegetation are the dominant controls of soil biota. The resulting maps also reveal the pattern of soil biota which can further be used for regional assessment of soil biodiversity and from which degradation induced by global changes can be monitored.

Forest-to-pasture conversion and cattle periodontal disease in the Brazilian Amazonia

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Aim:

Periodontal disease in ruminant livestock has been linked to deforestation for introduction of new pastures. Nonetheless, the ecological process triggering this disease has not yet been fully elucidated. Therefore, we took advantage of the deforestation scenario in Amazonia to understand which factors are related to this process.

Methods:

We assessed extensive livestock systems with recently reported cases of periodontal disease in cattle across a gradient of soil fertility in Western Amazonia. We characterized the soil, forage, and animals, as well as their bacterial communities. Pastures were classified as low and high severity level systems (LSL and HSL, respectively) based on the prevalence of animals with periodontal lesions.

Results:

HSL had increased bacterial alpha and gamma diversities in all components of the soil-plant-animal continuum, suggesting dysbiosis at the ecosystem level. Keystone taxa possibly related to microbial protection had their abundance decreased in HSL, disrupting microbial co-occurrence network stability. These systems also showed higher soil C:N, indicating a system's overall lower nutritional capacity. Better soil and forage qualities were observed in LSL, especially higher Zn and Cu content in forage and soil, respectively. Finally, in HSL, streptomycin biosynthesis genes were more abundant in soil, forage, and cattle.

Conclusions:

Our findings point out that land-use intensification seems to trigger a cascade-effect that, depending on the magnitude of the arrangement between biotic and abiotic factors, sets the ideal conditions for the emergence of oral infections.

Mating grapes with aromatics: one option to reach soil biodiversity conservation and new markets

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Aim:

Soil biota in vineyards face multiple stressors, e.g. frequent fungicide application and bare soil management that goes along with intensive mechanical disturbance, erosion and organic matter depletion. Permanently covered and mechanically undisturbed conditions, e.g. realized through the mixed cultivation of grapevines and aromatic plants (AP), may help to alleviate adverse impacts on soil biota and thus, protect soil biodiversity. Hence, this study aims to investigate the effects of intercropping grapevines with AP on vineyard soil biota.

Method:

In a field experiment, *Origanum vulgare* and *Thymus vulgaris* were introduced to grapevine rows of an organically managed vineyard in the Mosel area of Germany. Monocropped and regularly tilled grapevine rows served as control. Topsoil (0-10 cm) samples were taken over three crop cycles to analyse microbial community structure (16S and ITS metabarcoding), microbial biomass carbon (after fumigation-extraction), microbial activity (basal respiration, enzymes) and soil chemical properties.

Results:

There is evidence for an increase in soil organic matter in response to AP cultivation, whereas a significant decline of total microbial biomass, respiration and C-/N-cycling enzymes was observed. Other enzymes, e.g. those involved in S- and P-cycling increase under AP. This may be due to a higher abundance of specialized bacterial and fungal taxa in the chemically altered and mechanically undisturbed root zone of AP, such as arbuscular mycorrhizal fungi.

Conclusions:

Cultivating AP in vineyards constitutes a suitable measure to protect soil and increase habitat- and organism diversity. A higher probability of implementation can be expected from the economic value of AP.

Selection on the rhizosphere microbiome alters nitrogen use efficiency and seed yield in *Brassica rapa*

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Aim: Microbial communities in the rhizosphere influence several aspects of plant growth and development. In recent years, interest has grown in manipulating the rhizosphere microbiome to alter host plant traits and confer stress tolerance. Repeated selection for rhizosphere microbiomes associated with target plant traits could alter microbial community composition and interactions in the rhizosphere that impact the host plant. In the present study, we performed a multigeneration growth chamber experiment in which we applied selection pressure on the rhizosphere microbiome for consortia associated with enhanced plant productivity in *Brassica rapa* over nine generations of plantings.

Method: The experiment consisted of three selection treatments: a high biomass selection treatment where microbial communities were selected based on association with greater *B. rapa* biomass production, a random selection treatment where microbial communities were selected at random, and a control treatment consisting of no selection. Plant phenotypes and microbial community composition were compared between the three treatments after each generation.

Results: After nine generations of plantings, we found *B. rapa* plants in the high biomass selection treatment had significantly greater nitrogen use efficiency and seed yield compared to plants in the control treatment. Sequencing of rhizosphere microbial communities showed bacterial communities were distinct between the three treatments and extended local similarity analysis using sequencing data showed that bacterial interaction networks were altered in the high biomass selection treatment.

Conclusions: These data suggest microbial community composition and interaction networks in the rhizosphere could be modified to impact target traits of a host plant.

Soil Biodiversity and Plant Diversity Interactions and Consequences for Ecosystem Functions and Resilience

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AIM: Soil biodiversity is a critical contributor to terrestrial ecosystem functioning and resilience, regulating key soil processes including nutrient cycling. However, relative contributions of biotic interactions of soil- and aboveground biodiversity, and mechanistic understanding on impact of biotic interaction on ecosystem functions remain largely unknown. This presentation aims to (1) identify relative contribution of plant, soil biodiversity and their biotic interaction on individual ecosystem functions and multifunctionality, and (2) determine the role of soil biodiversity in shaping plant microbiome assemblages and consequences for ecosystem functions.

METHODS: This presentation combined data from global survey and manipulative glass house experiment which simultaneously manipulate soil and plant biodiversity.

RESULTS: We provide evidence that plant and soil biodiversity independently account for a unique portion of variation in above- and belowground ecosystem functioning and resilience. Further soil fungal and invertebrate diversity influence both soil and aboveground functions. In addition, we found the plant root microbiomes are strongly influenced by soil microbial diversity, but leaf microbiomes are driven by the host identity.

CONCLUSIONS: Overall, we provide evidence for complex but predictable interactions between plant and soil biodiversity, supporting the demand to conserve both above- and belowground diversity to sustain ecosystem functions under rapid global changes.

Climate resilient restoration of degraded dryland biodiversity and function with biocrusts

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Aim:

Biocrusts, diverse communities of bacteria, cyanobacteria, lichens, and bryophytes, provide key ecosystem functions in low productivity systems. Climate change and land use are leading to biocrust loss. We aimed to determine how biocrusts are affected by novel climates and how to do climate-resilient restoration.

Method:

1) We set up three reciprocal common gardens with mature biocrust transplants along ~3000 m elevational-climate gradient on the Colorado Plateau. 2) We set up a restoration experiment on the Colorado Plateau using biocrust collected across a climatic gradient (Sonoran, Mojave and Colorado Plateau). Biocrusts were cultivated on weed cloth, biodegradable paper or jute with ~1cm of soil in the presence or absence of and harvested in 3 m x 1m sods, transported and installed on field restoration sites. In both experiments we measured changes in biocrust visible cover, soil stability, exopolysaccharides, Chlorophyll a and bacterial community after 1-2 years.

Results:

In both experiments biocrusts preferred milder climate over home conditions. Biocrusts cultivated from the hotter deserts grew better than home sourced biocrusts, but establishment from all sources was similar in the field. All sources benefited from shade. Solid bottom sods were good at deterring weed establishment, and we saw some expansion of biocrusts into interspaces. The bacterial community showed fidelity to its home site in the common gardens, but not in the restoration experiment.

Conclusions:

Assisted migration of cultivated or mature biocrusts from hotter climates may be a viable method to restore biocrust communities and functions in degraded landscapes as climate change continues.

Disentangling mechanisms of co-adaption between trees and soil food webs in response to environmental perturbations

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Aim: We tested how drought and elevated CO₂ affect carbon flow from trees to soil food webs through two pathways, litter (the 'slow' pathway) and roots (the 'fast' pathway).

Method: We constructed mesocosms with four tree species: *Quercus robur*, *Quercus pubescens*, *Pinus sylvestris*, and *Pinus halepensis*. Trees were collected as saplings from the UK (*Q. robur* and *P. sylvestris*) and France (*Q. pubescens* and *P. halepensis*) and planted into pots with native soil. We maintained mesocosms under ambient moisture and CO₂ conditions, drought (50% reduction in watering), elevated CO₂ (550 ppm) and drought x elevated CO₂ in growth chambers for seven months. In a subset of mesocosms, we added ¹³C labelled litter (at the beginning of the experiment) and ¹³C pulse labelled (at the end of the experiment) to trace carbon flow from roots and litter, respectively, into soil food webs.

Results: Preliminary results show that trees exhibit several species-specific responses to perturbations. But in general, *Pinus* spp. had greater root biomass, while *Q. robur* and *Q. pubescens* had greater trunk and leaf biomass, respectively, under elevated CO₂. As well, microbial biomass decreased under drought x elevated CO₂ for all four tree species. Yet microbial communities derive more carbon from roots when under elevated CO₂; however, this effect was lost with drought.

Conclusions: Drought and elevated CO₂ can affect aboveground-belowground communities through several means. But importantly, elevated CO₂ can affect carbon flow into soil systems, which may impact ecosystem functions these communities provide.

Invasive earthworms alter microbiomes and carbon dynamics in boreal forest soils

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Aim:

The ongoing invasion of exotic earthworms in North American forests might alter ecosystem functioning and biodiversity. While most research on the topic has been carried out in the temperate biome, little is known on the impact of these invasive earthworms on soils of the boreal forest, the largest terrestrial carbon (C) reservoir. This study aimed at identifying and quantifying the impacts of earthworm invasion on soil microbiomes and soil organic matter (SOM) characteristics in boreal forests.

Method:

Using a space-for-time substitution, we compared earthworm-invaded and non-invaded soils across the Canadian boreal forest. Soil microbiomes were characterized using phospholipid fatty acid analysis and metabarcoding of the 16S rRNA gene and ITS2 region. After quantification of C stocks for forest floors and surface mineral soils separately, C stability was estimated with a one-year laboratory incubation and SOM chemical composition determined using pyrolysis-gas chromatography-mass spectrometry.

Results:

In forest floors, earthworm invasion caused a decrease in C stocks, not compensated in the mineral soils, where C stability was lower and microbiome composition shifted. Invasive earthworms increased fungal biomass, mainly through their positive impact on ectomycorrhizal fungi, and favoured copiotrophic (Bacteroidota) over oligotrophic (Acidobacteriota and Chloroflexi) bacteria. While total microbial biomass did not significantly increase, fungal and bacterial diversity indices were higher in earthworm-invaded soils, where SOM was overall more decomposed.

Conclusions:

By altering microbiome composition and SOM dynamics, invasive earthworms are likely to have a long-term impact on nutrient cycling and vegetation development as the invasion progresses in these boreal forests.

Diversity of true truffles (*Tuber spp.*) in European biodiversity hotspots, the role in soil bioremediation

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Aim: Truffles (*Tuber spp*) are the ectomycorrhizal fungi that produce highly valuable fruitbodies and are the only obligatory fungal symbionts that are successfully produced in man-made plantations. Few European species can be grown using special agroforestry practices that are also enabling the development of functional forest soils/ ecosystems. For these reasons, truffles have attracted the attention of the scientific consortium within the H2020-MSCA-RISE project INTACT, which is aimed at evaluating their diversity, natural habitats, plantation possibilities, novel production techniques, protection and policies in different countries.

Method: We analyze the state of the art of truffle diversity in three European biodiversity hot spots (Spain, Italy, and Serbia) as connected to different ecological characteristics. We explore possibilities for establishing truffle plantations in these regions as the rare exemplar of sustainable remediation of forest soils and ecosystems. We present a new tool for studying truffles and their habitats – Edaphobase, a database of soil biodiversity (<https://portal.edaphobase.org/>) that has been upgraded to be able to host also fungal taxa and connect them to other soil communities and common environmental traits.

Results: The significant diversity rates confirm the ecological suitability for different truffle production in three European regions. COST Action 18237 outcomes enabled, for the first time, the connection of specific fungal and soil mesofauna communities and their environments.

Conclusions: Managing techniques must be applied to natural truffle habitats in order to preserve truffle production and supportive soil biodiversity. Edaphobase tools will enable monitoring of soil biodiversity/environments not only in changing natural habitats (forests) but also in truffle plantations (agroforests).

Soil biodiversity at Swiss long-term monitoring sites: from prokaryotes to the eukaryotic micro- and mesofauna

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Aim: Soil biodiversity management and protection require the assessment of organisms from all three domains of life. This can be achieved at high-resolution with metabarcoding using specific markers. Analyses of responses to environmental changes may help to identify factors that promote or threaten specific communities or populations.

Method: Metabarcoding of five groups of soil organisms, i.e., prokaryotes, fungi, protists, nematodes, and arthropods, was performed on soil or arthropod DNA extracts derived from soil cores from 28 sites of the Swiss Soil Monitoring Network covering arable land, grassland, and forest.

Results: Overall, 15,387 prokaryotic, 7,852 fungal, 1,542 protistan, 384 nematode, and 9,205 arthropod amplicon sequence variants (ASVs) were obtained, of which 67.7%, 47.9%, 30.1%, 23.4%, and 50.2% remained unclassified below the family level revealing a large proportion of yet undescribed organisms. The proportion of unclassified ASVs differed among land-use types and sites, for instance, with higher proportions of unclassified fungi in arable land and higher proportions of unclassified arthropods in forest, indicating group-specific hotspots of undescribed diversity. Community composition significantly correlated among all groups ($\rho=0.47-0.76$, $p<0.05$), suggesting similar selective environmental factors for all groups. The main environmental factors that correlated to community compositions were the C/N-ratio, pH, total and organic carbon content, bulk density, and climatic factors.

Conclusions: Metabarcoding revealed a large diversity of prokaryotic and eukaryotic soil organisms, with group-specific hotspots of undescribed biodiversity. Larger and more detailed surveys are needed to identify environmental drivers of soil biodiversity that secure and promote specific ecosystem services.

Soil compaction persistently alters microbial diversity and its functional potential in agricultural fields

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Aim:

Soil compaction is a consequence of mechanized agriculture and affects approximately one quarter of the global agricultural land. There is insufficient understanding on how this disturbance affects soil microbiomes and ultimately sustainable crop production. In this study, we examined the microbial response to compaction under three farming systems over four growing seasons by using a long-term field experiment.

Method:

We assessed soil microbial diversity and its functional potential by metabarcoding and by shotgun metagenome sequencing, respectively. We also monitored changes in soil physicochemical properties and crop yield.

Results:

Soil compaction initially reduced crop yield (up to -90%), which largely recovered after three seasons. Soil compaction increased soil bulk density (+15%), decreased air permeability (-94%), and gas diffusion (-59%) without fully recovering after four seasons. Microbial diversity and its functional potential were consistently altered by compaction throughout the four growing seasons. Oxygen depletion in compacted soils favoured anaerobic taxa and genes associated with anaerobic metabolism. Adaptive strategies to improve metabolic efficiency (e.g., molecule transport and cofactors) or survival (e.g., mobility and sporulation) increased in compacted soils. Interestingly, shifts in microbial diversity were farming system dependent, whereas shifts in functional potential were uniform.

Conclusions:

We conclude that soil compaction induces long-lasting effects on the soil microbiome and that the change in microbial functional potential is uniform regardless of the compaction- and farming system-dependent change in microbial diversity. This consistent change from aerobic to anaerobic microbiomes raises concerns about altered nutrient cycling, reduced capacity to degrade pollutants, and increased greenhouse gas emissions in compacted agricultural soils.

Vegetation, Climate and Soil Properties Drive Soil Bacterial and Fungal Communities and Functions Across Europe

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Aim: Recent studies showed that factors like vegetation cover, climate, and soil properties drive the assembly of soil microbial communities, but it is still poorly understood how this impacts microbial-driven ecosystem functions, especially at large scales.

Method: Here, we analysed microbial taxonomic and functional diversity along a gradient of increasing land-use perturbation, detecting over 84,000 bacterial and 25,000 fungal OTUs from 715 sites across Europe.

Results: Bacterial and fungal diversity was lowest in less-disturbed environments (forests) and highest in highly-disturbed environments (e.g., croplands). Highly-disturbed environments contained higher proportions of bacterial chemoheterotrophs, harbored a higher proportion of fungal plant pathogens, and had less beneficial fungal plant symbionts compared to forests and extensively-managed grasslands. Patterns of microbial communities and predicted functions were best explained when interactions among major drivers (vegetation cover, climate and soil properties) were considered.

Conclusions: We propose tools for environmental policy actions and argue that both taxonomical and functional diversity should be considered for monitoring purposes.

Linking soil communities to arable management practices and soil functions using network analysis

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A key challenge is to increase sustainability in agriculture. Soil functions like nutrient cycling and disease suppression that could replace chemical inputs are driven by soil communities that are steered by arable soil management like crop rotation, tillage and fertilization. So, in order to enhance these soil functions, we need to understand the links between the soil microbiome, tillage, amount of organic inputs, nutrient cycling and disease suppression. Reduction of the immense bulk of sequencing data into one or two axes like alpha and beta diversity is probably too simplistic. Instead network analyses might be a usable tool to get insight in which clusters of taxa are shifting with specific management practices and enhanced nutrient cycling and disease suppression. We sequenced bacteria, fungi, nematodes and protists in arable fields in the Netherlands and have information on tillage, crop rotation and fertilization. We used network analyses to extract co-occurring communities and subsequently try to find links between these sub-communities and management practices and soil functions. We found that community composition of bacteria, fungi and protists differed between organic and conventionally managed fields in clay but not in sandy soils. We found multiple sub-communities of co-occurring species, although clusters are highly overlapping. Mostly, species from the same group tend to cluster together, but there are also mixed clusters. We hope to show links between management and functioning to clusters or to individual taxa. Our findings will yield important insights how arable soil management is related to the functioning of soil communities.

Resource sharing and mycorrhizal associations in the Mediterranean forest, from saplings to mature trees

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Mycorrhizal fungi can be associated with multiple root tips of different trees to form mycorrhizal networks. Much is known about the various network characteristics of forests in relatively wet regions. However, mycorrhizal networks in water-limited areas, such as Mediterranean forests, were given less attention.

Aim: To characterize the mycorrhizal community and the proportion of shared mycorrhizal species in semi-arid forests and quantify resource sharing among the trees.

Method: The mixed Mediterranean forest is composed of trees from different phytogeography origins in which different mycorrhizal guilds have evolved to live in proximity for many years. We characterized the mycorrhizal community and level of transferred ¹³C pulse labelled carbon under three experimental designs: (1) among five mature tree species in a diverse mixed forest, (2) among saplings of these same species growing in communal containers, or (3) among saplings growing in individual pots using soil from the mixed forest.

Results: The fungal communities of the different hosts were highly diverse, with higher diversity in *Pinus* and *Quercus*. Surprisingly, some supposedly arbuscular hosts, like *Cupressus* and *Pistacia*, were also associated with several ectomycorrhizal fungi (e.g., *Inocybe* and *Tuber*) in the forest and the communal containers. However, saplings potted individually are associated only with the presumed compatible functional mycorrhizal fungi guild. Finally, we show asymmetric belowground carbon transfer among the five tree species growing in the communal containers and the forest.

Conclusions: We investigated novel belowground interactions, potentially influencing forest connectivity and resistance to future, predicted hot and dry, climates.

Soil Legacy Effects of Plant and Drought on Aboveground-Belowground Interactions in Range-expanding Plant Communities

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Aim:

Soils contain biotic and abiotic legacies of previous conditions that may affect soil microbial communities and thus have induction consequences on aboveground biodiversities, such as plant biomass production and associated herbivores or pollinators. However, little is known about the belowground legacies relative strengths and interactions on the aboveground plant-insect interactions.

Method:

We used an outdoor mesocosm experiment, the soils were first inoculated with two soil origins seven years ago, then historically created plant community legacies and extreme summer drought legacies. This full-factorial experiment can allow us to investigate the legacy effects on the belowground soil microbial community composition, and the aboveground plants, aphids, and pollinators in range-expanding plant communities during the growing season.

Results:

We found the initial soil inoculation still affected soil bacterial, fungal and nematode compositions. The effect of plant legacy faded away throughout the growing season, whereas the legacy effect of previous years' summer drought continued to influence fungal community composition. The biotic-abiotic soil legacies also affected the aboveground dynamics. That the effects on plant biomass productions were plant species genus-specific, and the effects on the abundance of aphids were more strongly than pollinators which the pollinators were mostly driven by flower numbers.

Conclusions:

We conclude that climate warming-induced plant latitudinal range expansion and extreme drought can be 'memorized' in the soil and influence the aboveground plant performance and aboveground community interactions in the next growing season.

Plastic and Bioplastic Mulching: Relationship between Soil Properties and Microbiome After One Year

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The use of plastic mulches, aiming at improving crop productivity, has increased in recent decades. Despite their advantages in agriculture, plastic mulches left on soils can be fragmented producing microplastics (MPs). The effects of MPs on soil microbiome are still poorly investigated although microorganisms are involved in key ecological roles linked to matter turnover. Aim: The present study sought to compare the effects of polyethylene (plastic, P) and Mater-bi® (bioplastic, BP) mulches on soil microbiome. Method: In mesocosm trials, soils covered by P and BP mulches for 6 (6M) and 12 (12M) months were analyzed for DNA yield, eubacterial DNA, fungal DNA, microbial respiration and enzymatic activities such as hydrolase (HA), dehydrogenase (DHA), α -glucosidase (α -GLU) and urease (URE). The DNA amount was quantified by qPCR and sequenced by Novoseq. Results: Actinobacteriota and Proteobacteria were the most dominant phyla regardless by time and treatment. The bacterial microbiome of 12M-BP samples had the highest richness and diversity and the highest number of unique amplicon sequence variants (ASVs), and clustered separately by the other samples. Differently by the bacteria, the fungal microbiome showed significant differences due to the exposure time rather than the mulch types. The microbial activities did not vary according to mulch types but showed different temporal behaviors. In fact, microbial respiration, HA and α -GLU increased, whereas DHA and URE decreased. Conclusions: The application of bioplastic mulches after one year enhanced the richness and diversity of the soil bacterial microbiome and stimulated respiration, HA and α -GLU activities.

Plant diversity increases microbial resistance and resilience to drought in European grasslands

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Aim:

Higher plant diversity is thought to facilitate root niche partitioning, resulting in greater root densities, deeper root exploration and a more active rhizosphere. The ability of microorganisms to resist drying and recover after a drought, in turn, depends on the microbial access to rhizosphere carbon resources. Yet, the influence of plant diversity on the microbial responses to drought cycles remain unclear. We hypothesized that the microbial ability to resist drought and recover following drought would increase with higher plant diversity.

Method:

To test this, we investigated how microbial communities maintained their growth during dry conditions (resistance) and how fast growth rates recovered after rewetting (resilience). We used soil samples from the Jena Experiment in Germany (1-60 grassland plant species in experimental plots for 20 years) and two different soil depths (0-10 cm, 10-30 cm).

Results:

We found that the microbial resilience to drought increased with higher plant diversity in both soil depths, where surface soils recovered faster after rewetting compared to deeper soil layers. In addition, the microbial resistance to low moisture levels increased with higher plant diversity.

Conclusions:

The results show that microbial communities cope progressively better with drought as the plant diversity increases, and suggest that grasslands with higher diversity can favour soil carbon sequestration via microorganisms during drought.

What drives the changes of biotic communities after the global retreat of glaciers?

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Aim:

Glaciers show a pattern of retreat at the global scale. Increasing areas are exposed and colonized by multiple organisms, but lack of global studies hampers a complete understanding of the future of recently deglaciated terrains. Multiple factors can determine biotic colonization of terrains exposed after the retreat of glaciers, including time after glacier retreat, climatic differences, and the rapidly evolving abiotic and abiotic features of these environments. In our research we combine innovative methods and a global approach to boost our understanding of the evolution of soil communities in recently deglaciated areas.

Method:

We investigated chronosequences in glacier forelands ranging from recently deglaciated terrains to late successional stages of soil pedogenesis, considering 48 glaciers from five continents. Through environmental DNA metabarcoding, we identified species from multiple taxonomic groups, to obtain a complete reconstruction of soil communities along glacier forelands.

Results:

Soil features show strong modifications, with a consistent increase of carbon stock and organic contents, and a faster accumulation of organic matter in warmer areas. Environmental DNA provided information on all main components of soil biodiversity. Species richness tends to increase with age after glacier retreat, but the pattern is not consistent across taxonomic groups. Time since glacier retreat, microhabitat modifications and biotic interactions interplay to determine the biodiversity changes occurring along the colonization of glacier forelands.

Conclusions:

Environmental DNA allows an all-inclusive community ecology, which reveals how complex biotic interactions increase during primary successions, and will help to predict the impacts of climate change on the whole ecosystems.

THE IMPACT OF FIRE ON MICROARTHROPOD BIODIVERSITY VARIES WITH THE VEGETATION COVER

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Aim:

In Mediterranean area, fire is a recurrent factor of disturbance that affects soil biodiversity. Although microarthropods are considered as bioindicators, they are often overlooked compared to vegetation and surface species in studies focused on fire impact. The present research aimed at filling this gap evaluating the changes in the assemblage of soil microarthropods in burnt soils covered by trees and shrubs. Moreover, the functional traits and taxa resistant to fire were investigated.

Method:

To achieve the aims, surface soils were collected inside the Vesuvius National Park at unburnt and burnt areas covered by trees and shrubs. Microarthropod were extracted by soil cores, identified and described for some functional traits such as body length, mouthpart type and pigmentation linked to resource acquisition and dispersion.

Results:

The results highlighted that fire alone did not impact the microarthropod community, but its impact was strongly dependent on vegetation cover. In fact, fire reduced microarthropod density under burnt trees, and Shannon index under shrubs trees. The abundances of Acarina and Diplura increased under burnt shrubs and trees, respectively, whereas Symphyla and Pauropoda abundances decreased under burnt shrubs. Fire reduced the abundances of large microarthropods under burnt trees and shrubs and sucking mouth part type, typical of predaceous organisms, under burnt shrubs. By contrast, fire increased the abundance of pigmented organisms under burnt shrubs.

Conclusions:

These findings indicate that fire differently impacted microarthropod community under trees and under shrubs. Functional traits of microarthropods can be profitably used to evaluate the impact of fire on soil biodiversity.

The small-scale: Unravelling drivers of soil microbial diversity

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Aim:

The soil microbiome is immensely diverse. What promotes this microbial diversity, has been declared as one of the greatest challenges of soil ecology. To ultimately unravel drivers of microbial diversity, we set out to link microbial communities and their immediate environment by studying small soil volumes reflecting the scale of interconnected communities.

Method:

We collected 190 individual 2mm-sized aggregates from soil cores sampled in 0-5- and 15-20-centimetres depth along an 80-meter-long transect in a temperate Beech forest. Of each aggregate, we measured absolute abundances and composition of bacterial and fungal communities together with water content, and isotopic signature and content of carbon and nitrogen. We recorded spatial distance between aggregates, and obtained environmental variables like pH and microbial composition from homogenised soil cores.

Results:

Aggregates strongly varied in bacterial and fungal richness, composition, and bacterial biomass, as well as chemical-elemental composition. Compositional similarity was largest among microbial communities of aggregates drawn from the same core. Beyond the centimetre-scale, spatial distance did not affect community similarity, supporting our observation that communities are influenced by local environmental conditions like pH. Richness and composition of microbial communities, and bacterial biomass were strongly linked to aggregate-associated carbon and nitrogen content, and natural abundance of carbon-13.

Conclusions:

We show that microbial community structure at the millimetre-scale is intimately linked with microbial habitat characteristics. Our results strengthen the concept that the vast microbial diversity in soils is promoted by the small-scale chemical heterogeneity, which results in multiple microbial habitats and thus likely supports countless distinct microbial communities.

A Comprehensive Functional Classification for Soil Protists

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Aim:

Protists play a key role in influencing multiple ecosystem functions, although they are one of the least studied components of soil biodiversity. Our work aims to compensate for the scarcity of functional data and the lack of uniform guidelines, proposing a comprehensive functional classification suitable to characterise the majority of soil protists.

Method:

The functional classification was defined by selecting traits that are: sensitive to environmental drivers, easy-to-find in existing literature, and adaptable to most soil protists taxa. We then used the classification to build a functional database from 570 protists taxa obtained from a global eDNA survey including 1448 soil samples collected along 48 glacier forelands in five different continents. Functional information was assigned by consulting specific datasets, atlas, handbooks, monographies, and taxonomic articles.

Results:

The resulting classification consists of five broad functional typologies including eleven more specific functional traits. For each trait, we report: the definition, the potential ecological relevance, the functional categories, the availability in literature, and the main limitations. The assembly of the functional database allowed us to functionally characterise soil protist communities and to analyse the changes in functional diversity along the ecological successions occurring after glacier retreat.

Conclusions:

The proposed classification aims to be a basis for ecological studies concerning soil protists, allowing a functional characterisation of this essential but too often neglected component of soil biodiversity. Furthermore, the functional database represents a valuable collection of functional information including traits for most of the major supergroups of soil protists.

Spatio-temporal fungal dynamics along a land-use gradientKezia Goldmann¹, François Buscot^{1,2}*¹UFZ - Helmholtz Centre For Environmental Research, Halle (Saale), Germany, ²German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Leipzig, Germany*

Aim: Currently very little is known about how land-use intensity impacts the highly diverse group of soil fungi, which play a significant role in ecosystem functioning. They serve as symbionts, saprobes or pathogens. Changes in soil fungal communities is influenced by soil physio-chemical properties or plant composition at different scales. Yet, little is understood about functional shifts of fungal communities in spatial and temporal context along land-use gradients.

Method: We are studying fungal communities in three temperate study sites across Germany containing forests and grasslands. Our studies cover up to 300 experimental plots to understand large- and small-scale as well as temporal distributions of fungi with different ecological values. Those study sites were established by a large interdisciplinary consortium funded by the German Science Foundation (DFG) called "Biodiversity Exploratories". Furthermore, a broad range of land-use and management regimes varying from almost natural to highly managed forests and grasslands complete the design of the study sites. Targeting the fungal ITS2, we assessed the soil fungal communities using amplicon sequencing.

Results: We show that fungal functional groups differ in their response to changes of anthropogenic, biotic and/or abiotic factors. Plant-dependent groups, such as mycorrhizal or pathogenic fungi, respond stronger towards changes in vegetation or land-use intensification than saprotrophic fungi. Furthermore, fungi showed not just host plant preferences but also various temporal appearance patterns at plot, local and regional scales.

Conclusions: Like plants, soil fungal communities are strongly affected by land-use changes, which alters fungal-mediated functions and potentially weakens ecosystems.

Heathland management regime affects soil response to drought

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Aim: Drought events can have a strong impact on ecosystem functioning through changes in plant-soil interactions. This is particularly a threat for vulnerable ecosystems, such as heathlands, where ongoing nitrogen deposition is altering plant dynamics by increasing the dominance of grasses over the heather (*Calluna vulgaris*). These changes aboveground can, in turn, impact soil dynamics and heathlands' responses to drought. Here, we have determined whether legacy effects of drought on heathland soils depended on heathland management practices. Specifically, we assessed whether soil drought response differed under heather and grass, and under heather plants at different ages as a result of mowing.

Method: We sampled soil from control and drought plots that were part of a 20-year drought experiment in a heathland in Oldebroek, The Netherlands. Each plot was further subdivided into three different mowing treatments, which led to a young, intermediary and an old heather community. We measured nutrients and C pools and used amplicon sequencing to characterize soil microbial communities.

Results: Our results show that soil carbon decreased under drought conditions but only underneath grasses and old heather, while under young heather, soil C actually increased under drought when compared to control conditions. Overall, bacterial and fungal community composition differed between drought and control treatments and were not affected by plant species but by the age of heather, and were directly related to changes in soil C.

Conclusions: Our data thus suggests that a younger and more heather-dominated plant community might reduce soil C losses under drought conditions predicted by future climate change.

Protist-Bacteria Interactions within the Wheat Rhizosphere Microbiome

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Bacteria and fungi are known to drive the rhizobiome with a significant impact on plant growth, and the plant microbiome is predominantly studied as plant-bacteria-fungi interactions. Unicellular eukaryotic organisms as predatory protists are rarely included, despite they are significant members of the belowground microbiome and predate on bacteria and fungi. In contrast to the well-described impact of large predators on prey abundance and diversity above ground, much less is known of how micro-predators as protists affect the soil microbiome and plant growth.

To understand this role of protists and their diversity in the wheat rhizobiome, we examined rhizosphere, rhizoplane and soil collected from four winter wheat cultivars grown to the flag-leaf stage for 141-146 days in mesocosms. Samples collected were used for diversity profiling of protists and bacterial communities, and protist isolation. We isolated and identified >200 protists. Bacterial metabarcoding (16S rDNA) of the isolated protist cultures showed a dominance of *Pseudomonas*, while the protists *Cercozoa* had an influx of *Pedobacter*, and the protists *Ochrophyta* an influx of *Dyadobacter*, showing that protist predation drive the bacterial community.

Profiling protist communities using metabarcoding (18S rDNA) revealed effects on the protist diversity of rhizo-compartment and wheat cultivar with *Cercozoa* and *Ciliophora* dominating in relative abundance. *Excavata* and *Rhizaria* showed a higher relative abundance in taller wheat plants, suggesting positive effects on plant growth. Using correlation-based analysis, networks of the protist and bacterial co-occurrence indicated that bacteria (profiled by 16S rDNA metabarcoding) were driving the rhizobiome. Overall, our results highlight the importance of protists in the wheat rhizosphere microbiome and provide evidence that protists significantly correlate with bacterial communities and plant growth.

Succession in soil communities after glacier retreat: taxa replacement versus taxa addition

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Aim:

The analysis of ecological succession is one of the bases of ecological theory, yet the mechanisms driving succession are not fully understood. Succession is a complex process that can vary among successional trajectories, geographical zones, or taxonomic groups. Here, we assessed the succession of soil communities after glacier retreat to determine whether the differences in composition and the relative importance of taxa *versus* replacement, change in a predictable global pattern over time and among taxa.

Method:

We used environmental DNA metabarcoding to sample seven groups (plants, nematodes, bacteria, fungi, collembolans, insects, and oligochaetes) in 240 dated sites along chronosequences (representing 1 to 419 years of succession) in 46 forelands around the world. Compositional variation was measured and decomposed into richness differences or replacement processes.

Results:

For plants, nematodes, collembolans, insects, and oligochaetes taxa addition was the main driver of compositional differences, while replacement was the main driver for bacteria and fungi. Compositional differences, and the processes underlying it, varied progressively over time, without breaking points. For plants, collembolans and insects, we found a shift in the dominance of the processes shaping soil communities after ~50 years of succession.

Conclusions:

Succession was underlined either by a sequence of threshold-induced processes or linear processes, pointing out the complexity of succession in harsh environments after glacier retreat. Our study highlights the importance of global studies, covering both large spatial and temporal scales, to define whether the processes that govern community assembly during succession and, hence, generate biodiversity, can be generalised across successional sequences.

Cryptogamic Vegetation and Soil Development on Holocene Deposits on the Baltic Sea Coast

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Aim:

Biological soil crusts (biocrusts) are microecosystems consisting of prokaryotic and eukaryotic microorganisms growing on the topsoil. They are widely distributed pioneer communities in arid, cold, or temperate regions.

This study characterizes shifts in the community structure of biocrust phototrophic organisms, their areal coverage, and biomass accumulation along two dune chronosequence. The investigation area in Mecklenburg-Western Pomeranian represents Holocene deposits on the Baltic Sea coast. A further goal is a description of soil in its initial stages and further development.

Method:

A biodiversity survey on biocrusts followed by species determination was conducted. A drilling stick (5 cm diameter) down to a depth of 30 cm was used for sediment samples. The analyses include: analytical determination of basic pedological parameters like pH, moisture content, cation-exchange capacity, and nutrient contents (carbon, nitrogen, phosphorus). Further: wet-chemical determination of pedogenic oxides and sequential P-fractionations. The development of organic soil substances is characterized using high-resolution mass spectrometry.

Results:

The results highlight a varying phototrophic community composition of biocrusts regarding the dune successional stages. A shift from algae-dominated to lichen- and moss-dominated biocrusts in later successional dune types was observed. Moreover, the study shows an enrichment with soil organic matter, acidification and the formation of pedogenic oxides.

Conclusions:

The results enable a description of the effective weathering and soil genetic processes. The development of biocrusts suggests them as key players in geochemical processes supporting sediment moisture and stability. Moreover, it highlights these communities as ecosystem engineers playing valuable part in nature protection i.e., preventing sediment erosion in coastal dune areas.

Diversity of RNA Virome in SoilRumakanta Sapkota¹, Catia Carreira¹, Anne Winding¹¹*Aarhus University, Roskilde, Denmark*

Viruses are the most abundant entities in the soil ecosystem, yet their role in the soil food web is largely unknown. Soil viruses are suggested to shape the diversity and abundance of the soil microbial communities, and be significant in soil nutrient cycling. Studies of soil viruses are mainly focusing on DNA viruses, although there is an indication that the viral RNA community is quite diverse. In this study, we determined the genomic diversity of the RNA viruses in four soil types (beech and pine forest, grassland and agricultural) together with physicochemical variables. Viral abundances were highest in the beech forest soil ($4.1 \pm 2.4 \times 10^8$ viruses g^{-1}) and lowest in the agricultural soil ($1.8 \pm 0.4 \times 10^8$ viruses g^{-1}). Our results captured rather diverse viromes ranging from bacteria, plants, to invertebrates and contrasted DNA-based studies, which are dominated by bacteriophages. Pisuviricota, a phylum that includes plant and marine microbial hosts, was found in higher proportion in the grassland soil that is occasionally flooded with marine water. Lenarviricota virus dominated relatively in the forest and grassland soils, in particular the bacteriophage *Emesvirus*, while the phylum Kitrinoviricota (mainly plant hosts) dominated relatively in the agricultural soil. This study indicates that different soils harbor very different RNA viral communities, but their impact on plant ecology still needs to be determined.

Coupling of Soil Microbial Networks Increase Soil Functioning Under Diversified Crop Rotations

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Aim: We aimed to evaluate how crop rotation diversification (from monocultures to five species rotations) affects soil microbial networks (bacteria and fungi) within three different aggregate size classes (micro-, macro-, and mega-aggregates).

Method: We used a long-term rotational cropping diversity experiment located in the Kellogg Biological Station, Michigan, United States. Soil samples were collected when all treatments were under the same crop (corn). We measured the abundance of bacterial and fungal groups based on phospholipid fatty acid (PLFA) markers and used these data to build soil microbial networks at the treatment and aggregate size level (18 networks) applying the concept of coupling. Coupling is based on system-level correlations in absolute value and provides a measure of order within ecosystems. We tested the effect of crop rotational diversity and aggregate size class on coupling using a null modelling approach. We also investigated the association between the coupling of networks and soil functioning (hydrolytic and oxidative enzymes).

Results: Greater diversity of crop rotations altered the composition of soil microbial communities in micro and mega-aggregates. Against our expectations, we found no relationship between soil microbial network coupling and crop rotational diversity, although coupling networks of low-diversity treatments tended to be more coupled than the null model. We found a positive relationship between microbial network coupling and the activity of hydrolytic enzymes. Moreover, the main predictor of soil microbial coupling network was microbial biomass.

Conclusions: Our results suggest the important role of soil microbial interactions for soil functioning regardless of crop rotational diversity.

Untangling Belowground Food Webs with Machine Learning

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Aim: Studying food webs can reveal how biodiversity and ecosystem functioning may respond to environmental change. To answer such questions, however, we need time-efficient methods to identify who-eats-whom belowground. This is especially challenging for microscopic organisms, whose interactions are difficult to observe with classical approaches (i.e. behavior and gut contents analysis). In such situations, trait-matching and machine learning approaches are promising for successfully inferring feeding links.

Method: We tested six machine-learning algorithms for their ability to predict feeding links, based on species traits and taxonomy. By incorporating organism speed, size and abundance into the model predictions, we estimated the probability of feeding link to occur. Using an empirical case study dataset from *Sphagnum*-dominated peatlands, we cross-validated the predictions for feeding links observed for two testate amoebae species.

Results: We found that the boost-regression-tree algorithm predicted feeding links between microbes best. Sensitivity analyses further showed that predictions were robust against false feeding links and faulty predictors in the training set, and capable of predicting feeding links for empirical datasets containing up to 5% of new taxa. The feeding habits of the two testate amoeba species were comparable between microscopic observations and model predictions, although the model slightly overestimated predation on other testate amoebae for one of the two test cases.

Conclusions: Machine learning algorithms offer a means to develop robust models for studying microbial food webs. They offer a route to combine traditional observations with DNA-based sampling strategies to upscale soil biodiversity research along ecological gradients.

The Threat of Non-Native Flatworms to Soil Fauna

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Aim:

Terrestrial flatworms are predatory and feed on earthworms, molluscs and other soil invertebrates. Several non-native species have become established in Europe, which pose a potential risk to native soil fauna.

Method:

Pest Risk Analyses

Evaluating the potential impact of invasive flatworms on soil fauna is a prerequisite to establishing control and management approaches. The impact of three species will be discussed: *Arthurdendyus triangulatus* (an earthworm predator), *Obama nungara* (earthworm and mollusc predator) and *Platydemus manokwari* (mollusc predator).

Results:

A field-based manipulation experiment demonstrated that *A. triangulatus* reduced earthworm biomass by c. 20%, but more importantly anecic earthworm species were differentially predated with a loss of c. 75% biomass in the highest flatworm-infested plots. Data from France have demonstrated a rapid spread of *O. nungara*, throughout the country and in adjacent regions. *Platydemus manokwari* is responsible for severe declines in endemic snails in the Pacific Islands.

Conclusions:

Non-native flatworms have established and spread in several countries in Europe. The impact on soil fauna is largely unstudied, except for *A. triangulatus* – which reduces anecic earthworm populations. Non-native flatworms are covered by invasive species legislation. The main pathway for introduction and spread is containerised plants and plants-for-planting. There is a need for enhanced biosecurity and awareness-raising in nurseries and garden centres to prevent spread of these flatworm species and safeguard native soil fauna.

Pesticide Effects on Soil Fauna Communities - a Meta-analysis

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Aim: The wide use of pesticides to limit crop losses raises concerns about their impacts on biodiversity. Soil fauna communities represent a significant portion of global biodiversity and play crucial roles in terrestrial ecosystems, but there is currently no quantitative synthesis of their response to pesticide use.

Method: Here, we compiled the results of 54 studies and 294 observations of pesticide impacts on soil fauna communities and use meta-analysis to evaluate pesticides effects on their abundance and diversity across a wide range of environmental contexts. We analyse the effects of different types of pesticide application, exposure conditions and functional groups of soil fauna in order to identify the most detrimental scenarios.

Results: We found that pesticides overall decrease the abundance and diversity of soil fauna communities (Hedge's $d = -0.31 \pm 0.17$), and have stronger negative effect on their diversity than abundance. Scenarios with the most detrimental impacts involve multiple substances, broad spectrum substances and insecticides. Our results further highlight important research gaps that need to be filled to provide a full picture of pesticide effects on soil biodiversity.

Conclusions: Our findings demonstrate that pesticide use can threaten soil biodiversity. The detrimental effects of multiple substances revealed here are particularly concerning given that realistic pesticide use often involves combining several substances to tackle several kinds of pests and pathogens over the crop season. Our study highlights that pesticide application has significant detrimental non-target effects on soil biodiversity, eroding a substantial part of global biodiversity and threatening ecosystem health.

Warming and Top Predator Interactively Affect Above-Belowground Interactions in a Long-Term Experiment

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Aim: Climate change causes context-dependent responses of terrestrial ecosystems that may be prominently driven by biotic interactions. While several studies have addressed the effect of warming in simplified soil food webs, few have considered the effects of climate-induced aboveground trophic cascades. Here, we explore how a vertebrate top predator, the common lizard, modulates the effects of warming on above-belowground linkages.

Method: Using a seven year-long warming experiment in outdoor, semi-natural, mesocosms, we investigate the response of multi-trophic communities encompassing plants, aboveground arthropods, soil invertebrates and microbes (metabarcoding), over time. Our design enables to test the separate and interactive effects of lizards' presence/absence and of +2/3°C warming compared to present temperatures (IPCC projections for 21st-century).

Results: We found that strong responses of both the above and belowground communities to warming depended on the presence of the top predator. Top predators tended to buffer or even invert warming effects, depending on the taxonomic and functional group. Those shifts in community composition of aboveground arthropods and subsequent trophic levels suggested cascading effects of changes in top predators' diet in response to warming, in line with previous observation in our experiment.

Conclusions. Our findings demonstrate how trophic cascades can unravel the context-dependent responses of above and belowground communities to warming. A more holistic view of terrestrial communities will thus be crucial to improve future forecasts of the ecological consequences of climate change.

sOilFauna - a global synthesis effort on the drivers of soil macrofauna communities and functioning

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Aims:

Understanding global biodiversity change, its drivers, and its consequences on ecosystems requires to include soil macrofauna, a highly diverse group involved in numerous ecosystem processes. So far, our knowledge of both the factors that shape soil macrofauna communities and the ecosystem effects of these organisms is limited at the global scale, while numerous local studies exist.

Methods:

The project “sOilFauna” fosters the gathering of literature data on macrofauna communities and produced the most comprehensive soil macrofauna database - the MACROFAUNA database - which collates abundance and biomass data of 17 soil invertebrate groups assessed with a standardized method at ~8700 sites around the world.

Results:

This dataset allows testing many important theories in macroecology (such as latitudinal gradients and productivity/perturbation-diversity relationships), as well as quantifying the responses of functional and trophic groups of soil macrofauna to different climatic, edaphic, and human-induced drivers (e.g. land use type and change). We will display preliminary results on macrofauna abundance, diversity, and biomass, with the identification of their main drivers at a global scale.

Conclusions:

The sOilFauna project and consortium also aim at encouraging the global community of soil ecologists to use and share standardized data for future research that will allow even further increase of our knowledge on this understudied group.

Drivers of Soil Food Web Structure in the French Alps

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Aim: Soil food webs are crucial for ecosystem functioning and associated services, but we largely ignore what drives their spatial structure and complexity. While environmental conditions determine the local abundance of different soil groups, such as earthworms or different fungal guilds, it is not yet clear how this affects the overall structure of soil food webs. Here, we studied changes in soil food web structure across environmental gradients to identify the key ecological drivers and the importance of trophic interactions for group abundance.

Method: We apply network dissimilarity metrics to 451 local soil food webs along 24 elevation transects in the French Alps.

Results: We found significant variation in soil food web structure both within and across alpine habitats (grasslands, shrublands and forests). Across habitats, turnover of soil food webs was characterized by turnover of specific 'co-structures' related to feeding channels: the relative abundance of groups belonging to the "green channel" was higher in forests, while groups belonging to the "brown channel" predominated in grasslands. The main ecological factors driving structural variability differed between habitats. In forests, geographical isolation and physiological constraints were most important, while in grasslands it was rather the taxonomic composition of plants followed by physiological constraints.

Conclusions: Overall, our results showed that the spatial structure of soil food webs at large spatial scales is driven by environmental filtering (i.e. trophic (co-)group sorting), plant-soil interactions and geographic limitations, but is ultimately constrained by an universal backbone of soil trophic interactions.

USE OF -OMICS TO DETERMINE MICROBIAL DIVERSITY OF HYDROCARBON POLLUTED SOILS

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Aim:

The present study aims to characterize the microbial diversity in three polluted soils to obtain insights into the presence of active species involved in contaminants degradation.

Method:

Different omics technologies, namely 16S/18S amplicons sequencing, metagenomics sequencing and metaproteomics analysis were employed to assess the microbial diversity and activity in the studied samples.

Results:

We have analyzed microbial diversity (bacteria and fungi) in soils from distant locations with a long term pollution history, with hydrocarbon levels from 2 to 30 g/Kg of soil. Samples were taken from Spain (Site N), Ireland (Site C) and China (Site G). Soils microbiomes were determined by 16S DNA (bacteria) and 18S DNA and ITS amplicons (fungi) sequencing. Alfa diversity showed that the three soils had Shannon Indexes that were similar to those reported in the literature for clean soils. However, specific populations were altered, specially at family and genus level. These results allowed to determine a core community typical of polluted soils. Metagenomic DNA was also sequenced and the presence of genes encoding enzymes implicated in hydrocarbon degradation were shown to be very abundant in the three sites, suggesting that the soils have the microbial potential for hydrocarbon degradation. Virtually all the genes encoding activities for the initial degradation of aliphatic, aromatic and poly aromatic hydrocarbons were found in the three sites. This analysis was complemented with a metaproteomic study, which confirmed the presence of a number of enzymes being expressed in all contaminated soils involved in the contaminants degradation.

Conclusions:

Results presented here show that there are specific populations of microorganisms which harbour hydrocarbon pollution capacity in polluted soils, indicating that bioaugmentation with local microorganisms can be a successful strategy for bioremediation.

Are drivers of nematode communities in agricultural soils, stochastic or deterministic?

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Aim: While it is recognised that nematodes are one of, if not the, most prevalent and abundant phylum in agricultural soils, there is a knowledge deficit as to the drivers of their community structure. In agricultural soils, to date, assessment of drivers has primarily been under either controlled conditions (e.g., microcosms, mesocosms) or at a limited field scale and does not adequately capture the level of biological variability that exists at scale. Using nematode community data from agricultural soils collected at national scale (Great Britain), coupled with soil and agronomic metadata, the aim is to ascertain the drivers of nematode community composition in agricultural soils.

Method: Soil nematode communities from > 5000 agricultural soil samples were characterised using DNA methodologies. Soils were analysed for micro- and macronutrients and common soil chemical parameters (e.g., pH). A subset of soil samples (n=927) was characterised for a range of soil physical measures. Agronomic data for the sampled crop and 5 years prior to sampling was provided by farmers and included information on inputs, tillage management, and fertiliser type.

Results: A dual bioinformatic and statistical approach will identify whether the primary drivers of nematode community in agricultural soils are either deterministic or stochastic and which drivers have most influence in shaping nematode communities.

Conclusions: Knowledge gained will strengthen the evidence base to support and inform decision-making, practice and uptake for sustainable management and minimization of degradation and loss of agricultural soils.

Contribution of Plant and Soil Biodiversity to the Nematode-Associated Microbiome

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Aim: Nematode feeding on plant roots is accompanied by the changes in the root microbiota and microbiomes associated with different life stages of nematodes. Here we investigated whether the soil type and diversity of the host plants triggers specific nematode-microbiome assemblies that may dampen nematode performance on plants.

Method: In the first approach, we tested the effects of soil type on microbial attachment to the infective stages (J2s) of root-knot nematodes. We inoculated the J2s to tomato plants grown in soil from nine different fields and determined nematode performance on roots. We also exposed the J2s to the microbiome from different soils and characterized the composition of J2-attached microbiomes using amplicon sequencing. In the second approach, we inoculated the J2s to ten different host plants and collected different life stages of the root-knot nematodes. We used amplicon sequencing to characterize the microbiome that associated with the developing nematodes inside the roots over time.

Results: Microbiomes originating from nine fields differed in their ability to suppress nematode performance on plant roots. Amplicon sequence data revealed that J2-associated microbiomes from nematode-suppressive soils clustered together and were more diverse compared to the J2-associated microbiomes from nematode-conducive soils, which may affect the J2 ability to invade the roots. In addition, nematode infections altered the root endospheric microbiome.

Conclusions: The soil microbiome determines nematode survival and infectivity through attachment to nematode skin. During development in roots of different host plants, nematodes associate with a specific microbiome that have important functions in the nematode life cycle.

Do Millipedes Depend on their Gut Microbiome to Digest Leaf Litter?

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Aim:

Millipedes are an essential group of detritivores, eating voraciously to compensate for their poor diet. Millipedes are considered keystone macrodetritivores in many terrestrial ecosystems after termites and earthworms, devouring 10-36% of the annual litter. Therefore, they contribute to soil formation and are essential ecosystem engineers.

Despite their ecological importance, it remains unclear whether millipedes are cellulolytic and what is their microbiome's role in the diet.

Methods:

We evaluated to what degree tropical and temperate millipedes depend on their gut microbiome. First, we charted the microbiome of 11 millipede species and measured their guts' redox potential. Then, further experimented with two model species using chemical suppressors and RNA-SIP in conjunction with metagenomics and metatranscriptomics to elucidate the metabolic potential of key bacterial players in the hindgut.

Results:

Bacterial and archaeal communities were phylogenetically conserved while the fungi matched the diet. Random forest analysis partitioned the microbiome into three distinct groups, closely matching the gut's redox conditions. Chemical suppressors dramatically affected microbial functions, but with only minimal effect on the millipedes.

In total, 305 high-quality MAGs consisting of 18 prokaryotic taxa were obtained, including various novel bacteria. The results from reconstructed metabolic pathways indicate, in addition to fermentation, ammonia oxidation and nitrogen fixation.

Conclusions:

Our results suggest that while the microbiome benefits the millipedes and its composition reflects the prevailing conditions in the gut, it is not essential. As opposed to, e.g., termites or ruminants, millipedes seem to feed on microbial biomass instead of fermentation products.

Community Assembly in Response to Glacial Retreat: A Meta-AnalysisSatyendra Kumar Pothula¹, Byron Adams¹¹*Brigham Young University, Provo, United States***Aim:**

Our goal was to identify universal patterns and processes that drive ecological succession of soil ecosystems in response to deglaciation.

Method:

We conducted a global meta-analysis of 88 published studies focused on the succession of various taxa and soil physicochemical properties in glacier forefield soil communities along their chronosequence.

Results:

Key soil properties and the abundance and richness of biota followed two conspicuous patterns: 1) Some taxa and chemical properties demonstrate a persistent increase in abundance and richness over the entire chronosequence (Proteobacteria, Zygomycota, omnivorous and plant-feeding nematodes, springtails, mites, enchytraeids, Hymenoptera, lichens, vegetative cover, vascular and non-vascular plants; CNP); 2) other taxa increase in abundance and richness during the first 50 years of succession, then gradually decline 50 years onward (Acidobacteria, Chloroflexi, Planctomycetes, Ascomycota, Basidiomycota, bacterivorous nematodes, Coleoptera, Opiliones, Arachnida; EC)

Conclusions:

Soil properties and soil organisms intimately tied to vegetation followed the first pattern, consistent with the idea that aboveground patterns of vegetation are coupled with processes that drive belowground biodiversity. The second pattern may be due to an initial increase and subsequent decline in available nutrients and habitat suitability caused by increased biotic interactions, including resource competition among soil biota. A consensus view of the patterns of historical and contemporary soil ecosystem responses to deglaciation provides insight into the processes that generate these patterns and informs predictions of ongoing and future responses to environmental disturbance.

Soil biodiversity for educational diversity: Using soil organisms for diverse learning outcomes with diverse audiencesLoren Byrne¹¹*Roger Williams University, Bristol, United States***Aim:**

Conservation and management of soil biodiversity (SBD) depend on people having SBD literacy, defined as the scientific knowledge of soil organisms' ecological relationships and roles, and use of this knowledge for evidence-based decision making. Lack of such literacy is a threat to sustainable use of SBD. Increasing societal SBD literacy requires expanding SBD education beyond soil and environmental science classes. The objective of this presentation is to describe how SBD can be used for diverse learning outcomes in many settings for a variety of audiences.

Method:

Examples of teaching and communicating about SBD were gathered from the literature and online resources, and developed by the author as part of his teaching and outreach activities.

Results:

Because most people are unaware of many soil taxa or misunderstand their ecological relationships, many SBD educational materials and programs aim to simply introduce SBD, as through videos of living organisms, museum exhibits, and children's books. To reach diverse audiences, SBD has been connected to people's daily lives (e.g., food, clean water), and varied career and disciplinary interests (e.g., landscape architecture, anthropology). Soil life has been used to help non-science students explore general ecological concepts in courses focused on introductory biology, sustainability, and urban ecosystems.

Conclusions:

Helping more people become aware of the existence of SBD and its relevance to humanity should be a primary goal of the SBD science community. Hopefully, examples from this talk will provide inspiration for developing diverse educational efforts that increase everyone's SBD literacy around the world.

Epichloë Increases Root Endophyte Richness and Alters Root Endophyte Composition in a Changing World

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Aim:

Plants harbour a variety of fungal symbionts both above- and belowground, yet little is known about how these fungi interact within hosts, especially in a world where resource availability is changing due to human activities. Systemic vertically-transmitted endophytes such as *Epichloë spp.* may have particularly strong effects on the diversity and composition of later colonizing symbionts such as root endophytes, especially in primary successional systems. We ask: Does colonization of the host grass by *Epichloë* alter root endophyte species richness or community composition? And if so, does N addition intensify the effects of *Epichloë* on the root endophyte community?

Method:

Utilizing a long-term field experiment in North American Great Lakes sand dunes, we tested whether *Epichloë* colonization of the dune-building grass, *Ammophila breviligulata*, could alter root endophyte species richness or community composition in host plants and whether nitrogen addition intensified the effects of *Epichloë* on the root endophyte community. The root endophyte community was characterized by culture-based methods coupled with sanger sequencing.

Results:

We found that *Epichloë* increased richness of root endophytes in *Ammophila* by 17% overall, but only shifted community composition of root endophytes in nitrogen enriched conditions.

Conclusions:

These results indicate that this systemic endophyte is acting as a key species within *Ammophila*, changing diversity and composition of the root mycobiome and integrating above- and belowground mycobiome interactions. Further, effects of *Epichloë* on root endophyte communities were enhanced by N addition, indicating that this fungus may become even more important in future environments.

Long-term Effects of Wood-Ash Fertilization on Soil Microbial Diversity in Boreal Peatland Forests

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Aim: Wood-ash is a commonly used fertilizer in peatland forests of boreal region. Wood-ash is known to have long-term positive effects on soil properties promoting tree growth in peatland forests. Ash raises the soil pH resulting in increasing the cation exchange capacity and bioavailability of nutrients. It includes mineral nutrients required for tree growth but no nitrogen which is not the limiting factor in peatland forests. Changes in pH alter the soil microbiomes. However, still a very little is known about the effects of wood-ash on soil microbes even they are major regulators of nutrient cycling and carbon storage. Shifts in microbe participating in the GHG exchange, for instance, may eventually lead changes in soil carbon sink. For the first time, metagenomic data was applied to study the role of soil microbial diversity in boreal peatland forests applied with wood-ash.

Method: Samples were taken in autumn of 2021 from two boreal peatland forest sites applied with wood-ash in 1997 and in 1985, respectively. Altogether 24 samples including 6 replicates from wood-ash fertilized and control sites were taken both from the vicinity of total soil respiration measurement and heterotrophic respiration measurement spots where roots were removed. Samples were frozen at -20°C. DNA was extracted, and metagenomic libraries prepared and sequenced with Novaseq platform.

Results & Conclusions: Metagenomic analyses are still under the process. We expect to have groundbreaking knowledge about the role of compositional and functional soil microbial diversity including novel metabolic traits in peatland forests after long-term wood-ash application.

Drought legacy affects soil fungi and functions in arable ecosystemsEmilia Hannula¹¹*Leiden University, Leiden, Netherlands***Aim:**

The aim of this research is to quantify the effects of legacy of disturbances (drought and tillage) on soil fungal community and functions they provide in arable soils.

Method:

Mesocosm experiment in which four soil inocula with varying levels of fungal biomass were added to sterile soil was conducted in common-garden set-up. In a fully factorial design, half of the mesocosms were subjected to severe naturally occurring summer drought of 2020 (while half served as irrigated control). Another disturbance, tillage was performed in spring 2021 again to half of the units making the number of treatments 4 (across 4 soils). Fungal biomass, community structure and soil respiration were measured first monthly and later every 3 months throughout the experiment. Functionality was measured by plant growth and nutrient content, decomposition and finally by following the fate of ¹³C through the soil food-web (PLFA-SIP for microbes, EA-IRMS for collembola) and its stabilization in stable soil aggregates (EA-IRMS).

Results:

We show that the legacy of the drought on fungal community structure diminishes in time but that the changes in fungal community lead to difference in functions in long-term. Both decomposition rates and carbon sequestration differed between soils that were exposed to the drought year prior compared to well irrigated soils. The tillage/mixing affected the soils carbon budget further but the effect was smaller than for drought and no interactive effect was noted.

Conclusions:

Legacy of a drought has long-term effects on soil fungal communities and functions including decomposition and carbon sequestration.

Shotgun Metagenomics Reveals Decade-Scale Spatio-Temporal Dynamics of Entire Soil Communities: Microbes and Soil Invertebrates

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Aim:

We explore decade-scale spatio-temporal dynamics of soil community composition and function and their anthropogenic drivers.

Method:

We take advantage of a unique sampling scheme of the German Environmental Specimen Bank (<https://www.umweltprobenbank.de>) to obtain soil environmental DNA (eDNA) time series collected at 11 locations over Germany over 20 years. The sampling locations cover a variety of habitat types that are representative of German land-use conditions. We use shotgun metagenomics to representatively sequence eDNA fragments. Sequence assignment is supported by a newly generated soil invertebrate genome library containing genomes from over 250 central-European soil invertebrate species.

Results:

Soil communities react to outer conditions, such as temperature, water availability or pH-value. The dataset generated here promises to capture the spatio-temporal dynamics components of the entire soil biota. On the spatial scale, we expect a differentiation of soil biomes' taxonomic composition and function with land-use type, soil type and associated abiotic conditions. We also expect temporal change in community composition and function as land-use, climate and chemical use changed during the two decades of the sampling.

Conclusion:

The results allow to evaluate the ability of shotgun metagenomics to capture all living components of the soil ecosystem. Combined with our new reference database, this allows to gain massive amounts of comparable data rapidly and explore changes in soil invertebrate communities and their associated microbiomes for a full community-level picture of compositional and functional changes through time. The knowledge gained could refine predictions of future changes in soil community.

How does horticultural agriculture affect soil biodiversity? - a meta-analysis

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Aim:

Horticultural agriculture – growing fruit and vegetables – is both important for a healthy diet and (compared with mostly wind-pollinated cereals) more dependent on local biodiversity, including soil biota; but most research into the biotic impacts of agriculture has focused on cereal crops. We have synthesised comparisons of below-ground biodiversity in different horticultural agricultural systems and semi-natural baselines, using matched environmental data to test responses between regions, crops, and taxa.

Method:

Our literature search captured studies on horticultural agricultural systems and their effect on biodiversity in Europe. We used papers that measured below-ground biodiversity in at least two sites, comparing either different horticultural management types/intensities or horticultural agriculture vs semi-natural land. Further sources came from relevant reviews and meta-analyses. Effect sizes were calculated for each control-treatment pair. We constructed multi-level random effects models to account for variation within studies.

Results:

A total of 915 paired observations were available for modelling, from 55 articles. Response variables were abundance (84.04%, n=769), species richness (10.16%, n=93) and Shannon diversity (5.79%, n=53). A large proportion of heterogeneity was attributable to study-level random effects, but moderator analysis revealed that geographic effects, taxonomic identity of crop and study taxa were also important, as – to a lesser extent – was management type.

Conclusions:

Analysis is still ongoing, but even our preliminary analyses show how using meta-analysis for cross-study syntheses can complement synthetic multilevel modelling of raw biodiversity data. We will be able to present an analysis of whether the effects of management practices differ among taxonomic groups.

Seasonality Drives Soil Dynamics - Environmental DNA Metabarcoding Study on Soil Communities

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Aim:

The aim of our study is to investigate the effects of seasonality and other environmental conditions on the eukaryotic community richness and composition.

Method:

A floodplain in Germany was biweekly sampled to collect soil environmental DNA (eDNA) for over a year. Four different marker regions were amplified to and sequenced in a metabarcoding analysis: plant *trnL*, eukaryotic 18S rRNA, macroinvertebrate *cox1* and fungal ITS. Reads were clustered into operational taxonomic units (OTUs) to examine community changes over time using joint species distribution modelling.

Results:

We detected only a few abundant OTUs. Especially metazoan OTUs were rarely detected. Seasonality was a stronger driver of community composition and richness than mean temperature and precipitation of the two prior weeks. As expected, soil community richness was higher in summer and decreased towards winter. We observed strong dissimilarity in community composition even over short time periods. Consecutive summers differed greatly in soil community composition.

Conclusion:

Here we show that soil eDNA is able to capture seasonal signals in the properties of soil communities. Joint species distribution models, in combination with the temporal resolution of eDNA samples, promise a better understanding of soil communities, effects of abiotic factors, and the temporal dynamics of interactions among plants, fungi and metazoan. The results also highlight that further methodological improvements are necessary to capture soil biodiversity with eDNA, to improve rare species detection in particular.

Biogeography of soil fungi and their associations to plants

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Aim: Global soil biodiversity is driven by environmental factors such as soil pH, temperature and precipitation. In Switzerland, which is characterized by two mountain ranges, large gradients of pH (2.9-7.8), mean annual temperature (-3-12.2°C) and yearly precipitation (617-2,566 mm) exist over relatively short distances. Using a regular grid of sites across Switzerland, we assessed environmental drivers and plant associations structuring soil fungal communities.

Method: Fungal communities of 1,010 soil samples from 255 sites and the four land-use types arable land, meadow, alpine grassland and forest, were determined using metabarcoding. Plant communities were recorded at each site.

Results: In total, 28,085 fungal amplicon sequence variants (ASVs) were detected, of which one third was assigned to the genus-level. Although, on average only 20.7% of the ASVs were detected in all soil samples that were taken within few meters at a site, 78.7% of the soil samples nevertheless revealed a site-specific fungal community structure. Fungal community structures differed among land-use types (PERMANOVA; $R^2=8.8\%$). Fungal communities in forests were better explained by plants ($R^2=19.1\%$) than by pH, elevation and variation of temperature (together $R^2=12.0\%$). In alpine grasslands, plant communities were also stronger drivers of fungal communities ($R^2=21.1\%$) than pH ($R^2=7.0\%$), while in meadows plant communities ($R^2=14.4\%$) and pH as well as nutrient status (together $R^2=13.3\%$) explained similar fractions of variation.

Conclusions: Much of the diversity of soil fungi remains unknown and awaits detailed description. Sites included heterogeneous but specific fungal communities. Plant communities were better predictors of fungal communities than soil and climatic factors.

RNAseq analysis shows that Collembola affect Plant molecular processes.

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Aim

Biotic interactions taking place between above and belowground terrestrial ecosystems are considered the backbone of biodiversity and ecosystem functioning, but depicting and understanding such interactions is still a hot topic especially in soil ecology. Soil animals, like Collembola, are known to directly or indirectly regulate plant physiology, architecture, growth and flowering phenology. However, clear mechanisms through which a plant may respond to the presence of Collembola are not elucidated. We hypothesized that RNAseq analysis of plant tissues will help to understand molecular impact of the presence of Collembola microarthropods on plant morphological and physiological changes.

Method:

Within soil microcosms, seedlings of *Poa annua* were grown in presence or not of a Collembolan species (*Folsomia candida*) for 6 weeks. Transcriptomic analysis was performed on leaves, RNA was collected and purified according to standard methods. Differential expression of genes analysis has been conducted with DeSeq2. GO annotation and enrichment were performed using Blast2GO and visualization thanks to WEGO.

Results:

Our analysis showed only 6 Differentially Expressed Genes (DEG) up-regulated and 1080 DEG down-regulated for plants grown with Collembola. The 1080 DEG down-regulated are implicated in 75 biological processes with a high number of DEG implicated in organic substance metabolic process, stress tolerance or nutrient efficiency.

Conclusions:

Soil fauna, like Collembola, exerts a strong regulation on molecular processes taking place in plants by differentially regulating gene expression. It clearly demonstrates the predominant role that can play soil animals in driving vegetation development.

How Scale Influences Conclusions About the Effects of Soil Biodiversity on Carbon Cycling

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Aim:

There is a rich theoretical and empirical literature on ‘ecological inference fallacies’. These formal fallacies arise from decisions about scale of data collection and analysis. These fallacies obfuscate local effects of causes at broader scales. I test whether common design and analysis decisions for soil studies inadvertently fall into this inference trap, thereby underestimating the importance of biodiversity as an ecosystem control.

Method:

I collate four empirical datasets, where observations of soil carbon cycling, plant growth, abiotic, and biotic controls were collected at high local densities and fine scales at multiple sites across regional climate gradients. I use these data to quantify how decisions about scale of data collection and analysis affect estimates of soil biodiversity on process rates. Specifically, I examine decisions regarding observational grain, data aggregation, process knowledge and statistical modelling.

Results:

Common ways in which we design and analyse studies lead to false conclusions and often strong underestimates of the influence of soil biodiversity on ecosystem carbon dynamics. For example, I show that soil biodiversity effects can be entirely obscured through data aggregation – both as a product of experimental design and of data analysis – and erroneously attributed to other causes through process knowledge and statistical modelling decisions.

Conclusions:

There is high potential for awareness of ecological fallacies to reshape how we design and analyse soil studies. Reshaping our scientific approaches will help build a robust foundation of data on which to build policy and practice that leads to the sustainable use and conservation of soil biodiversity.

Biogeographical characterization of the rhizosphere microbiome of crop wild progenitors in their habitats of origin

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Aim: Harnessing plant-microbiome interactions is one of the most promising strategies to guarantee food security and agricultural sustainability. Exploring the microbiomes of crop wild progenitors and their abilities to establish beneficial relationships with soil microorganisms at their native habitats is an understudied avenue in this realm. We ecologically characterize the centres of origin of major staple crops (maize, rice, wheat, potato, bean, little millet, barley, sunflower, soya and cotton) and identify the core of the soil microbiome of the crop wild progenitors.

Method: We put together an international consortium (MICROWILD) and gathered a global database containing the amplicon sequencing of the 18s, ITS, and 16s rRNA genes from bulk and rhizosphere soil, as well as climatic and edaphic variables of ten crop wild progenitors. Each wild progenitor was sampled in ten different populations along a soil-climate gradient at its distribution range.

Results: We identified the core microbiome (representing 25-53% of all 18s/16s/ITS reads) of the crop wild progenitors that is ubiquitous (>50% samples) and represents less than 4% of the total number of phylotypes. The relative abundance of the core microbiome was similar in both

rhizosphere and bulk soil but showed unique patterns between different species and between microbial groups (bacteria, fungi and protists). This may suggest different environmental preferences of the core phylotypes of the ancestral crop microbiomes.

Conclusions: Our global, interspecific and multi-gene approach provides a valuable ecological understanding of the ancestral microbiomes of major crops and identify potential phylotypes that could be targeted for directing future research.

Yearly dynamics of microbial communities at the scale of an agricultural landscape

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Aim

Soil microbial communities play a central role for sustainable soil use: their extreme diversity supports soil functions and related ecosystem services. Today, non-random spatial distribution of soil microbial diversity is well established from global to landscape scale but few studies focused temporal variations. Here, the objectives were to evaluate if the spatial distribution of soil bacterial, archaeal and fungal communities changed through time and if this was related to changes in the subsequent environmental filters.

Method

Soil samples were collected at the scale of an agricultural landscape (1,200 ha, Fénay, France; sampling grid 215x215m, 264 sites) during two campaigns in 2011 and 2019. Soil bacterial, archaeal and fungal communities were characterized by a metabarcoding approach (Illumina®) targeting either 16S or 18S rRNA genes, and variations in community composition were confronted to soil physico-chemical characteristics, land-use and agricultural practices.

Results

Significant variations in microbial community compositions were observed between 2011 and 2019 while their spatial patterns remained stable. Per year, 15% to 34% of the spatial variations of soil bacterial, archaeal or fungal communities were explained, first by soil characteristics and then by land use type and agricultural practices. Between 2011 and 2019, soil physico-chemical characteristics experienced little variations and had stable spatial patterns. Therefore, yearly compositional changes in microbial communities could be related to changes in agricultural practices: e.g. tillage reduction, diversification in crop rotation, perennial plant cover.

Conclusions

Soil characteristics may strongly determine the spatial distribution of soil microbial communities while changes in agricultural practices contribute to temporal changes in community composition.

Exploring the biodiversity of the microbial resistome of pristine and anthropogenically disturbed soils

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Aim:

We assessed microbial antibiotic resistance in select local (Wyoming, USA) soils and how grazing activity, as a proxy for anthropogenic disturbance, affects the diversity of microbial communities.

Method:

Soils from three locations with different levels of grazing activity (cattle grazed, bison grazed, or glacier (no grazing)) were used for microbial culturing, qPCR, and high throughput and targeted sequencing approaches for select antibiotic resistance genes (ARGs). Cultured bacterial isolates were tested for antibiotic resistance using a minimum inhibitory concentration assay (MIC).

Results:

Multivariate analysis of gene quantity of 13 ARGs showed differences by disturbance (grazing) level, with cattle grazing locations being different from bison grazing and glacier soils. Several ARGs showed differential abundances by disturbance level: *intl1*, *intl2*, *intl3*, *blaVIM*, *qnrA*, and *tetW*. Genes in higher abundance represent resistance to several different classes of antibiotics and resistance mechanisms. Of six different antibiotics tested in MIC assays, only tetracycline MIC values were significantly different among different disturbance levels. Anthropogenically disturbed soils exhibited a trend of more resistance as measured by MIC than undisturbed soils.

Conclusions:

Abundance measurements of ARGs, combined with assessment of the level of resistance through MIC assays can help us to understand the historical levels of antibiotic resistance and measure the impacts of anthropogenic disturbance on the microbial community. There are limitations to using qPCR and MIC assays for the assessment of antibiotic resistant phenotypes from soil bacteria. Targeted sequencing results in a comprehensive view of the biodiversity of ARGs present in soil bacteria that may potentially threaten human or animal health.

Interactions Between Roots, Soil and Soil Biota in Agricultural Multi-Species GrasslandsKatie Martin^{1,2}, Fiona Brennan², Saoirse Tracy¹, Olaf Schmidt¹*¹University College Dublin, Dublin, Ireland, ²Teagasc Environment Research Centre, Johnstown Castle, Ireland*

The diversification of plant species sown within agricultural grasslands has been shown to have benefits compared to their monoculture counterparts. Lower fertiliser requirements, increased biodiversity and improved stress resilience have all been reported in these multi-species grasslands. However, changes to the plant communities has the potential to affect the soil structure as well as the abundance, diversity and activity of the soil biota.

Aim: This project aims to assess the soil structure, soil microbial communities and root traits of grassland plots within monocultures and mixtures of six grassland species.

Method: The soil, plant roots and microbial communities were assessed through X-ray computed tomography, root image analysis, and molecular analysis of microbial communities.

Results: X-ray computed tomography revealed changes in macroporosity associated with different grass communities as well as visualising biopore formation by root and earthworm activity. The overall percentage porosity in mixed-plant communities tended to be higher than grass monocultures. As the plant species included had diverse root architectures, root traits assessment was used to understand root impacts on soil structure and plant resource uptake. Whilst the highest root length density of monoculture plots was found in grasses, two and six-species mixtures were not significantly different indicating that fine root production associated with nutrient uptake was maintained. Further analysis of these samples aims to untangle the microbial diversity within these different grassland communities.

Conclusions: Altering plant species diversity affects not only grassland agronomic potential but has belowground effects on soil biotic interactions as well as soil physical properties.

The Resistance and Resilience of Soil Microbial Communities to drought in Multi Species Grassland Swards.

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Aim: To study the impact of sward composition on the resistance and resilience to drought of soil microbial community composition, diversity and function in agricultural grasslands.

Method: Microbial diversity and functional analyses were performed on soil samples taken from varying plant community combinations within a six-species system during an *in situ* drought treatment and six weeks after rewetting. Microbial drought resistance was defined as the ability of the microbial community to retain normal structure and function during a drought. Microbial drought resilience was defined as the ability of the microbial community to regain normal structure and function when water is no longer limited, following a period of drought. Rainfed controls were used in this study to define 'normal' conditions. Diversity Interactions modelling was used to analyse the data.

Results: Soil microbial community abundance, composition and nitrogen cycling functions in temperate agricultural grasslands were generally resistant and resilient to drought, regardless of sward composition. However, where effects of drought were observed, microbial resistance and resilience was in many cases mediated by plant identity. In contrast, plant interspecific interactions generally had no influence on soil microbial drought resistance and resilience. The microbiome of *L. perenne* monocultures with additional nitrogen fertiliser was found to be less resistant and resilient to drought suggesting that additional nitrogen can make grassland microbiomes more vulnerable to climate stress.

Conclusions: The soil microbiome in intensively managed, temperate, agricultural grasslands was generally resistant and resilient to drought, regardless of plant species composition but was impacted by N fertiliser application.

Farming Practices Shape Belowground Plant-Microbe Interactions with Consequences for Aboveground Plant Performance

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Aim: Our aim is to improve plant growth and plant health by understanding how agricultural soil legacies affect plant-microbe interactions.

Method: Root observation windows were installed in consecutive years in a long-term field experiment (Bernburg/Germany) comparing plough (MP) vs. cultivator tillage (CT) and intensive vs. extensive N-fertilization. Model crops were winter wheat and maize with the latter in addition receiving inoculation with a consortium of beneficial microbes (*Pseudomonas* sp., *Bacillus* sp., *Trichoderma* sp.). Besides non-destructive root exudate analysis and recording of plant growth, the expression of stress-induced genes and metabolites in leaf tissue and the rhizosphere microbiome were investigated.

Results: Compared to MP, winter wheat grown under CT had more fine roots and exuded more primary and secondary metabolites. Copiotrophic and potential plant-beneficial microbes (e.g. *Bacillus*, *Devosia*, *Trichoderma*) were enriched in the rhizosphere under CT pointing to a stronger plant selective effect. Tillage-affected belowground interactions resulted in differential aboveground stress levels with winter wheat grown in CT soils exhibiting lower stress gene expression and physiological stress indicators.

With respect to the inoculation, the agricultural legacy resulted in differential responses of the maize rhizosphere microbiome. Yet, the consortium improved maize biomass independent of farming history. Leave nutrient, metabolite, hormone and gene expression analyses pointed to a common, farming-independent stress likely induced by drought during early growing season, which was mitigated by the inoculants.

Conclusions: These multidisciplinary studies contribute to a better understanding of belowground plant-microbe interactions in agroecosystems, which can be harnessed for a microbiome-based sustainable crop production.

Elevation and Island Isolation as Drivers of Protist Endemicity

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Aim:

The island biogeography theory was developed based on the observation that species diversity of macro-organisms declined and their rate of endemicity increased in relation to smaller island size and higher distance to the nearest continent. It was latter applied to micro-organisms when the definition of island in ecology was extended to any type of isolated habitats (e.g., lakes, tree holes). To date, the original theory of MacArthur and Wilson was not tested for most eukaryotic micro-organisms (i.e., protists) over continental and oceanic islands.

Method:

Here we present results of elevation gradients diversity analyses of soil protists in two main land mountain ranges and five islands by soil eDNA HTS. The two main hypotheses evaluated are the increase proportion of endemic taxa i) with increasing distance to continents, following the classical island biogeography theory, and ii) at low elevation (i.e., in forest vs. alpine habitats) due to increase wind-exposure and higher dispersal ability of soil protists.

Results:

The distance to the nearest continent appeared to be a strong driver of endemicity rate, which was significantly higher in the forest than in the alpine habitats. Most clades also displayed a significant linear increase in endemicity with distance to continent in forests, while only clades of larger protists such as Ciliophora and Imbricatea showed also this trend in the alpine habitats.

Conclusions:

These results support the idea of a higher dispersal ability and adaptability of smaller protists in alpine habitat, while most forest soils protists have restricted geographical distribution.

Critical Needs of Soil Biodiversity Science in the Age of Global Monitoring

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Aim:

Monitoring to quantify soil biodiversity change is increasing worldwide and some governmental bodies, such as the European Union, now recognize that soil biota are critical for human well-being because their activities underpin soil resources and the delivery of major ecosystem services. These monitoring programs are the first step toward developing effective policies and land management practices for the protection and restoration of soil biodiversity. Joint program efforts target the lack of specialized taxonomic knowledge, protocol standardization for effective monitoring, logistic complexities of large-scale monitoring, and navigation of legal procedures, such as those resultant from the Nagoya Protocol. I will explore the impact of the GSBI transnational scientist volunteers and policy-driven projects on the missions to raise awareness and develop transorganizational ties to aid in research, monitoring, and protection of soil biodiversity, and recent efforts to mobilize data. What monitoring programs are out there? How are different programs integrated? And what research areas and capacity-building strategies do we need to hasten monitoring?

Method:

Analysis of the monitoring programs, their integrated collaborations, and “Centers of Excellence” for capacity-building that can be accessed for training and funding.

Results:

These findings are important for further advancement of large-scale soil biodiversity monitoring and protective policies for soil biodiversity, which have been ignored up until recently.

Conclusions:

After, we suggest that future advancements include:

1. Development in taxonomic methods to ensure inclusive participation
1. Integration of advanced machine learning into data collection methods
2. Co-operation between monitoring programs to standardize and share knowledge

Impact of various fungicides on the number and species abundance of fungi in podzolized chernozem

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Aim: The aim of the study was to determine the effect of fungicides on the soil fungi community.

Method: In laboratory experiment the soil in containers was treated with the fungicides in recommended doses. Six treatments were designed comprising three chemical fungicides based on carbendazim, tebuconazole, azoxystrobin, and two biological fungicides based on antagonistic fungi Trichodermin and Chaetomic, and control. The number of fungi was counted 5, 20, 40 and 110 days after treatment using the Petri dish method. The species affiliation of the isolates was determined by microscopy.

Results: After 20 days after treating, there was a significant decrease in the number of fungi by 25-41%, after 40 days, their number remained smaller, after 110 days it approached the control. The number of fungi decreased less and recovered faster when the soil was treated with biofungicides. 5 days after treating under the influence of carbendazim and Trichodermin, the abundance of dominant species decreased slightly. Tebuconazole, azoxystrobin and Chetomic significantly changed the structure of the fungal community, the abundance of species dominating in the control decreased, and other species became dominant.

Conclusions: Studied fungicides temporarily reduced the total number of fungi in the soil and had effect on structure of soil fungal community. The direct effect of fungicides is to suppress phytopathogenic fungi in crop production. However, non-target fungi also may be affected. Some fungicides have an adverse effect on the entire soil fungal community. This may lead to undesirable changes in soil properties and a decrease in its fertility.

Understanding abiotic stress effects on plant-microbial interactions of an endangered habitat

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Aim:

We aim to elucidate the ways that natural stressors – fire and allelopathy – can affect the structure and function of microbial communities, as well as their subsequent impact on plant performance. Plants in this habitat comprise a range of natural histories and can be common, endemic, or endangered; therefore, a better working knowledge of microbial effects on their function under native stress can translate into important applications for their preservation and restoration.

Method:

We performed two independent studies determining 1) the direct effects of fire or allelopathy on soil microbial communities, and 2) the subsequent stress-selected microbiome effects on plant germination, productivity, and biomass allocation. We utilized a prescribed burn in the field for our fire treatment, or the direct application of the dominant allelochemical to native soils. We sequenced for soil prokaryotic and fungal communities and used computational tools to identify functional shifts, and finally carried out two large (>1,200 pots each) factorial grow room studies with >11 native plant species.

Results:

Fire and allelopathy shifted bacterial but not fungal community composition, and allelopathy increased bacterial nitrogen fixation gene abundance. Ultimately, prescribed fire selected a microbiome that strongly decreased plant productivity across plant species, while allelopathy selected a microbiome that weakly increased plant productivity.

Conclusions:

We propose an important way to approach plant-microbial interactions responses to stress through the guiding principle of local adaption, where historical stress frequency linearly relates to the strength of microbial-mediation of plant response.

Harnessing native soil microbes to reconnect plant and soil biodiversity and improve restoration outcomes

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Aim:

Global environmental changes such as drought, intense fire and land degradation are rapidly transforming the structure and functioning of ecosystems worldwide. These changes are leading to a severe loss of above and belowground biodiversity and increased soil degradation. Soil microorganisms control important ecosystem functions such as nutrient cycling, plant productivity and climate regulation. Thus, microbially assisted conservation and restoration has the potential to reconnect above and belowground dynamics, creating functional ecosystems that are more resilient to climate change impacts.

Method:

In this research, we (i) assessed the responses of soil microbial communities to disturbance, e.g., severe fire, and extractive activities such as mining, and (ii) developed bioinoculants composed of locally sourced soil bacteria from the rhizosphere and biocrust cyanobacteria, to promote plant growth and soil fertility and enhance ecosystem capacity for global change adaptation.

Results:

This presentation will showcase some key findings of these studies conducted in contrasting Australian ecosystems (shrubland-grassland in the arid zone, and subtropical/temperate forests). These outcomes include the successful translocation of whole-soil communities for inhibiting weeds, and the effective use of indigenous microbes (rhizobacteria and cyanobacteria combinations) for soil carbon sequestration, nitrogen fixation, and growth promotion of key arid and temperate plant species.

Conclusions:

Overall, our research demonstrates the benefits of using native microbial communities as bioinoculants in ecosystem restoration. The emerging technologies used in our research, i.e. seed enhancement through seed biopriming and biopellets, have a large potential for landscape-scale conservation and restoration programs in the context of global change.

The role of molecules, morphology and methodology in determining patterns of soil mite diversity

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Aim:

Mites are among the most diverse and abundant taxa in soil ecosystems; however, due to their minuscule size, they are rarely included in soil biodiversity research. Metabarcoding is increasingly proposed for studying soil biodiversity more comprehensively, yet many questions about best practices remain. This research aims to explore methodology with respect to primer choice, extraction method and DNA source to determine the most accurate and practical approach to assessing soil mite diversity.

Method:

To assess the impact of biomass and primer bias, soil mites were extracted using Berlese funnels, pre-sorted, non-destructively DNA-extracted, and Illumina sequenced using multiple primer sets. We also compared metabarcoding results from eDNA extracted directly from soil with that of bulk mesofaunal samples. Voucher specimens were also identified morphologically. Finally, we compared soil DNA extraction methods to determine if standard microbial techniques would successfully capture mesofaunal diversity.

Results:

Pre-sorting had minimal effect on the taxonomic coverage compared to mixed samples. While 18S and COI provided similar OTU numbers, COI taxon assignment was more accurate due to more comprehensive reference databases. Soil eDNA and bulk mesofauna sequencing both effectively characterize sites; however, eDNA requires greater sequencing depth to fully capture mesofaunal diversity. Standard microbial DNA extraction methods do not include enough soil to sufficiently characterize the mesofauna.

Conclusions

Choice of method depends on the biodiversity research goals; however understanding the advantages and limitations will assist researchers in making practical decisions. Ultimately, we hope to contribute to standard protocols that encourage the exploration of soil mite diversity worldwide.

Digitization and Automatic Characterization of Soil Invertebrates Community Samples Using Macrophotography and Deep-Learning

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Aim:

Soils communities of tiny invertebrates are essential to the functions of soils. Characterizing those communities in terms of species diversity and species abundance is part of investigating soil functions and response to perturbation. It involves an enormous amount of time, straining the workflow of soil zoologists. Deep learning-based computer-vision approaches can assist in automatizing the repetitive tasks of samples characterization.

Method:

We present an open-source prototype for such a computer-vision workflow. It includes a macrophotography system for acquiring high-resolution pictures of small animals in fluid and a deep learning-based application to train and evaluate models for the detection and classification of those animals. We evaluated the workflow using a mix of specimens belonging to 12 species of springtail and mite to train and test a Faster-RCNN object detector and classifier.

Results:

Our system is affordable and easy to build from parts. It allows the rapid digitization of soil samples in a streamlined. The deep-learning model achieved good levels of Precision (0.940) and Recall (0.918). The model showed a lower Recall for one species, but was performant on all others.

Conclusions:

Our prototype offers an operational workflow for the creation of soil fauna picture datasets needed to train deep learning-based classifiers. Scaling up to the effective diversity of soil invertebrates will require a large collaborative effort. Example of applications are: automatization of taxonomic collection digitization, of soil biodiversity analysis and monitoring and assessment of bio-indicators.

Terrestrial Diatoms as Indicators of Soil Conditions

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Aim: While diatoms (Bacillariophyta) are widely used as indicators of freshwater quality, their role and presence in terrestrial systems are deeply neglected and poorly documented. We explored diatoms (Bacillariophyta) as soil quality indicators, aiming to use these communities to indicate anthropogenic disturbance levels and soil fertility classes.

Method: Traditional microscopic analysis and high-throughput sequencing (HTS) metabarcoding (*rbcL* gene) techniques of four hundred forty-six samples collected in Luxembourg during the years 2018, 2019, 2020 and 2021 were analysed. Samples come from several localities with different land use (i.e., arable, grassland and forest), soil textures and farming practices (i.e., BIO vs conventional CONV).

Results: A total of 2552 amplicon sequence variants (ASVs) were identified as Bacillariophyta. Their distribution is significantly controlled by soil texture and farming practices; the ecological optimum and tolerances to nutritional parameters are shown. The congruence between the genetic information and microscopic analysis was used to identify some key 'unclassified' taxa. The surprising diversity and importance (in terms of genetic variants and total reads) of the genus *Mayamaea* are highlighted.

Conclusions: The establishment of ecological preferences of ASV's for measured environmental parameters and the development of an index that considers soil fertility classes and integrates diversity components is discussed. Diatom responses can potentially inform the development of nutritional criteria and decisions regarding manure management, land use and management practices that target, for example, nutrient load reduction. Diatom measurements using relative abundances of gene sequence readings could be incorporated into soil monitoring programmes.

Cellulase genes are widespread in soil invertebrates

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Aim:

We evaluated the taxonomic spread of endogenous (genome-encoded, not microbiome-conferred) cellulases in soil invertebrates.

Method:

We screened ~250 newly generated soil invertebrate genomes (springtails, mites, myriapods, nematodes, enchytraeids) for protein domains characteristic of cellulase genes already confirmed in arthropods. We evaluated the presence of recorded cellulase genes among fungi and metazoa, and reconstructed phylogenetic relationships of the cellulases.

Results:

We recorded the wide-spread presence of cellulase genes of the glycoside hydrolase family 45 in the genomes of oribatid mites and springtails. We also recorded cellulase genes in nematodes and tardigrades. The genes were completely missing from myriapods and enchytraeids. As expected, cellulase genes were missing from the genomes of chordates, but they were frequently found in different fungal families. Gene tree topology indicates independent horizontal gene transfers from fungi into springtails, oribatid mites, and insects.

Conclusions:

Our results provide first evidence that endogenous cellulase genes are wide-spread across soil invertebrates. The ability to decompose cellulose without support from microbial symbionts seems to be common among these animals. The relative importance of microbial *versus* invertebrate cellulase activity in soils remains to be evaluated, but our results raise the possibility that soil invertebrates might play a role in terrestrial carbon cycling.

Scientific assessment of buried underpants as soil health indicator and awareness-raising using citizen science

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Aim:

Soil life is a driver of ecosystem functioning. However, studying soil organisms and their activity can be a tedious process, making large-scale investigations challenging. Moreover, awareness of soils as living systems among land managers and the wider society is often rare. We conducted a citizen science project systematically investigating soil biological activity and major driving factors on 1000 sites across Switzerland.

Method:

We adapted the idea of so-called ‘Soil Your Undies’ campaigns for the first time in a scientifically structured way. We shipped 2000 standardized Cotton underpants and 12000 teabags to over 1000 citizen scientists (50% farmers and 50% private gardeners) from all parts of Switzerland. Participants buried underpants and teabags in soil and collected soil samples following standard protocols and entered site and management information into a specially designed App. After 1 or 2 months, underpants and teabags were retrieved, dried and returned to the lab. Underpants degradation was assessed using gravimetric and imaging methods and teabags were used to calculate the Tea Bag Index (TBI), an established method to assess soil decomposition processes. Soil samples were comprehensive analyzed.

Results:

Results showed that management practices and soil properties were the strongest factors explaining soil biological activity.

Conclusions:

Underpants degradation and TBI performed equally well as indicators for soil quality. Underpants, in addition, provide a visual and haptic experience of living soils and serve particularly well for raising awareness of soil biodiversity. The project aroused global media attention and communicated the importance of healthy and living soils across the planet.

Land topography shapes AMF biogeography besides spatial distance and soil conditionMengting Yuan¹, Anne Kakouridis¹, Erin Nuccio², Jennifer Pett-Ridge², Mary Firestone¹¹University Of California Berkeley, Berkeley, United States, ²Lawrence Livermore National Laboratory, Livermore, United States**Aim:**

Arbuscular mycorrhizal fungi (AMF) are significant root biotrophs that promote carbon and nutrient transfer across the plant-soil interface. But few reports have disentangled the drivers of AMF biogeography from those of their plant hosts. We excluded host influence by studying AMF associated with closely related plants, and evaluated the contributions of environmental filtering vs. stochasticity on the beta-diversity of AMF.

Method:

We collected 156 soil samples (14 cm to >548 km apart) from areas dominated by closely related host plants – *Avena spp.* (Wild Oat) – from three California Mediterranean grasslands that differ in annual precipitation, soil conditions and land topography. *Avena*-associated AMF communities were surveyed using ribosomal small subunit (SSU/18S) primers WANDA/AML2.

Results:

AMF communities differed significantly among grasslands; only 10% of the 1263 AMF OTUs were present at all three sites. Community similarity exponentially decayed with distance. A null-model analysis revealed dispersal limitation (35%) and other stochastic phenomena (56%) are the most important assembly processes shaping AMF communities across grasslands. Differently within each grassland (<1.7 km), AMF beta-diversity was significantly correlated with pH, soil texture, mineral nutrients and microclimate. Dispersal limitation ranged from unimportant (<5%) in two of the grasslands to surprisingly high (37%) in the other site, possibly mediated by variations in local elevation and slope.

Conclusions:

Dispersal limitation of AMF is influenced by distance and land topography; it tends to be strong across large spatial distances and heterogenous landscape. Environmental filtering by edaphic conditions can directly influence AMF communities associated with the same host species.

Site and plant or soil niche strongly influence *Lolium perenne* pasture microbiota in New Zealand

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Aim:

New Zealand's primary-export driven economy relies on perennial ryegrass as the feed base for most livestock farms. Microbiota have been demonstrated to be critically important for many soil and plant functions, but the communities associated with perennial ryegrass in NZ are largely unknown. This study aimed to determine ryegrass microbiota across several farming sites (and soil types) and between plant and soil niches to determine to what extent they were drivers of community structure.

Method:

Forty plots of three-year-old perennial ryegrass plants were sampled from each of four sites across New Zealand. Samples were separated into below- (soil, rhizosphere soil, root) and above-ground (shoots and phyllosphere) niches (ie 800 subsamples). Microbial communities were determined by extracting DNA and analysing using 16S and ITS MiSeq amplicon sequencing.

Results:

Ryegrass bacterial alpha diversity was strongly influenced by niche with rhizosphere being the most and phyllosphere the least diverse. Site had a significant effect on bacterial alpha diversity only for bulk soil and shoots. Fungal alpha diversity was significantly driven by both niche and site with bulk soil and rhizosphere being more diverse than shoots. Both bacterial and fungal beta diversity showed a clear separation between below- and above-ground communities. There were few microbial taxa shared across sites and niches.

Conclusions:

This work is a first step in understanding the below- and above-ground microbial diversity of an important forage grass in NZ. It opens targeted approaches to manipulating microbiota for improved ryegrass persistence via plant breeding, microbial isolations, or soil amendments.

Microbes that Matter: Stable Isotope Probing of Active Soil Microbiomes Throughout the California Water Year

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Aim:

Soil microorganisms are frontline managers of the terrestrial carbon cycle and play key roles in soil carbon turnover and stabilization but water availability constrains the structure and function of soil microbial communities, and their impacts on soil C.

Method:

To understand how altered precipitation regimes in semi-arid systems affect the microbial ecophysiological traits associated with soil organic matter formation, we are using quantitative stable isotope probing (qSIP) to interrogate *Who is where?* and *What are they doing?* in wild soil communities collected during multiple points in the Mediterranean climate water-year, from sites with a range of soil moisture conditions.

Results:

Our SIP results indicate only a fraction of the microbial community is active at any moment or location. At the growing season start, the growing portion was 28%, 48% and 58% at wet, intermediate and dry sites. Taxonomic identity was a strong predictor of growth; a taxon's growth at one site predicted its growth at others. During plant growth, soils with restricted moisture had lower microbial growth rates, significantly fewer active taxa (particularly eukaryotes), less formation of new mineral-associated organic matter, and lower enzyme activity. During the 'wet-up' at the end of the summer drought, only 4% of the community was immediately active (but responsible for ~10% of ecosystem C mineralized) and viral-based bacterial mortality doubled in the 24 hours post rewetting.

Conclusions:

Together, these findings show how changes in the timing and amount of rainfall can modify microbial interactions and functions that shape C flow belowground.

Assessing the soil microbiome's role on soil health in the context of Napa Valley terroirs

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Aim:

Soil microorganisms are protagonists of essential soil processes for plant growth including nutrient cycling and carbon stabilization. However, we lack depth in understanding how soil microbial diversity could influence functions for building healthy soils. In recent interviews, wine grape growers expressed strong interest in learning about the soil microbiome diversity, especially about their role in vineyard soil health. With today's changing climate and all its associated challenges for sustainable agriculture like intense drought and rainfall events, growers are willing to adopt more sustainable management practices if practical information about soil microbial diversity is provided. Our study aims to evaluate how soil microbial diversity influences soil health indicators across different soil types of Napa Valley American Viticultural Areas.

Method:

Soils were sampled from 0-10 cm of depth from two locations, (vine row and interrow), across 32 red wine grape vineyards. The soil microbiome was assessed using 16S rRNA and ITS high throughput amplicon sequencing. Soil health indicators analyzed include soil mineralizable carbon (C), microbial biomass carbon, permanganate oxidizable C, aggregate stability, inorganic N, and potentially mineralizable N. Supplemental information about soil taxonomy was collected from the US Soil Web Survey.

Results:

We expect to see increased soil health values, especially for soil carbon indicators, in soils with higher soil microbial diversity.

Conclusions:

This project will help growers learn about their vineyards soil microbial diversity and its relevance for building healthy soils for wine-grape production.

Microbial diversity and soil quality across a range of cropping systems and soil texturesThomas Jeanne¹, Joël D'Astous-Pagé, Richard Hogue¹*Institut de Recherche et de Développement en Agroenvironnement, Québec, Canada***Aim:**

The microbiome composition and diversity are linked to the soil quality and reflect the effects of crop management in agricultural soils including the type of fertilization or the diversity of cultivated plants. Pedoclimatic properties are major drivers of soil microbiome diversity which limits the transfer of long-term experimental studies to producers' fields. It is important to document the notion of variability of soil microbial diversity to allow the development of new omics-based models to facilitate the monitoring of the impact of sustainable cropping systems on soil quality.

Method:

The soils of 1500 observed sites were characterized and categorized in terms of tillage, fertilization management and cropping system. We evaluated the prokaryotes and fungi diversity using MiSeq amplicon sequencing and assessed the diversity with the Shannon's index and weighted UniFrac distance. On a sub-sample of 12 sites, we determined the technical, spatial and temporal sources of variability in potato, field crops and grassland agricultural contexts.

Results:

A technical variability threshold was determined for Shannon index and weighted UniFrac distance for both prokaryotes and fungi. This variability threshold allowed to compare spatial and temporal variability and to observe a greater effect of the variability in grassland. Data from all sites made it possible to determine the influence of soil types, pedoclimatic conditions and cropping system on microbial diversity.

Conclusions:

The use of omics data at amplicon sequence variant, taxonomic and functional levels combined with the evaluation of several machine learning approaches will allow developing predictive models of soil quality.

Forest Restoration Treatments Alter Function and Community Composition of Soil Mesofauna and Fungi

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Aim:

Restoration of frequent-fire-adapted forests is a high priority for land managers in the western United States, but effects of restoration treatments on soil communities and their ecological functions remain largely unexamined. We aimed to illuminate responses of soil mesofauna and fungi to thinning and prescribed fire in a *Pinus ponderosa* forest and to untangle direct and indirect effects of these organisms on decomposition.

Method:

We used field mesocosms to manipulate soil mesofauna communities at the driplines of *P. ponderosa* trees in untreated and thinned/burned forest management units. Our mesocosms (N=96) were constructed to restrict the recolonization of defaunated soil according to animal size while minimizing treatment side effects. After two growing seasons, we measured mass loss of standard recalcitrant (wood) and labile (cellulose) substrates placed in the mesocosms and characterized mesofauna and fungal communities.

Results:

Five years post-fire, the management units hosted different fungal and mesofauna communities. Notably, ectomycorrhizal fungi were reduced in the thinned/burned unit. Structural equation models indicated that mesofauna had no direct effect on decomposition, consistent with reports from other moisture-limited systems. However, in the thinned/burned unit only, microarthropod abundance correlated positively with the ratio of ectomycorrhizal to saprotrophic fungi ($\lambda=0.35$), which correlated negatively with wood decomposition rate ($\lambda=0.53$)—consistent with the Gadgil effect.

Conclusions:

Forest restoration treatments can have lasting effects on soil fungi and their mesofauna consumers, with potential implications for biogeochemical cycling. Our results add to existing evidence that the Gadgil effect is dependent on both substrate recalcitrance and fungal community composition.

Analyzing the Fragility of Soil Microbial Biodiversity and Its Contributions to C and N Cycling

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Aim:

Even though the interactions among members of the soil microbiome, which include viruses, bacteria, archaea, fungi, and protists, are recognized as essential for ecosystem functioning, their responses to environmental change and resulting impacts on nutrient cycling are poorly understood. Here we will discuss the responses of microbial trophic interactions to soil degradation and how top-down control by protists and nematodes shape carbon and nitrogen availability.

Method:

Multi-marker metabarcoding, genome-resolved metagenomics, and network analyses were applied to analyze the responses of soil microbial biodiversity to soil retrogression. ¹³C-labeling field experiments coupled with quantitative isotope probing (qSIP) and laboratory trophic manipulation assays were used to study the contributions of protists and nematodes to the distribution of plant-derived C through the soil and to changes in N dynamics.

Results:

We show that soil biodiversity, community complexity, and metabolic potential decline with soil retrogression. Prokaryotic and micro-eukaryotic metagenome-assembled genomes allowed identifying putative key players and their genetic capacities for nutrient cycling. Our results also indicate that bacteria, fungi, protists, and nematodes follow different community assembly mechanisms across soil sites with different degrees of degradation. Finally, we also show that all of these microbial groups contribute to the distribution of plant-derived carbon and that the top-down control of protists and nematodes on prokaryotic communities increases ammonia oxidation and nitrogen availability.

Conclusions:

Our results show that soil microbial biodiversity and microbial trophic networks are susceptible to soil deterioration and provide proof of the critical contributions of protists and microfauna to shaping C and N availability.

Shining light on the belowground eukaryotes: an EU-wide metabarcoding analysis on environmental drivers

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Aim

Knowing the baseline of diversity is crucial for capturing the changes in diversity and prioritising conservation efforts. Since few large-scale studies exist for soil eukaryotes other than fungi, we assessed soil eukaryotes and their environmental drivers in an EU-wide study.

Method

We sequenced the 18S-rDNA gene for 787 samples across the European Union (EU). We assessed the effect of environmental variables (soil properties and climatic variables) on diversity of protists, fungi and soil fauna (split into micro-, meso- and macrofauna), and consider the ecosystem type (cropland, grassland and woodland), and biological activities (basal respiration, microbial biomass).

Results

We found edaphic properties to better predict α - and β -diversity compared to climatic variables. With the exception of macrofauna, α -diversity was significantly different between ecosystem types, with the highest diversity and richness found in croplands. Overall, environmental variables explained 6 (protists) to 34% (macrofauna) of the β -diversity and 2 (macrofauna) to 18% (fungi) of the α -diversity. Reasons for low macrofauna diversity and high data dispersion could be related to the small volume of soil analysed (0.2g per sample). We found diversity overlaps in taxa between ecosystem types (21-47%) which mirrored the gradual land use change from woodland over grassland to cropland that occurred in Europe over the last centuries.

Conclusions

We conclude that the higher diversity in croplands is the result of a legacy of dormant and dead organisms since their DNA can remain in soils over centuries. This study sets an important baseline for comparisons in monitoring activities and future conservation activities.

Plant diversity and drought effects on community composition of Cercozoa and Oomycota

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Aim: Due to climate change, European grasslands are increasingly affected by heavy droughts during summer. Drought is known to negatively affect ecosystem functioning. On the other hand, plant biodiversity is associated with increased ecosystem functioning. We investigated how plant species richness and drought treatment influenced the diversity of two protistan taxa, Cercozoa (Rhizaria) and Oomycota (Stramenopila), and whether increased plant diversity would lead to resistance against the drought effects. These two protistan groups are functionally diverse and include a wide range of plant parasites.

Method: The “Jena Experiment” is a long-term field experiment consisting of experimental plots with varying plant communities ranging from 1 to 60 species. In 2008, a sub-experiment was established that emulated repeated summer drought. On all plots, transparent roofs were installed for six weeks in summer from 2008 to 2016. Soil was sampled one year after the last drought period. Cercozoa and Oomycota were sequenced by amplicon sequencing (metabarcoding).

Results: Alpha diversity indices of Cercozoa decreased with increasing plant species richness and increased in the drought treatment. Diversity indices of Oomycota also decreased with increasing plant species richness but were unaffected by drought. These changes were mostly explained by changes in evenness. Both protistan community compositions were strongly influenced by plant species richness, but only the cercozoan community was significantly affected by drought. Overall, no buffering effect of plant diversity against drought was observed.

Conclusions: Our results indicate that ecosystems will be increasingly challenged by plant pathogens due to more frequent summer droughts and biodiversity loss.

Wide metatranscriptomic overview of seasonal changes in soil microbial food webs in the Alps

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In alpine zones, soil microbial diversity and activity are strongly dependent on the annual patterns of snowpack formation. It is under the insulating winter snowpack that a large and stable winter microbial community thrives, which is believed to die during thaw, when temperatures start fluctuating again. We investigated the dynamics of soil microbiomes along altitudinal gradients above the tree line in three mountains in the Swiss Alps by an unusually large-scale metatranscriptomics study covering the whole soil diversity. Soil sampling (160 samples in total) took place before, during and immediately after snowmelt, and later in summer. Also vegetation, and relevant edaphic and climatic parameters were recorded. We used Illumina Novaseq high-throughput sequencing of RNAs (metatranscriptomics) to assess the whole community composition, e.g. prokaryotes (Archaea, Bacteria) and eukaryotes (fungi, protists, nematodes, microarthropods). From the c. 400 million sequences obtained, we found an overall diversity differing from that usually retrieved using metabarcoding: Amoebozoa was the most abundant protistan lineage, followed by Rhizaria and Alveolata. We annotated functional traits to the taxonomic output, in particular feeding modes and living styles, to track soil food web dynamics. We found a superactive food web under snow that differed strikingly from summer communities, strong evidence for protists as major fungal consumers and myxobacteria being THE major bacterivores in microbial food webs.

Symbiotic Control of Canopy Dominance in Forests

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Aim:

Subtropical and tropical forests are some of the most species rich plant communities on Earth but are at risk from pressures of land-use. Tropical and sub-tropical forests in Asia often have a distinct structure whereby the canopy is dominated by a limited number of tree species that form symbioses with ectomycorrhizal fungi, and an understorey comprising many species of arbuscular mycorrhizal forming species. Here we explore how different types of mycorrhizal fungi, including the hyphal networks they form, in addition to root-pathogenic fungi shape the structure of sub-tropical and tropical forests.

Method:

We established field based and laboratory experiments to test how seedlings that form ectomycorrhizas and arbuscular mycorrhizas respond to different forms of phosphorus, and survive and grow in situations where the potential to form shared fungal networks with neighbouring adult plants was manipulated. We also measured the presence of pathogens on seedling roots.

Results:

We found that ectomycorrhizal plants have greater capacity to use organic forms of phosphorus than arbuscular mycorrhizal forming species, and the ability to form shared fungal networks also had greater positive effects on their growth.

Conclusions:

We propose that ectomycorrhizal trees a) gain greater benefit from integration into shared fungal networks in terms of survival and growth, b) have the capacity to acquire phosphorus from a range of compounds including organic forms not available to arbuscular mycorrhizal plants, c) gain protection from pathogens, and d) in reaching canopy dominance the superior photosynthetic capacity enforces processes highlighted (a-c) through provisioning carbon to ectomycorrhizal fungi.

Non-native earthworms improve diet quality and population size of a woodland salamander in Eastern Canada

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Aim:

Earthworms did not survive the Wisconsin glaciation period, which ended about 10,000 years ago. Consequently, all species currently found in Eastern Canada were introduced by European settlers over recent centuries. Studies show that non-native earthworms had substantial impacts on soil microbial communities, nutrient cycling and plant diversity. Less is known, however, about their impacts on higher faunal species. Here, we investigated the effects of non-native earthworms on *Plethodon cinereus*, a common woodland salamander. We hypothesized that earthworms could adversely affect *P. cinereus* by consuming the forest floor, thereby decreasing soil moisture and the abundance of native preys. On the other hand, earthworms could positively affect *P. cinereus* by providing refugia in their abandoned burrows as well as by being a nutritious novel prey.

Method:

In 2019, we installed 25 cover boards in 38 mature sugar maple (*Acer saccharum*) forests. Over the next two years, we visited each site on nine occasions to quantify earthworm and salamander populations, using hot mustard extractions and visible implant elastomers, respectively. At a subset of four sites (i.e., with and without earthworms) we determined salamander diets using gastric lavage techniques.

Results:

Forest floor depth decreased, whereas population density and body size of *P. cinereus* increased, with earthworm abundance. Earthworms composed most of the salamander diet at sites with high earthworm densities, volumetrically accounting for more than all other prey groups combined.

Conclusions:

Non-native earthworms improve diet quality and population size of *P. cinereus* in Eastern Canada, which may in turn affect above and belowground food webs.

Carbon Supply by Arbuscular Mycorrhizal Fungi Shapes the Hyphosphere Community

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Aim:

Arbuscular mycorrhizal fungi (AMF) consume up to 20% of plant photosynthetic carbon (C); transfer of this C into soil shapes the composition and function of AMF-associated microbial communities.

Method:

We used ¹³CO₂-labelled plants to track C from the host *Avena barbata*, a widespread annual grass, into the soil via *Rhizophagus intraradices* in two-chamber microcosms designed to isolate AMF in soil. Hyphosphere DNA was analysed by both amplicon sequencing and Stable Isotope Probing (SIP) metagenomics to identify metagenome assembled genomes (MAGs) that incorporated ¹³C.

Results:

After 6 weeks, we tracked AMF-¹³C flow into different fractions of soil, and found that a significant portion went into the heavy fraction (25%). Amplicon sequencing indicated that AMF significantly modified the soil prokaryote community, but not diversity; nineteen amplicon sequence variants (ASVs) significantly increased in the presence of AMF, including *Arthrobacter sp.*, *Caulobacter sp.*, *Rhizobium sp.*, *Dongia sp.*, and *Verrucomicrobia*. SIP-metagenomics of hyphosphere soil identified that the primary consumers of ¹³C imported via AMF hyphae were highly enriched (10-33 atom% ¹³C). Of the 212 ¹³C - MAGs, the taxa that assimilated the most ¹³C were from the phyla *Myxococcota*, *Fibrobacterota*, *Verrucomicrobiota*, and the ammonia oxidizing archaeon genus *Nitrososphaera*.

Conclusions:

AMF rapidly transported ¹³C into both soil organic matter pools and the microbial community. While amplicon-analyses yield a more representative fingerprint of the total soil community composition, SIP and metagenomics allow us to focus on the specific taxa that are beneficiaries of AMF-transported plant C and unravel the potential trophic interactions among these organisms.

Core microbial communities and their associations in sub-alpine *Pinus cembra* forests

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Aim: Soil is a complex ecosystem that harbours a wide range of microbial communities. These microbial communities affect soil functioning as well as nutrient turn-over and availability. Especially in high-altitude alpine regions, the microbial communities are quite diverse and dynamic, i.e., they likely follow a distinct seasonal pattern. However, there is limited knowledge on the latter. From core microbial communities, i.e., microbes that are present in multiple ecosystems across regions, and their associations and dynamics we can gain an understanding of the alpine soil ecosystem. Therefore, we studied the effect of seasonal dynamics and environmental factors on these microbial communities.

Method: We collected soil samples from 9 different locations (n > 180 soil samples) across high-altitude sub-alpine *Pinus cembra* forests in and around Tyrol in both, summer (snow-free) and winter (snow-covered). We then analysed the soil properties and identified the microbial communities and their core using Illumina sequencing. Using network inference tools, we identified microbial co-occurrences associated with the two different seasons.

Results: Our results demonstrate that different microbial communities reside under the snow cover compared to the snow-free period. Although the microbial composition varied among habitats, there was a large core community across regions, which revealed a range of cross-phyla and –kingdom interactions.

Conclusions: Our results emphasize the dynamics and specificities of high-altitude sub-alpine microbial communities. From their core, dynamics, and associations, we can gain an understanding of how the soil ecosystem deals with seasonal and climatic changes.

Root Exudation in Crops and Their Wild Relatives

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Aim:

Crops and wild plants are known to differ in many aboveground traits, but the effect of domestication on roots is far less well studied. Root exudates are involved in many interactions with the abiotic and biotic components of the soil, and investment in root exudation is predicted to be lower in crops due to a trade-off with maximising yield. The aim of this study was to investigate the composition and quantity of root exudates in crops and their wild relatives.

Method:

We set up a greenhouse experiment with 20 species, including 10 crops and their 10 respective wild relatives. Plants were grown individually until maturity, when they were removed from the soil, roots were cleaned, and then placed in aqueous solution to collect exudates. Exudate composition was measured with non-targeted metabolomics analysis and exudate quantity was measured as total organic carbon.

Results:

We will discuss if there is an overall domestication effect on exudate composition and quantity, or if different crops respond in diverse ways. It will be of particular interest to see if compounds involved in increasing nutrient availability in the soil are less prevalent in crops.

Conclusions:

Our results will be discussed in the context of searching for new beneficial traits in crop relatives that could improve the sustainability of agricultural systems. Knowledge about root exudates that interact with soil nutrients could lead to lower fertilizer use in the future.

Co-cultivation of Mortierellaceae with *Pseudomonas helmanticensis* affects both their growth and volatilome

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Aim: Volatile organic compounds (VOCs) might mediate microbial interactions, especially in spatially structured environments, such as soil. However, the variety and specificity of volatilomes, i.e. all VOCs produced, are poorly understood. Here, we investigated a potential phylogenetically conserved relation of both, growth behaviour, and volatilome of different soil fungi during fungal-bacterial-interactions, which these soil fungi might naturally encounter.

Method: We studied 25 Mortierellaceae strains belonging to the widespread genera *Linnemannia* and *Entomortierella* in both pure and co-culture with the ubiquitous soil bacterium *Pseudomonas helmanticensis* under laboratory conditions. We analysed both, the fungal growth depending on co-cultivation, and the cultures' volatilomes, applying proton-transfer-reaction time-of-flight and gas chromatography-mass spectrometry (PTR-ToF-MS and GC-MS).

Results: In a strain-specific manner, we found the fungi's radial growth rate, biomass production, and colony morphology to be affected by the presence of *P. helmanticensis*. The fungus seemed to generally reduce the bacterial growth. The volatilomes of the fungal and bacterial pure and co-cultures were diverse. While the fungi frequently consumed VOCs, *P. helmanticensis* produced a higher diversity and amount of VOCs than any fungal strain. Our results support that both, the pure and co-culture volatilomes are taxonomically conserved. Moreover, the changes in volatilomes induced by the co-cultivation of *P. helmanticensis* were correlated to the corresponding changes in growth behaviour.

Conclusions: Taken together, our data support the relevance of VOCs in Mortierellaceae-*P. helmanticensis* interaction. We also discuss individual VOCs that appear relevant in the interaction.

Fungal-bacterial interactions in glacier forefields around the world

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Aim:

Bacterial-fungal interactions in recently deglaciated ecosystems promote biogeochemical cycles, mineral soil fertility, and pioneer plant growth, but the diversity of keystone microbes and the quality of their interactions remain largely unexplored. Here, we investigated the diversity of both fungal and bacterial communities to predict core microbial networks and to estimate conserved interactions across comparable deglaciated systems.

Method:

We studied the soil fungal and bacterial communities at the early stages of soil development (0-25 years) in four receding calcareous glaciers of the Alps (>200 samples). High-resolution marker-gene (16S and ITS) analysis were performed alongside detailed soil geochemical analysis. Furthermore, we included 13 datasets from publicly available projects on forefields of receding glaciers (world-wide) whose sequencing libraries resembled the criteria of our own dataset. Network analysis (FlashWeave) was performed for each dataset. Then, core microbial interactions were identified across glacier forefields.

Results:

Bacterial and fungal communities differed in a location-specific manner, sharing remarkably few common taxa. We found extremely dense networks in all locations, with fungi clearly dominating the keystone nodes for all major interactive clusters. We speculate that conserved interactions across glacier forefields are rather based on trophic preferences than on phylogenetic diversity.

Conclusions:

Our data emphasize (i) the unique diversity of soil microbial communities in glacier forefields likely depending on stochastic processes of dispersion, but provide (ii) evidence for common ecological roles based on conserved microbial interactions.

A report of *Haplotaxis gordioides* from subsoil and first analysis of its trophic position

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Aim:

Haplotaxis is an enigmatic genus of annelid worms. While it has a cosmopolitan distribution, it is only sporadically recorded and it is believed to be predatory. There also is a debate reaching back more than 150 years of whether these worms are aquatic or terrestrial. The aim of this study was to report the discovery of *Haplotaxis* specimens from a terrestrial subsoil and to test its trophic position.

Method:

Deep soil pits (0–60 cm) were excavated manually in a dry agricultural meadow soil in the Pieniny Spiskie region, southern Poland. Soil samples were collected in layers from 0–60 cm, and soil properties were measured (pH, texture, organic C, total N). *Haplotaxis* sp. and Lumbricidae were collected manually, while other soil fauna (including Enchytraeidae) were extracted with suitable laboratory methods. Freeze-dried animals were analysed by stable isotope ratio mass spectrometry.

Results:

During two sampling campaigns in spring and autumn 2022, *Haplotaxis* sp. were recorded at about 60 cm depth in mineral soil layers of this Luvisol. Based on existing keys, the worms were identified as *Haplotaxis gordioides* (they were donated for DNA based analysis and an ongoing taxonomic revision of the Haplotaxidae). C and N stable isotope compositions will be used, for the first time, to compare the presumed predatory trophic position of *Haplotaxis* sp. with that of co-existing detritivorous worms.

Conclusions:

This paper presents a new, fully documented record of *Haplotaxis* sp. from subsoil layers of a terrestrial mineral soil, plus isotopic comparisons with other oligochaetes.

How applied reclamation treatment affects soil fauna in the novel ecosystem

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Aim:

What is the relationship between the applied reclamation treatments, plant cover and soil fauna in novel ecosystems?

Method:

The research was carried out on a mining spoil heap in Upper Silesia, Poland. Studies were conducted on two types of materials bare rock (BR) and topsoil (TS) that covered BR during the reclamation. Four variants were investigated: natural forest regeneration, i.e. succession on BR (Succession_BR) and TS (Succession_TS), afforestation (Reclamation_TS) and afforestation with *Robinia pseudoacacia* (Robinia_TS). Basic soil properties such as pH, soil organic carbon (SOC), total nitrogen (TN) content, and soil texture were measured in 0-10 cm layers. Earthworms were collected using the hand sorting method, and enchytraeids were collected using wet extraction with the heating method.

Results:

The investigated soil had a varied pH from 5.3 in a Succession_BR to 7.2 in Robinia_TS. The highest content of SOC and TN was in Succession_BR, and the lowest was in Succession_TS. Enchytraeids density was in the following increasing order 275, 2982, 3001 and 4548 ind m⁻² for Succession_BR, Robinia_TS, Succession_TS and Reclamation_TS, respectively. Earthworms' density ranged from 0 ind. m⁻² in the Succession_BR through 109 ind m⁻² and 134 ind m⁻² in Reclamation_TS and Succession_TS, respectively up to 178 ind m⁻² in the Robinia_TS.

Conclusions:

Investigated soil fauna was positively related to pH value and clay content. The most stimulating variant for the development of earthworms and enchytraeids was the topsoil application and afforestation.

This study was financed by the National Science Centre, Poland (Grant No. 2020/39/B/ST10/00862).

Microbial Community Composition Impacted by Land Use Along a Precipitation Gradient of the Central USA

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Land use (LU) change from native prairie to agriculture has modified the original soil carbon and microbial community composition. Many studies have focus on the changes of soil microbial community on the topsoil, however, few have addressed the association between soil carbon and microbiome at deeper layers. Eight native and eight agriculture sites were sampled across a long-term gradient of precipitation ranging from 455 mm yr⁻¹ to 1040 mm yr⁻¹ in the central Great Plains, USA. The LU change from native to agriculture affected the soil carbon and nitrogen content up to a depth of 75 cm, but the mean annual precipitation at deeper layers (75-120 cm). Soil carbon and nitrogen were greater in the native prairie than in agriculture site. Overall, soil carbon decreased with MAP at 75-120 cm. The microbial biomass, gram +, gram -, actinomycetes, AMF and fungi were greater at native prairie than in agriculture, but just gram – and fungi: bacteria ratio were affected by MAP at 75-120 cm. In general, strong LU effects of both the SOC, total N, and soil microbial community composition and the lesser impact of the MAP on soil microbial community composition were observed. The soil microbial community composition also responded strongly to LU in deep soil.

Role of small RNAs in Plant-Associated Bacteria, *Azospirillum brasilense* under Abiotic Stress Conditions

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Background:

For a long time, RNA was considered to be important as an information carrying intermediate between DNA and the proteins, and as transfer and ribosomal RNA involved in protein synthesis, but not to have any regulatory function. This view has changed dramatically in the last couple of decades. Today, we know that RNAs can carry out many functions in the cell, such as catalysis and gene regulation. In eukaryotes, processes such as gene silencing and developmental regulation, all largely depend on such regulatory RNAs. Bacterial regulatory RNAs were identified prior to their eukaryotic counterparts in *Escherichia coli*. This opened up a whole new field; that of small RNAs (sRNAs) in bacteria. Most sRNAs base pair to the mRNAs to affect its translation and/or stability. Now it appears that the majority of the sRNAs are stress-related, helping bacteria to respond to changes in the environment. Different studies have been carried out to discover small RNAs in plant associated bacteria (PAB) and have shown to play essential roles under abiotic stress conditions like iron limitation, oxidative and salt stress, heat and cold shock, and accumulation of glucose-phosphate.

We have undertaken a study to explore the presence of sRNAs in selected PAB, *Azospirillum brasilense* Sp245 and the differential expression of the identified sRNAs in abiotic stress. Their role in plant growth promotion has also been explored.

Results and Conclusion:

In our study, expression-based sRNA identification (RNA-seq) revealed the first list of ~ 468 sRNA candidate genes in *A. brasilense* Sp245 that were differentially expressed in nitrogen starvation versus non-starved (control) conditions. Altogether, putative candidates were stringently curated from RNA-seq data based on known sRNA parameters (size, location, secondary structure, and abundance). In total, ~ 59 significantly expressed sRNAs were identified in this study of which 53 are potentially novel sRNAs as they have no Rfam and BSRD homologs. Sixteen sRNAs were randomly selected and validated for differential expression, which largely was found to be in congruence with the RNA-seq data. In parallel, *in silico* tools also identified two of the above as candidate sRNAs, sSp_p4 and sSp_p6, which were further selected for their functional characterization.

Plant microbe interactions are generally not an outcome of standard gene interactions but are usually a part of a multigenic response involving a multitude of sRNAs and their associated mRNA targets. Target gene expression analysis of sSp_p4 confirmed that it influenced gene regulation and plant growth-promoting traits such as poly-hydroxybutyrate synthesis, indole acetic acid production, and biofilm formation. sSp_p4 was overexpressed, knocked-down and complemented to characterize its physiological functions, and importance in plant growth-promoting traits. Its expression in wild type and mutant strains studied in different nutrient conditions revealed variable regulation of different targets. sSp_p6 expression was found to be modulated in carbon and nitrogen stress while forming an interactive network with the target genes, *vnfG* (encoding vanadium-dinitrogenase) and σ -54 (sigma factor, interaction region) thereby establishing an essential role of this sRNA in biological nitrogen fixation by the strain. Additionally, plant-microbe interaction studies between the host plant, sorghum and sRNA mutant strains, revealed increased

root length, lateral root growth and germination rate of the host plant, thus displaying improved plant root morphology.

This study established the *A. brasilense* Sp245 sRNAs, sSp_p4 and sSp_p6 as the potential candidates for improving abiotic stress enduring capability in this strain. Since this bacterial strain is plant-growth promoting in nature, the modulation of the identified sRNAs will help improve the PGP potential of the strain by its improved stress response and eventually contribute to sustainable agriculture. With the change in the global climate, it is presumed that the existing abiotic stresses faced by the plants will increase many folds and cause the development of complex environments such as extreme temperatures, draught, salinity, accumulation of toxic compounds in the soil, hypoxia, and exposure to UV and eventually cause substantial crop damage. The microbial communities inhabiting the plant rhizosphere are known to aid plant survival and their ability to withstand environmental stress attacks.

The 'other' mycorrhizas: Mucoromycotina 'fine root endophytes' form functional mycorrhizal associations with flowering plants

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Aim:

The majority of land plants form mycorrhizal associations with certain groups of soil fungi. Through these partnerships, photosynthetically-fixed carbon is transferred from the plant host to the fungus in return for fungal-acquired nutrients. Recently, it was shown that the fungal associates of plant roots are more diverse than assumed, extending to Mucoromycotina fungi previously identified as 'fine root endophytes'. These Mucoromycotina 'fine root endophytes' (MFRE) are widespread, spanning a variety of habitats and plant hosts. MFRE generally co-colonise plant roots together with Glomeromycotina arbuscular mycorrhizal fungi (AMF). Until now, co-colonisation with AMF and reliance on non-sterile, soil-based experimental systems has hindered direct determination of the function of the MFRE symbiosis.

Method:

To overcome this major barrier, we developed new techniques for fungal isolation and culture and established the first monoxenic *in vitro* cultures of MFRE, isolated from a lycophyte, colonising a flowering plant - white clover. Using radio- and stable-isotope tracers in these *in vitro* systems, we measured transfer of ³³P, ¹⁵N and ¹⁴C between MFRE hyphae and the host plant.

Results:

Our results provide the first unequivocal evidence that MFRE fungi form nutritional mutualisms in a flowering plant by showing that clover gained both ¹⁵N and ³³P tracers directly from the fungus in exchange for plant-fixed C in the absence of other microorganisms.

Conclusions:

Our findings and methods pave the way for a new era in mycorrhizal research, firmly establishing Mucoromycotina 'fine root endophytes' as both mycorrhizal and functionally important in terrestrial ecosystems.

A field exclusion experiment to assess the role of soil fauna in microbial community assembly

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Aim: While a large body of research showed how plants are affecting microbial communities, less attention has been given to microbe-fauna interactions. We aim at determining how interactions with the micro- and mesofauna influence bacterial and fungal community assembly.

Method: We used exclusion microcosms with windows covered with mesh of different pore sizes (31, 50, 100, 250, 500, 1000 µm) and filled up with sterilized soil. Microcosms were buried in grassland soil following a randomized design across adjacent blocks and harvested after 3, 9 and 12 months. Bacterial, fungal and faunal community composition in the exclusion microcosms was monitored using high-throughput sequencing of the 16S and 18S rRNA genes.

Results: Bacterial, fungal and faunal phylogenetic diversity (PD), species richness and evenness (Pielou index) increased and stabilized after 9 months. In comparison to the initial colonization of the sterile soil, effects of mesh exclusion treatment were more pronounced for microcosms with mesh pore size lower than 1000 µm after stabilization of the communities (9 months). We found that mesh exclusion mostly increased the relative abundance of OTUs belonging to protists, while the opposite was observed for bacterial and fungal OTUs. Network inference revealed that more than 90% of mesh-specific negative links involving Cercozoa were connected to bacteria from the *Bacteroidetes* phylum.

Conclusions: Altogether these findings provide important insights on how the soil fauna is shaping microbial community assembly in a grassland field.

Ungulate effects on root fungi community at Mediterranean montane areas.

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Aim: The ability of herbivores to alter the microbial communities of the soil and rhizosphere has been the subject of study in recent decades. The ungulates can modify the fungi associated with the roots directly by the consumption of plants, or indirectly by changing the soil physical and chemical characteristics. In several areas of Spain, there is a high density of red deer that has led to the construction of exclosures that allow the development of vegetation.

Method: In this study, the community of fungi associated with roots of plants with different palatability has been analysed by Next Generation Sequencing, comparing areas excluded from livestock for a long time (15 years), areas with controlled densities for 3 months and free grazing areas at three different vegetation types. Sequences obtained from Illumina amplification of root DNA from the ITS regions were used to calculate alpha diversity index and beta diversity was analyzed by nonmetric multidimensional scaling (nMDS) method.

Results: No effects were found on alpha diversity. However, the long-term exclosures presented more obvious differences in their fungi composition. Interestingly, three months under various grazing regimes are sufficient to affect the fungal communities of the root, for both highly consumed species and less palatable species.

Conclusions: Ungulates have a strong impact on the composition of the fungal community associated with plant roots in Mediterranean ecosystems. Short periods of intense grazing are enough to affect the community of rhizosphere fungi.

Functional significance of Mucoromycotina ‘fine root endophyte’ fungi in plant nitrogen nutrition

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Mucoromycotina ‘fine root endophytes’ (MFRE) are widespread mutualistic fungal symbionts of plant species. MFRE fungi facilitate host plant N acquisition from soil, but their capability to access diverse sources of N remains unresolved. Similarly, the ‘costs’ to plants of hosting MFRE in terms of photosynthetically-fixed carbon are also unknown. Using stable- (¹⁵N) and radioisotope tracers (¹⁴C) we investigated the capacity and preference of MFRE in accessing, assimilating and transferring ¹⁵N to their host plant, *Plantago lanceolata*, across a range of organic and inorganic N sources. Initially, an axenic compartmentalised fungal ‘choice’ microcosm, was used to investigate the symbiosis in the absence of confounding microbes. We found significantly more glycine was transferred to host plants than all other N sources trialled in return for greater 14C allocation than fungi treated with inorganic N sources received.

We used the same isotope tracers in non-sterile, soil-based experimental systems to investigate the effect of a soil microbiome on C-for-nutrient exchanges between MFRE and *P. lanceolata* across the same range of ¹⁵N sources as our previous experiment. We found that symbiotic transfer of 15N to host plants does occur in soil systems. Our research provides new insights into the importance of diverse soil fungal symbionts in plant nutrition, defining a new role for MFRE in accessing and assimilating soil N by plants.

Revisiting microbial soil DNA pools and reevaluating the stories told

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Aim: The soil microbial metagenome is defined as the totality of the microbial genomes, or as the entire microbial genetic material recovered from soil samples. This total soil DNA pool (totDNA) is composed of its intracellular (iDNA) and extracellular fraction (exDNA) - actively or passively released into the environment. exDNA can be further divided into free DNA, and DNA that is weakly or tightly bound onto organic or mineral soil particles. Routine approaches based on totDNA are potentially biased by a masking of iDNA by exDNA, affecting the gathered information on current microbiome composition and activity.

Method: Here, we sequentially extracted all aforementioned DNA fractions (differently strong bound exDNA vs. iDNA) from three different soil types with varying physico-chemical characteristics and performed a comparative analysis with the directly extracted totDNA. We applied high throughput NGS on all DNA types (exDNA vs. iDNA vs. totDNA) and correlated the respective results with RNA-cDNA-based and dehydrogenase-based microbial activity proxies.

Results: DNA types varied in their quantity and molecular weight, with totDNA and iDNA achieving the highest yields, and the exDNA fractions the lowest. Nonetheless, the exDNA fractions make up a quantitatively and qualitatively important part of the soil totDNA that might blur the information derived from iDNA.

Conclusions: Our findings will add to the correct interpretation and understanding of results from previous and future microbial community studies.

Plant-Parasitic Nematode Infection Impacts The Quality And Quantity Of Plant-Carbon Exchanged With Arbuscular Mycorrhizal Fungi

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Aim:

Plants interact with many biotrophic symbionts simultaneously, from mutualistic arbuscular mycorrhizal fungi (AMF) to parasitic potato cyst nematodes (PCN). As obligate biotrophs, AMF rely exclusively on their hosts for carbon in the form of carbohydrates and lipids. The impact of competing symbionts on the regulation of carbon transfer from plant to AMF is unknown.

Method:

We examined the movement of host-fixed carbon resources to AMF symbionts of potato with concurrent PCN infection, using a combination of radioisotope labelling, LC-MS and transcriptomics.

Results:

We found that host resources were partitioned towards AMF-colonised, rather than PCN-infected root tissues of the same plant. However, PCN infection disrupted movement of recently-fixed carbon from plant roots to AMF, with AMF-colonised roots withholding recent photosynthate rather than deliver to their beneficial fungal partners. LC-MS revealed that when PCN infected an AMF-colonised host, the delivery of monosaccharide-based carbon to their fungal partners was dramatically reduced, whilst delivery of carbon as fatty acids was maintained. Transcriptomic analysis indicates that differential delivery of carbon resources to AMF is potentially plant-led rather than AMF-regulated.

Conclusions:

When roots are concurrently parasitised by nematodes the supply of monosaccharides to AMF is dramatically reduced yet lipid delivery is maintained. This may have evolved as a potential mechanism for the host to promote beneficial symbiosis by supplying specific compounds to specific regions of the root system where benefit is perceived. Assessment of AMF function alongside additional soil organisms is vital to effectively determine their role in plant and soil community structure and function.

Impact of Potato Cyst Nematodes on the Function of Mycorrhizal Networks

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Aim:

Plants typically interact with multiple, co-occurring symbionts, including arbuscular mycorrhizal fungi (AMF) which can connect plant neighbours via hyphal networks. The most studied aspect of plant symbioses with AMF is the exchange of plant carbon-for-fungal-derived nutrients, with recent findings suggesting that the presence of competing organisms such as aphids or potato-cyst nematodes (PCN) can disrupt this exchange. However, the role of mycorrhizal networks connecting multiple host plants, alongside additional competing organisms remains unknown.

Method:

We grew two neighbouring plants in the same container pot, separated by a root-excluding mesh which allowed AMF hyphae to grow through. All plants were inoculated with AMF, but not all were infected with PCN. We employed established isotope tracing techniques to track ³³P allocation from the fungus to the plant and ¹⁴C from the plant to the fungus.

Results:

In the treatment where one plant was infected with PCN, but its neighbouring plant was not, we found evidence of preferential allocation of ³³P to the PCN-free plant. Conversely, plant carbon provision to the fungus did not differ between the treatments, suggesting there was no preferential allocation to particular symbionts by the plants in any of our experiments.

Conclusions:

Our work suggests common mycorrhizal networks may be important in mediating multi-symbiont interactions in plant-soil systems. Our findings highlight the importance of employing experimental designs of increasing ecological relevance to more fully understand the carbon-for-nutrient dynamics in AMF-plant networks.

Weak Effects of Long-term P Fertilization on Soil Nematodes in Agricultural Soils from France

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Aim: Soil nematodes are key components of the soil food web and play major functions at the soil-plant interface. They are known to be affected by phosphorus (P) supply, and that this impact is dependent to soil texture. While most of the studies investigated the short-term responses, here we aimed at characterizing the long-term effects (more than 30 years) of soil nematode communities to P fertilization.

Method: We studied the soil nematode communities from soil samples collected along two long-term P-fertilization trials in southern France. Both field trials showed contrasting soil types (i.e. sandy and clay-loamy texture) which will allow us to evaluate nematode response according to soil texture.

Results: The abundance and alpha diversity of soil nematodes exhibited weak and insignificant responses to P treatments in both field experiments. Similarly, the nematode indices (Maturity Index, Enrichment and Structure indices) did not vary significantly among the P treatments. We plan to analyze nematode functional traits (e.g., mass, P content) to account for other important nematode metrics.

Conclusions: Our results show that, irrespective to soil texture, soil nematodes are highly resilient against P addition at least at the community level. However, further deeper analyses based on traits are required to validate this statement.

Grassland Degradation-Induced Declines in Soil Fungal Complexity Reduce Fungal Community Stability and Ecosystem Multifunctionality

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Aim:

Soil microorganisms are major regulators of ecosystem functioning and are under threat from human-induced disturbances. Among these threats is grassland degradation, which is estimated to affect 49% of the grassland area worldwide, threatening biodiversity and ecosystem functioning. We aimed to test how grassland degradation influences belowground microbial communities, their stability, and functioning, and how effective restoration efforts are for the recovery of these important belowground properties.

Method:

We assessed soil fungal network complexity and a suite of ecosystem functions along a well-characterised gradient of grassland degradation and restoration on the Qinghai-Tibetan Plateau, and conducted an accompanying microcosm experiment designed to test the effects of complexity on stability in soil fungal communities.

Results:

We found that with increasing levels of grassland degradation, soil fungal communities became less complex and were less compositionally stable when confronted with drought under laboratory conditions. Moreover, this degradation-induced reduction in fungal community complexity was associated with lower ecosystem multifunctionality. However, fungal communities and ecosystem multifunctionality failed to recover even after ten years of grassland restoration.

Conclusions:

Our results indicate that degradation-induced simplification of fungal communities can impair fungal community stability and ecosystem multifunctionality, thereby highlighting the need to protect and restore healthy grasslands with complex belowground microbial communities.

Evidence of ecological critical slowing-down in temperate soils

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Aim:

The resilience of ecological systems is crucially important, particularly in the context of climate change. We present experimental evidence of critical slowing-down arising from perturbation of a key function in a complex ecosystem, using a basic soil biological function (respiration) as an exemplar.

Method:

Soils collected from across England and Wales were exposed to multiple drying:rewetting cycles and respiration measured continuously during the wet stages. Data was analysed to look for changes in variance and autocorrelation over 4 cycles. These metrics were used to classify soils into different functional behaviours which were then compared to covariates to understand drivers of resilience and map these at a national scale.

Results:

We found soils that could be classified as adaptive, resilient, fragile or non-resilient. The latter involved increasing erratic behaviour (i.e. increasing variance), and the propagation of such behaviour (i.e. autocorrelation), this was interpreted as a critical slowing-down of the observed function. Soil microbial phenotype and land-use were predominantly related to variance and autocorrelation respectively. No relationship was found between biodiversity and resilience, but the ability of a community to be compositionally flexible rather than biodiversity *per se* appeared to be key to retaining system function.

Conclusions:

Some soils from England and Wales have low levels of resilience to D:RW cycles, and that yet more have potential to lose resilience when challenged by climate change. If this is true of English and Welsh soils it will also likely be the case for other soils in other temperate regions, especially those under intensive management.

Contribution of forest fungi to fungal necromass decomposition and soil carbon storage

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Aim: In forests, a large part of the carbon from plant organic matter is incorporated into the microorganisms responsible for its decomposition, in particular fungi. These fungi produce a necromass corresponding to a large stock of C in the soil. Our aim is to contribute to the characterization of the microorganisms involved in the decomposition of fungal necromass and to assess the impact of forest management on the functional diversity of fungi in terms of input or export of carbon in soils.

Method: Through different tools (metabarcoding, transcriptomic, isotopic and enzymatic approaches), we will shed new light on the potential role of fungi, in particular ectomycorrhizal (EcM) fungi, in the decomposition of fungal necromass in soil forest.

Results: Through different experiments, we revealed that some EcM species had high nitrogen mobilization capacities from exogenous fungal chitin, providing evidence that EcM fungi can efficiently i) degrade fungal necromass, and ii) transfer organic N to their host plant. In this communication, we will also illustrate the consequences of massive forest biomass export on the diversity of microbial communities in soil forest and the associated functional changes. Following this forest management, we have highlighted differences in fungal decomposition dynamics related to changes in the structure of microbial communities (e.g. copiotrophic/oligotrophic bacteria ratio and EcM/saprotrophic fungi ratio), as well as to the chemical quality of the necromass (stoichiometric changes).

Conclusions: All these results reveal that soil fungi are central actors in the carbon input / output, or its stabilization, in the forest soil.

Describing Succession of Decomposer Fungi on Coarse Woody Debris in a Central European Virgin Forest

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Aim:

Species composition and interactions among species of decomposer fungi are constantly changing during sequential decomposition of wood. Succession is not unidimensional - after a particular decomposing species reaches its peak, it is not always replaced by the determined species. Instead, succession follows different decomposition pathways. The aim of this study was to describe the fungal succession in the decomposing wood in a virgin temperate forest (Rajehnavski Rog) in Slovenia.

Method:

Following a 6-class description of decomposition stages, samples from coarse woody debris (CWD) were collected from the first five stages. The wood dust was collected ex-situ and used for DNA extraction. Fungal ITS2 region was used for amplicon sequencing on Illumina MiSeq.

Results:

Early decomposition stages were characterized by a higher relative abundance of Basidiomycota compared to Ascomycota (average 62% in the first decomposition stage), while Ascomycota dominated in the later stages (average 93% in the last stage). While the genera *Aureobasidium* and *Purpureocillium* (Ascomycota), both common soil fungi, were present in all decomposition stages, genus *Bjerkandera* (Basidiomycota), comprising mainly white-rot species, was among the more dominant genera in the first decomposition stage. In the second and third decomposition stages, a greater relative abundance of the genus *Fomes* (Basidiomycota), which also consists of wood-decomposing fungi, was observed.

Conclusions:

Our results complement previous records and provide great insight into understanding the succession of fungal communities in decomposing wood and the limitations of different methods.

Do Soil Conservation Agriculture Permit Soil Biodiversity and Soil Properties Restoration. Results from Farm Network

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At farm scale, soil conservation agriculture includes several agricultural practices such as mechanical reduced soil disturbance, use of cover crops, long crop rotation and organic matter management. These systems are expected to be good alternatives to conventional systems which have led to a decrease of soil biodiversity and multi-functionality. Many studies worldwide have analyzed the impact of these systems on different soil properties, but most of them focusing on isolated properties (physical, biological or chemical properties). Moreover, many studies have used Long Term Experimental sites, where the effect on one or at least two practices (e.g. mechanical reduced disturbance, organic matter management) are assessed, while an integrated view of the impact of all practices applied under soil conservation agriculture is still lacking, especially in “real” life. One aim of SoilMan project (<https://ecobiosoil.univ-rennes1.fr>) was to study how soil conservation agriculture managed by farmers impact on soil biodiversity (earthworm community, microbial biomass), soil properties (aggregate stability, nutrient content, hypha length) and ecosystem services (water regulation, yield). Twelve fields managed by farmers and located in Brittany (France) were studied in 2018, allowing the comparison of direct seeding and conventional ploughing systems. The results highlighted that, despite the heterogeneity of soil texture, direct seeding systems positively impacted earthworm abundance, biomass and diversity as well as anecic abundance, and in a lesser extent epigieic and endogeic community ($p > 0.05$). These systems also improved microbial biomass, nitrogen and carbon rates in the first 10 centimeters of soil. They increased aggregate stability at both depths [0-10; 10-20cm] for the fast wetting and breakdown tests, linked to microbial biomass, carbon content, and length of hypha (for fast wetting). Despite an increase of hydraulic conductivity at the first 10 cm [0-10 cm] for -0.5hPa, no real effect was noticed for the water infiltration. Regarding provisioning service, wheat yields obtained in direct seeding systems were not lower than those under conventional ploughing system, demonstrating the capacity under direct seeding to maintain the yield. As a conclusion, direct seeding systems by improving several soil functions and by the way several ecosystem services such as soil biodiversity conservation, nutrient cycling and soil structure maintenance, provide resilience capacity of this agroecological system and resistance against soil erosion. Moreover, by maintaining yield, it reinforces the idea that these agroecological systems based on three major pillars (no mechanical disturbance, length and divers crop rotation, fertilisation) give a real opportunity for developing sustainable practices.

Soil Remediation Methods after Decades of Nitrogen Deposition

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Nutrient-poor sandy soils (mostly spodosols) are susceptible of acidification by atmospheric deposition. After decades of sulphate deposition, which declines now, deposition of oxidised and reduced nitrogen, however, continues. Next to an acidifying aspect, nitrogen deposition has also a nutrient unbalancing aspect, as N:P ratios increase. Traditional restoration methods such as sod-cutting on heathlands increase the N:P ratio even more, while the usual method to combat acidification, liming, binds phosphorus, resulting overall also in an increase of the N:P ratio. Currently, we are investigating new methods to overcome both the acidification effect as well as to restore a more balanced N:P ratio together. Rock dust application, especially those having a significant amount of apatite as P source, seems a good candidate in fulfilling above promises, as it has both the effect of pH increase as well as a slow-release of essential minerals which were leached in the acidification process in soil. Moreover, the apatite containing sorts can supply the limited amount of P in these soils. In a number of experiments we compared to addition of P, traditional liming and addition of various types of rock dust by measuring the abundance and diversity of soil microarthropods, all identified to the species level and grouped in life-history strategies, size-classes or feeding guilds. The results revealed significant increases of herbivores after P addition and like-wise declines after liming even on the long run. Rock dust application seems to fulfil both the promise of pH increase (depending on the given amount) as well some restoration of the nutrient balance. Long-term experiments, however, suffer from the continued N deposition, which let positive initial effects disappear again. Moreover, we discuss, the potential loss of species, essential in decomposition processes, during decades of unsuitable habitat and food provisioning, due to a lower abundance of especially mycorrhizal fungi.

COMPARATIVE GENOMICS and EVOLUTIONARY HISTORY of NOD GENES of 38 BRADYRHIZOBIUM STRAINS SYMBIONTS of LEGUMES

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The genus *Bradyrhizobium* stands out among the symbiotic N₂-fixing bacteria due to the high diversity and economic and environmental importance of its hosts in the Leguminosae family. The genomes of 38 *Bradyrhizobium* strains and isolated from soybean (*Glycine max*), lima bean (*Phaseolus lunatus*) and forage peanut (*Arachis pinto*) of different Brazilian biomes were sequenced for comparative genomic analysis and molecular phylogeny in comparison to the type strains of the already described species of the genus. Strains from each of the three legume species were assigned to clades with known *Bradyrhizobium* species as well as independent clades likely representing novel species. The similarity matrix based on the average nucleotide identity showed similar results to the phylogenetic tree constructed based on universal genes, and allowed the identification of three new species isolated from the forage peanut, a new species from the soybean and a new lima bean species. The phylogeny of each of the nodulation genes *nodA*, *nodB*, *nodC*, *nodD1*, *nodI*, *nodJ*, *nodN*, *nodZ* and *nodW* showed very similar topologies and all strains were grouped according to the host plants from which they were isolated. Besides, there was no apparent effect of geographic origin on the tree clustering patterns. Therefore, the strains showed a very similar evolutionary history based on whole-genome and nodulation genes, indicating limited horizontal transfer of the latter genes. Collectively, our analysis showed high diversity among *Bradyrhizobium* strains and species that are native to Brazilian soils and establish symbiosis with different species of native or exotic legumes.

What are the Key Drivers (Environmental and Anthropic Parameters) of Earthworm Community at Watershed Scale

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Soil biodiversity dynamic and spatial distribution are strongly influenced by anthropic parameters (land use, agricultural practices) and by environmental factors (pedological, climate contexts). Many researches have studied the drivers of earthworm community at fine scale (field) and by modelling have identified drivers at large scale (European, Global). However, there is still a lack about the drivers at medium scale such as watershed scale reflecting the heterogeneity of agricultural landscape, and models still need to be developed. In this context, SoilServ project (ANR project 16-CE32-0005-01) carried in Brittany (France), collected biological, environmental and agronomical data at watershed scale (5 km²) in order to identify which are the main drivers that affect earthworm distribution. In march 2018, 92 points were sampled at Kervidy-Naizin watershed which is part of ORE *AgrHys* supervised since 1993 by research institute INRAE and characterized by mixed crop-livestock farming systems. Earthworms were sampled by hand-sorting combined by AITC application. Earthworm communities were characterized the abundance, biomass, ecological diversity (epigeic, epi-anecic, strict anecic, endogeic) and species diversity. Moreover, each sampling point was characterized by i) soil properties (pH, C, N, P contents, texture, bulk density, hydromorphic state), ii) land use (crop, inter-crop, permanent or temporary meadow), and iii) agronomical past history since 2012 (crop rotation, ploughing actions, number of years of meadows). Different models (RandomForest, Gradient Boosting Trees, Cubist, Generalised linear mixed models) were applied and compared to test the relevance of the different drivers identified. The application of these different models provided robust results and permitted, at watershed scale, to i) reinforce the role played by pH and texture in earthworm spatial distribution, previously noticed at European scale, ii) highlight new key drivers (bulk density, hydromorphic state), iii) precise agricultural managements which affect biological distribution (land use, rotation), demonstrating the crucial importance of the field agronomical history. It appears that the knowledge of agronomical drivers (e.g. nb of years of meadow in crop rotation) is a real tool which could be addressed to farmers in order to maintain/improve earthworm community and associated ecosystem services at watershed scale.

Modest microturbellarians: revealing the undocumented biodiversity of limno-terrestrial Rhabdocoela in the British Isles

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Aim:

Most surveys of soil invertebrates focus on cuticle-bound organisms, but soils also contain soft-bodied organisms, dominant among which are the microturbellaria, free-living flatworms <2 mm in size. Their taxonomy is based principally on their internal reproductive organs, which are best studied in live specimens. This fact, and a difficult taxonomic literature, has discouraged research: most of the ca. 50 known species are type locality endemics. They are to date effectively unknown in the British Isles.

Method:

We have sampled throughout the UK, mostly centred in SE England and greater London, extracting meiofauna using a Whitehead-Hemming tray method. Live microturbellarians are isolated and vouchered with photomicrograph series. These specimens will be subjected to a bespoke transcriptome amplification method, producing pools of up to 96 libraries for sequencing using the latest nanopore chemistry, which we anticipate will yield 100s of high-confidence gene sequences which we intend to exploit for phylogenetic inference and multilocus species delimitation.

Results:

We have studied over 200 specimens, which fall into at least 35 provisional morphospecies, many likely new to science. The validity of these species, and the prevalence of cryptic species, will be tested using the aforementioned transcriptome-skimming protocol. This may be seen as a case study for an accessible, cost-effective protocol for multilocus DNA taxonomy, suitable for a wide variety of organismic groups.

Conclusions:

Microturbellarians are a ubiquitous but universally overlooked constituent of soil communities. Rarefaction curves suggest that considerable diversity still remains to be observed. We hope to highlight these organisms as worthy subjects for future research on fundamental, applied, and conservation biology.

Dispersal Patterns of Oribatid Mites Across Habitats and Seasons

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Aim:

To understand temporal and spatial shifts in biodiversity it is fundamental to investigate dispersal patterns and species' dispersal limitations structuring mesofauna communities. The aim of this study was to investigate the importance of oribatid mite dispersal using Malaise traps to exclude sole passive wind-dispersal. We hypothesized (1) that oribatid mite communities in the traps differ between habitats, indicating habitat-limited dispersal. Further, we hypothesized (2) that oribatid mite communities differ among seasons suggesting that dispersal varies due to changing environmental conditions.

Method:

Oribatid mite communities were collected over a three-year period from five different habitats (coniferous forests, deciduous forests, mixed forests, meadows, bog/heathlands sites) and three different seasons (spring, summer, autumn) across Sweden. Mites entered traps either by walking or by phoresy i.e., by being attached to flying insects.

Results:

The majority of the collected species were not typically soil-living species but rather from habitats such as trees, lichens and mosses. Oribatid mite communities differed significantly between forest habitats and bog/heathlands and meadows, i.e., species were restricted to their local habitats. Oribatid mite communities were further significantly different across all seasons.

Conclusions:

The predominance of not typically soil-living species indicates that walking into the traps or entering them via phoresy are of greater importance for aboveground than for soil-living species. Oribatid mite communities collected in the traps likely originated from the surrounding local habitat suggesting that long distance dispersal of oribatid mites is scarce. Significant differences among seasons indicate higher dispersal during warm and dry periods of the year.

A DNA barcode reference library for terrestrial enchytraeids in Europe

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We created a DNA barcode reference library for the majority of common European terrestrial enchytraeid species.

The library is result of the joint work of several authors and laboratories. Backbone is the Scandinavia Clitellate Library, established in the framework of National Taxonomy Initiatives of Sweden and Norway. It covers 2267 specimens in 322 species hypotheses with 2262 COI sequences, 1382 of 16S, 1087 of ITS, and 941 of H3. It is enriched by libraries of several hundred specimens stemming from other research projects at the European level (e.g., EcoFinders, SoilMan), apart from DNA sequences in the published databases. The specimens are from Sweden and 13 further European countries.

Animals were heat-extracted from soil samples and identified to species. DNA was extracted from the posterior half of each individual, the anterior half was maintained as voucher for further morphological studies. Cytochrome oxidase I (COI) was sequenced in all specimens, ITS I, ITS II, 16S and/or H3 only in a subset of them.

Tagging of names to sequences was not always straightforward, and thorough taxonomic work is ongoing, integrating new DNA-analytical methods and refined morphological investigations. Paramount is the anchorage of a sequence in an extant physical specimen. Especially challenging is the high number of new species, many of them cryptic. The most common nominal species, *Enchytraeus buchholzi*, is also the most diverse, with so far 26 species hypotheses. These species must be named, because only named species gain reality in biodiversity assessments.

From the Coast to the Andes; Analysing Pedology on Litter Decomposition and Soil Microbial Decomposers.

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Soil nutrient availability can regulate shifts in plant species distribution patterns often predicted by climate change models. However, soil nutrient availability can result from unbalanced rates of two ecological processes; litter production (and quality) and litter decomposition.

Therefore, a mechanistic understanding of decomposition processes is key to making predictions about future ecosystem dynamics. The inclusion of soil microbial decomposers is key if we aim to predict changes in soil nutrient availability, ecosystem processes (e.g. litter decomposition), and shifts in species distribution patterns. Accordingly, in this study, we evaluated the extent to which litter traits have regulatory controls on soil microbial communities, litter decomposition and potentially on soil nutrient availability.

For this, we established a longitudinal litter decomposition experiment using litter of 57 species collected across 28 sites across Chile's forest ecosystems. Forests on the Andes and the Coastal Range have contrasting soil nutrient availabilities (due to contrasting pedology) and share several dominant woody species. We quantified litter biomass loss, extracellular enzymatic activities, and soil microbial composition via analyses of fungal and bacterial groups (e.g. DNA extractions and analyses of 16s and ITS).

Our results show a strong effect of soil nutrient availability on litter decomposition, mainly via litter quality. This suggests that living leaf tissues can have an "after life" effect on decomposition processes. However, DNA analyses show that decomposers have high metabolic flexibility for degrading plant litter irrespective of its origin and that several plant species (or ecological strategies) select for microbial communities that preferentially decompose their own litter.

Fondecyt-Regular 1201643

Prairie restoration of marginal croplands does not increase diversity but shifts composition of soil microfauna

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Aim: Restoring native ecosystems in marginal lands of agricultural farms can recover biodiversity and the provision of ecosystem services. Whereas the effects of ecosystem restoration on aboveground diversity are well-known, effects on soil biota, particularly soil fauna, are less clear. Here, we studied how grassland prairie restoration of marginal croplands affects the diversity and composition of soil microfauna (protists, nematodes, tardigrades and rotifers).

Method: We analysed crop and neighbouring prairie sites in 5 productive farms from Ontario, Canada. In each site, we collected soil samples (0-15 cm) from 5 randomly selected quadrats. After DNA extraction, we carried out high-throughput sequencing targeting the 18S rRNA V4 region. Amplicon sequence variants (ASVs) were classified taxonomically using the PR² database and non-target reads were removed.

Results: Depending on the farm, prairie restoration decreased or did not affect microfaunal ASV alpha diversity. ASV community composition was affected by restoration, farm and their interaction. Communities were dominated by Nematoda and protists from Cercozoa, Chlorophyta and Conosa. Other less dominant taxa were Tardigrada and protists from Ciliophora, Lobosa, Apicomplexa and Pseudofungi. Among crop soils, coarser textures presented higher dominance of Chlorophyta and lower of Nematoda and Tardigrada. According to differential abundance analyses, prairie restoration reduced Conosa and Lobosa (Amoebozoa), Discoba (Excavata) and Filosa-Sarcomonadea (Rhizaria-Cercozoa). We will further explore how these changes in microfauna relate to microbial communities.

Conclusions: Even though prairie restoration did not recover soil microfaunal diversity, it caused marked shifts in community composition that could have functional implications, particularly for the soil food web.

Standard metadata collection and data sharing via the National Microbiome Data Collaborative

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Aim:

The microbiome is a critical component of soil biodiversity. Modern omics technologies allow us to assay multiple aspects of soil microbes, including their genome, the expression of gene products, and metabolite profiles, giving us an insight into species composition and interactions. When combined with other environmental and biodiversity data this is a powerful tool for understanding soil biodiversity and community dynamics. However, the size and complexity of the data produced presents huge challenges, particularly when it comes to integrating datasets together.

Method:

FAIR data principles, including the use of standardized metadata elements to describe soil characteristics and sample processing, as well as standard ontologies such as the Environment Ontology (ENVO) for soil types, are necessary to integrate these complex datasets. In this presentation we describe the National Microbiome Data Collaborative (NMDC), a collaborative effort to harness microbiome data in order to better understand the role of microbial communities in environmental systems such as soil. We describe our work in the context of the Genomics Standards Consortium (GSC) to harmonize soil data and metadata.

Results:

We invite discussion on how these standards can work hand in hand with broader FAIR data efforts in soil biodiversity, including standards like Taxonomic Databases Working Group (TDWG, Biodiversity Information Standards).

Conclusions:

This effort paired with community feedback will improve metadata capture, which in turn will elevate science and the elucidation of soil biogeochemistry and biodiversity.

Posters

Long-term effects of phytomanagement with *Populus sp.* on soil biodiversity

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Aim:

Soil metal contamination is a worldwide problem of great magnitude. Phytomanagement is based on the use of plants to reduce and control risks arising from soil pollution while at the same time restoring and generating other wider site services. The PHY2SUDOE project maintains a network of contaminated sites that have been under phytomanagement for many years in Portugal, Spain and France. The aim of this study was to evaluate the long-term effects of phytomanagement with *Populus sp.* on soil biodiversity and complexity at different levels of the trophic web.

Method:

Composite soil samples were taken in the contaminated sites ST Médard D'Eyrans (Gironde, FR), Chaban-Delmas (Gironde, FR), Borralha (Montalegre, PT), Ariñez (Vitoria-Gasteiz, ES) and Touro (Galicia, ES), both under phytomanagement and non-phytomanaged controls. Then, metabarcoding analyses of 16S rRNA, ITS, 18s rRNA y COI genes were carried out.

Results:

The diversity, composition and complexity of the soil prokaryotic, fungal and invertebrate communities were affected by the long-term phytomanagement practices. Site-specific soil characteristics also had a significant influence on the edaphic biota.

Conclusions:

Given the essential functions it performs in contaminated soils, phytomanagement practices should aim to restore soil biodiversity.

A Case Study on Restoring Soil Biodiversity: TalamhBeo's Soil Biodiversity Literacy and Enhancement EIP Project

Bridget Murphy¹,

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Aim:

This one-year project assess how farmers can successfully work towards soil biodiversity restoration themselves if they are given access to knowledge, equipment, scientific support, and each other.

Method:

The project was designed by farmers (a ground-up approach), led by farmers, and implemented by farmers, with support from a soil scientist.

16 Irish farms were selected, covering different land & soil types and condition, geographical locations and production systems. The farmers undertook a choice of educational courses, including a microscopy certification component. A series of online Knowledge Transfer meetings linked them to each other, and each farm hosted an event demonstrating their physical context and journey to soil biodiversity regeneration. The soil scientist delivered soil sampling and testing, and where farmers identified specific issues, she designed and assisted them running field trials.

Results:

The farmers can sample soil for chemical, physical and biological analysis, and physically identify soil for health. They can interpret the scientific data and decide how to implement the recommendations or experiment with amendments (eg bio-complete compost, inoculated biochar, compost teas) or innovations to remediate. They have a group to share and refine their experiences. The soil scientist has a list of research areas identified by need from the direct engagement.

Conclusions:

Empowering farmers with knowledge, tools and access to scientific support helps them to restore soil biodiversity and soil health. Topics requiring scientific research and support are identified by need.

Overcoming Linnean shortfall in soil biodiversity: the case of soldierless termites from the Amazon basin

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Aim:

This is an in-depth taxonomic study of soldierless termites (Apicotermatinae subfamily), to overcome the Linnean shortfall in this group. It was estimated the bias of undescribed species, as well as potential indicator species in Amazonian habitats.

Method:

Termite samples of the CATAC-SINCHI institute, Colombia, were examined. Samples were collected using transect protocol, active search, and TSBF monoliths in 171 localities from the Colombian Amazon, in seven natural and intervened habitats. Soldierless termites were identified based on enteric valve and gut morphology. Most effective method for soldierless termites according to their sampling effort were evaluated by rarefaction. Soldierless termite species as indicator species of one or more habitats were obtained using *IndVal* values.

Results:

From 4.089 termite samples revised, 992 were soldierless (25%). From them, 201 termite species were identified, being 54 soldierless (27%). From soldierless species, 29 were undescribed genera and/or species. Rarefaction curves confirmed that TSBF (46 species, 53% undescribed) is the best method for sampling soldierless termites and other soil-inhabiting termites, however, this implies a very high sampling effort. In contrast, the transect method (33 species, 48%, undescribed) is better when considering all termites species (no only soldierless). Analysing the *IndVal* results, 19 soldierless species were identified as indicator species for one or more habitats. From those, 10 species (53%) are still not yet described, and being found mainly as indicators of disturbed habitats.

Conclusions:

The unknown diversity of soldierless termites estimated by our study is high (54%), with 35% of these undescribed species being potential indicators of different habitats. This highlights the importance to study these species in soil ecology studies, where they are currently ignored. TSBF method captures a high soil fauna diversity of undescribed species in the Amazonian habitats, although the great sampling effort required.

The Importance of Soil Biodiversity in Sustainable Agriculture, Threats and Ways to Conserve it

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Soil biodiversity is the variety of life that exists within the soil, including bacteria, fungi, Earthworms and termites. We critically highlight some evidence for the importance of soil biodiversity and its Sustainable management to sustaining (agro-)ecosystem. Soil biodiversity plays a critical role for agriculture and food security through the services it Provides to the ecosystem. For example, microorganisms in the soil convert organic and inorganic compounds, releasing Nutrients that plants can feed on. These transformations are also necessary for the filtration And decomposition of pollutants in water and soil. There is evidence that soil microbial diversity confers protection against soil-borne disease, but crop and soil type and management also play a role. But human activities, climate change and natural disasters can threaten the important role of Soil biodiversity in ensuring sustainable agricultural food systems. The overuse and misuse of agrochemicals continues to be one of the main causes of soil Biodiversity loss, thus reducing soil biodiversity potential for sustainable agriculture and food Security. Preserving biodiversity requires many efforts, agricultural land degradation must stop so that Agriculture can protect and restore biodiversity within and around agricultural ecosystems. And organic Reducing the wasteful use of pesticides and chemical fertilizers because of its Negative impact on biodiversity loss . Environmental awareness and education may be among the important factors for the Protection of soil biodiversity, by teaching farmers to use clean agriculture or integrated Control methods to reduce pesticides and chemicals used and because of their harmful Impact On the environment and health.

Plant roots fuel tropical soil animal communities

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Belowground life is traditionally considered to rely on leaf litter as the main basal resource, whereas the importance of roots remains little understood, especially in the tropics. Here, we analysed the response of 30 taxonomic groups of soil animals to root trenching and litter removal in rainforest and plantations in Sumatra and found that roots are similarly important to soil fauna as litter. Trenching effects were stronger in soil than in litter with animal abundance being overall decreased by 42% in rainforest and by 30% in plantations. Litter removal little affected animals in soil, but decreased the total abundance by 60% both in rainforest and rubber plantations but not in oil palm plantations. Litter and root effects on faunal abundance were explained either by the body size or vertical distribution of specific animal groups. Our findings provides the basis for animal-cantered carbon modelling, ecosystem-friendly agricultural management, and conservation of soil animal biodiversity in the tropics.

Distribution of Major Plant Parasitic Nematodes Associated with Tree Fruits within Niagara/Southern Region of Canada

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Aim:

In Ontario, the fruit industry has a farm gate value of over \$225 million, with the Niagara region being the largest and most important fruit-growing area. Recently, fruit growers in the region are witnessing considerable yield losses and the death of fruit trees which necessitated the need for surveying for the presence of PPNs. Therefore, this study was conducted in year of 2019 and 2020 to determine the frequency of occurrence, prominent value (predominant species), and population density of plant-parasitic nematodes in selected fruit orchards.

Method:

Soil samples were collected from different orchards and extracted using sieving and decanting, followed by sugar centrifugal flotation method. Nematodes were morphologically and molecularly identified.

Results:

The survey revealed the presence of *Mesocriconema xenoplax*, *Pratylenchus penetrans*, *Paratylenchus* sp., *Tylenchorynchus* sp., and *Helicotylenchus* sp. The species *Mesocriconema xenoplax* was the most predominant species found across the fruit crops. 100 % of surveyed fruit orchards came positive with *Mesocriconema xenoplax*, where 83% had more than 200 nematodes per kg. For the first time, the genera *Paratylenchus* is reported from fruit trees as the second most predominant and abundant except in plums, where *Xiphinema americanum* was predominant and abundant.

Conclusions:

Our data indicate that the Niagara region is witnessing an increase in the population of plant-parasitic nematodes associated with fruit crops which requires attention. Generating awareness among growers about the presence of plant-parasitic nematodes in their orchards and potential yield loss due to this issue is ongoing.

Soil biodiversity and the regenerative farming movement in the UK

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Aim: Understanding UK farmers' perspective on soil biodiversity

There is an increasing interest in soil ecosystems in UK agriculture. A number of farming movements and groups has emerged around the concept of 'soil health', promoting methods such as regenerative agriculture. This paper present results of qualitative social science research with farmers in the UK which investigated, firstly, what soil health related land management practices are being taken up by farmers in the UK, and, secondly, how farmers understand and engage with the concept of soil ecosystems.

Method: Survey and interview data, UK farmers

The paper presents data collected through 1. semi-structured interviews with 35 farmers in the UK in 2017-2019, and 2. a survey of over 300 farmers in the UK conducted in 2019.

Results: A range of practices with no systemic focus; a desire to learn

The survey finds a wide uptake of soil health related land management practices in the UK. The practices are not, however, combined to achieve systemic outcomes. Interview data indicates that farmers in the UK have a strong interest in investigating soil ecosystems on their farms, and that they use a variety of information and advice to strengthen their understanding. However, there is a lack of place-specific support which would allow the farmers to achieve their learning objectives.

Conclusions: Mechanisms to enable greater collaboration between farming and research communities

In conclusions, I outline a multi-scalar platform for intensifying farmers' own research on soil ecosystems while connecting with scientific research on soil biodiversity.

Tillage Effects on Ground Beetles in Temperate Climates

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Aim: Ground beetles (carabids) constitute an important functional component of biodiversity in agroecosystems, mainly because of their role as predators of pests, but also as consumers of weed seeds and as prey to other organisms. Over the past few decades, there has been a marked and continuous decline of ground beetles in Europe, and many species of this insect family are threatened by intensive agricultural practices. The effect of soil tillage, a standard technique in arable farming, on carabids has been investigated in many experimental studies.

Method: review-study

Results: We show that the effects of intensive tillage on ground beetles—especially the use of mouldboard ploughing—are extremely variable. Nonetheless, on balance across multiple studies, greater tillage intensity tends to have a negative effect on abundance, species richness, and diversity. The observed variability may partly be attributed to a change in species-specific food availability or habitat conditions, induced by tillage. Tillage effects on dominant species tend to have a strong impact on total carabid abundance. The high variability of carabid responses to tillage is also a consequence of various modifying factors such as cover cropping, rotations, and variations in weed control associated with tillage.

Conclusions: Because different modes of tillage tend to affect different carabid species, the diversification of tillage operations within a farm or region may contribute to the overall diversity of carabid communities.

Organic matter additions to horticultural soils: Management for enhancing soil microbial functionRachel Hasler¹¹*Cranfield University, Machynlleth, United Kingdom*

The type of soil organic amendment selected for addition to soil can have profound implications for carbon cycling processes. Understanding the link between this choice and its effect on the soil microbiome will improve our understanding of the capacity of these materials to improve carbon sequestration and cycling dynamics. This research focused on utilising organic amendments to alter the indigenous soil microbial community composition and function to improve the capacity of the soil to cycle and store carbon in horticultural soils. The effects of the annual application of various organic fertilisers (peat, bracken, bark, horse manure, garden compost) in a long-term (10year) field experiment were explored. The response of soil microorganisms was assessed as microbial biomass, community composition (Phospholipid Fatty Acid profiles), arbuscular mycorrhizal fungi (neutral lipid biomarker 16:1 ω 5) and carbon functional cycling profiles (Multiple Substrate Induced Respiration: MSIR); carbon was also quantified as total and hot water extractable fractions. Microbial biomass measurements in soils amended with compost and horse manure were significantly higher in quantity and composition to all other treatments and the control. Peat provided the greatest shift of microbial community composition, bark increased the proportion of arbuscular mycorrhizal fungi. All treatments significantly differed to the control in an analysis of multiple substrate induced respiration. All treatments had a significant positive effect on hot water extractable carbon and total carbon. More targeted application of resources will reduce waste and ensure the legacy effects of organic matter applications are positive and support soil function.

Impact of subsoil warming due to electric transmission lines on soil organisms and their activity

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Aim:

In the future, electricity from wind power stations in the North Wadden Sea will be transported through Germany via 380 kV underground electric transmission lines (UTL) at a soil depth of 140cm.

Naturally, soil temperature decrease with depth in line with respective temperature amplitudes. During operation, UTL emit heat, thereby leading to temperature anomalies within the soil profile. The study's aim was to determine the impact of such operational subsoil warming on soil organisms, microbes and earthworms.

Method:

The impact of UTL on soil temperature and moisture was modelled for a variety of soils and evaluated against an existing UTL system. We determined soil microbial properties at various soil temperatures and investigated earthworm burrowing activity by use of 2D Evans' boxes of 160cm high.

Results:

Temperature increase through UTL operation relative to a control was on average 0.6, 1.1, 3.1 K in 30cm, 60cm and 140cm depth, respectively. As expected, microbial properties were subsequently slightly enhanced. No significant differences were found for earthworm numbers, biomass, and species composition. Results from Evans' boxes revealed that anecic earthworms reduced burrowing activity in heated subsoils (90 – 140cm) but increased their activity in the overlying soil. However, no difference in burrowing activity was found.

Conclusions:

Operational soil warming by underground electric transmission lines has no significant impact on soil micro-organisms and the earthworm community. Deep burrowing species, however, might be affected in their burrowing activity. An overall evaluation scheme for the impact of soil temperature on earthworms will be presented.

Organic Amendments Alter Soil Hydrology and Belowground Microbiome of Tomato (*Solanum lycopersicum*)

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Aim: Test the hypothesis that manure-based vermicompost promotes plant growth at least as well as mineral fertilizer and is superior to windrow-based dairy manure compost or heat-treated poultry pellets.

Method: Conducted a greenhouse experiment to grow tomato (*Solanum lycopersicum*) with three organic amendment treatments (dairy manure compost: DMC, dairy manure-derived vermicompost: VC, dehydrated poultry manure pellets: PP) and a conventionally fertilized control (C). We measured plant growth and soil physical properties and characterized the bacterial and fungal communities of the compartmentalized root microbiome using high-throughput amplicon sequencing of 16S rRNA and ITS-1 spacer genes, respectively.

Results: Of manure-derived fertilizers amendments, only VC led to vigorous tomato growth throughout the experiment, whereas DMC had mixed impacts on plant growth and PP was detrimental. Organic amendments increased soil porosity and soil water holding capacity, but delayed plant maturation and decreased plant biomass. Composition of bacterial communities were affected more by organic amendment than fungal communities in all microhabitats. Composition of communities outside roots (bulk soil, rhizosphere, rhizoplane) contrasted those within roots (endosphere). Distinct microbial communities were detected for each treatment, with an abundance of *Massilia*, *Chryseolinea*, *Scedosporium*, and *Acinetobacter* distinguishing the C, VC, DMC, and PP treatments, respectively.

Conclusions: Plant growth is affected by the application of organic amendments not only because of the soil microbial communities introduced, but also due to a synergistic effect on the physical soil environment. Furthermore, there is a strong interaction between root growth and the spatial heterogeneity of soil and root-associated microbial communities.

Effects of Microarthropod Density on the Composition of Soil Fungal Communities in Nutrient-poor Ecosystems

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Aim:

Our aim was to study the effects of microarthropod (i.e. mites and springtails) density on fungal communities in nutrient-poor ecosystems like heathlands and grasslands. This is highly relevant for ecosystem functioning due to the contributions of such interactions to organic matter decomposition during succession. Whereas microarthropods are likely to affect both the structure and function of soil microbial communities, underlying processes remain poorly understood.

Method:

We conducted a 3-month in situ mesocosm experiment to determine the effects of soil microarthropod density (low or high) on microbial decomposition and community composition of soil fungi across a range of grasslands and heathlands in Belgium.

Results:

The mesocosms with higher microarthropod densities were characterized by a higher fungal species richness and a higher number of fungal indicator species (i.e. 29 vs. 2). Moreover, fungal community composition was clearly distinct from the low density treatment, regardless of ecosystem type. However, the relative abundances of fungal functional groups and decomposition rates remained unaffected by microarthropod density.

Conclusions:

Our study provided essential insight on the interactions within belowground communities. These results suggest that microarthropods alter decomposition processes via alternative pathways, and may thus eventually translate into practical management approaches favouring the development and functioning of belowground communities.

Soil Microbial Community Responses to Two Years of Water Limitation in Scots Pine Mesocosms

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Aim: We assessed the response of prokaryotic and fungal communities to different levels of prolonged water deficit over two growing seasons of young Scots pine trees.

Method: A greenhouse experiment was conducted with mesocosms consisting of natural forest soil and young Scots pine trees (*Pinus Sylvestris* L.). The mesocosms were adjusted to three soil moisture levels for two years – control, intermediate, and severe water deficit (40% and 75% reduction compared to control, respectively). DNA metabarcoding of fungal and prokaryotic taxonomic markers combined with measurements of tree growth parameters and soil physicochemical conditions was used to evaluate changes to water limitations on a seasonal basis.

Results: Our results show that prokaryotic communities were less resistant to water limitation than fungal communities. Water limitation promoted the proliferation of taxa known to be tolerant to desiccation and prefer oligotrophic conditions, such as Acidobacteriota. Severe water deficit led to a decline in the relative abundance of genera involved in nutrient cycling (e.g., *Nitrospira*) and plant-growth promotion (e.g., *Tuber* and *Paenibacillus*). Moreover, a decrease in fresh carbon inputs and an increase in residual complex organic compounds under water limitation induced a shift from symbiont- to saprotroph-dominated communities. Water limitation favored the abundance of saprotrophic Ascomycota (e.g., *Penicillium*) capable of decomposing dead plant material.

Conclusions: Our findings indicate that water limitation in forest soils will likely lead to a decrease in the relative abundance of symbiotic microbial taxa, with cascading consequences for tree health and forests affected by prolonged periods of drought.

Trophic interactions of Collembola at the soil pore scaleJingzhong Lu¹¹*University Of Goettingen, Goettingen, Germany*

Aim: Soil pores serve as habitats for soil organisms interconnected by trophic interactions. Although trophic interactions are essential for soil functioning, the drivers of trophic interactions remain largely unknown. We studied how the physical structure of soil determines the trophic interactions between food resources and consumers.

Method: In a microcosm experiment, we tested how the localisation of food resources at the soil pore scale drives their accessibility to Collembola. We placed ¹³C-labelled sugar in four pore classes (2–10, 10–50, 50–300, and >300 μ m) using the soil matric potential. Four collembolan species with contrasting body sizes were incubated for four weeks, and their bulk and compound-specific isotope composition in fatty acids were measured to assess the extent to which they accessed food resources from pores.

Results: We expect that (i) soil pores < 50 μ m limit resource accessibility to all collembolan species; (ii) resource accessibility varies with species, with larger species being more limited to pores than smaller species, and (iii) fungi are the main food resource for Collembola and enable them to access to resources in smaller pores via fungal hyphae.

Conclusions: Our interdisciplinary approach integrates soil physics and soil food web ecology to test how size-based segregation of consumers and food resources drives trophic interactions in dark and opaque soil.

Soil microbial community structures are shaped by agricultural systems revealing little temporal variation

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Aim:

To determine if any differences in soil microbiome structures between both sharply contrasting, slightly differing and quite similar agricultural systems persist through changing growth conditions.

Method:

Under field conditions, soil samples were taken from different agricultural systems; a sown grassland to maize rotation (MC), an intensively managed permanent grassland (INT), as well as extensively managed permanent grasslands with high (EXT_HP), low to sufficient (EXT_LP) and deficient available P (EXT_DP), six times throughout the 2017 growing season. Soil DNA was extracted, with the fungal internal transcribed spacer region (ITS2) and bacterial 16S rRNA gene being PCR amplified and an amplicon-based Illumina Miseq sequence analysis conducted.

Results:

For both fungal and bacterial community structure, the influence of agricultural system ($\sqrt{CV} = 0.256$ and 0.145 , respectively, both at least $P < 0.01$) was much greater than that of temporal progression ($\sqrt{CV} = 0.065$ and 0.042 , respectively, both $P < 0.001$). Importantly, nearly all agricultural systems persistently harbored significantly distinct fungal community structures across each of the six sampling events (all at least $P < 0.05$). There were not as many pairwise differences in bacterial community structure between the agricultural systems, but some did persist (MC and EXT_HP ~ EXT_DP, all $P < 0.001$).

Conclusions:

These results highlight the temporal stability of pairwise differences in soil microbiome structures between established agricultural systems, even those with comparable management. This is a highly relevant finding in informing the sampling strategy of studies in soil microbial ecology and for designing efficient soil biodiversity monitoring systems.

Assessing taxonomic pipelines for analyses of soil metagenomic data

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Soil is recognized as one of the most diverse microbial habitats on earth. The soil microbiome is critical to plant health, stress resistance, drought tolerance, and antimicrobial resistance, among other things. With shotgun metagenomic sequencing it is now possible to detect and characterize microbial species in unprecedented ways. The current state of the art for taxonomic classification of shotgun metagenomes uses a variety of approaches resulting in different results or different levels of identification depending on the sequenced environment. And as of now, pipelines for complex datasets such as soil with a large number of uncultured microbes and much diversity are still in the early stages.

In this study, we classified shotgun metagenome data from 133 soils collected across Ireland using dominant taxonomic profilers including Kaiju and Kraken, as well as a custom Kraken database built from GTDBTK genomes, and found that the results differed according to the pipelines used. When standard pipelines for Kraken and Kaiju were compared, Kraken performed better at species-level classification and at a lower computational cost. Creating a custom database increased the percentage of reads classified to 34% per sample, compared to 17% and 19% for Kraken and Kaiju. As a variety of software tools are currently available for taxonomic classification, it is vital to develop, refine, and validate computational methods and bioinformatic tools to investigate soil microbiomes effectively. Through fine-tuning pipelines available for soil metagenomics, we can gain hitherto unattainable insights into the soil microbiome.

Evaluating the Impact of Conservation Agriculture on Soil Health

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Aim:

Many conventional agricultural practices, such as tillage, have been strongly linked with substantial degradation of soil health. Conservation Agriculture (CA) is an agricultural system designed to manage agro-ecosystems for improved and sustained productivity by conserving and enhancing soil health and biota. The system is predicated on three key management principles: no-tillage crop planting, permanent soil cover with crop residues or cover crops, and use of diversified crop rotations.

Soil microarthropods play a vital role in soil ecosystem service provision, and thus its composition can be used as an indicator for soil health. Here we apply the QBS-ar index to investigate the impact of CA on soil health, compared to conventional methods, using a systems-level field experiment with the aim of quantifying the impact of the different approaches on this soil health metric

Method:

A systems-level field experiment has been established across 10 ha using two different cropping systems (CA and conventional plough based), each managed independently by professional agronomists with expertise in each system, with each system replicated five times across two fields. Here we will focus on the results of microarthropods extracted from the soil will be used to calculate EMI values to apply the QBS-ar index. This data will be used to test the hypothesis that QBS-ar will indicate higher levels of soil health within the CA system. This will provide important information on the impact of CA on soil health.

Plasma treated nitrogen enriched manure and the living dudes in the soil

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Aim: Plasma treatment of animal manure is a new technology, enriching the manure with plant-available nitrogen. Therefore, the product is termed Nitrogen Enriched Organic fertilizer (NEO). The producer (N2Applied) claims that NEO can be a sustainable alternative to conventional fertilizers used in agriculture. However, the effect of this product on soil-dwelling organisms is unknown.

Method: This study investigates and compares the effects of NEO on changes in soil fauna feeding activity, the abundance of springtails, and the abundance and weight of earthworms to mineral fertilizer and organic fertilizer (cattle slurry) in pot and field experiments with sandy clay loam.

Results: Early effect evaluation (week 7) indicated influences on soil fauna feeding activity; among treatments, higher amounts of fertilizers went along with lower feeding activity, regardless of fertilizer type. However, the initial fertilizer application stimulation was transient and stabilized with time after fertilization towards mid-term (week 14) and late effect evaluations (week 21).

Accordingly, differences between feeding activities were less than five percent at late effect evaluation. Similarly, none of the fertilizers used imposed adverse effects on the abundance of springtails and the abundance and weight of earthworms; these parameters were almost identical among all fertilizing treatments.

Conclusions: After two years of application in field trials and in a pot experiment, NEO and the other used fertilizers seem not to harm the selected soil-dwelling organisms.

Microbial communities from different soil types respond differently to different digestate fractions input

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Biogas digestates are more and more used as organic fertilizers. However, their effect on soil microbial quality is still debated. Moreover, little is known on how the response of soil microbial community to a given digestate may depend on the fraction (whole (FYM_WD), liquid (FYM_LD) or solid (FYM_SD)) of digestate applied, and/or on the physicochemical properties of the soil receiving the input. Here, we performed a microcosm experiment (42 days of incubation) to compare the effect of different fractions of the same digestate, each applied to 3 different soils types (contrasted physicochemical and climatic characteristics), on the abundance and diversity of the soil microbial communities. The experiment contained also three other modalities: cattle manure (CM), slurry (CS) and mineral fertilizer (MIN). At the end of experiment, microbial biomass (MB) of coarse textured soils was lower when FYM_WD or _LD was applied compared to FYM_SD ($P < 0.001$). The effect of FYM_LD and _WD on MB was similar to CS, and CS and MIN respectively. These variations were explained by the quality of input (C/N) and soil parameter (clay content). Soil prokaryotic diversity of coarse textured soils was higher when FYM_WD was applied compared to FYM_SD ($P < 0.001$). The effect of FYM_WD on soil prokaryotic diversity was similar to CS, CM and MIN. These variations were explained by total organic carbon content of input. Our results suggest that microbial communities of soils with a poor clay content would be more vulnerable to digestates input, particularly the liquid fraction.

Effects of post-fire wood mulch on biocrust-forming mosses and soil fungal community recovery

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Aim:

The study aimed to evaluate the effects of the application of wood-based mulches on the aboveground and belowground soil communities after a wildfire in a Mediterranean semiarid forest. Despite the effectiveness in soil stabilization, the wood incorporation repercussion in soils is rarely studied, in particular the effects on the biocrust-forming mosses and the fungal community compositions, and the implication for the post-fire ecosystem recovery.

Method:

Two rates of wood soil cover (65% and 100%) were studied, during one year of application, in soils affected by a wildfire and subsequent salvage logging, where an emergent moss biocrust demonstrated to positively drive the ecosystem recovery in the short term. Fungal community composition was studied based on ITS2 amplicon sequencing.

Results:

Mulch adversely affected biocrust development. The fungal community was altered in richness and structure, and reacted to the application rates, in particular through changes in the soil moisture, aggregate stability, nitrogen, and phosphorous. The dissimilarities thanks to the moss biocrust disappeared after the mulch application, communities became more similar after one year. The study of the dominant taxa revealed the strong legacies of the fire, the moss biocrust presence, and the mulch application.

Conclusions:

The mulch application interfered with the passive restoration of soils by mosses. The effects of biocrust on microbial diversity were diluted after the mulch application, and fungal communities become transitorily highly stochastic and less diverse. Despite preventing soil erosion, wood mulch did not help to restore microbial community and preserved ecosystem functionality after the wildfire.

Diversity and Functionalities Hidden Within the Mycorrhizal Fungal Microbiome

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Mycorrhiza is a soil fungus that establishes a mutualistic symbiotic association between a fungus and host plant roots. Mycorrhizae contribute significantly to plant nutrition, particularly to phosphorus uptake. They also contribute to the selective absorption of immobile (such as Zn) and mobile (S, Ca, K, Fe, Mn, and N) elements from plants along with water uptake while providing resistance against abiotic and biotic stresses. Bacteria are very closely associated with mycorrhizal microbiome (as AMF-associated bacteria or AAB) and act as a third partner involved in mycorrhizal-plant symbiosis. They are involved in influencing plant hosts directly and indirectly as well as interact at varying levels to enhance mycorrhizal activity, nutrient uptake, and provide resistance against various stresses. As part of the presented research work, we screened 33 geographically diverse AMF species from *in vitro* and *in situ* co-cultures. We isolated, purified, characterized 231 AABs from the AMF microbiome based on 16S rDNA analysis. Ten plant growth-promoting functional traits were tested with 109 AABs and it was observed that bacterial strains possessed multifarious traits. Through microscopic techniques, the association of AABs with AMF was confirmed in the form of aggregates, biofilms and as endobacteria.

AAB association was recreated with the model AMF, *Rhizophagus irregularis* using *in vitro* plant experiments with hairy roots of *Daucus carota* to examine their effect on mycorrhization of plant roots. The AABs were found to be associated with *R. irregularis* and were able to migrate along with growing AMF hyphae and spores. AABs differentially influenced the growth of the AMF and its functional capability of biofilm formation, phosphate solubilization, and nitrogen fixation. We identified interaction as well as the synergistic relationship between the two cross-kingdom microbial partners.

Understanding the role and mechanism of the functional co-existence of the mycorrhizal microbiome diversity with host plants will aid in developing superior performing biofertilizers for sustainable crop production. This will also help us in bringing the naturally existing microbial diversity into functional applications for benefits to agriculture.

Soil BON Foodweb: A Global Standardized Monitoring of Soil Animal Communities

Anton Potapov¹, The SBF Team²

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²*Core team of 43 researchers from the following countries: , Germany, Australia, Japan, France, Netherlands, Brazil, Italy, Spain, China, Georgia, Ireland, Czechia, Canada, Argentina, Russia, Greece, South Africa, Poland, New Zealand, Taiwan, Finland, Thailand, UK, Switzerland, US, Morocco, Portugal, Chile, Croatia, Kenya, Malaysia, Luxembourg*

Aim: Here we introduce the Soil BON Foodweb Team (SBF Team), a cross-continental collaborative network that aims to deliver open global knowledge on the status and changes in soil animal biomass, diversity, and functions.

Method: We established a network of volunteer researchers from over 30 countries who selected sites for novel quantitative assessment of soil micro- meso- and macrofauna. These sites were selected from the Soil BON pool and thus our animal assessment is linked to data on soil properties, functions, and microbial communities with perspective of long-term monitoring (every three years).

Results: At the initial phase, the SBF Team developed standard protocols to assess communities of nematodes, enchytraeids, microarthropods, earthworms and other macrofauna by adapting traditional and easy-in-use methods. The protocols supplemented with videos are openly available online: <https://soilbonfoodweb.org/protocols-and-manuals/>. We further established a pipeline to streamline counting, rough identification, and measurement of soil invertebrates using image analysis. During 2022-2023, over 100 sites were assessed globally across the above-listed animal groups using our standard protocols.

Conclusions: The SBF Team is established as a unique initiative in monitoring soil animal communities across size classes and across the globe in association with soil functioning. It represents a network to build transcontinental observation and experimental projects in soil ecology and conservation. We advocate for the use of standard methods across different projects and intend to deliver tools to streamline global soil ecological research.

Multifunctionality of Belowground Food WebsAnton Potapov¹¹*German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Leipzig, Germany*

Aim: Belowground consumers create complex food webs that regulate functioning, ensure stability and support biodiversity both below and above ground. My aim is to develop trait-based approach of 'multichannel' soil food-web reconstruction that accounts for empirical evidence, tackles the soil food web complexity, and delivers indicators related to animal functions.

Method: I build on a comprehensive state-of-the-art review of the feeding habits of soil-associated consumers and infer weighted interactions among trophic guilds using feeding preferences, prey protection, body size and spatial distributions, and biomasses. I then calculate energy fluxes to quantify 'trophic functions' of soil animals and propose bulk indicators such as 'trophic multifunctionality'.

Results: The approach allowed me to connect soil protists, micro-, meso- and macrofauna (invertebrates), and soil-associated vertebrates in a single interaction network, being reproduceable across different communities. The multichannel reconstruction differed from traditional food-web reconstruction and calculated trophic functions were consistent with some independently measured ecosystem functions (e.g. herbivory, decomposition).

Conclusions: The 'multichannel' soil food-web reconstruction is a powerful, realistic, and reproduceable approach. Further empirical validation of the food-web indicators in laboratory and field experiments will establish this approach as an effective tool for understanding animal diversity–ecosystem functioning relationships in soil.

Impact of soil faunal necromass on soil organic matter and microbial diversityStefanie Maaß^{1,2}, Shin W. Kim^{1,2}, Daniel R. Lammell^{1,2}, Matthias C. Rillig^{1,2}*¹Freie Universität Berlin, Berlin, Germany, ²Berlin-Brandenburg Institute of Advanced Biodiversity Research, Berlin, Germany*

All animals, regardless of trophic position, will ultimately have their biomass recycled in an ecosystem upon their death, directly by their decomposition or indirectly by the decomposition of the predator that consumed them. Most studies of faunal necromass refer to the decomposition of vertebrates or aboveground animals, but little is still known about the necromass of soil fauna in this context. Due to the high abundance of especially soil invertebrates, we have to expect a huge input of faunal dead biomass throughout the year. We here discuss potential impacts that dead faunal biomass can have on the soil and the soil community. Especially the provision of short-term, high quality food sources for the microbial community does play a major role, as the presence of available chitin might increase certain bacteria and fungi that are able to break down this component. In addition, the microbial community originating from the cuticle and from the gut system of the dead individual might, at least in the short-term, affect the soil microbial community. Overall, due to its high numbers, dead faunal biomass has to be taken into account in local nutrient turnover scenarios.

Community structure of known and previously unknown endobacteria associated with spores of arbuscular mycorrhizal fungi

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Arbuscular mycorrhizal fungi are ubiquitous plant root symbionts providing vital mineral nutrient to their host while also housing their own endosymbiotic bacteria. Two different AMF endobacteria have been characterized to date: *Ca. Moenioplasma glomeromycetorum* (CaMg, Tenericutes) and *Ca. Glomeribacter gigasporarum* (CaGg, β -proteobacteria), however, little is known about the distribution and population structure of these endobacteria in natural AMF populations and whether AMF can harbour other endobacteria. We isolated AMF spores from a natural dune ecosystem and an agricultural grassland and surveyed the surface-sterilized spores for presence of endobacteria. We found that CaMg were extremely common, found in 80% of spores and their populations were highly diverse within AMF individuals. CaGg, on the other hand were very rare (2% of spores) and their populations were homogenous within AMF individuals. Unexpectedly, we discovered an additional and previously unknown level of bacterial diversity within AMF spores which extended beyond the known CaMg and CaGg endosymbionts. We detected as many as 277 other bacterial Operational Taxonomic Units (OTUs) in individual spores. These reads belonged to diverse groups of free-living, parasitic or plant-symbiotic bacteria which likely represent transient hitchhikers that exploit the lipid-rich AMF spores as a source of shelter.

SOIL BIODIVERSITY ON PIANOSA ISLAND: PRELIMINARY RESULTS OF SOIL EVOLUTION AFTER AN INTENSIVE AGRICULTURAL MANAGEMENT

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Aim: The purpose of work was identify data gaps on soil biodiversity, applying a set of new tools for monitoring biodiversity at the taxa at functional level, so to ensure that the right information is available to scientists and end-users of biodiversity information. We focus for the first time on soil quality and biodiversity of Pianosa Island, an excellent training ground for validating monitoring tools and understanding the biological evolution of soils after intensive agronomic management.

Method: Pianosa is an island included in the National Park of Tuscan Archipelago in the Tyrrhenian Sea that has been a correctional agricultural colony for more than one century. The Island is a scientific research base and an eLTER site. Agricultural fields have been abandoned at the beginning of the 90's, and the natural vegetation is now expanding. Three main ecosystems have been identified in Pianosa: 1) abandoned agriculture fields, 2) abandoned pastures and 3) mediterranean natural macchia at the island's borders. Considering past studies, we focus on soil quality and biodiversity identified along a renaturalization gradient. A set of soil quality indicators (chemical and physical) were analyzed to soil characterization. In terms of biomonitoring, microbial activity and mesofauna functional adaptation are extremely interesting thanks to the speed of analysis and the related information.

Results: The work shows preliminary results from the first sampling campaign of "PianosaLAB2" - Soil ecosystem hub Project of the Institute of Bioeconomy of National Research Council (IBE-CNR).

Conclusions: Data obtained confirm how Pianosa Island is a perfect laboratory to study the soil evolution after soil intensive management and detect threats on biodiversity. Results clearly support the use of microbial activity and mesofauna adaptation to have qualitative and quantitative functional information to allow for evidence-based, data-driven policy and management decisions

Scanning soil biodiversity in a Silvopastoral system in Mediterranean area: results from central Italy

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Aim: Agroforestry, one of the most ancient agricultural practices of the Mediterranean culture and partly lost due to agricultural intensification, has recently been reintroduced for its positive effects on the SOC sequestration (FAO and ITP 2021). Long-term agroforestry (LTA) studies in Mediterranean climate focusing on of the ecological drivers of organic carbon dynamics are extremely interesting and deserve to be analyzed. This survey aims to provide monitoring tools for the assessment of soil quality and to define appropriate biodiversity indicators useful for providing functional information relating to ecosystem services.

Method: We analyzed mesofauna and microbial fungal communities in an LTA Silvopastoral farm. The methodology was developed along a gradient based on land use (Mediterranean forestry, Silvopastoral and Grassland) and on the intensity of grazing as a function of the maximum distance that animals usually reach from the main feeding stations (high density pastures with lower distance from the station feeder and low-density pasture at greater distance). Particular attention was given to fungi and possible relationships with soil abiotic e biotic components.

Results: The first results showed a substantial trend in how some silvopastoral practices can better preserve soil biodiversity, with a high level of abundance of mesofauna and fungal biodiversity, as well as soil biological quality and ecological stability, if managed in a way rational. If forest pasture is not properly managed and livestock is persistently on the ground, biodiversity levels drop dramatically and the benefits of silvopastoral practice are not realized.

Conclusions: Further analyses will be necessary to 1) deepen understand and highlight the complex interactions between biological communities and physicochemical variables, all of which contribute to the overall quality of soils; 2) explore if interactions can be reliable enough to be applied for soil quality monitoring and management.

The role of biodiversity for ecosystem functioning in forests

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Uncertainty in the behaviour of the carbon (C) cycle is one of the biggest limiting factors in accurately predicting Earth's temperature into the 21st century. Forests are important ecosystems for global C cycling because they sequester approximately half of the world's atmospheric C; while decomposition is the process by which the C locked up biomass is transferred to different pools in the atmosphere, the soil, or the tissues of decomposer organisms. Yet, despite its importance for carbon budgets, decomposition remains poorly understood compared with other key ecosystem processes such as primary production. Surprisingly, we lack a fundamental understanding of the mechanisms driving differences in decay rates across the globe. In this talk, I will: 1) demonstrate the importance of termites in decay processes, showing that they create hotspots of decay in canopy gaps and are able to decompose more than half of deadwood in tropical rainforests and 2) introduce a new large-scale, long-term project designed to further our understanding of the role of belowground biodiversity in mediating soil processes and ultimately tree productivity and C storage in European forests.

Microbial functions after the application of nanostructured bio stimulant: activity from "TERRE" project

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Aim: The National Research Council project "TERRE" proposes innovative strategies for plant growth, based on a combination of nanostructured bio-stimulants from organic waste and sensors to improve technological infrastructure of agricultural practices while preserving natural resources and soil ecosystem. In the framework of a specific work package, we are planning an experiment to evaluate the effect of such nanostructured bio-stimulants on soil ecosystem quality and plant growth with an eco-functional approach.

Method: After the chemical transformation of agro-industrial waste (e.g., dried fruits shells) into nanostructured materials, microcosmos experiments will be set to detect the impact of these nanomaterials – in different concentrations, on the ecological functions of the microbial consortium of the growth substrate and on plant growth. We will use the innovative community level physiological profile (CLPP) as a tool to evaluate the average metabolic response (AMC) and the community metabolic diversity (CMD), and plant growth indexes.

Results: Although the results are still not available, the application of such bioactive products could be powerful in improving the knowledge on how microbial consortium can act on plant and soil relationships, but also in offering a circular and sustainable solution to crop productions, contributing in fulfilling the demand for healthy and sustainable food.

Conclusion: We are hopeful that the results obtained from the experiments with organic nanostructured materials will demonstrate a potential solution for preserving soil ecological functions in crop productions, as this is the key for the transformation of actual agricultural systems into more sustainable and competitive managements.

Effects of P-availability on Root Exudates and Rhizosphere Community of a Phosphite-metabolizer *N. tabacum*Isabel Siles Asaff¹, Luis Herrera-Estrella^{1,2}¹*CINVESTAV, Irapuato, Mexico*, ²*Texas Tech University, Lubbock, United States*

The use of GMOs in agriculture has become necessary because they can improve crop yield, as well as reduce the use of fertilizers and pesticides. Nonetheless, understanding plant-soil interactions of these modified organisms is crucial to determine the impact they can have on agroecosystems.

Therefore, we analysed the changes on root exudate composition and rhizosphere microbial community across different phosphorous concentrations for phosphite metabolizer, *ptxD-36 Nicotiana tabacum* and its wild type counterpart.

Plants were grown in a growth chamber for 21 days, and later transfer to rhizotrons filled with a soil/sand mix under different P-concentrations. After 28 days root exudates and soil rhizosphere DNA were collected and DOC, MBC, and root morphology were quantified for each treatment.

Soil biodiversity on urban farms: composition and relationship with foodborne pathogen survival

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Urban farming has potential to provide a diverse set of social and ecological benefits. Soils on urban farms are often degraded and, in some cases, contaminated. Urban farmers apply lots of organic amendments such as compost to help restore degraded soils and supply nutrients, dramatically altering many soil properties. The impact of these changes on the composition of soil fauna and their capacity to carry out critical processes such as mediating the survival of foodborne pathogens is not well understood. To address this knowledge gap, we collected soils from a diverse set of 18 urban farms in 5 cities across the state of Indiana in the United States. Soils were collected from both unmanaged and managed areas and characterized using a diverse set of soil physical, chemical, and biological assays. The composition of soil bacterial, fungal, and nematode communities were determined using next-generation sequencing and several bioinformatic programs. A subset of the soils were amended with an attenuated strain of *Escherichia coli* O157:H7 labeled with green fluorescent protein to determine how the soils could influence the survival of this foodborne pathogen using laboratory mesocosm assays. Survival of the pathogen was quantified using plate counts and qPCR. Preliminary results indicate that pathogen survival varied dramatically among soils. Efforts are underway to identify potential correlations between pathogen survival and soil physical, chemical and biological properties. Results will provide new insights on how to manage urban soils on urban farms for soil, crop and human health.

Regenerative Agriculture Practices Changed Soil Microbial and Nematodes Communities in a 29-years Long-Term Experimental Site

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Aim:

Increasing crop productivity and profitability, while keeping production environmentally sustainable, is a challenge for agriculture worldwide. As a result of agriculture intensification, many soils are highly degraded and depend on the massive use of chemical inputs. Agricultural systems have significantly contributed to the perturbation of natural habitats and losses of biodiversity in addition to being a major contributor to global anthropogenic greenhouse gas emissions. Economic and environmental costs of fertilizers and pesticides are increasing, while yields have reached a plateau, warranting a transition to more sustainable practices.

Method:

Here we took advantage of long-term (29 years) corn (*Zea mays L.*)-soybean (*Glycine max L. Merr.*) rotation to measure impacts of two regenerative agriculture practices – no-till and variable P- and N-fertilization levels – on soil bacterial, fungal and nematodes communities.

Results:

While no-till led to no change in bacterial and fungal biodiversity levels, it did greatly shift the structure of the communities with potential impacts on soil functions. Although less pronounced, different levels of N-fertilization led to changes in both soil microbial biodiversity and structure while different levels of P-fertilization did not have any impacts on soil microbial communities. The effects on nematodes were more subtle but specific families were affected, revealing a change in the structure of the micro-food web. This was further supported by co-occurrence correlation network analyses.

Conclusions:

Because microbial communities are carrying a plethora of functions in soils, assessing long-term impacts of regenerative practices on these communities is key to evaluate the impacts of those practices on agroecosystems functions

Multi-trophic interactions between microbivorous and herbivorous mesofauna: implications for N cycling and plant growth

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Aim:

Soil nematodes are composed of multiple feeding groups that control distinct energy channels and strongly interact with plant growth, but to date most studies focused on bacterivorous nematodes, largely neglecting the contribution of herbivorous and fungivorous nematodes. We conducted a mesocosm experiment to investigate whether and how herbivorous and microbivorous microfauna, separately and in combination, enhance N mineralization and plant growth.

Method:

Nutrient-poor loamy sand soil was selectively sterilized by gamma irradiation (6 kGy) and pre-incubated for one month to recover the indigenous microbial community caused by the irradiation effect. *Pratylenchus zaeae*, *Aphelenchus avena*, and *Rhabditis oxycera*, representing herbivorous, fungivorous, and bacterivorous nematodes respectively, (abbreviated as Hn, Fn, and Bn) were inoculated in soils alone and all combinations, and *Lolium multiflorum* was used as a model plant. After two months, plants were harvested and analyzed, and the soil was analyzed to explain the mechanisms by which the trophic interactions affected plant growth.

Results:

The combination of all trophic groups of nematodes significantly increased the shoot and root biomass (by 11.4 and 45.2%, respectively), but decreased total N concentration significantly by 15% for both shoot and root as compared to the control treatment (without nematodes). The root/shoot ratio was higher in the HnBn and BnFnHn treatments than in the control. Contrary to our expectation, there was no effect on the soil N mineralization and no significant change in microbial activity (dehydrogenase, β -glucosaminidase, basal respiration) and MBC for all treatments.

Conclusions:

Combination of the three trophic channels increased plant growth but did not do so through increased N mineralization. This unique study highlights the vital importance of taking into account interactions between organisms explicitly when studying their roles in nutrient cycling and plant growth.

Uncovering Trophic Variations in Collembola With Elevation Using Species Specific Bulk Stable Isotopes

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Changbai Mountain extends along the border between the Chinese provinces Jilin and Liaoning, and North Korea, where the "Changbaishan National Nature Reserve" was designated in 1979. Due to its poor forestry history, the northern slope of the mountain to a large extent is covered by primary forests. The temperate climate and the undisturbed forests make this mountainside attractive for studying changes in forest ecosystems with increasing altitude allowing insight into potential consequences of climatic changes on forest ecosystems. A number of invertebrate groups receive increasing attention regarding their reactions to climate change, however, potential effects on forest soil invertebrates are poorly investigated. Springtails (Collembola) dominate the microarthropod community in litter and soil of forest ecosystems. They are important decomposers and changes in temperature and soil moisture might alter their trophic interactions in the soil food web. We investigated changes in the trophic structure of Collembola along a gradient of seven altitudinal sites between 800 and 1700 m at Changbai Mountain. We measured bulk stable isotopes of the most abundant species of Collembola and compared the results with previous studies in which we measured bulk stable isotopes, and neutral lipid fatty acid and amino acid stable isotopes of Collembola at the group level. As basis of the decomposer food web we also investigated changes in potential food resources, such as bacteria and fungi, along the altitudinal gradient using phospholipid fatty acid analysis and substrate induced respiration.

BioDivSoil - Unveiling the Food Spectrum of Epigeal Predators (Coleoptera: Carabidae) using DNA Metabarcoding

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Aim

Carabids are important predators in soil ecosystems. They regulate the abundance of many invertebrates and contribute to ecosystem stability. Previous studies mainly focused on barcoding of individual carabids or targeted specific prey organisms. However, approaches to fully map the dietary spectra of carabids are lacking. DNA metabarcoding of predator gut contents offers the possibility to study predator-prey interactions in more detail.

Methods

Throughout the vegetation period in 2021, carabids were captured at 26 sites using pitfall traps. Individuals were sorted on a species-specific basis. All individuals were washed in 13 % chlorine bleach to remove external DNA. Beetles < 10 mm were processed completely, of beetles > 10 mm only the guts were used. Nonspecific arthropod primers were applied.

Results

In addition to non-target organisms like earthworms and snails, consumption of a variety of carabid species was also detected. A more diverse carabid community also resulted in a broader prey spectrum. Further results promise insights into the food spectra of specifically foraging ground beetles and should reveal possible interactions between above- and belowground biodiversity.

Conclusion

The results suggest that while earthworms and snails make up an enormous proportion of the ground beetles' diet, the number of other prey species should not be underestimated. For example, other carabid species make up an enormous part of the prey spectrum, which has not yet been described. However, this is in accordance with the idea that the food of polyphagous carabids is strongly related to the most abundant organisms of a site.

BioDivSoil – Evaluation of Patterns in Soil Animal Communities as a Method for Indicator Development

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Aim:

Soil animals are involved in important soil processes and thus provide multiple ecosystem services, such as crop growth and soil formation. In agroecosystems, soil organisms are directly exposed to the impact of management, e. g. tillage and pesticide applications. The aim of the project is to identify typical patterns in the species composition of several soil animal groups in different agrarian habitat types. Subsequently, these patterns are evaluated to derive indicators that can be used for the assessment of soil biodiversity, in order to support a sustainable agriculture.

Method:

Data sets of different arable sites, grasslands and field margins in various regions of Germany were evaluated. They consist of data collections from previous projects as well as newly conducted samplings from the year 2021. These included pitfall traps (Araneae, Carabidae), soil cores (Collembola, Oribatida) and standardised hand sortings (Lumbricidae). In addition, various habitat parameters were recorded, and literature data was taken into account.

Results:

The result is a close dataset containing the species spectra of different soil animal groups, that were simultaneously recorded at the same sites. The overall pattern of the different taxa will be presented exemplarily in relation to habitat parameters, management intensity, landscape heterogeneity etc. Interrelationships among the various taxa, if apparent in the data set, are also shown.

Conclusions:

The observed patterns allow conclusions to be drawn about the extent to which certain parameters are suitable indicators of soil quality and biodiversity for use by the farmers or in scientific research projects and monitoring programmes.

Unpredictable events and disturbance: probabilistic approaches to study the responses of soil biodiversity to perturbations

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Aim: We synthesise how multiple sources of stochastic fluctuations contribute to soil biodiversity and how these fluctuations can be modelled to improve our ability to predict the response of soil biodiversity to global change factors, especially environmental unpredictability.

Method: we use the theory of stochastic processes and error propagation, and existing ecological research that have used this theory, integrating it to our current understanding of the processes that generate patterns in soil community structure and functions

Results: Major sources of stochasticity in soil are measurement errors and environmental fluctuations. Measurement errors are due to the small size, high abundances, and broad distributions of soil organisms, which limit sampling in space and especially over time. We argue that positive autocorrelation is a main characteristic of soil environmental properties, which may have important consequences on the response of soil biota to perturbations. This has consequences also on aboveground-belowground interactions, for example plant-soil feedback (PSF) dynamics. At a local scale, large populations of soil organisms also imply a minor role of demographic stochasticity. Yet, we show that demographic stochasticity can be sizeable in some datasets, but still much smaller than environmental stochasticity.

Conclusions: In general ecology, stochastic approaches mean probabilistic predictions in terms of population growth, extinction, species coexistence and community structure. In soil, stochasticity implies very variable responses to perturbation and soil feedback (e.g. PSF). Future studies will have to identify the major sources of environmental stochasticity with a particular focus on the interaction between multiple global change factors.

Soil Restoration with Organic Amendments at the Long-Term: A Case Study Focused on Microbial Communities

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Aim:

The application of organic amendments into soil has been proposed as an effective way of improving the quality and fertility of degraded soils and protecting the environment because their use could be a strategy to eliminate and recycle massive amounts of waste. The lasting periods of organic amendment effects on soil microbial communities have not been sufficiently investigated.

Method:

Here, a degraded soil located in a Mediterranean semiarid region was characterized 18 years after being amended with sludge or compost (different stabilization degree) regarding: (i) physicochemical properties, (ii) basal respiration and enzyme activities, and (iii) abundance (fatty acids), taxonomic composition and functionality (shotgun metagenomics) of microbial communities.

Results:

Soil contents of macronutrients, basal respiration, β -glucosidase and phosphatase activities, and bacterial and fungal abundances were higher in the amended treatments in comparison with the unamended control soil. Differences between the two types of amendments were not observed. Most of the annotated sequences in the metagenomic study were of bacterial origin. Although some differences in taxonomic community structure between treatments were observed, the same microbial phyla dominated in the three treatments. Differences in functional community structure between treatments were not that large as initially expected. However, amended soils showed a higher abundance of functions related to nutrient cycling at the lowest SEED subsystem levels.

Conclusions:

The beneficial effects of soil amendment application on nutrient contents, microbial abundance, and enzyme activities remain after 18 years. However, the impact of soil amendments on microbial taxonomy composition and functionality dilutes with time.

Soil Ciliated Protist Communities from Natural Sites and Agroecosystems in Italy

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Aim:

In this study, and for the first time in Italy, we have investigated the diversity and the community structure of soil ciliates from natural sites and agroecosystems in Marche Region (Italy). The main aims were: i) to evaluate the capacity of ciliates to discriminate between different types of land uses; ii) farming management practices; and iii) to assess relationships among ciliate community and abiotic parameters.

Method:

Soil samples were collected twice from 10 sites [5 natural sites: FORest (virgin soils); and 5 agricultural fields: 3 ORGanic (minimum tillage) and 2 CONventional (sod seeding)]. Ciliate communities were studied by means of qualitative (*non-flooded Petri dish* method) and quantitative methods. Soil chemical-physical parameters (texture, CEC NPK, OM, C/N, soil moisture, temperature) were also measured.

Results:

Qualitative ciliate analysis allowed us to identify a total of 59 species representing 29 genera and 12 orders (including 10 species new to science). ORG sites were the richest in species followed by CON and FOR. Multivariate analysis showed statistically significant differences between natural sites (FORest) and agricultural sites, as well as between the ORGanic and CONventional management farming systems. CCA analysis showed correlations between the distribution of species with environmental parameters indicating the importance of these parameters in shaping the ciliate communities in the different type sites.

Conclusions:

Altogether, these results showed the bioindicative potential of ciliate communities in discriminating between natural sites (FORests) and agroecosystems, as well as their capacity to discriminate, *at least preliminary*, between different soil management systems (ORG vs CON).

Energy Flux of the Belowground Food Web in Conventional and Organic Farm

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Aim: This study aimed to investigate the energy flux of the belowground food web in conventional and organic farms for quantitatively assessing the effects of agricultural management practices on soil biodiversity.

Method: Ten soil cores (diameter: 10 cm and height: 10 cm) were randomly collected in conventional and organic peach farms located in Korea, respectively. Sampled soil cores were transferred to the laboratory and individually placed in Tullgren funnels with a single 40-watt incandescent bulb for the extraction of soil fauna. The extracted individuals were identified and counted. Identification was done to order or family level, allowing the assignment of the animals to trophic groups such as predators, herbivores, and decomposers. Additionally, the body lengths of each individual were measured for calculating individual metabolic rates and energy flux of the belowground food web.

Results: There was no significant difference in the density and biomass of predators, herbivores, and omnivores between conventional and organic peach farms. However, significantly higher density and biomass of decomposers were observed in the organic farm than in the conventional farms. In energy flux analysis results, significant differences in energy flux related to decomposers were detected between the farms that applied different agricultural management practices.

Conclusions: Our results suggested that agricultural management practices can affect not only the biomass but also the energy flux of the belowground food web. Investigating the energy flux can be a promising tool for assessing soil ecosystems.

Responses of Soil Arthropod Biodiversity to Extreme Events: First Signs of Change After "Vaia" Storm

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Aim:

Climate change will increase the frequency and impacts of catastrophic events like "Vaia", a storm that hit the eastern sector of the Italian Alps in 2018, provoking extensive damages to forests. Subsequent changes in habitat and resource availability are expected to affect soil living communities and related ecosystem services. This research aims to highlight the shift in soil arthropods community in "Vaia" impacted forests, to understand if it is moving toward a conversion to meadow or if the wooded features still prevail.

Method:

Soil chemical parameters (pH, soil organic matter - SOM) and edaphic arthropod community (abundance, biodiversity – Shannon and Simpson indices, composition) were studied, in Italian Dolomites forests affected by the storm (W), in Intact forests (IF, control condition) close to W, and in meadows (M) in the two years following "Vaia" storm (2019-2020).

Results:

In both years after "Vaia" event, SOM and arthropod total abundance were lower in M than in IF and W. No differences in biodiversity indices were observed. However, the arthropod community differed between M and forests (W and IF) in 2019 but differences in arthropod communities persisted only between IF and M in 2020.

Conclusions:

The storm did not appear to have radically changed soil arthropod community one year after "Vaia", despite upheaval to vegetation cover. However, in impacted forests, results suggested that community composition, unlike abundance and biodiversity, is prone to a progressive shift from the woods to meadow condition, just two years after the catastrophic event.

Effect of cover crops on modern agricultural production of vineyard and cherry trees in Chile

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Aim:

The LivinGro® Chile project is based on the development of protocols to create optimal conditions to enhance biodiversity above and below ground and safeguarding the soil for future generations using cover crops. This study seeks to determine the effect on the use of cover crops in the inter-row in three cherry orchards and three vineyards, located in the central Valley of Chile. LivinGro® considers the effect of cover crops on biodiversity, soil health, nutrition, pathology, and crop quality. In this presentation, we focus our research on the effect of cover crops on the soil invertebrate biodiversity.

Method:

Monitoring was carried out by pitfall and subterranean soil traps every two months among Sept.2020–Jul.2022. The abundance and diversity of individuals were determined for each field and both treatments: control and cover crop.

Results:

Preliminary results show that cover crops have shown a very positive effect on soil fauna and beneficial insects present in the area.

Conclusions:

The implementation of cover plants in agricultural landscapes results in biodiversity enhancements through the attraction of soil fauna.

Greater Relative Increase of Ectomycorrhizal vs Saprotrophic Fungal Biomass with Tree Stand Density

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Aim: Forest management has been identified as an important tool to mitigate climate change through storing carbon in trees and soils. Yet, relatively little is known about how different harvest intensities affect soils and their carbon cycling. Ectomycorrhizal fungi play a major role in soil organic carbon stabilization in European forests, and are likely strongly decreased in abundance by tree harvesting. This negative impact may be reduced by only moderately reducing tree stand density through thinning instead of clearcutting. Here, we studied how stand density affects the biomass of ectomycorrhizal versus saprotrophic fungi. **Method:** In 15 Dutch 1-ha forest stands (covering European beech, Douglas fir and Scots pine) located on poor sandy soils, four different tree stand density treatments were created: 0%, 20%, 80%, and 100% of biomass harvested. We used fungal in-growth bags to determine ectomycorrhizal biomass with ergosterol. From bulk soil samples we measured total fungal biomass and calculated saprotrophic biomass. **Results:** Both ectomycorrhizal and saprotrophic fungal biomass increased with tree stand density. However, the effect of stand density is stronger for ectomycorrhizal fungi, leading to a greater relative increase from clearcut to no-harvest treatments compared to saprotrophic fungal biomass. The effects are most pronounced in the Scots pine and European beech. **Conclusions:** Tree harvesting leads to a loss of fungal biomass which may lower rates of soil organic carbon stabilization, but this can be minimized by applying low-intensity forest thinning.

Exploring alpine soil fauna communities: composition, biodiversity and functional groups in a highly changing environment

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Aim: Although soil biodiversity studies are increasing, (high) alpine habitats, as can be found in the European Alps, remain understudied. We aim to close these knowledge gaps by conducting basic and experimental research on alpine soil fauna and species interactions with a highly changing environment. Here, we give an overview on community and functional composition of soil invertebrates, as well as biodiversity patterns.

Method: To assess the soil fauna, we used standard soil fauna samples and pitfall traps. Our study sites are covering large parts of the European Alps, including more than 200 unique plots covering 20 habitat types. Further, methods such as stable isotope analyses, molecular approaches and functional trait analyses were applied.

Results: The community composition seems to remain similar with increasing elevation, but show decreasing abundances (i.e. density and activity). Biodiversity patterns differ for taxonomic groups (linear vs. hump shaped) but generally taxa numbers decrease with increasing elevation; however, rare taxa/species can be found predominantly in high elevation sites. As shown by stable isotope analyses, taxa in high alpine soils show a high degree of omnivory.

Conclusions: Alpine soil fauna research still lacks data, especially for remote high elevation habitats. However, putting together the available data, we identify some general patterns and discuss responses to the fast-approaching climate and land-use changes. Against prevalent perceptions, we found a quite high and well-adapted mountain soil fauna biodiversity, confirmed by several rare and new species records for the regions.

The Differences in Soil Microarthropod Diversity Between Old Permanent Forests and Young Forests

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Aim:

It is expected that many soil microarthropod species are benefitted by habitats that have been around for a long time and encounter little disturbance. In order to learn more about pattern, we studied datasets collected from old (permanent) forests and young forests (~150 years) across the Netherlands and aimed to answer the following hypotheses:

- Old forests have a higher diversity than young forests
- Old forests have a higher number and density of fungivorous species
- Old forests will be able to support more large microarthropod species

Method:

We used datasets for 3 old forest stands, 10 old hedge rows (also permanent forest sites) and 19 young forests and compared the species richness, Shannon index and Simpson index across those locations. Mite species and genera were assigned a feeding guild and size for a trait analysis across the locations.

Results:

Old permanent forests had a higher species richness than young forests. However, we saw no difference in the two diversity indexes across locations. Furthermore, there was a decrease of fungivorous grazers from old forests to young forests. Lastly, hedge rows were able to support a higher number of large species compared to old forest stands and young forests.

Conclusions:

Older forests have a higher species richness in microarthropods and the higher number of fungivorous grazers is expected to benefit the decomposition process in the soil. These results show that for the soil microarthropod diversity, it is important that soils are allowed to be stable for a long period.

LivingGro™ a Holistic Approach to Enhance Soil Biodiversity and Conservation in Agricultural Landscapes

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While above-ground biodiversity has been a topic of significant public interest over the last decades, soil biodiversity has not generated wide attention beyond the scientific and agronomic world until recently. Syngenta's initiative, LIVINGRO™ takes a holistic approach to improving all dimensions of soil biodiversity related to agricultural activities in a given ecosystem.

The aim is to generate robust, comprehensive scientific data that reliably measures how agricultural technologies and best farm management practices applied on crops grown in proximity to multifunctional areas consisting of indigenous annual flowering plants, can boost both sustainable food production and healthy, diverse ecosystems above and below ground, in and beyond the field. Together with scientists from public and private research organizations, a comprehensive cross regional, multidisciplinary project was initiated to study all soil fauna from the surface and below ground. In addition, the soil microbiome and structure as well as its ability to make nutrients bio-available for plants and to sequester carbon was assessed.

By taking a holistic view of biodiversity, including the soil microbiome, LIVINGRO™ has the potential to provide scalable measures for sustainable farming systems and improved food production sustainability in biodiverse, thriving, and healthy ecosystems, protecting our most precious agricultural resources - soil and water.

Plant diversity and soil history effects on community assembly of arbuscular mycorrhizal fungi

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Aim:

Research has shown that the relationship between plant biodiversity and ecosystem functioning (BEF) strengthens over time. One potential underlying mechanism is the interaction with soil-borne fungi, in particular arbuscular mycorrhiza (AMF), but further insight is scarce. It is unclear whether the effect of plant diversity on AMF communities changes and the AMF-plant relationship strengthens over time.

Method:

We made use of the long-term biodiversity study The Jena Experiment, by re-establishing its grassland plots. The grasslands, varying in composition along a gradient of 1-60 species and 1-4 functional groups, were split to study common soil and plant history: We used existing plots (19 years shared history of plant and soil) and split-plots with new re-sown plants in old soil and others with new re-sown plants and new soil. We sampled bulk soil from all split plots, and roots, rhizosphere and root-free soil from 16 plant species all in old plots.

Results:

At the community level, alpha diversity of AMF increased with plant diversity, and this slope flattened over time. Communities became more homogenous. Community structures were robust to absence of common soil and plant history and plant diversity, but some genera, like *Paraglomus*, accumulated over time. However, trends in root-associated AMF differed from bulk and rhizosphere AMF: In roots, AMF diversity decreased with increasing surrounding diversity and roots, but not soils, hosted species specific communities.

Conclusions:

These results demonstrate temporal changes in plant diversity on AMF communities. However, this relationships looks different depending on the soil compartment and needs to be further examined.

Cascading effects of global change on plant invasion reshaped soil oribatid mite community in alpine-tundraLichao Feng^{1,2}, Zhiqi Du¹, Karel Tajovský², Ting-Wen Chen^{2,3}, Qingfan Meng¹¹*Beihua University, Jilin, China*, ²*Czech Academy of Science, České Budějovice, Czech Republic*,³*University of Göttingen, Göttingen, Germany*

Global changes have promoted invasion of *Deyeuxia angustifolia* (Kom.) to cold regions (from low to high altitudes/latitudes) with changes in microbial communities by altering soil physicochemical properties. However, little is known about structure of soil fauna associated with plant invasion. In this study, we focused on the effects of microbial-mediated changes due to plant invasion on soil oribatid mites. We demonstrated that invasion of *D. angustifolia* reduced oribatid mite diversity and reversed the altitudinal pattern of richness. Furthermore, altitude limited distribution of some oribatid mite species but increased abundances of others. As compared with soil physicochemical properties, soil microbial diversity explained more variation in oribatid mite community compositions. Overall, changes in soil microbial compositions due to plant invasion determined oribatid mite assemblages. Responses of alpine tundra ecosystems to global change should be considered with bottom-up cascade effects of plant invasion on soil food web structure and environments.

BioDivSoil - In Search of a More Complete Approach to Describing Ecological Soil Quality

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Aim

Increasing human populations lead to intensive land use in agriculture, which has direct and indirect effects on soil organisms. A biodiverse soil community protects against the loss of necessary soil functions. Conservation and assessment of soil organisms is complex but essential. A combined approach of morphological- and DNA-based methods will provide a suitable data basis for the assessment of soil biodiversity in agricultural systems.

Method

Twenty-six sites were sampled throughout the 2021 growing season using soil cores, pitfall traps, and search by hand. Samples were processed using either morphological identifications or DNA-based approaches. Oribatids, springtails, lumbricids, carabids, and spiders were morphologically determined. In addition, bycatches in the traps, stomach contents of carabids and further soil cores were subjected to metabarcoding. Furthermore, data on management practices and vegetation occurrence were collected, soil mapping and aerial photo analysis were conducted and existing datasets from previous data collections were included in the analyses.

Results

The combination of these methods opens up the possibility of a spatially, temporally and methodologically condensed soil monitoring. It includes above- and below-ground interactions, the enlightening of food webs, and the analysis of characteristic soil communities. The results are used for functional assessment of communities based on their structure and composition.

Conclusions

This multidimensional approach provides the data basis for deriving indicators of ecologically good soil quality and biodiversity. Furthermore, the integration of DNA-based methods into monitoring studies is discussed and recommendations for sustainable agriculture or integrative nature conservation will be developed.

Steering microbiomes by organic amendments towards climate-smart agricultural soils

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Aim:

Increasing carbon sequestration while lowering greenhouse gas emissions and maintaining crop yields is one of the biggest societal and scientific challenges. We assessed the use of organic fertilizers and mixtures thereof, to steer microbiomes towards higher contribution to carbon sequestration and lowering of GHG emissions.

Method:

We executed mesocosm as well as field trials and assessed diversity and abundance of Archaea, Bacteria and fungi as well as a large range of functional guilds involved in nitrogen and carbon cycling under application of single or mixes of various organic residues (e.g. compost, digestate, covercrop residues). GHG fluxes as well as soil physico-chemistry was assessed in parallel.

Results:

All organic amendments induced a shift in the diversity and abundances of key microbial groups demonstrating the potential to not only lower GHG emissions by modifying the microbial community abundance and composition, but also favor crop growth-promoting microorganisms. Interestingly, some of these effects were facilitated by microbes already present in the residues. The latter was most pronounced for the uptake of atmospheric methane uptake in agricultural soils, which was significantly stimulated by compost application and the methane oxidizing bacteria already present in the compost. Extensive molecular analysis showed that the methanotrophic species dominantly present in compost, are significantly enriched in the methanotrophic communities of organic residue-amended soils.

Conclusions:

Collectively, our results show that microbiomes can be modulated by sustainable green fertilizers with positive implications for the global warming potential of agricultural soils.

Global Change Effects on Earthworms

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Aim:

Earthworms play an important role in maintaining several soil functions and are suitable bio-indicators for soils. Many environmental factors can affect earthworm activity and abundance. Due to global change, some new factors have emerged or increased in strength (elevated soil temperature, biochar, microplastic, agricultural management, etc.). However, our knowledge whether and to which extent earthworms are affected by these factors is still limited. The presentation gives a summary of several experiments in which the effects of these factors on earthworms were studied.

Method:

Within several experiments in micro- and mesocosms, as well as in the field, we investigated the influence of elevated soil temperature and atmospheric CO₂ concentration, biochar and microplastic, and field management practices on the activity and abundance of predominantly endogeic earthworms. Furthermore, we investigated the contribution of earthworms on the emission of greenhouse gases under the influence of some factors and whether anecic earthworms contribute to the plastic input into soil.

Results:

We found that anecic earthworms transport plastic bag fragments into soil, that biochar has no or negative effects on endogeic earthworm biomass and abundance and that the previous year's field crop has more impact on earthworm abundance than a three-year pesticide abandonment.

Conclusions:

The presented effects of global change factors show that some are influencing earthworms but also that earthworms can partially interact with them (plastic distribution in soil). However, this indicates that earthworms are good bio-indicators of altered environmental conditions induced by global change.

Short-term Effects of Cultivation Systems Without Chemical Synthetic Plant Protection on Soil Organisms

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Aim:

The use of pesticides is increasingly criticized due to its significant impact on the environment. The possible decrease in abundance and diversity of soil organisms might lead to a loss of soil biological functions. The project “NOcsPS – Agriculture 4.0 without chemical synthetic plant protection” is aiming to develop a sustainable, environment-friendly, yet productive cultivation system.

In 2020, a field experiment with different cultivation systems was established at the University of Hohenheim: (1) a conventional system with pesticide and mineral fertilizer application, (2) NOcsPS systems without pesticide application, but mechanical weeding and mineral fertilizer application and (3) an ecological system without pesticide application, but mechanical weeding and no mineral fertilizer application.

Method:

The field experiment consists of a six-part crop rotation. Samplings of soil (0-20 cm) and soil animals were conducted during the winter wheat vegetation period for three years. Soil samples were analyzed regarding microbial abundance (CFE) and respiration (RMS), community structure (PLFA) and enzyme activity (enzyme assay). Furthermore, the abundance of Collembola und Gamasina as well as the abundance and diversity of earthworms was examined.

Results:

Soil microbial abundance, activity as well as community structure were not significantly influenced by the cultivation system. Collembola abundance was highest in NOcsPS systems while earthworms showed a higher abundance in conventional systems.

Conclusions:

In short-term, the cultivation system rather affected the soil animal than the microbial properties. While some soil animals might benefit from not applying synthetic pesticides, others might in turn be harmed by the consequently increased mechanical weeding.

Microbial Biodiversity Recovery after Steam Treatment of Nursery Soil.

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Aim:

Healthy soils are important for producing healthy plants. Whereas some soil microbes support plant growth, many pathogens can kill plants or reduce yield and quality of crops. We developed a steam-treatment method to control the invasive pathogen *Phytophthora ramorum* (Oomycetes), causal agent of Sudden Oak Death in the US and Sudden Larch Death in Europe, in soil mixes used at nurseries. We are interested to test the effects of our method on bacterial and fungal soil communities and the dynamics of their recovery over time post-treatment. In addition, we analysed the effect of steaming on plant nutrients present in the soil mix, which might impact not only plant growth, but also microbial communities' composition and ultimately function.

Method:

A soil mix was heat-treated using a top-down approach. Soil samples were collected at four time points post-steaming (1-day, 30-days, 60-days, and 150 days). DNA was isolated from thirty-two soil samples and 16SrRNA gene and ITS1,2 markers were used for amplicon-based sequencing (metabarcoding) of bacterial and fungal soil communities.

Results:

Microbial diversity and composition changed overtime. On day 1 post-steaming the bacterial community was dominated by endospore producing Firmicutes including the genus *Bacillus* spp., whereas 2 months and 5 months post-steaming a wide variety of phylogenetically diverse bacteria were recovered. Fungal communities were mainly dominated by ascomycetes, but heat-resistant Geminibasidiomycetes yeasts were abundant 2 months post-steaming.

Conclusions:

Soil steaming does not eliminate, but reduces the microbial soil biodiversity which will 'bounce back' to pre-stress levels after a prolonged period of time.

A Diversified Cropping System: Benefiting to Crop Production and Soil Health in Southern Ontario, Canada

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Including cover crops in the cereal rotation would not only benefit the crop yield but also could improve soil health. Cereal rotation, such as soybean-winter_wheat-corn rotation, is popular in southwestern Ontario; however, this rotation leaves the soil bare for 15 – 16 months in one cycle of rotation (3 years). While the soil is bare, it not only make nutrients (e.g. N and P) left in the soil vulnerable to leaching, but it also destroys valuable organic matter in the soil. So this rotation is not an ideal cropping system in term of soil fertility and biodiversity. A feasible way to help farmers achieve the dual benefits of crop production and soil health is to grow crops, such as cover crops, between the cash crops. Here, we investigated an evergreen farming practice in southern Ontario, which included two seasons of legume cover crops in a 3-yr organically managed soybean-winter_wheat-corn rotation. In this rotation one legume season (including crimson clover, hairy vetch, and red clover treatments) were seeded after winter wheat harvest and another legume (a mix of above three legumes) were inter-seeded into corn field at corn V5-7 stages. In this production system, legume cover crops were used as the primary N source for the grains (corn and winter wheat), also included was a conventional control (with synthetic fertilizers) without legume cover crops as check. Growing two seasons of winter-hardy legume cover crops in rotation yielded a system of 5 crop seasons in 3 years which provided year-round cover on cropland. Results showed that compared to no cover crop CK, cover crops left less residual soil nitrogen (~50 kg N/ha less) in the soil by late November, which were normally lost through over-winter leaching in the region. In early May before corn planting, significant amounts of above-ground biomass N (150 - 200 kg N/ha) were incorporated into the soil as primary N nutrient for corn from the legumes seeded into wheat stubble, and the same time about 5.5 - 8.5 Mg/ha biomass were incorporated into the soil. The legumes seeded into corn fields showed a variable covering, some years with a full cover and other years a patchy cover dependent open the weather (~40 kg N/ha and ~1.5 Mg biomass/ha per year). In the three-year transition period, average corn grain yields (14.5% moist) were 13.1 and 13.0 Mg/ha for hairy vetch and red clover which were similar to check (13.8 Mg/ha). In the four-year organic period after the transition, average corn grain yields were 11.3 Mg/ha, 11.1 Mg/ha and 9.9 Mg/ha for hairy vetch, crimson clover and red clover which were about 72 – 82% of corn yield in check (13.7 Mg/ha). Soybean yields were similar among treatments in the year of transition and by the four years after the transition, with an average of 3.2 Mg/ha. Over 8 years (2022 data included) of the experiment, the average conventional winter wheat yield has been 5.1 Mg/ha and 4.1 Mg/ha for organic. The effects on selected soil health parameters are under study will be presented at the 3rd Global Soil Biodiversity Conference. This study highlighted the impacts of diversified and legume-based cropping on grain production and soil health in southwestern Ontario.

Characterization of Soil Microbial Communities in Different Soil Profiles

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Aim:

Soil microbial communities participate in biogeochemical cycles and therefore provide essential ecosystem services. The drivers of soil microbial communities are well-known. Specific microbial communities correlate with forest type, at least partly via the effect of forest stands on biochemical conditions of the topsoil. For example, forest type is reflected through soil nutrient availability, with deciduous forests having nutrient-rich soil compared with coniferous forests. However, soil biodiversity between different topsoil remains poorly described, especially the associated soil microbial communities. Our study aims to compare soil microbial community characteristics of different topsoil types, which will be interpreted in terms of the ecosystem functions of their composite microbial taxon.

Method:

We collected soil samples in two European temperate forests, measured their biochemical properties, and used in-depth sequencing to produce microbial profiles. Microbial community composition, structure and diversity were compared among topsoil types.

Results:

Despite acidic soils in both sites, microbial profiles differed between topsoil types. Relative abundances of dominant bacterial and fungal phyla changed, reflecting both the nutrient status and the chemical properties of the soil.

Conclusions:

This study contributes to the characterization of topsoil types based on their microbial profiles. With climate change, monitoring ecosystem functions is important and the soil profile could give a quick answer to the current status of a site.

Linking the Soil Microbiome to Crop Yield and Quality in a Long-term Intensive Potato Trial

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Aim:

The current study investigates impacts of different potato cultivation methods on the soil microbiome and its influence on yield and quality.

Method:

Practice-oriented treatments running from 2001 until 2019 differed in the order of the pre-crop (winter wheat, silage maize), positioning of oil radish as cover crop within the crop rotation, and type of fertiliser (mineral, straw, manure, slurry). Crop yield and quality data were obtained for all rotation cycles, while soil samples were taken after the last potato harvest in 2019. Basic soil physical, chemical, and microbiological parameters such as abundances, activities, and amplicon sequence variances (ASVs) of prokaryotes, fungi, and protists were determined.

Results:

Long-term results indicated higher potato yields after wheat+oil radish. Pathogen-induced quality losses were highest after maize. There were no differences in soil basic parameters and microbial abundance, activity, and α -diversity. An exception was fungal abundance, which was highest after wheat+oil radish with straw+slurry application and lowest after maize. β -diversity showed strongest differences between treatments with wheat+oil radish as pre-crop fertilised with manure or straw+slurry and maize as pre-crop. Fungi (4–38% of the sequences) and protists (11–18%) were stronger drivers than prokaryotes (1.3–3.0%). Several ASVs identified as being associated with the different treatments (59, 205, and 127, respectively) could be classified taxonomically.

Conclusions:

Potato yield was determined by the positioning of the cover crop within the crop rotation, while potato quality was probably influenced by the microbial community composition. Thus, cultivation techniques affect quality parameters via impacts of the soil microbiome.

The impact of re-rooting on soil rhizosphere microbiota at the level of amplicons and proteomics

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Aim: Soil is a diverse domain that exhibits extensive diversity throughout its distinct strata. Global warming and climate change have caused a significant impact on soil horizons. The idea of re-rooting a cash crop using the deep root canals of a cover crop was to overcome a deficit of nutrients in the topsoil and an increased risk of drought. The rhizospheres of a cash crop like maize (*Zea mays*) and cover crops each have their own microbial identities and nutrient mobilities.

Method: Maize was grown in tandem with several cover crops, and noticeable differences are visible in the rhizosphere between maize and the mixture of maize and cover crops when cultivated in the same plot. In this study, these variants are investigated at the nucleic acids' level using 16s amplicon sequencing.

Results: The first results from amplicon sequencing data indicated a shift in the alpha diversity between time points of the growth phase, treatment types, and root depths after testing nine treatments against control (maize).

Conclusions: The variations amongst those combinations are mainly due to growing maize by re-rooting using the remaining cover crop roots in the sub-soil layers, separate growth phases of maize, and the depth of the root length influencing the functionality, the composition, and the role of the existing microbiota. Further analysis of the soil proteome will provide information about the dynamics of the bacteria and pathways in which they play a role in soil.

Response of Forest-floor Foodweb to Peregrine Earthworms in the American NortheastTimothy McCay¹, Sophie Pedzich¹, Coco Xie¹, Joy Tang¹¹*Department of Biology, Colgate University, Hamilton, United States*

Aim: Colonization of previously glaciated North America by exotic earthworms has been implicated in changes in ecosystem structure and function. However, our understanding of the ways in which earthworms interact with other members of the forest-floor food web is poor. Two waves of peregrine earthworms have been introduced to North America: European lumbricids and Asian megascolecids. We aimed to better understand the effect of both types of invasive earthworms on animals of forest-floor food webs.

Method: We sampled locations in central New York State, USA, which was glaciated during the Wisconsin Glaciation. At each location we sampled the earthworm community using fixed-area mustard vermifuge and the forest-floor food web using extraction from litter. Sites included those inhabited by lumbricids, megascolecids, and few (or no) earthworms.

Results: We found a strong, negative relationship between the biomass of earthworms and abundance of other invertebrates in the litter layer. This pattern was true across a variety of taxa and was likely mediated by the abundance of organic litter. Sites with only *Bimastos rubidus* had a high mass of leaf litter and large numbers of leaf litter animals despite high densities of this putative native earthworm.

Conclusions: Previously glaciated forests in North America were probably inhabited by few if any earthworms in the years since deglaciation. The addition of peregrine earthworms into these systems can lead to decreased diversity and abundance of other invertebrate animals. The continued expansion of peregrine earthworms in the US Northeast may continue to have negative consequences.

Dynamics of hypolithon development in the Namib Desert

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Aims:

Type I hypolithons are Cyanobacteria-dominated desert microbial communities that reside on ventral surfaces of semi-transparent rocks such as quartz, where they find shelter from the abiotic stresses of the desert soil surface. These communities are seen as key players in the nutrient cycling of soils in desert biomes. However, despite their importance, very little is known about hypolithon growth rates and community development pathways. The aim of this study was therefore to understand the dynamics of hypolithon formation in the pavements of the Namib desert.

Methods:

Replicate arrays of sterile translucent (Quartz and Marble) and non-translucent (Travertine) rocks was established in two areas of the Namib desert pavement with different annual precipitation regimes, and annual sampling was done over a period of seven years. This was coupled with eDNA extractions and 16S rRNA gene amplicon sequencing.

Results:

Our results show that in the area with higher precipitation, evidence of hypolithon formation could be observed in the translucent rocks three years after the arrays were established. This observation corresponded to a Cyanobacterial “bloom” in the microbial communities attached to these rocks at year three, when compared to the communities under non-translucent rocks and control soils. By comparison, no hypolithon development was observed in the area with lower precipitation, which corresponded to an absence or low abundance of cyanobacterial taxa.

Conclusions:

This study showed that hypolith development is dependent on cyanobacterial “blooms”, which in turn are driven by precipitation regimes. This study also determined three years to be the minimum time required for hypolithon development.

Supporting a Sustainable Transition from Peat-Use in Mushroom Cultivation

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Mushrooms are an important crop within Ireland. Due to the role of peat in current cultivation practices, the industry is under increasing pressure to become more sustainable. Peat is a non-renewable resource; its extraction damages bog habitats, driving biodiversity loss and releasing greenhouse gases.

Peat functions as “casing”, gradually releasing moisture to the fungal mycelium. This is essential for mushroom growth. Therefore, further to being sustainable, it is paramount that peat-alternatives produce comparable mushroom yield and quality to that of industry standard. Such a material will require similar physical, chemical and biological characteristics to peat. Despite previous efforts assessing the performance of novel casing media, the general suitability of peat-alternatives remains largely uncertain.

This research aims to determine the efficacy of peat-alternatives and how this may impact commercial mushroom production. Trials to date, conducted at an experimental scale, but reflecting commercial production practices, have focused on bark amended with chalk and sugar beet lime (5% by mass). Initial results from two replicated experiments have been promising but inconsistent and unpredictable. Mushroom biomass and quality were statistically comparable to peat-based casing ($P = <0.05$). However, from a commercial perspective, the bark-based casing has affected the timings of the mushroom emergence and the presence of other contaminant fungi, which are not acceptable from a commercial perspective. Studies are continuing to refine the experimental casing, focusing on better consistency of bark feedstock. Results obtained will contribute to ongoing research to reduce the dependency of mushroom production on peat.

Assessing the Total Microbial Population and Soil Characterizations of Former Mining Land for Agricultural Sustainability

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Aim

The purpose of this research is to identify the limiting factors on degraded land after mining activities that affect to soil biodiversity, as a basis for providing appropriate actions in the implementation of land reclamations.

Method

The sampling method used is a semi-detailed survey with a scale of map 1: 100,000 and characteristics of land assessment used Matching and Scoring method. The variables observed in this study are 1) Total Microbial population (TMP) 2) Land Use; 3) pH; 4) Soil Texture; 6) Soil Physic and Chemistry Properties.

Results

This research comparing the samples from the land-use categories, they are community plantations, forestry, and former mining land. According to Government Regulation of Republic of Indonesia Number 150 of 2000 concerning Control of Soil Damage for Biomass Production, TMP threshold is 10^2 cfu/g. The TPM results for each land category are lower than the threshold, which at 10^{-9} cfu/g. The former mining land sample (P.35) had a lowest result of 972×10^{-9} cfu/g. While the highest result (P.21) at 4×10^{-3} cfu/g. This is coherent with the pH results, P.35 (4.99) and P.21 (5.24), which indicate that a lower pH can have an impact on the biodiversity of the soil.

Conclusions

The output of this study is a land damage status map which can be used for the next step of land degraded improvement. The results demonstrated that soil biodiversity was significantly under the threshold in all land use categories. It is concluded that continuous land activities have an impact on soil biodiversity.

Effect of Increased Plant Species Diversity on Soil Nematode Faunal Assemblage in an Intensively-Managed Grassland

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Aim: Plant productivity, decomposition and nutrient cycling are controlled by plant-soil-biota interactions. Previous studies have shown that increasing plant species diversity results in increased biomass yields in intensively managed grasslands. In this study, we investigated how plant species diversity affect the soil nematode community and their associated indices in an intensively-managed grassland with the aim of studying aboveground-belowground interactions.

Method: Nematodes were extracted from 66 experimental plots differing in plant species diversity, comprising of six plant species within three functional groups (FGs). The FGs included grasses: ryegrass (*Lolium perenne*) and timothy (*Phleum pratense*); legumes: red clover (*Trifolium pratense*) and white clover (*Trifolium repens*); herbs: chicory (*Cichorium intybus*) and plantain (*Plantago lanceolata*).

Results: Results showed that the composition and diversity of the soil nematode differed significantly among the levels of plant species diversity. Specifically, plots with all six-plant species had a significantly higher nematode diversity, maturity index and proportion of sensitive taxa (omnivore and predators) than the others. In addition, the abundance of plant-feeding nematodes (herbivores) were significantly lower in the six species plots than in the monocultures. Also, increased biomass yield were obtained from the high-diversity plant communities.

Conclusions: Overall, our results support the hypothesis that increasing plant diversity in intensively managed grasslands will result in a positive effect on the belowground soil biota. Our findings contribute to knowledge of the positive effects of increased aboveground plant diversity on the belowground diversity of soil biota. This creates a pathway towards sustainability with reduced fertilizer inputs.-

Home-field advantage effects in litter decomposition is largely linked to litter quality

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Aim:

Climate change affects plant communities, potentially decoupling links between plants and their associated soil microbial communities. This may in turn affect processes like litter decomposition, hence nutrient and carbon cycling and many other ecosystem processes. Microbial decomposers have been proposed to specialise, being able to decompose easier litter from its 'home' community than litter from other communities, in what is termed the home field advantage (HFA).

Method:

We carried out a litter decomposition experiment including four alpine meadow communities ranging from the Atlas in Morocco to the Iberian Peninsula to the Swiss Alps. The experiment had a factorial design, including soil and litter from all four high-elevation communities. We tested whether litter decomposition rate would differ depending on litter and soil origin, expecting to find HFA in all of four alpine communities.

Results:

HFA ranged from very negative to neutral to positive along our geographical gradient, which could be attributed to the interaction between soil microbial communities, soil and plant traits, and climate. Litter decomposition depended on litter quality and on the fungal community, which seemed adapted to deal with poor-quality, recalcitrant litter, leading to positive HFA. Phyllosphere communities competed with soil communities when in interaction, a fact that may have blurred results of some previous HFA experiments.

Conclusions:

There seems to be positive HFA in systems with low-quality litter that requires a specialised fungal community to maximize decomposition. By contrast, high-quality, easy to decompose litter would be dealt with by any decomposer community, not showing positive HFAs.

Understanding the Drivers of Belowground Functional Diversity Across Europe

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Aim:

The recent trend of land use intensification within Europe poses a threat to the ability of the soil community to sustain soil functions (nutrient cycling, carbon sequestration, water regulation, disease suppression, and primary production). In order to predict soil functions and their resilience to disturbance across the heterogeneous landscapes of Europe an increased understanding of the drivers of the spatial distribution of belowground organisms is needed. Soil food-web dynamics and community traits are much stronger predictors for soil functions than species diversity. Therefore, shifting the focus from biogeography to functional biogeography could facilitate the link to soil functions. Nematodes are present throughout the soil food-web and can thus function as indicators for soil food-web dynamics. Within this study I aim to uncover how soil forming factors (climate, organisms, relief, parent material and time) drive belowground functional diversity across Europe, using nematode-based indices of soil food-web dynamics as a proxy of functional diversity.

Method:

Data on nematode diversity was obtained from open-source databases of nematode community studies across Europe. Additionally, soil maps were consulted to gather data on environmental and soil physical properties. I used structural equation modelling to assess the relative importance of different soil forming factors in driving the functional diversity of nematodes.

Results:

The relationship between soil forming factors and nematode functional diversity differs for the different nematode-based indices of soil food-web functioning.

Conclusions:

Soil forming factors play an important role in driving belowground diversity.

Soil microbes are passengers in the community development of early successional dune ecosystems

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Aim:

We aim to answer the research question on plant-soil interactions: whether soil microorganisms are “drivers” or “passengers” of ecosystem dynamics

Method:

A field experiment was conducted in an early successional dune ecosystem. We manipulated the soil community by adding living and sterile soil inocula, originating from natural ecosystems, and examined the responses of soil and plant communities to the soil inoculation treatments during three years.

Results:

The experimental manipulations had a persistent effect on the soil microbial community with divergent impacts of living and sterilized soil inocula. Plant community was also affected by soil inoculation, but there was no difference between the impacts of living and sterile inocula.

There was also an increasing convergence of plant and soil microbial composition over time.

Conclusions:

Based on these results, we concluded that the soil microorganisms acted more as “passenger” (soil microbial community dynamics followed changes in the plant community) rather than as “driver” (soil microbial community patterns drive host plant community). These findings give valuable insight into the further understanding of the community assembly of plant and soil microorganisms under natural conditions, and are directly relevant for ecosystem management and restoration.

Impacts of climate change and land use on soil energy fluxes

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Soil organisms and their diverse interactions provide essential ecosystem functions and services through a variety of mechanisms, making them an important resource for human well-being. However, global change drivers such as climate change and modern land use threaten to alter this critical role, as they do not act in isolation from each other, making ecosystem consequences difficult to predict. To address this knowledge gap, we used a large-scale field experiment to investigate the interactive effects of climate change and land use type on the belowground food web. We measured soil microbial activity, identified soil nematodes, mesofauna and macrofauna, and measured their length and width to determine the energy flux of the belowground food web. We tested food web responses in an ambient and future climate scenario (+0.6°C temperature increase and changing precipitation patterns) in four land use types (conventional cropland, organic cropland, intensive grassland and extensive grassland) to draw conclusions about changes in key ecosystem functions such as decomposition, pest control, and belowground herbivory.

BioDivSoil: Evaluation of an eDNA Based Approach in Ecological Soil Monitoring

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Aim:

Currently, determining the composition of soil biodiversity often still ends at the boundary of endogeic life. Lack of expertise and the high time effort, besides the disregard of endogeic organisms, are the main reasons for this obvious gap in many monitoring projects. By directly comparing a classical survey of endogeic soil organisms (oribatids, collembolans) and the extraction of eDNA from soil cores, we aim to evaluate a possibility for a faster and less time-consuming procedure for soil monitoring.

Method:

For the comparison of the two methods, a subset of five soil cores were pricked four times at each of 26 sites, which were subsequently used for the extraction and sequencing of the eDNA. In addition, 10 soil cores were taken at each site, from which oribatids and collembolans were extracted and identified morphologically to species level.

Results:

Through the results, general statements can be made about the quality of the molecular biological approach (eDNA) compared to the classical method used so far. Furthermore, due to the different spatial proximity of the soil cores to each other, further conclusions for a standardised collection of eDNA samples from soils can be derived to contribute to improved and comparable study designs in the future.

Conclusions:

Correctly applied, eDNA sampling can play an important role in ecological research and conservation. Due to the faster generation of results and the less stringent demands on the user's prior training, this eDNA approach has promising and decisive advantages over current practice.

Effects of Enchytraeids on N Mineralization from Crop Residue in a Japanese Organic FieldRisako Kato¹, Koki Toyota¹¹*Tokyo University of Agriculture and Technology, Koganei, Japan*

Aim: To supply more N which is the main factor restricting yields of organic farming, promoting N mineralization is one option. In preliminary experiments comparing 10 fields, there was a significant relationship between enchytraeid population and the amount of available N, suggesting that enchytraeids may promote N mineralization. In this study, we focused an organic field that had the highest population of enchytraeids and amount of available N and aimed to evaluate the effects of enchytraeids on N mineralization by microcosm experiments.

Method: We added 0.2% mung bean residue as a model organic matter and 6 individual (ind) enchytraeids/45 g of soil and then set up 4 treatments: 1)(-)Enchytraeid, 2)(+)Enchytraeid, 3)Mung bean(-)Enchytraeid, 4)Mung bean(+)Enchytraeid. After 4 and 12 weeks of incubation at 25°C, we destructively analyzed NO₃-N, NH₄-N, faunal populations (enchytraeids, nematodes, rotifers), available N and mean weight diameter (MWD) of soil aggregates.

Results: Enchytraeids promoted N mineralization in the treatment added with mung bean by 23% at 12 weeks, but not at 4 weeks. The number of enchytraeids increased from 0 to 4 weeks and then decreased from 4 to 12 weeks (236±102 ind/20g, 4±2 ind/20g, respectively). The addition of enchytraeids had no effects on available N and MWD.

Conclusions: We concluded that enchytraeids promoted N mineralization from crop residue and it took a long time such as 12 weeks. Furthermore, enchytraeids did not promote N mineralization from soil organic matter. These results suggest that soils with diverse fauna including enchytraeids have a high N-supplying ability.

Root Traits Explain Multitrophic Interactions of Belowground Microfauna on Soil N Mineralization and Plant Productivity

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Aim

Both herbivorous and bacterivorous microfauna have been proven to influence root development, soil N mineralization, and plant productivity. Yet, our limited knowledge on these effects is mainly based on investigations ignoring multitrophic interactions. Here, we aimed to investigate whether and how herbivorous and bacterivorous microfauna, separately and in combination, affect plant biomass through root traits and/or soil N mineralization.

Method

To do so, Italian ryegrass (*Lolium multiflorum*) was cultivated in a full factorial experiment with the absence and presence of herbivorous nematodes (*Pratylenchus zeae*), bacterivorous protists (*Acanthamoeba castellanii*), and bacterivorous nematodes (*Poikilolaimus oxycercus*).

Results

Our results showed that root traits coordination in response to soil microfauna was consistent with the root economics space concept with its two main dimensions: root diameter and specific root length (RD-SRL); root nitrogen concentration and root tissue density (RNC-RTD). Bacterivorous nematodes increased while herbivorous nematodes decreased plant productivity. The negative interaction between herbivorous and bacterivorous nematodes on plant productivity at high herbivorous nematodes infestation could be explained by reduced N mineralization and variation in the RNC-RTD axis aligned with herbivorous nematode density in roots. Further, no conclusion could be drawn on the effect of bacterivorous protists due to unsuccessful soil colonization.

Conclusions

This study revealed that herbivorous and bacterivorous nematodes interactively affect plant performance via root traits coordination and N mineralization, and for the first time suggests the value of the root economics space concept for interpreting phenotypic root plasticity and functioning in response to local biotic factors.

Forest management impact on soil food web: the key role played by the understory vegetation

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Aim: Forest management methods contribute to maintain sustainable forests notably by increasing their resistance and resilience to climate change. Forest thinning, one of the main management practices, induces change in understory vegetation and microclimatic conditions which can have cascading effects on soil biodiversity. This thinning treatment can be coupled to an understory vegetation removal. During the past decades, a strong attention was paid on the responses of soil microbial communities to these forest management practices, while our knowledge on their impacts on soil fauna still very limited.

Method: we studied the whole soil food web (microorganisms-microfauna-mesofauna-macrofauna) in a *Pinus halepensis* forest located in southern France along a tree cover gradient made up of three pine densities (control, medium and high thinning intensities) with or without the presence of an understory vegetation. In addition, we sampled the soil organisms in spring and at the end of the summer period to study in which extend forest management practices mitigate the negative impact of the summer drought period.

Results: First results highlight a decrease in soil fauna abundance and diversity with the increase of thinning intensity. Whatever the thinning level considered, the presence of an understory vegetation increases soil fauna abundance and diversity. Soil fauna community is more negatively affected by the summer drought period in thinned plots while the presence of the understory vegetation alleviates this negative effect.

Conclusions: These results point out the key role played by the understory vegetation in structuring the soil food web and mitigating the negative impact of summer drought period.

Mycotron Experiment: a Common-garden Approach for the Quantification of Mycorrhizal Interactions and Impacts

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Aim: Mutualistic relations between plants and soil fungi, mycorrhizae, control carbon fluxes between atmosphere and soil. Mycorrhizal types differ in eco-physiological traits making ecosystems dominated by vegetation featuring a particular mycorrhizal type to exhibit specific biogeochemical properties. Due to the complexity of field studies, quantitative relationships between mycorrhizal abundances, intensity between mycorrhizal interactions, and mycorrhizal impacts on ecosystem functioning remain poorly understood. We present a field experiment “Mycotron”, where we established vegetation series featuring three mycorrhizal types - Ericoid (ERM), Ecto- (ECM) and arbuscular mycorrhiza (AM), in varying plant biomass proportions, to quantitatively assess mycorrhizal impacts on ecosystem functioning.

Method: The experiment is located at Hoge Kempen National Park, in Belgium. Plant species featuring AM, ECM, and ERM are planted in different combinations, creating the following experimental treatments: three pure mycorrhizal types; six mixtures of two mycorrhizal types, varying in levels of dominance; one mixture of three mycorrhizal types. Plant species were selected to vary only in mycorrhizal types, but to feature similar eco-physiological traits.

Results: This experiment constitutes a unique testbed for quantitative assessments of mycorrhizal impacts on a large variety of ecosystem functions. Examples of possible targeted experimental assessments and techniques, enabled through this experimental setup, include soil food web analyses, assessments of biochemical cycles, as well as functioning and abundance of mycorrhizal fungi themselves.

Conclusions: Our approach allows addressing knowledge gaps of mycorrhizal functioning which are impossible to cover with current field studies, and will aid quantitative assessments of the significance of mycorrhizal types and their interactions.

Influence of graphene oxide nanoflakes on microbial communities of a metals and hydrocarbons co-contaminated soil

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Nowadays, nanomaterials are widely used as remediation approach. However, the effect of some nanomaterials on soil components, whether biological or physicochemical, has not been well clarified. In this regard, graphene oxide (nGOx) is a novel extremely oxidative form of graphene with known capacity to remediate metals in different environments. Although, many studies have reported that nGOx could have different effects over isolated microorganism, there are only few studies describing the global changes on soil microorganisms. In addition, taking into account the direct effect that nGOx may have on soil microbiome, it is also important to analyse how the microorganism communities are affected by physicochemical changes caused by graphene oxide addition. The main objective of this study was to conduct an in-depth study of microbial communities changes caused by GOx addition in a co-contaminated soil. In order to elucidate interactions mechanism of nGOx, polluted soil and microorganism, several assays were performed. Four microcosms experiments with metals, arsenic and hydrocarbons co-contaminated soil were designed (control, addition of nGOx, addition of nutrients, and combined addition of nutrients and nGOx). Changes on pollutants and microbial communities were monitored for 90 days. The results should facilitate a better understanding of the effects of GOx on soil and an advance in the analysis of its usefulness in remediation technologies.

Textile Composting: An Avenue for Clothing Waste Management, Mitigating Climate Change, and Regenerative Agriculture

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Abstract.

The average American throws away 82 pounds (lbs.) or 37 kilograms (kgs) of clothing per year for a total of 17 million lbs./7.7 million kgs annually; 15% of that is donated or recycled while the other 85% is landfilled or burned, leaching toxins into the air, soil, and groundwater. Ericka Leigh of Sewn Apart is leading a pilot project to explore solutions to textile waste management.

Aim.

Rather than landfilling fabrics or shipping them overseas, Sewn Apart in partnership with the Patel College of Global Sustainability (PCGS) at the University of South Florida (USF) started a textile composting project at Rosebud Continuum Sustainability Education Center to explore reducing textile waste by composting it instead.

Method.

Textiles were composted two ways, one used whole cotton sheets as landscape fabric; the other method used shredded fabric pieces mixed with food scraps, shredded paper, and mulch in a compost pile.

Results.

Shredded bamboo fabric decomposed the quickest in the compost heaps and cotton landscape fabric disintegrated in three months. At the time of this writing, we have composted 300 lbs/136 kgs of textiles and 500 lbs/226 kgs of food and created over 250 lbs/114 kgs of soil organic carbon. The composted clothing soil was tested and showed high levels of calcium, magnesium, and zinc.

Conclusion.

More testing needs to be done to determine carbon sequestration levels. All data suggest that scaled appropriately, unwanted textiles made of natural fibers could be composted rather than landfilled and have a net positive impact on the environment.

Microbial Communities in Different Components of an Alpine Grassland Ecosystem

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Aim:

Biodiversity is a central keyword of the 21st century and is gaining even increasing attention in the light of global change. Whereas traditional concepts of studying microbial diversity consider individual components or taxa in a given habitat (e.g. bulk soil, plants, earthworms), these concepts neglect that complex interactions and co-occurrences of microbial communities may exist between these components.

Methods:

The prokaryotic and fungal community composition of different sample types (components), including bulk soil, rhizosphere soil of *Carex* spp. and *Festuca* spp., members of the micro- (nematodes), meso- (collembolans), and macro- (earthworms, ground and rove beetles) fauna, as well as fecal samples of wild mammals (hare, deer) and domestic livestock (cattle, equids) are investigated by amplicon sequencing along an elevational gradient from 1000 to 2500 m a.s.l. A meta-dataset of soil properties, soil microbial and meteorological data contributes to the interpretation of the community data of the almost 2000 samples within the alpine grassland ecosystem.

Results:

Soil, rhizosphere and faunal samples each have unique microbial communities, but these microbiota overlap to different degrees, depending on functional traits, trophic relationships and elevation. Our data indicate connections between microbial communities of different ecosystem components and that certain animals can serve as vectors for various microorganisms. Generally, results reveal key drivers for the microbial biodiversity within the different components of alpine grasslands.

Conclusions:

Our data prove – even across the elevation gradient – connected microbial communities in alpine pastures and allow conclusions about the sensitivity of the complex interactions especially in light of climate change.

EUdaphobase - building bridges between cohabiting soil communities, environments, and methodologies

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Aim: Edaphobase is a database previously constructed by the Senckenberg Natural Museum in Görlitz in Germany for the purpose of connecting soil invertebrate taxa to their environment. To extend Edaphobase into a warehouse for data on soil biodiversity at the European level and improve its usefulness, COST Action “EUdaphobase” was launched. Action gathers a network of European specialists working on enlarging existing capacities, and improving the technical capabilities, to provide a unique database that would be used by the different levels of stakeholders (from farmers, research and education institutions to decision makers). Taxonomists, ecologists, modelers of soil ecosystem processes, financial and IT specialists joined to form a holistic picture of soil biodiversity and introduce it into the decision-making process in Europe.

Method: WG 7 of EUdaphobase is focused on two goals - to enable a framework for integrating the data on fungi, bacteria and microeukaryotes, and collating the data derived by molecular methods (metabarcoding, NGS-based, environmental DNA/RNA), on all soil organism groups.

Results: The highly demanding technical problems of incorporating fungal and molecular data into the already existing framework of Edaphobase were resolved. The joint work of researchers working on different soil organisms and techniques resulted in the unique possibility for a variety of users to provide/analyze/use data that include cohabiting taxa, their environments, and mutual relationships.

Conclusions: The outcome will enable the usage of the upgraded Edaphobase for holistic soil state evaluation and monitoring, as well as monitoring of the dynamics of soil communities/environments involved in different ecosystem services on the European level.

The impact of drought on the wheat microbiome and its consequences for soil functioning

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Aim: Frequency and severity of drought are projected to increase due to climate change. Drought can affect soil microbial communities, which are crucial to maintain soil functions that are relevant for crop production. Conventional and conservational agricultural management systems promote contrasting soil microbial communities with potentially different capacities to buffer soil functions against drought. This project aims to better understand the effects of drought on the soil microbiome and its cascading effects on soil functions under different agricultural management practices to ultimately improve the climate resilience of cropping systems.

Method: An on-field drought simulation with rainout-shelters and a controlled climate chamber pot experiment have been established to investigate effects of drought on the taxonomic and functional diversity of root-associated microbiomes in wheat using metabarcoding and shotgun metagenomics. The field experiment will assess the resilience of root-associated microbiomes to drought in conventional and conservational agricultural systems. The plant, soil and microbiome interplay during drought will be studied using stable isotope labelling and plant metabolome profiling. To quantify the microbial contribution to plant drought tolerance, untreated and γ -irradiated soils were compared in the climate chamber experiment.

Results: Data on both experiments have been generated and are currently analysed. Preliminary results from the climate chamber experiment showed that microbial community composition gradually shifted with a 50% and 75 % water reduction compared to the control.

Conclusions: The results from this project will help to elucidate the potential of different agricultural systems to promote soil microbiomes that improve the climate-resilience of crop production systems.

Temperate Alley-cropping Improves Soil Micro-arthropod Biodiversity and Biological Quality on Arable Farms in Eastern England

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Aim:

Conventional agriculture places unsustainable pressure on soil microarthropod communities, threatening the essential soil processes and services they underpin. Alley-cropping, an agroforestry practice incorporating parallel tree rows into agricultural fields, has been shown to enhance biodiversity on agricultural land. However, there remains a distinct paucity of information on how tree rows influence soil microarthropods despite their invaluable role in soil functioning, a literature gap this study aimed to address.

Method:

Three composite soil samples ($n = 6$ per treatment) were collected in April–June 2022 from paired arable alley-cropping and monoculture fields on five UK farms. Soil microarthropods were extracted using Berlese-Tullgren funnels and identified morphologically to order/family level. Samples were assigned a biological quality score according to the QBS-ar index. Microarthropod abundance, diversity, and biological quality were compared between land-uses and as a function of tree row distance (i.e., 0, 2, and 24 m).

Results:

Alley-cropping systems supported higher soil microarthropod abundances, α diversity, and biological quality compared to their monoculture counterparts, with gains primarily concentrated in the tree rows but extending into the crop alley. Multiple soil physical and chemical parameters influenced by tree row presence regulated microarthropod communities.

Conclusions:

Tree rows improve soil biological quality and microarthropod biodiversity on arable farmland. This is likely to be through reduced disturbance and beneficial alteration of soil environments by trees. The greater potential for biological activity associated with higher soil biodiversity positions alley-cropping as a more sustainable practice for arable farmers, capable of concurrently delivering multiple ecosystem services.

Above- and Belowground Biodiversity Following Herbicide Application Post WildfireTanner Hoffman¹, Linda van Diepen¹¹*University Of Wyoming, Laramie, United States***Aim:**

Our aim is to understand responses of the soil microbial community structure and function to the application of a pre-emergent cellulose biosynthesis inhibiting herbicide (indaziflam) immediately post wildfire in a sagebrush steppe/shortgrass prairie ecosystem.

Method:

Following a wildfire in southeast Wyoming, USA, 21 sites were selected for soil sampling representing burned and unburned ecosystems that have either been treated or not treated with the herbicide indaziflam. A variety of biological, and chemical analyses are being performed to compliment a surveying effort by the United States Department of Agriculture Forest Service, who are looking at species level vegetation cover in order to observe the effectiveness of this herbicide, and measure any unintended consequences on native vegetation. The soil analyses being performed include amplicon sequencing to capture bacterial and fungal diversity, phospholipid fatty acid analysis for microbial biomass analysis, extracellular enzyme assays for microbial functional traits, and soil available nutrients, pH, and organic matter content.

Results:

Preliminary results from three months post herbicide treatment indicate minimal changes in soil biological, chemical and physical properties. Alpha, and beta diversity for bacteria and fungi was not affected by herbicide application, although the relative abundance of the bacterial phylum Nitrospirae is negatively influenced by treatment with indaziflam.

Conclusions:

Soil Microbial diversity and function does not appear to be heavily impacted by the herbicide indaziflam in the short term. Additional analyses over time will reveal potential residual effects of indaziflam application on soil microbial and native plant community recovery following wildfire.

From Darwin to SOC-D: building rich earthworm metadatasets for predicting soil biodiversity, functions and health

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Aim: The project aimed to build a compendium of data sources and rich metadatasets on earthworms and associated environmental conditions in the British Isles and Ireland, to support data analysis and modelling, and provide an open resource for the research community.

Method: Several international initiatives have collated earthworm and environmental data but none have systematically gleaned the available data sources covering the British Isles and Ireland. A systematic literature search was conducted to find data sources using Web of Science and Google Scholar, as well as directly from original authors/data holders where possible. Meta-data recorded covers the type of quantitative earthworm data (i.e. incidence, abundance, biomass, taxa), methodological details (e.g. sampling method/s, location/s, whether sampled plots were natural or experimental, sampling year/s), and environmental information (e.g. habitat/land-use, inclusion of climate data and basic soil properties).

Results: The initial compendium of field-based earthworm data sources and associated meta-data from across the United Kingdom and Ireland was published as an open resource ('WormSource'). It contained 257 sources published from 1891 to 2021. The most common habitat category across data sources was grasslands (62%), followed by arable (32%) and woodland (22%). An R Shiny app has been developed for researchers to explore the metadata in more detail.

Conclusions: Understanding how earthworms may respond to land use and climate change is vital to predict impacts on soil functions and health. Our approach to systematically glean available data sources has facilitated data extraction and synthesis for modelling, mapping and benchmarking of earthworm communities.

Interaction Between Root Phenotypes and Microbiomes in Maize Under Nitrogen Deficiency and Drought

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Aim: Plant performance under stress is influenced by the interaction between roots and associated microbial communities. However, the synergism between root phenotypes (i.e., root architecture and anatomy) and microbiomes has been poorly explored. The aim of this study was to identify and characterize maize (*Zea mays* L.) genotypes with potentially favourable combinations of resource-efficient root phenotypes and beneficial microbiomes under nitrogen deficiency and drought.

Method: We screened 28 maize inbred lines and 6 landraces for plant performance, root phenotypes, and rhizosphere microbial community composition under nitrogen deficiency and drought in the field. Laser ablation tomography for the evaluation of root anatomical traits and metabarcoding of ribosomal markers for microbiome characterization were used. Promising associations between root phenotypes and microbiomes identified in maize genotypes with improved performance will be further characterized in greenhouse mesocosms by analysing plant and soil metabolites, root phenotypes and functional traits of microbiomes under nitrogen deficiency and drought combined.

Results: Preliminary results show that bacterial diversity in the rhizosphere decreased under drought compared to the control conditions, and increased under nitrogen deficiency compared to the optimally fertilized plots, with variability between genotypes. Moreover, drought had a stronger influence on bacterial community structure compared to nitrogen deficiency.

Conclusions: Targeting potentially beneficial associations of root phenotypes and microbiomes might be implemented in the future to develop more resistant and resilient cultivars under resource-limiting conditions in the context of sustainable agriculture.

Global Soil Atlas: Bridging Biodiversity and Biotechnology with NGS

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Aim:

Basecamp Research is a company built on the belief that nature has already designed solutions to our planet's greatest challenges. We are mapping global soil microbial biodiversity to ethically discover biology-based solutions for a wide range of sustainable industries. While doing so, we build academic, national, and land management partnerships to help partners better understand and manage the biodiversity their land encompasses.

Method:

We partner with biodiversity guardians to develop ethical access and benefit sharing (ABS) agreements to sequence DNA from around the world. Our field team uses mobile laboratories to generate whole genome sequencing (WGS) data and environmental metadata (e.g. climate, land use, soil chemistry) - this builds a knowledge graph for the identification of novel industrially-relevant proteins.

Results:

We have collected >1000 samples with 40 different stakeholder groups across 16 countries to build an open-source atlas of soil bacterial diversity, which we use to draw inferences on drivers of soil microbiome composition and productivity. We have completed some of the largest microbial biodiversity studies across National Parks internationally, such as the Azores - in which both terrestrial and marine environments were sampled. We also work with specific landowner questions, for example with rangeland landowners in Oregon, USA we are sampling soils in various annual invasive grass colonisation states to address the impacts on soil microbial communities.

Conclusions:

We believe that connecting biodiversity and biotechnology will allow us to build a world that both recognises the value of our planet's biodiversity and learns from nature to build a cleaner, greener future for all.

Linking Community, Trait and Phylogenetic Ecology in Soil Animal Diversity Research

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Aim:

Recent developments in molecular methods, phylogenetics and functional trait ecology have overcome the perplexity of studying biodiversity in cryptic ecosystems, such as soil. Here I demonstrate an analytical pipeline in R that integrates community, trait, phylogenetic and environmental data in testing following hypotheses: (1) Traits are functional and informative, i.e., they differ in communities across environmental gradients or among different habitats. (2) Assembly processes (e.g., filtering and partitioning) are revealed by similarities of traits in local communities, but results depend on trait types and environmental contexts. (3) Different combinations of traits represent multidimensional niches of species, revealing both filtering and partitioning processes at work in the same communities. (4) Evolutions of traits are random processes, i.e., no specific directions but following the Brownian Motion model, that result in a non-random phylogenetic signal in trait values across species, but species evolutions in multidimensional trait space show convergent patterns. (5) In multidimensional trait space rare species occupy niches left behind by abundant species. (6) Partitioning over filtering processes drive community assembly of rare species and especially in stable habitats with ample resources.

Method:

I used trait-based approaches in community ecology and phylogenetic comparative methods in evolutionary biology to demonstrate both ecological and evolutionary processes of traits underlying contemporary soil animal communities.

Results:

The results will be presented with several empirical datasets of soil animals.

Conclusions:

By providing complementary information to traditional taxonomy-based studies on soil biodiversity, functional traits and phylogenetics of species help to predict soil animal responses to environmental changes.

Root-associated microbiome network connectivity and composition linked to disease resistance in strawberry plants

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The diversity and interactions between root-associated microorganisms could play an essential role in plant health and promote the resistance to soil-borne diseases in commercial crops. Yet, evidence of these interactions under field conditions, relevant to commercial production, and understanding of their main drivers is still scarce. By characterizing the prokaryotic and fungal community (via 16S rRNA and ITS, respectively) in the rhizosphere and roots of three strawberry cultivars with different resistance to the soil-borne fungal pathogen *Macrophomina phaseolina*, we tested the hypothesis that resistant cultivars assemble distinct bacterial and fungal communities that foster microbial connectivity and mediate disease resistance. Our results show that the soil-borne pathogen, *M. phaseolina*, does not perturb the rhizosphere and roots microbiome of three different strawberry cultivars with varying degree of resistance to *M. phaseolina*. Microbiome comparative analysis indicated that the highly susceptible cultivar Sweet Ann assemble a distinct microbiome that shows poor network connectivity, whereas more resistant cultivars were enriched in potential beneficial microbes and showed higher network connectivity. Collectively, these results suggest of genetic traits in the plant host that could be involved in the assembly of beneficial microbiome members. Our study reinforces the eminent role of the plant microbiome as trait of selection in breeding programs and stresses further understandings of the genetic and biological mechanisms that mediate microbiome assembly. Uncovering these mechanisms will be key for future plant breeding programs and susceptibility in agriculture.

Soil Macrofauna State of Knowledge in the World Using Science Data Tools

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Aim: Estimate the state of knowledge of soil macrofauna in the world. **Method:** A dataset with 14,947 article records was obtained from a bibliographic search performed in Web of Science between 2011 and February, 2022. A database with these records was built in PostgreSQL and connected with the R statistical program enabling customized queries with keywords of interest and elimination of redundant articles. The Microsoft Excel version 2019 was used to build graphs and maps based on analysis of 8044 article records of authors from 94 different countries. **Results:** USA and China stood out with >1000 articles, followed by India and Brazil with > 600 articles and European countries such as France, Germany, United Kingdom and Italy. South Africa and Australia appeared within the top 20 countries, but many African countries showed no records on macrofauna studies. Earthworms are the most studied soil macrofauna organisms so far, present in 52% of the articles analyzed, followed by coleopterans (18%), ants (11%) and termites (6%). Earthworms are mainly used as indicators, in soil quality, taxonomy, bioturbation and composting studies and are also the most used in molecular studies and ecotoxicology. Coleopterans are the most frequent in articles on biological control and pitfall method. **Conclusions:** The results reveal there is a need to fill soil macrofauna knowledge on different taxons and especially in the tropical region.

Effect of *Epichloë* endophyte on ryegrass plant and soil microbiome - a field studyShengjing Shi¹, Sandra Young¹, Emily Gerard¹, Russell Croy¹, David Hume¹¹*Agresearch, Selwyn District, New Zealand***Aim:**

Perennial ryegrass (*Lolium perenne*) is the most common livestock forage species for pastures in New Zealand and other temperate countries. It can form mutualistic symbiosis with a shoot endophytic *Epichloë* fungus which produces a diverse range of alkaloid metabolites protecting plants from invertebrate pest damage. There is limited understanding of the effect of *Epichloë* on plant-associated and soil microbiomes. We aimed to address this knowledge gap and examine whether such effects are *Epichloë* strain dependent.

Method:

A field trial was established with six ryegrass cultivar/ *Epichloë* strain combinations, enabling comparison of *Epichloë* strain specific effects as well as cultivar/strain interactions on plant and soil microbiomes. Samples were collected when plants were 4-month-old and at the peak of alkaloid production. Microbiomes associated with bulk soil, rhizosphere soil, endophytic roots and shoots were processed and analysed using MiSeq 16S and ITS sequencing. The microbiomes associated with seeds used for the trial were also examined.

Results:

Strong *Epichloë* effects were detected for seed and ryegrass shoot microbiomes, and different strains of *Epichloë* showed various impacts on specific microbial phylum and classes. *Epichloë* effects were also detected in root, rhizosphere and soil microbiomes, particularly for bacterial communities.

Conclusions:

The aboveground shoot endophyte *Epichloë* not only impacted shoot microbiome but also belowground microbiomes (root, rhizosphere and soil). Some of the impacts were strain specific. Other samples from various time points were collected to further investigate whether such impacts are transient (e.g., during peak of alkaloid production) or long-lasting.

Spatial and temporal variation of soil microbiome across NZ dairy farms

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Aim: The soil microbiome plays critical roles for many soil functions. However, managing soil microbiome for agriculture gains is a serious challenge, partly due to the highly dynamic nature of soil microbes and unclear drivers of such variation. We aimed to understand soil microbial variations in dairy farms across New Zealand (NZ).

Method: Soils from thirty farms over three regions across NZ were sampled. Two farms from each region were sampled seasonally. Detailed spatial variability was determined from 32 soil cores taken from a single field (100 × 50 m) in one region. DNA was extracted from soils and analysed using MiSeq 16S and ITS sequencing.

Results: High microbial diversity was detected within NZ pasture soils. Region had a strong influence on both soil bacterial and fungal communities, while seasons had a minor impact. Approximately 15% of bacterial OTUs and 19% of fungal OTUs were present in all 30 sites. Spatial variation of soil microbiome within a single field was greater than the seasonal variation in that region. Several soil properties (e.g., soil pH, moisture, Olsen P and C/N ratio) and nematode population significantly correlated to soil microbiomes.

Conclusions: Our study revealed the different scales of soil microbial variations and potential drivers for soil microbiomes in NZ dairy farm soils. Common microbial taxa present across 30 sites were also identified. This knowledge is important in designing robust sampling strategies for soil microbiome studies and for moving towards managing soil microbiomes for productivity and environmental gains.

The Importance of Organic Layers for Soil Microbial Diversity Preservation: The Case of Brazilian Amazonia

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Aim:

Despite its role as a source of energy and nutrients in tropical forests, soil organic layers have been overlooked as essential habitats for soil microbes. We argue that bacterial diversity has been underestimated by not taking them into account. We used a tropical forest in Eastern Amazon and an adjacent pasture as model systems.

Method:

Seven distinct layers were identified on the forest floor, including the unfragmented and fragmented litter, a transition between the fragmented litter and the H horizon (subdivided into three layers), and the soil mineral layer. Four layers were identified in the pasture: the unfragmented and fragmented litter, the soil mineral layer, and the rhizosphere soil. DNA was extracted, and the 16S rRNA gene was sequenced with the Illumina platform. Functional groups involved in the N cycle (nitrifiers, N₂-fixing bacteria, denitrifiers) were quantified by qPCR.

Results:

Our results show a community composition gradient from the litter toward the soil mineral layer. Taking the organic layers into account significantly increased the diversity estimated in both systems. The most striking finding was the organic layers' higher bacterial diversity and abundance. In the pasture, virtually all functional groups were more abundant in the fragmented litter; in the forest, they were abundant in the H horizon, except for nitrifying bacteria, which were more abundant in the litter.

Conclusions:

The results show that the organic layers in forest and pasture harbor significant bacterial diversity and may be crucial for maintaining the N cycle in these systems.

Comparison of Microarthropod Faunal Indices Calculated from Urban Gradient Data

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For soil quality assessment - several methods based on use of faunistic indices have been proposed. For soil microarthropods there exists two groups of methods: methods based on a single taxonomic group such as Rusek's method for Collembola, Beger-Parker index for Oribatida, Ruf's maturity index for Mesostigmata, and methods using data from two or wider spectrum of taxonomic groups such as Bachelier's density ratio index, QBS, QBSar, and F'c. No comparison of these methods has been performed so far. We compared various methods and faunistic indices calculated from small sample sets collected in 21 urban habitats along the urban-rural gradient in the city of Riga (Latvia). The vector of axis calculated by NMS, describing the effects of urban environment on microarthropod community, was used as a measure of strength of anthropogenic pressure on microarthropod community. Of all the tested indices, statistically significant ($p < 0$) correlations with this axis were found only for three indices ($R_{F'c} = 0.946$, $R_{QBS} = 0.625$, $R_{Berger-Harper} = 0.542$). Although F'c showed the best results, it's use can be limited by the high labour intensity connected with the identification of the collected material to the species level. QBS was the most optimal in this respect because its calculation for more easily identifiable higher-level taxa are used.

Species-specific eDNA analysis of the bioindicator species in soil ecosystem, *Allonychiurus kimi* (Collembola: Onychiuridae)

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Aim:

Since the identification and counting the collembolans in the soil is a laborious and costly procedure, environmental DNA (eDNA)-based biomonitoring was proposed as an analysis tool of collembolan species found in the soil.

Method:

In this study, standard primer sets for the species-specific eDNA analysis using *Allonychiurus kimi*, a soil bioindicator species was selected. Then, the primers were tested for specificity and sensitivity from the soil samples. Two different eDNA samples were tested: 1) eDNA samples were extracted from the soil with *A. kimi* individuals (intra-organismal eDNA). 2) the samples from the soil without *A. kimi* individuals (extra-organismal eDNA).

Results:

The two primers were confirmed in their sensitivity and specificity to the two types of eDNA samples selected. Ct-values from both intra- and extra-organismal eDNA showed the significant correlations to the number of inoculated *A. kimi* (adj. R² = 0.7453 – 0.9489).

Conclusions:

These results suggest that in excretion, egg, and other exuviae had a significant effect on eDNA analysis from soil samples taken. Furthermore, our results suggest consideration of variables for other inorganic environmental factors that should be considered when analyzing eDNA collected from soil.

Assessing relationships between microbial communities and soil carbon across depths in perennial cropping systems

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Aim: Microbial communities in soils have a tremendous influence on soil biogeochemical cycles, yet much remains unknown about their role in carbon sequestration, especially in subsurface soil layers. Recent work suggests subsurface soil layers have a larger potential for long term carbon sequestration due to differences in mineral composition and microbial community composition and activity. However, these potential relationships have yet to be explored. In this study, we seek to investigate how soil microbial communities along with soil carbon shift across subsurface layers in two perennial semi-arid agroecosystems in California.

Method: Using Next-Generation Sequencing methods, we will compare bacterial and fungal taxonomic composition and diversity across four soil layers (0-15cm, 15-30cm, 30-60cm, 60-100cm) in grape and almond production systems. We will also measure CO₂ respiration, microbial biomass carbon, particulate organic carbon, and mineral-associated organic carbon to understand linkages between soil microbial communities and soil carbon across these depths.

Results: Given the differences in soil physicochemical properties at different depths, we expect microbial community composition, diversity, and activity will be altered at deeper soil layers with corresponding changes to carbon sequestration potential. Specifically, we hypothesize with lower microbial diversity and activity, the potential for carbon sequestration will be greater in deeper soil layers in both production systems.

Conclusions: These data will yield insight into the linkages between soil microbial communities, soil carbon pools, and land use histories at different depths in the soil environment, providing mechanistic understanding of the factors that influence soil carbon sequestration at different depths in agroecosystems.

Linking Volatile Organic Compounds from Agricultural Soil to the Microbiome

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Aim: Linking Volatile Organic Compounds From Agricultural Soil to the Microbiome

Microbes emit volatile organic compounds (VOCs) that may be plant growth promoting or plant growth inhibiting. Most studies are conducted with a single microbial species and focus on a single VOC, however VOC emission may be affected by interactions among microbial species. There is limited literature examining the associations between the soil microbiome and the VOC's emitted from agricultural soil. Our aim was to establish the potential for developing a device that land managers could use to give an accurate 'real-time' indicator of soil microbial diversity and activity.

Method: Detecting Microbial VOCs & Microbiome Characterisation

The first experiment was based on soil in pots, and microbial activity manipulated by moisture stress. The second experiment was based on a field trial of cover crops and mulches in an apple orchard. Volatile detection was carried out via GCMS. Soil microbiomes were characterised by DNA amplicon sequencing.

Results: In the pot experiment, changes in fungal and bacterial community composition, enzyme activity and substrate utilisation linked to soil type and moisture content were reflected in changes to soil VOCs. Preliminary results from the field trial show, measuring microbial biomass carbon (MBC), a treatment effect on the size of the microbial communities, and on the composition of the VOC's detected.

Conclusions: VOCs offer the potential for real-time monitoring of soil microbial activity, though analysis using artificial intelligence and calibration for soil type and land use will be needed.

Identification of Geocological Factors Determining Truffle Sites in Central Europe

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Truffles (*Tuber spp.*) live as hypogeous symbiotic fungi in most European soils. Recent reports show the existence of wild truffles with the species *Tuber aestivum* in Denmark, Germany, Poland, Serbia and Sweden. Most recent studies have focused mainly on the optimization of truffle cultivation in orchards, while little is known about the microbial and spatial environment of truffles in its natural habitat. To close this gap, our research will provide an overview of the interactions of truffles (*T. aestivum* and *T. uncinatum*) and its environment.

Literature Review, Mapping, Sampling, Analysis

Our methods are divided in four sections. The research design of the first section involves data collecting from literature including soil and site parameters influencing the natural distribution of *T. aestivum*. Section two provides a concise analysis of the site conditions with field work and samplings to confirm literature data. To enrich the data, part three is dedicated to laboratory analysis of C_{tot} , C_{mic} , N_{tot} , N_{mic} , P_{tot} , P_{mic} , $CaCO_3$, pH, K_{tot} , S_{tot} , Mg_{tot} in soil samples as well as PCR analysis of the sample surroundings. In section four we identify the key factors behind the geocology of truffles and develop a species distribution model based on soil, vegetation, topography and climate for Central Europe.

Poster Results and Conclusion

Our poster will show the outcome from the literature review. The results will enhance our ability to identify suitable truffle sites and accurately determine site characteristics.

Can We Preserve Biodiversity in Extremely Touristic Areas?

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Aim:

It is estimated that at most 10% of the populations of soil microarthropods have been explored and little is known about the drivers of the community composition. Noted the growing interest in using them as bioindicators, there is a need in understanding how communities respond to different disturbances. In this study, we investigated how microarthropods populations respond to anthropic pressure in two neighbouring Italian coastal areas: the natural reserve of Porto Caleri and the extremely touristic Albarella island.

Method:

We sampled 10 biotopes per area: 8 samples were taken along a transect from shore to forest across the Mediterranean dunal system, and the last 2 samples in unique site-specific non-matching biotopes. From each sample, edaphic microarthropods were extracted and their community analysed.

Results:

Statistical analysis revealed no significant differences in arthropod abundance, taxa richness, community composition, community diversity and QBS-ar index between the studied areas, suggesting that soil microarthropods are more dependent on the complexity of the ecosystem rather than on the level of anthropization.

Conclusions:

Natural habitats in Albarella island are extremely fragmented and eroded but scarcely mechanically disturbed and this has been revealed to be sufficient, in this site, for the preservation of the microarthropod community. This study suggests the importance, in artificial habitats, of the maintenance of some areas of preserved natural vegetation that act as hotspots for soil biodiversity. Further studies are needed to understand the minimum area necessary to preserve a vital community and the potential of spatial colonization of edaphic microarthropods.

Impact of contrasting root architectures of spring wheat on soil microbial community structure and activity

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Aim:

Wheat variants with contrasting root architecture might play an increasing role in agriculture due to their differences in hydraulic properties and the exploitation of nutrients. The aim was to investigate the influence of root architecture of *Triticum aestivum* L. on the main microbial groups and the enzymatic activities in top- and subsoil.

Method:

Two experimental spring wheat genotypes with strongly contrasting seminal root angles (UQR012: RA° = 110°; UQR015: RA° = 66°) were grown as monocultures in RhizoTubes and destructively sampled on a weekly basis from four weeks after sowing to seven weeks. Zymography was performed on top- and subsoil samples to detect the spatial distribution of enzymatic activity and to determine the location of microbial hotspots. Additionally, the PLFAs, NLFAs, and microbial biomass (C_{mic}) were investigated.

Results:

The root system has a considerable effect on β -glucosidase activity. While the shallow-rooted genotype showed a higher microbial activity in the topsoil than in the subsoil, the exact opposite was observed for the deep-rooted genotype after 7 weeks of plant growth. During plant growth, an increase in microbial activity was observed in the topsoil for the shallow-rooted genotype as well as an increase in the subsoil for the deep-rooted genotype. The deep root system also led to an increased formation of microbial hotspots in the subsoil compared to the shallow root system.

Conclusion:

The spatially explicit data on microbial function as well as abundance of soil microorganisms will be used to integrate microbially controlled processes and properties into a rhizosphere-microbiome model.

The Effects of Geographic Origin and Genotype on Fungal Diversity of Silver Birch (*Betula pendula*)

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Aim:

Fungi and plants interact to improve each other's fitness and survival. Although plant genetic variation affects ecosystem processes and functions, little is known about how interspecific genetic variation of plants affects fungal diversity. Thus, we wanted to explore the existence and magnitude of plant genotype effect on root fungal communities.

Method:

To determine the effect plant origin and genotype have on root fungal communities, we sequenced roots from 64 clonally propagated silver birch (*Betula pendula* Roth) trees representing 16 genotypes from four different geographical origins across Finland, grown together in a common garden.

Results:

We found that alpha and beta-diversity but not community composition of root fungi differ by *B. pendula* genotype.

Conclusions:

Birch genotypes may vary in their plasticity with regard to their fungal interactions, and individuals that are more plastic could thus be more robust against environmental changes.

Plants play a crucial role in revitalising remediated substrate after EDTA washing of metal-contaminated soils

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Aim: To evaluate the importance of different factors (e.g. soil type, plant cover, inoculum) for secondary succession and soil fungal community in remediated substrate.

Method: Two types of metal contaminated soils (calcareous and acidic) were washed with EDTA (ethylenediamine tetraacetic acid) for soil remediation. The pots were seeded with perennial ryegrass (*Lolium perenne*) and some were left without plant cover. Abundance of the total fungal community, determined by ITS fungal marker genes, and root colonisation by arbuscular mycorrhizal (AM) fungi were quantified.

Results: Four months after the start of the experiment, the abundance of ITS genes in the soil clearly showed that the presence of plants was the main factor affecting the total fungal community, which increased in most treatments in soils with plant cover, while it remained at a low level in soils without plants. While fungal ITS genes were detected in the soil at the end of the first growing season, arbuscular mycorrhizal (AM) structures were scarce in plant roots in all treatments throughout the first season. However, in the second season, AM fungal colonisation was detected in plant roots in virtually all treatments, with the frequency of colonised root length ranging from 30% to > 75% in some treatments, including those with remediated soil.

Conclusions: This study demonstrates the importance of plants and rhizosphere in the development and secondary succession of fungal communities in soil, which has important implications for the revitalisation of remediated soils.

Changes in carabid species distribution, body traits and associated microbiota along an elevational gradient

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Aim:

Climate warming is affecting Alpine habitats through an above-global average increase in temperature. Such rapid environmental change can affect biotic interactions, impacting ecosystem stability and functionality; however, these processes in mountain regions are not well understood. We used an elevation gradient ranging from 1000 to 2500 m a.s.l. as a proxy for climate change to examine the diversity of carabid beetle species, body traits and microbiota.

Methods:

On 12 grazed pasture sites (3 replicate sites every 500 m of altitude), we installed and checked pitfall traps for 24 hours every two weeks throughout the growing season. Almost 6000 individuals were morphologically identified to species, and body length, wing development and sex were noted. In June 2020, 182 carabid beetles were captured by hand, and used for microbial community analysis.

Results:

Community composition, diversity, and the ratio between winged and wingless species of carabid beetles changed significantly with elevation, but not in a linear pattern (ie. highest species biodiversity at 1000 m; lowest diversity and largest body size at 2000 m). Carabids established individual-specific but still elevation-dependent patterns in prokaryotic and fungal communities. Prokaryotic communities were similar below 2000 m but changed at higher elevations and fungal diversity was highest at 2000 m.

Conclusions:

We discuss how changes in species assemblages and body traits may alter the functional role of carabid beetles in mountain ecosystems, and how alterations in their microbiota might impact their ability to adapt to rapid environmental perturbation.

The European Atlas of Soil Fauna as a tool for the conservation of soil biodiversity

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Aim: The protection of soil biodiversity is essential for ensuring soil functioning and provisioning of related ecosystem services, as well as the conservation of species *per se*. *Designing efficient policy regulations, conservation, management and monitoring schemes requires transformation of existing knowledge into a guiding tool. Attempting to fill this gap, we initiated the “European Atlas of Soil Fauna”.* We aim to summarize current information, collect existing data, and map the distribution of soil micro-, meso- and macrofauna taxa across biomes, soil types and land uses.

Method: We developed collaboration within the Cost Action EUdaphobase/CA18237. We structured the Atlas into two parts: First part for summarizing current information and second part for creating soil fauna maps based on available data. A platform/warehouse for data storage/analysis (Edaphobase) is available. For identifying possible data sources we performed literature searches and developed a questionnaire to approach possible data holders.

Results: Collaboration among over 20 motivated researchers was very efficient resulting into an initial draft of the first part of the Atlas within few months. For the part concerning the maps, we found through the literature search over 2000 soil fauna study sites across Europe. Most of them have not yet been included in global reviews or meta-analysis studies.

Conclusions: The transformation of available data into soil fauna maps is a laborious task. It is however feasible if data holders join this initiative and become co-creators of the Atlas. We ask for contribution to this effort! The twitter account @soilfaunaAtlas serves as gate to join!

Community composition, habitat and soil associations of oribatid mites in Great Britain

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Soil structure, community composition and abiotic variables such as moisture and temperature are key determinants for species distribution and thus food web structure. Whilst mites are some of the most abundant microarthropods in soils, their diversity and functionality remain poorly understood. In undisturbed and organic-rich soils, oribatid mites tend to be the more abundant free-living mite group. Their biological activity helps to maintain soil structure, and their life-history traits - particularly slow development, low fecundity, and long adult lifespan - makes them sensitive to soil disturbance and structural degradation. In this study, we investigated data on oribatid species communities, alongside vegetation and soil parameters collected during national surveys and other extensive monitoring programmes (e.g. Countryside Survey). We aimed to determine the characteristic oribatid community composition of different British habitats and identify which biotic or abiotic variables and soil associations might clarify the value of oribatids as indicators for habitat and biodiversity monitoring. We applied multivariate techniques (IndVal, PermANOVA and PCA) to analyse oribatid community composition and relation to environmental variables, model presence-absence of prevalent taxa across soil property gradients, and integrated current knowledge of oribatid trophic status. Our findings include the key environmental variables and species with indicator potential which can be used in the monitoring of priority habitats, as well as the maintenance and enhancement of biodiversity according to national policy frameworks.

Improving soil macro- and meso-fauna diversity of Mediterranean agrosystems: Application to maize crops and vineyards

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Aim: In a context of global change, Mediterranean agrosystems, already weakened by conventional management practices (overuse of chemical fertilizers and pesticides, monoculture farming...), are subject to increasing environmental pressures (*i.e* extreme heat events, depletion of water resources). To face this climate crisis, it is essential to encourage agricultural practices that contribute to the improvement of soil biodiversity, as a key attribute of a sustainable agricultural system. In this context, ReCROP is an European project that aims to identify sustainable and resilient agricultural production systems in the Mediterranean region through the combined use of biotechnological tools, such as bioinoculants, and environmentally friendly agronomic practices. A positive influence of mulching and organic farming is expected on soil fauna. The effect of various bioinoculants will be compared since their influence on soil arthropods community has been little explored.

Method: Two types of crops (vineyards, maize), subjected to a wide range of practices (organic farming, bioinoculant, mulching, crop rotation), were investigated during spring 2022. A multi-taxa approach (*i.e* springtails, ants, spiders) was used to assess the influence of these practices on the abundance and diversity of soil fauna.

Results: We will present here the main results obtained on abundance, biomass, species richness and diversity, by focusing also on functional traits.

Conclusions: Soil fauna have a key role in ecosystem processes leading to essential functions, like predation of pests. This work will thus contribute to identify which practices are beneficial for the resistance or resilience of soil fauna, thus improving the functioning of Mediterranean agricultural soils.

Characterisation of a brown infrastructure for earthworm preservation in urban fragmented areas

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Ecological continuities were widely studied for the aerial biodiversity through the concept of blue-green infrastructure but the equivalent concept for soil biodiversity, the “brown infrastructure”, remains unclearly identified especially for species with low dispersal rates such as earthworms. Thus, we suggest defining the brown infrastructure as made up of pedological reservoirs and corridors allowing the movements of species living all their life stages in the soil and with limited dispersal abilities. In urban areas, the brown infrastructure is highly influenced by anthropic activities which modify and fragment soils. We proposed a methodological approach of characterisation and cartography of the brown infrastructure in urban areas in order to favour its preservation or restoration in urban planning projects:

- (1) A preliminary study from available georeferenced data aims to identify and to characterise the built and unbuilt surfaces to draw the contours of a potential brown infrastructure. This first location allows to define (i) reservoirs and corridors for earthworms, degrees of (ii) anthropisation and (iii) isolation of soils of the study site;
- (2) A field study aims to confirm and precise the previous cartography including (2.1) the description of soil profiles and anthropic discontinuities allowing to cartograph types of soils of the potential brown infrastructure, and (2.2) earthworm samplings allowing to cartograph earthworm abundance and diversity;
- (3) The cross-checking of the soil and earthworm data allows to discuss hypotheses made at the first step and to provide a characterisation of the functionality of the existing brown infrastructure.

Soil biodiversity monitoring as a useful tool on the way to a sustainable, biodiversity-friendly agriculture

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Aim:

With installing a Soil Biodiversity Monitoring across a representative set of agricultural sites we aim (1) to understand the effect of land-use type and intensity on soil biodiversity in general, (2) to evaluate whether a soil module within a biodiversity monitoring program can be a useful tool to identify sustainable agriculture practices that support soil biodiversity, and (3) to test whether land use intensification effects can be detected already on a higher taxonomic level

Method:

For the northernmost province of Italy, South Tyrol, a biodiversity monitoring program has been set up in 2019, including a module on soil and soil biodiversity. For the here presented study we evaluated samples from 73 agricultural sites between 2019-2021, including apple orchards, crop fields, vineyards, meadows of different management intensity and pastures. We installed two pitfall traps on each site twice a year. Animals were sorted and identified to family level; spiders were identified to species level.

Results:

Preliminary results show no differences in diversity indices on family level. However, community composition varied between land-use types. Ongoing analysis will further define which taxa drive community changes and test if higher a taxonomic resolution better detects land-use effects.

Conclusions:

Sustainable agricultural practices can help to weaken or even reverse the ongoing loss of soil biodiversity resulting from intense land-use; however, changes over longer time periods have rarely been studied. As a first step, our study allows to test which level of taxonomic resolution is required for receiving a useful tool to a sustainable, biodiversity-friendly agriculture.

Biodiversity in mountain soils: current knowledge and research needs

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Aim: Mountain soils fulfil important ecosystem functions, such as water filtration for lowlands and carbon storage, but little is known about their soil biota diversity and related functions. The working group “Mountain Soil Biodiversity” within the Global Mountain Biodiversity Assessment (GMBA) platform aims to evaluate the current state of knowledge and identify future research needs.

Method: We established an analytical literature search tool to obtain an overview of available data for biodiversity in mountain soils above the treeline in temperate zones for invertebrates, non-vascular plants and microorganisms. We analysed the coverage of different regions and taxonomic groups in existing studies. Further, we collated the data to provide a broader picture on diversity distribution patterns.

Results: We showed that soil biodiversity studies are available mainly for the European Alps and Tibetan Plateau, and some more for Australasia and the Scottish Highlands. Therefore, many mountain regions remain un- and understudied (e.g. Rocky Mountains, Caucasus, Andes). Biodiversity was found to be still high at high elevation, with many specialist taxa that have developed adaptations (e.g. omnivory, life under snow) to cope with the more extreme environmental conditions.

Conclusions: Knowledge on organisms living in and on mountain soils is still sparse. With the current initiative, we aim to bring more attention to these habitats, as they represent a relevant livelihood for many countries and people. The outcome of this first review allows us to define open research questions and give recommendations for policymakers on the current status of soil biodiversity and its preservation.

Modelling connectivity of microhabitats: You can run, but can you hide?Sean Darcy^{1,2}, Christina Kaiser¹, Ksenia Guseva¹¹*Centre Of Microbiology And Environmental System Science, University Of Vienna, Vienna, Austria,*²*Doctoral School in Microbiology and Environmental Science, University of Vienna, Vienna, Austria***Aim:**

Soils are complex systems made up of microhabitats of varying resource composition that are colonized by diverse locally interacting communities. Habitat accessibility and suitability are key for the propagation and thereby survival of soil microbes. Both are inherently linked to habitats spatial arrangement and heterogeneity. We developed a theoretical model to explore how microbial community composition is impacted by the spatial structure of habitat networks. We investigated varying levels of network connectivity, resource diversity and distribution, as well as dispersal mechanisms and transfer our analyses to real soil structure networks.

Method:

Our model simulates Generalized Lotka-Volterra population dynamics in local communities - patches which make up nodes in a spatial network. Varying forms of repeated dispersal were implemented and tested as well as levels of patch resource diversity, abundance and heterogeneity. Our main focus was relating simulated habitat networks structure to community composition. Analysis was also applied to soil pore networks constructed from micro-CT scans.

Results:

We found that connectivity impacts both diversity and community composition. Analysing the model allowed us to characterize how dispersal dynamics influence communities on local and system scales. Dispersal type, resource diversity and heterogeneity all shifted the shape of the relationship between connectivity and communities.

Conclusions:

Our results show a strong impact of physical connectedness on community patterns and predict that structural changes heavily influence community dynamics. Applying our model to soil pore networks was exploratory, but more detailed data on the structure and heterogeneity of soil at the microhabitat-scale could enable more realistic parametrization and interpretation.

The Impacts of Land Management on Soil Characteristics and Belowground Diversity in a Coastal Ecosystem

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Aim:

The study aimed to uncover the impacts of land management and hydrology on soil characteristics and belowground biodiversity in a coastal sand dune system.

Method:

Soil samples were collected in autumn 2021 from sixty-three locations encompassing a range of microhabitats in the Ainsdale Sand Dunes National Nature Reserve (dry dunes, dune slacks, coniferous woodland, birch woodland and dune grassland cleared of trees in the 1990s). The organic and mineral layers of soil cores were examined separately to build a robust dataset. Soils were characterised by pH, bulk density and LOI. Nematodes and microarthropods were extracted using Baermann and Tullgren funnels, respectively, and enumerated. Soil blocks were also examined at the same locations across the site to collect earthworms for identification.

Results:

Regarding soil characteristics, the organic horizons of the coniferous woodland samples had the lowest pH with no significant difference between the organic and mineral horizons in the other microhabitats. LOI values were higher in organic horizons while bulk density was typically higher in the mineral horizons for all sampled locations. The organic layers were also distinctly richer in soil invertebrates with dry dune locations displaying the lowest soil mesofaunal diversity overall.

Conclusions:

This study highlights the importance of measuring and analysing distinct soil horizons separately to account for varying profiles in coastal sand dune ecosystems. Furthermore, it also suggests that different habitats maintain distinct conditions that may harbour unique soil biodiversity composition in the sand dune landscape.

The Genome-based Diversity and Ecological Plasticity of Truffles From Their Natural Distribution Area

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Aim:

Truffles are among the most prominent edible fungi and are considered as best characterised non-timber forest products. *Tuber aestivum* is a broadly distributed commercial truffle species. Its taxonomic diversity is well known while there were little correlations established between its ecological variants and the genomic potential. The whole genome resequencing aimed to correlate the basic genomic differences with selected environmental parameters relevant to truffle distribution and cultivation of this species.

Methods:

A genome sequencing using Illumina approach was used to re-sequence 60 whole genomes of *Tuber aestivum* from 8 different countries, three climate types and most of its ectomycorrhizal hosts. Various bioinformatic tools were applied for analysis of the obtained genome sequences.

Results:

The whole genomes sequence analysis resulted in a draft phylogenetic relationship among analyzed samples. The origin of analyzed truffle was strongest selection parameter in separating truffles. On the other hand, climate and ectomycorrhizal tree partner did not play role in separation of genomes, in both cases with geographic distance as a co-variable.

Conclusions:

This is the first example of a whole-genome resequencing study in commercial truffle species. The whole genomes comparison indicated the geographic distance of samples as the most important criterion in diversification of *Tuber aestivum*. The ectomycorrhizal tree partner, however expected, did not play a role in diversification. Based on these results, the crucial aspect a selection of truffles for seedling inoculation and cultivation in agroforestry systems should focus on their geographic origin and not necessarily on ectomycorrhizal tree.

Drought Legacy Effects on Grassland Functioning and Responses to a Subsequent Drought

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Aim: Drought can have long-lasting effects on ecosystems, altering their functioning and responses to subsequent droughts. How drought intensity mediates soil drought legacies is unknown. Our aim was to determine how soil drought legacies across a gradient of drought intensity affect soil functioning and plant growth in response to a subsequent, summer drought.

Method: We studied soil drought legacy effects in two model grassland communities with contrasting resource acquisition strategies (fast/acquisitive and slow/conservative) that experienced a gradient of drought intensity in summer 2020. We measured soil microbial community structure, potential extra-cellular enzyme activities (EEA) related carbon (C) and nitrogen (N) cycling, and plant productivity in the spring following the drought (2021), as well as during and after a summer drought in 2021.

Results: We found that drought legacies mediated plant community resistance to and recovery from the summer drought, and that this response differed between communities with contrasting resource acquisition strategies. Increasing intensity of the 2020 drought decreased resistance to the 2021 drought in the slow community only. Seven weeks after the 2021 drought ended, we found that increasing intensity of the 2020 drought decreased recovery of the fast community, while recovery of the slow community was unaffected. Drought legacy effects on EEAs were moderate - N-acetylglucosaminidase decreased with increasing intensity of the 2020 drought- and effects on soil microbial community structure are yet to be analysed.

Conclusions: Based on our preliminary results we conclude that drought intensity influences soil drought legacies, altering soil functioning and plant community resilience.

Legume-rhizobium symbiosis and synthetic communities production for increasing crop production under climate change challenges

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Aim: importance of rhizobium- legume symbiosis in climate change

In the last few years, climate change has gained importance due to its severe environmental consequences. A promising strategy is represented by the rational use of the wide genetic and functional diversity of the microorganisms that colonize plants. The rhizobia-legume plant symbiotic interaction is a fundamental part of the input of fixed nitrogen in the agroecosystems. The application of rhizobia as bioinoculants can be improved by the creation of synthetic microbial communities.

Method: importance of systems biology and predictive models

The development of host-microbiome model systems for crop plants is needed to translate laboratory-scale evidence of synthetic microbial communities to field application. Studies should be extended to climate-resilient nonmodel crops, such as *Amaranthus* spp., *Chenopodium quinoa* (quinoa), *Eragrostis tef* (teff) and *Setaria italica* (foxtail millet). Studies on core microbiome through meta-omics approaches represent a valid tool for the understanding the most recurrent taxa associated to a certain host phenotype. Multi-omics approaches, metagenome wide association analysis, network analysis, genome mining reconstruction of transcriptional and regulatory networks and statistical modelling approaches should be used to integrate different data.

Results: SynComs improving nitrogen fixation

Research projects are testing out consortia of rhizobia and PGPR for improving legume growth and resilience toward climate change-related stress. The rationale of many of these very small-scale synthetic communities (indeed only two strains, a rhizobium and a PGPB) is to combine a good nitrogen-fixing rhizobium with a plant hormone producer.

Conclusions: Perspectives and future challenges

predictive modelling and rational design of synthetic communities are critical and obliged steps to accelerate the progress in bioinoculants development for increasing nitrogen fixation in harsh conditions.

The Impact of Cover Crops on Microbial Activity and Community Composition in Stockpiled Soils

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Aim:

To examine the effect of cover crops on microbial activity and community composition over time in stockpiled soil, and its relationship with carbon and nitrogen sequestration.

Method:

Soil was arranged into 12 windrow shaped piles sized approximately 6 x 4 x 2m. Piles were randomly sown with one of 3 treatments; an amenity grass mix, a herbal ley seed mix or no seed. Half of each stockpile were covered with a thin layer of mulched wood chip. Soil samples were taken from each replicate (n=24) at depths of 0-30cm and 90-100cm, taken at T0, 1, 2, 4 and then at 4 weekly intervals. Microbial activity in the soil was assessed by measuring CO₂ flux in situ and performing fluorescein diacetate assay (FDA) on the same day. Soil was processed for total nitrogen, total organic carbon, pH, and soil organic matter. Microbial biomass and community composition were measured at T0 and 4 weekly, using a Microbiometer in field kit and Minlon DNA sequencing.

Results:

The experiment is in early stages with final samples to be taken March 2023. Hypothesis is that herbal ley cover crops will have the most diverse microbial communities, enhancing or retaining soil biodiversity in a situation where soil usually degrades.

Conclusions:

The impact of stockpiling soils on soil biodiversity is poorly understood; this study begins to address this knowledge gap. The implications of our results could be incorporated into policy and best practice advice for the sustainable use of soils on construction sites.

Determination of soil invertebrate diversity using morphological and DNA-based methods at 25 sites in Germany

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Aim:

In Germany, no regional coverage and comprehensive information regarding the biodiversity of soil invertebrates is available. To improve this situation, the German Federal Environmental Agency started a project in 2018 to develop recommendations for a standardized, comprehensive and efficient programme to monitor selected soil invertebrate groups all over Germany.

Method:

Sampling was performed at 25 permanent soil monitoring sites, representing different soils, land use forms and regions, for Lumbricidae, Enchytraeidae and Collembola, using ISO standards. Species were identified morphologically and by metabarcoding of community DNA (comDNA) and environmental DNA (eDNA).

Results:

For Lumbricidae, there was strong agreement between morphological and COI comDNA species identification, with the latter also being able to identify lineages and cryptic diversity. 16S eDNA metabarcoding on average yielded a similar number of species per site as the other two methods.

For Enchytraeidae, COI eDNA on average detected a slightly and not statistically significantly higher number of species per site than morphological identification and COI comDNA metabarcoding.

For Collembola, preliminary results suggest that morphological identification has a lower agreement with COI comDNA and eDNA species identification than found for oligochaetes.

Conclusions:

No final conclusions can yet be given as the project is still in its final stages of evaluation (finished by the time of the GSB conference). However, metabarcoding of eDNA is a promising method for routine soil biodiversity monitoring of oligochaetes but its applicability for Collembola is currently unclear. Some issues with the reference databases in particular for Enchytraeidae and Collembola need to be resolved.

Seasonal effects of sward functional diversity on soil microbiological properties associated with nitrogen mineralisationYahaya Jebril Amanor^{1,2}, Fiona Brennan¹, David P. Wall¹, Nabla Kennedy²¹*Teagasc, Environment Research Centre, Johnstown Castle, Ireland,* ²*Department of Science, SETU Waterford, Waterford, Ireland*

Aim: There is lack of knowledge about soil microbial processes (e.g. nitrogen mineralisation) driving the agronomic and environmental benefits of mixing plant species of different functional traits in temperate managed grasslands. This study investigated seasonal effects of plant functional diversity on soil microbiological properties associated with nitrogen (N) mineralisation. **Method:** The study used three experimental trials on different soil types in Ireland (Johnstown: Gley soil; Curtins: Brown earth; Lyons: Gleyic brown podzol) that consisted of swards of different functional diversity levels: grass monoculture, grass-legume mixture and grass-legume-herb mixture. The fields were sampled across four seasons as per grass growth pattern in temperate grasslands: Declining (DG), No (NG), Increasing (IG) and Peak (PG) growth seasons, and analysed for potential net N mineralisation (PNM), microbial biomass N (MBN) and C/N cycling enzyme activities (C: β -glucosidase; N: Leucine aminopeptidase). **Results:** PNM was affected by both season and functional diversity for the lighter and freer draining soils of Curtins but by season alone for the heavier and more poorly draining soils of Lyons and Johnstown. Seasonally, PNM values for Curtins were 1.1-1.5 fold and 1.8-2.0 fold greater than Johnstown and Lyons, respectively. Regardless of functional diversity level, PNM values in DG and NG were generally lower than IG and PG. The changes in PNM were strongly reflected in the MBN pool and to a lesser extent in β -glucosidase activity. **Conclusions:** The results show microbial activity responded more strongly to season than plant functional diversity and that seasonal plant growth stimulated changes in microbial activity.

Grassland Degradation and Possibilities for Restoration in Inner Mongolia

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Aim:

To analyse changes in vegetation and soil biota communities and relationships between aboveground and belowground communities during degradation caused by overgrazing in the grassland of Inner Mongolia, China, and explore the possibility of degraded grassland regeneration.

Method:

The experiment was established in 2014 with four grazing treatments in triplicate: 'No grazing', 'Light grazing' with 4 sheep per plot, 'Moderate grazing' with 8 sheep per plot and 'High grazing' with 12 sheep. The sheep had an individual body mass of 50 kg when treatments started. Grazing lasted 170 days per year. Each plot was 1.33 ha. In each plot, 32 subplots were set up, each with a 2 m x 2 m cage for sampling. From June to July, the vegetation was surveyed within the 4 m² quadrant in each plot. Five random soil cores were pooled for chemical analysis and per plot three soil samples were taken to assess the soil microbe communities.

Results:

Continuous grazing reduced the converge of palatable species but increased the coverage of unpalatable species. Plant community diversity showed a 'U' shape with the lowest at light distribution. The soil biota communities varied among different grazing intensities and had correlation with the aboveground changes.

Conclusions:

- The vegetation coverage declined significantly with an increase in grazing intensity and changed the composition.
1. Vegetation diversity in higher grazing intensity treatments did not support the intermediate disturbance hypothesis.
 2. The light grazing disturbance promote the spatial homogeneity but strength the heterogeneity in moderate grazing intensity treatment.

Mycorrhizal Fungi Dynamics and Drivers After Glacier Retreat Around the Globe

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Aim: Early development of soil is heavily dependent on mutualisms such as arbuscular mycorrhiza and ectomycorrhiza, the two most widespread plant-fungal symbioses. The nutrient-poor and harsh environments occurring in glacier forelands provide a unique model for studying primary succession of early mycorrhizal fungal communities.

Method: To explore the dynamics and drivers of mycorrhizal fungi in primary succession, we conducted a comprehensive inventory of 1251 plots in 265 forelands of 46 glaciers around the globe, with sites spanning from 1 to 483 years since glacier retreat. For each plot, we assessed fungal community using metabarcoding of soil environmental DNA. For a subset of 32 glaciers, we also estimated plant community, productivity and microhabitat conditions.

Results: Both types of mycorrhizal fungi colonize the substrate a few years after the retreat of the glaciers, although with a delay compared to the whole fungal community. Diversity of arbuscular mycorrhizal fungi is largely driven by time and plant community, while microclimate and productivity influence more strongly ectomycorrhizal fungi.

Conclusions: The establishment of mycorrhizal fungi is rapid with local dynamics driven by time after glacier retreat but also plant community, productivity and microhabitat conditions. Changes in the rate of ice melt and conditions such as microclimate could disrupt biotic colonization, potentially by causing a mismatch between mycorrhizal partners which would slow soil development and associated ecological processes. Further analyses using multi-trophic surveys are needed to predict ecosystem-level impacts.

Land-use Changes Alter Multidimensionality of Diversity in Overwintering Collembola Communities

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Aim:

Human activities have largely transferred natural vegetations to crop systems in the past decades, resulting in decreases in biodiversity. Due to immigration policy natural wetlands and forests in Sanjiang Plain (north-east China) have been transferred to arable fields and forest plantations, with some natural habitats scattering in the mosaic landscape and likely functioning as refugia for soil biota. Using trait-based and community phylogenetic approaches we investigated responses of the overwintering Collembola communities to the land-use changes.

Method:

We sampled entomobryomorph and poduromorph Collembola under snow layer from typical habitats of the region: wetlands, secondary natural forests, arable fields and forest plantations. We used trait community weighted mean and pairwise phylogenetic and trait distance as community attributes. We especially investigated responses of six traits to land-use changes: body length, furca-to-body ratio, ommatidia number, surface brightness, color pattern and colors in RGB model. We built an eco-morpho-space for traits and explored species evolution in the multidimensional niche space.

Results:

Traits are functional – they differ in communities among habitats. Community assembly processes depend on traits and habitats. Even in same communities, combinations of traits (representing multidimensional niches) reveal both filtering and partitioning processes at work. Rare species usually occupy the niches left behind by abundant species. Species evolutions in the multidimensional niche space were convergent.

Conclusions:

Land-use changes threat soil biodiversity not only taxonomically but also functionally as represented by community traits. Complementary to traditional biodiversity indices, trait and phylogenetic parameters are informative in prediction of diversity loss resulted from human impacts.

Investigating the function, persistence and biosafety of constructed microbiomes for improved bioremediation of petroleum-impacted soil

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Aim:

This project will construct an oil-degrading bacteria consortia and analysis for their safe use in the environment, investigate the fate of the consortia in the soil and its effects on the soil microbiome, and determine the key genes that are involved in the oil degradation process.

Method:

Analyzing the contaminated soil microbiome and the oil-degrading consortia microbiome to determine the major bacterial members of these communities. Assessing the Biosafety /ecotoxicity of the bacterial consortia. Inoculation of the consortia on trial plots. Examine the correlations of the diversity and abundance of key degradation genes with the microbial microbiome. Transcriptomic analysis of functional biodegradation genes.

Results:

Analysis of the Ecopile microbiome data and compare the changes in the Bacterial, Fungal, and Nematoda communities in seven Ecopiles over a two-year period. Results show that in most Ecopiles an increment in biodiversity was observed along the bioremediation process. Five types of highly efficient Diesel degradation bacteria have been isolated and cultured in individuals, carrying out degradation studies on individual bacterial and bacterial consortia. (ongoing)

Conclusions:

The Ecopiling method was successful in the biodegradation of hydrocarbon pollutants. The TPHs' values decreased by 95.91% and 76.78% on average for aliphatics and aromatics, respectively. For bacteria, the phylum *Proteobacteria* and more precisely the class *Gammaproteobacteria*, for Fungi, the genera *Mortierella*, for Nematoda, the genera *Rhabditida* and *Diplogasterida*. Whose relative abundance varied obviously with the TPHs' levels and was the most abundant taxa, could have played a major role in the degradation of these pollutants.

How does differentiated fertilization in organic farming affect soil biodiversity?

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Many edaphic species are important ecosystem service providers (e.g. decomposers) or valuable soil quality indicators in agricultural ecosystems. However, many soil-dwelling species and their habitat and resource requirements still remain largely unknown. In particular, the effect of different types of fertilizers on soil diversity is presently poorly understood. Current studies either focus on a small number of different fertilizers or a limited range of taxa.

Aim: In the project DüNaMed we use two locations to study the effect of six different solid and liquid fertilizers (cattle manure and slurry, straw, biogas digestate, compost, and mineral NPK) on different edaphic organism groups and compare them to unfertilized controls.

Method: The meso- and macrofauna are sampled with pitfall traps, emergence traps, Berlese-Tullgren funnels, and environmental DNA (eDNA), targeting a diverse group of taxa (mainly Diptera, Coleoptera, Hymenoptera, Araneae, Collembola, and Acari).

Results: Preliminary results of the first sampling year show significant higher abundance of Collembola in the plots with straw fertilization and Nematocera in the plots with cattle slurry fertilization. Moreover, differences in carabid diversity are higher between locations than within different fertilization treatments.

Conclusions: We expect that further identification at deeper taxonomic levels in combination with eDNA metabarcoding will allow us to get a more comprehensive view of the relevance of fertilizers for the conservation of edaphic biodiversity.

Restoring Polluted Soils Microbial Diversity with ECOPILES

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Aim: Ecopiling is a biodegradation method for hydrocarbons in soils. It derives from BIOPILES but phytoremediation is added to biostimulation with nitrogen fertilizer and bioaugmentation with local bacteria. We have constructed eight ECOPILES with soil heavily polluted with hydrocarbons in Carlow (Ireland). The aim of the study was to analyze changes in the microbial community during ecopiling.

Method: We have used metagenomic analysis of 16S (18S) amplicons to analyse the composition of the microbial community

Results: In the course of 18 months, hydrocarbon values decreased in 95.91% and 76.78% on average for aliphatics and aromatics, respectively, indicating a successful biodegradation. Community analysis showed that microbial alpha diversity (Shannon Index) increased with the degradation of hydrocarbons, with starting average value of 7.59 and final average value of 9.39. For beta diversity, a PCoA ordination was performed using Bray-Curtis, where the two first principal components (PCs) explain the 17% and 14% of the variance, respectively. Results show that samples cluster by sampling time rather than by Ecopile. This clustering pattern is supported by hierarchical clustering analysis, where most samples from the same timepoint clustered together. We determined the differential abundance of bacterial populations in Ecopiles at the beginning and end of the treatment. While TPHs degraders are abundant at the beginning, these populations are substituted by populations typical of clean soils by the end of the process.

Conclusions: All data indicate that the bacterial community follows a succession along the bioremediation process. This succession starts with a TPH degraders enriched community, and finish with a bacterial community typical of clean soils.

Fungi as an Important Ecological Driver in a Panamanian Rainforest

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Aim:

Reveal species-specific relationship of fungi taxa in soil and above-ground plant communities.

Method:

The study was performed in a permanent research plot (800 x 480 m) in Peninsula de Gigante of Barro Colorado National Monument, Panama, Central America. Eleven different tree species were surveyed, Soil (0-20 cm) and litter (O^{i-e} horizons) were separately collected from the four cardinal directions of each tree and pooled for each sample. DNA extraction and PCR amplification, the ITS marker gene was sequenced using the Illumina HiSeq platform. Bioinformatic analysis was done to separate the ITS sequence reads into grouping of amplicon sequence variants (ASVs). The ASV table was provided as input into FUNGuild. Our analysis focused on: mutualist, decomposers, and pathogens. A pairwise PERMANOVA (Permutational Analysis of Variance) test evaluated differences in fungal communities across tree species.

Results:

Plant pathogens were more abundant in litter samples than in soil samples, AMF (arbuscular mycorrhizae) were more abundant in soil samples than in litter samples, and saprotrophic fungi (decomposers) were roughly equal across both layers. Pathogenic and saprotrophic fungi (decomposers) appear to exhibit the strongest patterns of tree host-specificity. Ordination plots for these groups exhibited a high degree of within-group clustering and inter-group separation across the 11 tree species.

Conclusions:

These results suggest that fungal pathogens and decomposers show strong patterns of community divergence across tree species, thereby potentially validating their roles in shaping aboveground plant community structure.

Novel Carbon Foam Amendments and Their Effects on Soil Prokaryotic Communities

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Aim:

Nowadays, different amendments are being developed to stabilize heavy metals in severely contaminated soils, reducing metal availability and contributing to the restoration of soil ecosystems. While some of these amendments were proven to be effective in chemical soil remediation, several studies have confirmed their negative impact on soil biodiversity. This study focuses on assessing the effects of novel carbon foam amendments upon soil prokaryotic and fungal communities while proving that they can effectively reduce heavy metals availability in a contaminated soil.

Method:

In this study, we applied two types of carbon foams (non-impregnated and impregnated with goethite nanoparticles) obtained from molten sucrose in an environmentally realistic dose to a heavy metal contaminated soil in a microcosm experiment. Changes in the metal availability were monitored using the Toxicity Characteristic Leaching Procedure (TCLP) method and effects on autochthonous prokaryotic and fungal communities were assessed by Automated Ribosomal Intergenic Spacer Analysis (ARISA) and 16S/18S rRNA gene amplicon sequencing.

Results:

Results indicated not only significant changes in the mobility of some of the heavy metals, but also slight shifts in the composition of microbial communities, as well as changes in alpha diversity and taxonomic composition, depending on the applied amendment.

Conclusions:

This study emphasises further need to analyse specific interactions and possible cytotoxicity of these new amendments for them to be effectively applied in contaminated soils at a larger scale.

The effect of deep-rooting cover crop mixtures on subsoil carbon allocation and microbial hotspots

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Aim: The subsoil is an important carbon (C) pool with a large potential for C sequestration. Deep-rooting cover crops can accumulate organic C in their root pores and induce the microbial hotspots of C turnover in the subsoil. However, there is still a knowledge gap about the niche complementary effect of multiple cover crop species on root C allocation in the subsoil. This study aims to optimization of deep-rooting and shallow-rooting cover crop mixtures (red clover, white clover, tall fescue, ryegrass, oil radish, summer rapeseed) on C allocation and the microbial hotspots in the maize rhizosphere.

Method: We used a ¹³C-pulse labelling approach to quantify the C allocation. The activities of soil enzymes (β -glucosidase, leucine-aminopeptidase, and acid phosphatase) were measured by fluorometric microplate assays. The soil hydrophobicity of the root channels was measured by the sessile drop method.

Results: The ¹³C assimilated more in the three mixtures than the monocultures in cover crop growing seasons. The ¹³C enrichment was significantly lower in the topsoil in the mixture of radish and grass, and in red clover at maize growing stage BBCH 33, but the mixture of clover and grass assimilated more ¹³C to the subsoil. Cover crops grown in monoculture had less effect on the activities of maize rhizosphere C-, N- and P-cycling enzymes than cover crops grown in mixtures.

Conclusions: We quantified the C allocation in the subsoil optimized by cover crop mixtures and proved the beneficial effects of cover crop derived-C on microbial hotspots of maize.

Is soil a source for deadwood-inhabiting fungi?

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Aim:

Deadwood decomposition is a main process in terrestrial carbon cycling and is mainly attributed to specialized wood-colonizers such as fungi. As lying deadwood is located on the forest floor and thus is in direct contact with the soil surface it is considered as a main source for the diversity of deadwood-inhabiting fungi. However, little is known about this relationship and its relative strength. Here, we test whether the deadwood fungal community is correlated with the present soil community, whether this potential relationship consistently exists for different deadwood substrates and which drivers affect this relationship.

Method:

In order to explore these questions, wood blocks of three tree species (*Fagus sylvatica*, *Pinus sylvestris* and *Picea abies*) were put on the floor of 150 forest and 150 grassland sites for one year. The wood blocks had been sterilized for the inactivation of endophytes and thus to ensure colonization activity only at the field site. Amplicon sequencing was applied to DNA extracts of these wood blocks and soil samples taken from the respective site to identify fungal colonizers. These two community matrices are used for Procrustes analysis to explore their relationship.

Results:

We expect a close association between both communities. Given a significant relationship, the vector of Procrustean residuals will be used to test if the microclimate, the macroclimate or land-use intensity explain the association between soil and deadwood fungi.

Conclusions:

This study contributes to better understand fungal colonization mechanisms and the role of soil fungal diversity to the deadwood-inhabiting fungal community.

Soil-borne Plant Pathogens, Soil Microbiome and Disease Control

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Aim:

Soil-borne plant diseases are a major obstacle to agriculture and especial difficult to manage. Many soil-borne pathogens have very resilient survival structures . A prominent example is clubroot, a global disease of Brassica crops, with no available efficient control and spores that survive in the soil for decades. We aim to identify disease suppressive and disease conducive microbiome members, including bacteria, fungi and protists.

Method:

We are performing complex plant and soil physicochemical analyses to decipher underlying drivers of taxonomic and functional changes in the rhizobiome to clubroot infection including of trans-European field samples and greenhouse experiments. A focus is on the identification of potential predatory species of clubroot that could be involved in top-down control.

Results:

In this presentation we will provide the framework of the research and findings that provide first ideas on the importance of the plant-clubroot-soilbiome connections. This includes the core-Eukaryotic microbiome in connection to clubroot.

Conclusions:

By identifying pathogen suppressive and conducive soil biota and predator-prey relations, new biocontrol applications can be developed that will also be useful to control other soil-borne pathogens.

III Health of Ash Trees Causes Shift in Soil Communities

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The hedgerow network of Northern Ireland covers some 11,648 km and consists of a mixture of shrubs (mainly hawthorn (*Crateagus monogyna*)) and emergent trees (mainly common ash (*Fraxinus excelsior*)). The presence of ash dieback, caused by the fungal pathogen *Hymenoscyphus fraxineus*, means that many of the ash trees are expected to decline and disappear due to disease in the short to medium term future. The soils of intensive agricultural farmland are often biologically impoverished and characterized by high nitrogen inputs, rapid turnover rates and poor soil structure. In many areas, however, extensive networks of hedgerows acting as field boundaries exist and they form strips of soil with increased spatial structuring and more diverse and complex food webs, influenced to some extent both by the species composition and structuring of the hedgerows and the micro-environmental conditions they create. The health status of hedgerow trees may also have an influence on associated soil communities.

This poster describes an early study of soil food webs under ash trees declining from a variety of causes other than ash dieback. Soil samples were taken from under both healthy and declining ash trees in hedgerows in order to examine fine-scale community structuring within the hedgerow and the effects of poor tree health over four time points – two in summer and two in winter. Several groups of soil biota from microbial to macro-arthropods were examined. While most groups showed only subtle differences between soil communities associated with healthy and declining ash trees, a notable increase in phospholipid fatty acid (PLFA) markers for arbuscular mycorrhizal fungi (AMF) was found. Although this study was rather limited in scope it suggests that ash trees often respond to ill health by investing in below-ground symbionts, a relationship which can be further investigated through future studies.

Biosensing Rhizosphere for the Biodiversity FinanceDrago Indjic^{2,3}, Milorad Plavsic¹*¹Tata-Cornell Institute, Ithaca, USA, ²Oxquant, Oxford, United Kingdom, ³University College London, London, United Kingdom*

Aim: The EU Soil Directive, various national and private funding policies are calling for significantly improved assessment of soil health, state, and productivity. We anticipate availability of the soil moisture and in-vivo microbiota sensing devices, capable of the autonomous operation. We target the robust indicator species detection, facilitating the production of crops under the organic label and assessing the microbiota distance to the pristine soil condition.

Method: Our initial study indicates that a swarm of the off-the-shelf biosensors integrated into Small Robot Company (UK) and QualiSpot Biosens (Serbia) robotic vehicles can cost-effectively cover the multi-Ha fields, performing fast, active soil health sampling targeting the required uncertainty bounds. The economic soil production function is conditioned on the biodiversity, but soil and biodiversity are not necessarily fungible from investment perspective.

Results: Targeted microbiota of particular interest is identified, that enhance soil health, either through chemical reactions or through mechanical soil transformation. Such soils present vital precondition for resilient and highly productive agriculture and improved capacities for carbon storage.

Conclusions: The identified soil parameters are used to calibrate the soil quality and biodiversity adjusted farmland valuation, producing the science-based, sustainability compliant investment rate of return (IRR) estimate. In addition to soil biodiversity, the study of the farmland valuation is expected to augment data on physical and chemical features of the plots. The combined approach to investment addresses the main objectives of the EU Strategies 2030 as well as financial instruments proposed by the Common Agricultural Policy.

Contribution to the understanding of invasiveness in Mediterranean ant species, *Tapinoma darioi* and *T. magnum*

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Aim: Biological invasions in urban areas often have negative consequences for both human activities and local biodiversity, which is already heavily affected by urbanisation. On a global scale, ants are among the invasive species with the worst environmental impact and the highest economic cost. Recently, two other species of ants belonging to the *T. nigerrimum* group have been identified as invasive at the European scale, and in particular in the Mediterranean region: *Tapinoma darioi* and *Tapinoma magnum*.

Method: In order to relate the foraging activity of each of the species with the temperature in the soil and on its surface, we measured these three parameters in the field at several colonies of both species in Montpellier Region (France), repeatedly throughout the winter and summer of 2022 in order to cover a wide range of values for the measured parameters.

Results: An almost continuous activity have been observed for the two *Tapinoma* species compared to other species such as *Pheidole pallidula*, which could give them an advantage in the field. The difference between *T. darioi* and *T. magnum* seemed more complex to identify than expected.

Conclusions: The acquisition of information on the biology of these species will make it possible to identify the factors that are favourable or unfavourable to them, and therefore, in the long term, to act to limit their spread.

The BISES project: Urban soil biodiversity and ecosystem services

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Aim:

In order to remediate the negative impacts of urbanization, development policies are moving towards sustainable cities. To achieve this, a leap in the knowledge of urban socio-ecosystem is essential and critical. The BISES project (*Biodiversity of urban soils and sustainable cities: state of the art, interactions between productive and non-productive systems and importance for the provision of ecosystem services*) aims to understand the ecology of urban soil communities.

Method:

The project uses two complementary approaches based on academic collaborative and participative research. For the academic collaborative part, our aim is to compare soil organisms between productive (allotments, urban farms) and non-productive (parks, roadside linear and roundabouts) vegetated areas and their indirect flows using spatially explicit methods. We selected ca. 200 sites located in 4 different French cities located under contrasted climates (Montpellier, Nantes, Nancy and Paris) based on their use and location along the urbanization gradient. For the participatory science approach, we developed a new community science programme entitled QUBS (www.qubs.fr). QUBS seeks to encourage city dwellers to set up, in their garden or those of the community, simple and rigorous protocols to monitor macro-biodiversity (i.e. earthworms, ants, spiders) and organic matter decomposition.

Results:

For the academic approach, preliminary results showed a contrasted response to urbanization features. For the participatory science approach, participation will be analysed.

Conclusions:

The BISES Project already provides insights in the field of soil and urban ecology and will make it possible to set a dashboard of indicators of the ecological quality of urban soils.

How Non-Tilling Practices Impact Soil Health across different Crops: a Microbiome Approach

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Aim

Healthy soils are of utmost importance to pave the way for global sustainable agriculture. Soil health quantification is still dominated by physico-chemical analysis, neglecting the fact soil functions as a living biodiverse ecosystem. Hence, microbial communities should be considered as a novel indicator of soil health status. No-tilling practices have been shown to decrease soil erosion, while enhancing soil health and biodiversity. The aim of this study is to determine how contrasting tilling practices impact soil microbiome composition and functional potential during three time points when using different crops (wheat, pea and sunflower).

Method

A wide panel of Biome Makers soil health indexes (regarding biodiversity, hormones, biocontrol, nutrient metabolism or stress impact) were modeled in terms of tilling practices, crop and time. Next, a differential abundance approach was applied to profile beneficial and pathogenic taxa which changed their abundance due to tilling practices over time in each crop.

Results

Our results showed that the effect of non-tilling is crop-dependent. Wheat index responses tended to differ from pea and sunflower ones, especially those related to biocontrol agents and stress adaptation. Non-tillage management increases fungal taxa, with a different effect on the abundance of beneficial/pathogenic taxa depending on the crop. However, no-till practices significantly affected carbon cycling index in a crop-independent manner.

Conclusion

The results presented here provided insights into non-tilling practices impact on soil health from a novel microbial perspective. This may serve to better guide farmers and agribusiness decision-making.

Effects Of Agricultural Management Practices On Soil Microbial Biodiversity

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Aim:

Within the framework of the international LivinGro® project, promoted by Syngenta, this research focuses on the effect of different soil practices that could preserve or increase biodiversity and soil health on agricultural ecosystems.

Method:

This study was conducted on selected experimental plots of stone fruit and olive orchards located in different geographical areas of Spain. In each area different management practices (treatments) were considered. For each one, soil samples were collected during the two-years' experiments to unravel the soil characteristics, organic matter, basal respiration, nitrates, and porosity. Moreover, the microbial biodiversity was also obtained from the same soil samples and estimated by the relative abundance of Prokaryotic and Eukaryotic microorganisms. The alpha- and beta-diversity was analysed, and putative microbial indicators of specific fields and soil management were proposed.

Results:

Preliminary physico-chemical results indicate that both nitrate and basal respiration can be affected by treatment. Biodiversity analysis showed higher Prokaryotic than Eukaryotic biodiversity in areas with LivinGro® treatment, where all microorganisms were typical genera associated with agricultural soils. Our first results pointed to a higher effect of the tree irrigation systems on microbial biodiversity. However, some occasional effects of the soil practice in the microbiome community have been observed.

Conclusions:

Despite the relevance of the irrigation in the soil microbial biodiversity, the proposed soil management pointed to an effect on soil characteristics, with an increase in the relative abundance of some specific microbial genera that could have a potential beneficial role for soil and plants.

Agricultural practices, bacterial and fungal diversity, and their interaction

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Aim:

In agricultural fields, the soil microbial diversity is impacted at multiple spatial and temporal scales. Yet, the effect of agronomic management is controversial, and a holistic understanding of such influence is needed. In the present work, more than 300 soil samples were taken from apple orchards under conventional and organic management across an area of ~100 square kilometers. Our objectives were first to investigate the effect of different agronomic managements on soil bacterial and fungal alpha-diversity. Secondly, we aimed at finding a robust apple-related core soil microbiome and redundant modules in microbial communities consistent among the apple orchards or responding to the different edaphic conditions.

Method:

We investigated the soil biodiversity via DNA metabarcoding of the bacterial 16S rRNA gene and the fungal ITS2. We paired these analyses with the assessment of chemical-physical soil properties (e.g., pH, soil texture, soil organic matter, total nitrogen, total heavy metal content, and available mineral nutrient content).

Results:

Preliminary results show no difference in soil chemical composition between conventional and organic management. Specifically, only a limited pool of soil parameters distinguished soils based on their management (i.e., soil pH, Fe, Ca) (p -value < 0.01). On the other hand, soil bacterial communities had higher alpha diversity values (i.e., richness and Shannon, p -value < 0.01) in organic apple orchards than the conventional ones.

Conclusions:

Further analysis will focus on the bacterial and fungal beta diversity. Additional analysis will elucidate the species more consistently associated with conventional and organic farming through multi-kingdom species ecological co-occurrence networks.

A *Pseudomonas chlororaphis* Synthetic Community as Model to Study Bacterial Compatibility and Plant-Bacteria Interactions

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Aim:

The aim of this work is to study the compatibility of three different *Pseudomonas chlororaphis* (Pc) strains (PCL1606, PCL1601 and PCL1607) isolated from avocado rhizosphere, to study their interactions between them and with the plant rhizosphere to be considered as a potential synthetic community (SynCom).

Method:

Phylogenetical analysis, comparative genomics and blast-based search of PGP related genes was made. Compatibility and competitive *in vitro* and *in vivo*, phenotype dominance in colony morphology and biofilm formation were analysed. Confocal laser microscopy was used to visualize Pc distribution in biofilm and avocado roots. The biological control and stability of the Pc strains in the avocado rhizosphere allowed determination of colonization and persistence abilities.

Results:

Even isolated from the same habitat, the selected Pc strains were genetically different. Compatibility assays revealed competitive index (CI) modulated by the assayed medium or the avocado root. The biofilm and colony morphology phenotypes were different between strains and phenotype dominance correspond with the CI obtained *in vitro*. Strains can colonize and persist in avocado roots as single inoculant but PCL1607 are excluded when inoculated together as SynCom. No synergy among Pc strains was observed during biocontrol.

Conclusions:

CI values of Pc strains are modulated by environmental conditions (different *in vitro* and *in vivo*), and compatibility of strains depends on environmental conditions and dominances between strains. PCL1606 and PCL1601 are compatible and stable in avocado roots and can be established as base for future SynCom studies, however PCL1607 is finally excluded.

Effects of multiple pesticides on soil microorganisms and glyphosate degradation

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Aim:

In the last years, the pressure on farmers to produce high quantities of high-quality food increased. This often leads to intensive use of pesticides to ensure adequate yields. Next to the beneficial effects of pesticides for the farmer, they can harm the environment and non-target organisms. While studies on the effects of single pesticides are ample, studies that investigate the effects of multiple pesticides are rare. As part of the Horizon2020 EU project SPRINT, we investigate the effects of pesticide mixtures.

Method:

We incubated soil spiked with mixtures of 2-methyl-4-chlorophenoxyacetic acid (MCPA), Difenconazole and labelled Glyphosate for 56 days using concentrations close to field applications. At seven timepoints, soil (pH 7.0, SOC 12.1 g kg⁻¹ and silty loam) was analysed for microbial biomass, phospholipid fatty acids (PLFAs), pesticide residues and functional genes, as well as ¹³C-partitioning in microbial C, CO₂ and PLFAs.

Results:

We found a significant negative effect of the pesticide mixture on bacterial abundance and CO₂ release after 56 days. Although the Glyphosate degradation kinetics were similar in all treatments, the addition of MCPA stimulated the ¹³CO₂ release from labelled Glyphosate. Data on ¹³C incorporation into microbial biomass will show whether this result is coupled with a change in carbon use efficiency of microorganisms.

Conclusions:

Increased ¹³CO₂ release from Glyphosate in combination with MCPA indicates an additional stress induced response to a second pesticide. Therefore, mixtures of low concentrations of pesticides exert stress on the microbial community in soils with different magnitudes depending on the pesticide combinations.

Investigating changes in microbial diversity and abundance caused from phytoremediation of petroleum hydrocarbon contaminated soil.

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Aim:

Contamination of soil caused by petroleum hydrocarbons is an ongoing issue of serious ecological concern. Microbial and plant communities in affected soils are radically impacted by such contamination, disrupting the ecosystem services that they supply and resulting in biodiversity loss. Established methods for treatment of contaminated soil such as chemical or thermal treatment are expensive and provide no benefit to the microbial communities or destroy them completely. Phytoremediation is a passive, ecologically friendly and relatively cheap approach to remediating contaminated soils. Selected plants are used for the process and by means of direct degradation, co-metabolism and stimulation of the microbial community, work to degrade or sequester environmental pollutants. It is becoming increasingly clear that understanding the complex plant-microbe interactions, especially around the rhizosphere, are key to improving the efficacy of phytoremediation. This project investigates the impact of phytoremediation on the microbial communities in the soil before, during and after the process.

Method:

A randomized pot trial was established, consisting of a control, a high yield variety of perennial rye grass (*Lolium perenne*), white mustard (*Sinapis alba*) and common chicory (*Cichorium intybus*). The soil used was co-contaminated with petroleum hydrocarbons and heavy metals. Composite soil samples were taken three times during the trial. DNA extractions were performed on the soil and sent for 16s and 18s amplicon metagenomic sequencing. Oil was extracted from soil samples via Soxhlet extraction and total petroleum hydrocarbon concentration was determined by GC/FID. The microbial data was analysed using the dada2 pipeline and Qiime2 to identify organisms based on Amplicon sequence variants (ASVs). Further analysis was done using Rstudio packages such as DESeq2 and pheatmap to create visualisations of changes in Alpha and beta diversity. The microbial communities of the different treatments were investigated for microbes potentially beneficial to the remediation process, such as plant growth promoters and saprotrophs.

Results:

Preliminary analysis of results showed increase in the abundance of both 16s and 18s organisms throughout the progression of the trial. The mustard treatment, which saw the best overall degradation of petroleum hydrocarbons by a statistically significant margin, also contained the most unique ASVs compared to other treatments. Principle co-ordinate analysis of each treatment showed difference in the microbial community between treatments.

Conclusion:

This pot trial suggests that there are significant differences between the microbiomes of different plants species used in a phytoremediation pot trial. These difference in microbiomes could be the key difference in phytoremediation performance outcomes. This is indicated by the strong performance of the mustard treatment which contained the most unique 16s and 18s ASVs. The alpha diversity of the of the mustard treatments also increased at a more rapid pace than the other treatments, suggesting it may improve soil conditions more optimally that the other treatments.

Biodiversity of green roofs: current state of knowledge

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Aim:

The objective of this study is to carry out a systematic review of the scientific literature on the whole of the biodiversity of green roofs to (i) elucidate the role of green roofs in supporting biodiversity in the city by focusing on quantitative data, (ii) and to explore the factors influencing the biodiversity of green roofs.

Method:

We conducted our search in Web of Sciences using all available databases. The key words used are: ("green roof*" or rooftop* or greenroof*) and (biodiversity* or plant* or fauna or wildlife). In total, 2392 articles came out as search results. A first selection was made based on titles and abstracts, or even the entire article, to identify the articles that really fall within the subject. In total, 154 articles were considered relevant for our study.

Results:

Our review shows:

- The lack of knowledge on the biodiversity of green roofs with recent consideration (around 2010).
- The important contribution of green roofs in maintaining urban biodiversity through three influencing factors: characterization, uses, design.
- That there are very few studies concerning soil biodiversity, unlike aerial biodiversity (e.g. plants, bees, birds) within green roofs.

Conclusions:

Green roof construction guidelines should integrate soil communities into their design and aim to be heterogeneous at roof and landscape levels, with the aim of supporting soil biodiversity and creating sustainable habitats.

Arbuscular Mycorrhizal Colonization and Root Exudation in Wheat Varieties Released between 1965 and 2020

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Aim: to study arbuscular mycorrhizal colonization between 0 and 60 cm depths and carboxylate exudation from root systems of wheat varieties released between 1965 and 2020.

Method: the study was carried out at the Santa Rosa Experimental Station (INIA, Chillán, Chile). Fifty-six plots (14 treatments with 4 replications) were established in an Andisol. The soil parameters were: pH 5.6; organic matter: 5.8%; available N: 32 mg kg⁻¹; P-Olsen: 30 mg kg⁻¹; available K: 278 mg kg⁻¹. To evaluate arbuscular mycorrhizal colonization, soil samples were taken using a tractor-mounted hydraulic sampling tube (3.5 cm diameter), which reached a depth of 60 cm. Subsequently, roots were characterized and clarified with KOH (2.5 % w/v) and HCl (1% w/w), and stained with trypan blue (0.05% w/v). Mycorrhizal structures were observed and quantified by the line intercept method. To analyse root exudation, root systems were taken, the roots were washed and incubated in CaSO₄ (0.2 mM). The solution with exudates was filtered at 0.22 µm and frozen at -20°C to be lyophilized. Finally, the lyophilized samples were resuspended in chromatographic water and quantified in HPLC equipment (Hitachi Primaide).

Results: roots belonging to the first 20 cm of soil showed the lowest percentage of arbuscular mycorrhizal colonization, with the Talafen and Tukan varieties having the lowest percentage (approximately 3.5%) and the highest carboxylate exudation (9.4 and 7.3 µmol g⁻¹ FW h⁻¹).

Conclusions: plant genetics moderated arbuscular mycorrhizal colonization. Increased arbuscular mycorrhizal colonization decreases carboxylate exudation. In addition, these processes are promoted under nutrient-limiting soil conditions.

Interplay of tree genetics and soil heterogeneity regulate intraspecific growth in Norway spruce (*Picea abies*)Taina Pennanen¹, Matti Salmela¹, Leena Hamberg¹, Sannakajsa Velmala¹¹*Natural Resources Institute Finland, Helsinki, Finland*

Aim: Trees interact with a vast selection of associated microbes, and we have found a positive relationship between the ectomycorrhizal fungal (EMF) diversity and the growth rate of Norway spruce (*Picea abies*) genotypes. As this correlation does not confirm any mechanistic link between growth rate and EMF diversity, we studied fungal interactions of genetic representatives of seedlings before any phenotypic differences in their growth rates were visible.

Methods and Results: We did not find inherent differences between EMF richness of small seedlings, implying that their compatibility with EMF symbionts was not the reason for the differences in later growth rates. Instead, we found a genetic control of the host on the early root development; future fast-growing genotypes possessed more explorative root systems. Therefore, we studied the legacy behind resource utilization of spruce genotypes and their progeny under variable selection pressures; performance, microbial associates and root architecture of spruces planted in “home” and “foreign” ecosystems i.e. spatially heterogeneous forest soil and homogenous agricultural soils. This enabled us to measure genotypic variation and its dependence on the environment in the field, as well as seedling functional trait variation in a subset of genotypes grown in controlled treatments. Growth of saplings and adult trees showed genotypic variation in the field, and significant genotype × location interactions indicated that location affected genotypic rank order and the magnitude of genotypic variance.

Conclusions: Characterization of functional traits of progeny seedlings suggested that variation in belowground conditions is likely to have brought about plastic responses in divergent shoot and root traits also in the field.

Ecosystem services of soil biota in agriculture - Results from the SoilMan Project

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Aim

Soil biodiversity is pivotal for delivering food, fibre, biofuels, clean air, drinking water and carbon storage to society. However, as stated by the European Commission Soil Thematic Strategy and the Soil Framework Directive our understanding of how soil biodiversity is linked to soil functions and ecosystem services is still very limited. SoilMan aimed to identify supporting impacts of land use vs. soil biodiversity.

Method

Framed within the simple equation: A for B = B for A (if agriculture cares about soil biodiversity, soil biodiversity will work for agriculture) SoilMan identified and quantified detracting vs soil biodiversity supporting agricultural practises as well as threatening vs. beneficial impacts of soil biota on arable farming.

Results

SoilMan was especially focused on agroecosystems as the majority of the European land area is used for agriculture and land use is among the main global change factors detrimentally affecting biodiversity. Via a broad ecological, economic and political valuation of soil biodiversity soil biota was placed into a social-ecological context. SoilMan worked in 5 European countries and based on the A for B = B for A – matrix transdisciplinary activities were carried out to mediate the win-win-impacts of land use and soil biodiversity to stakeholders and policy.

Conclusions

SoilMan outcomes were presented in the Biodiversa - Policy brief: "How soil biodiversity can strengthen resilience and ecosystem services in agricultural landscapes" summarising a number of beneficial soil biodiversity impacts on sustainable land use

(www.biodiversa.org/1982)

Carrot Health, Storage Loss and Soil Microbial Communities of Carrot Fields

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Aim: Crop rotation, variety selection and timing of harvest are important means of carrot *Daucus carota* disease control. The harvest is often cold stored to ensure a year-round supply, but storage diseases can cause significant losses. The importance of the soil's biological activity and microbial communities in disease control has been emphasized, but not yet studied in boreal croplands. Furthermore, the optimization of crop rotation cycles that support natural mycorrhization of carrot, and the potential of soil "microbiome engineering" are linked to carrot health in various agricultural soils.

Method: Carrot, rhizosphere and soil samples were collected from altogether 28 carrot fields from three different cultivation areas. Storage loss and disease agents were evaluated twice during storage. Fungal and bacterial microbial communities were assessed by amplicon sequencing of ITS and 16S barcoding regions.

Result: The preservability of carrots varied considerably between the fields; the proportion of healthy carrots varied between 35 and 95 percent. The composition of microbial communities varied between fields and according to sample type. The microbiota of carrot fields suffering from storage diseases included a large number of pathogens e.g. *Mycocentrospora acerina* and molds belonging to the *Mucor* genus. In the soil that produced healthy carrots, molds of the genus *Trichoderma*, AM mycorrhizal fungi, saprotrophic fungi of the *Hygrophoropsis* genus, fungi belonging to the *Chytridiomyces* and *Nectriaceae* groups, and actinobacteria of the Streptomycetaceae family were more abundant.

Conclusion: A diverse soil microbial community is resilient and seems to support crop plant health.

Influence of Organic and Conventional Management Systems on Soil Microarthropods in Protected and Non-Protected Areas

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Aim:

The EU Biodiversity Strategy 2030 aims to increase land-protected areas at 30% and organic farming at 25% of agricultural lands. But which measure could be more effective in preserving soil biodiversity? The aim of the study is, therefore, to assess soil health of arable lands under organic and conventional managements in Non-protected (NPAorg) and Protected (PAcon) areas of Marche region (Italy) and compare the influence of the applied farming practices on soil microarthropods in two seasons, characterized by different intensities of soil management practices: spring (lower) and autumn (higher).

Method:

Soil health has been assessed through the Biological Quality of Soil index based on arthropods (QBS-ar). Novel approaches (QBS-ab and FAI indices) which consider microarthropods' abundance in the index calculation, have been also applied. Density (ind/m²), Acari/Collembola ratio, % of Oribatid mites on total mites, biodiversity indices, correlations with chemical-physical parameters, and ordination analysis (nMDS) have been evaluated.

Results:

In both seasons, different communities have been found according to management and, particularly, PAcon sites showed significantly higher levels of biodiversity compared to NPAorg. However, in autumn, microarthropod communities present higher stability in NPAorg sites, showing an opposite trend and fewer fluctuations of the indices compared to PAcon.

Conclusions:

PA, even in conventional managed soils, seem to enhance soil biodiversity, while organic farming in NPA, confers a higher resilience to soil, making microarthropod communities more stable. Results showed that agricultural intensity reduction combined with the increased integration of agroecosystems in protected areas may represent an effective, and sustainable measure to preserve soil biodiversity and its ecological services.

Toward a National Assessment of Soil Biodiversity: A Framework for Microbiological Data Collection

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Soil microbes play a key role in global nutrient cycling and provide various ecosystem services. While biodiversity is known to vary by ecosystem and soil type, it has not been captured by most soil and ecosystem hierarchies. Soil survey traditionally collects data related to physical and chemical properties. There is growing interest in soil biology and biodiversity as a part of conservation planning for soil health. US soil survey has expanded past traditional properties and interpretations to include ecosystem hierarchies, ecological site information, and dynamic soil properties that change with land use and management. However, to meet the increasing demand for biological soil data there is a clear need for the development of efficient and cost-effective methodology that can be used by the National Cooperative Soil Survey (NCSS). Methods considered must be repeatable, economic, and produce data interoperability across laboratories and locations. This presentation aims to provide a framework for the collection of soil microbiological data across the conterminous US. Wide-ranging soils and land uses will be targeted to provide consistent results across regions. Potential products and insights from this work will be discussed.

Geographical Signal and Morphological Variability in Guadeloupe Endemic EarthwormsSamuel James¹, Damhnait McHugh²¹*Maharishi International University, Fairfield, United States*, ²*Colgate University, Hamilton, United States*

Aim: investigate processes contributing to earthworm diversity

Method: Field collection of earthworms in the forested areas of Basse Terre, Guadeloupe, French West Indies, followed by integrated taxonomic analysis of the material, including the standard DNA barcode sequence.

Results: Analyses of DNA barcode sequences from 85 individuals belonging to ~12 putative species of *Dichogaster* show a geographical pattern consistent with the ages of volcanic eruption surfaces (older to younger from north to south on Basse Terre). The morphological variation within these species is not always consistent with the barcode lineages detected, suggesting that conventional taxonomy will be difficult.

Conclusions: This pattern indicates that colonization of younger surfaces by earthworms from older surfaces occurred independently in several lineages. Many of these lineages occur today in arboreal habitats (bromeliad leaf tanks, palm leaf axils, epiphyte-created suspended soils), a habit which does not necessarily predispose the worms to travel on or within ordinary soils. Recent earthworm diversification on these relatively young surfaces has not yet reached a state at which conventional taxonomic methods can clearly differentiate taxa.

Effects of Land Use on Soil Health in Tropical Montane Forests

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Land use, predominantly logging and forest conversion to agriculture, can affect soil health due to modification of soil physicochemical and biological properties. Here, we used a land use gradient consisting of six sites in Malaysian Borneo to understand how land use change can affect soil properties and canopy structure. We asked: (1) do canopy and soil physicochemical properties vary across land use types? and (2) does soil microbial community composition differ across different land use types? We measured soil (top 5 cm) physicochemical and microbial (next generation DNA sequencing) properties, and estimated understory and overstory canopy properties including percent ground cover and canopy closure. Our results show that old growth forests accumulated greater soil organic matter, had greater soil carbon and nitrogen ratio, were less acidic, and harbored greater bacterial and fungal diversity compared to logged forests and agricultural sites. Logged forests had soils that were more acidic and held the largest abundance of acidobacteria in comparison to old growth forests and agriculture sites. Agriculture sites had open canopy, greater soil temperature, greater percentage of grass ground coverage, and lower soil water content as compared to logged and old growth forests. Our results suggest that land use not only affects the soil microbial diversity, but also the microbial community composition.

Long-term mineral fertilizer application influences soil bacterial community structure, diversity and functioning

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Aim:

How does the long-term (46 years) application of mineral fertilizer to a production grassland influence bacterial community structure, diversity and functioning?

Method:

In 1972, a split-plot experiment was established in the Jura region (Switzerland), with four treatments (n = 6). These included a non-fertilized control (Cont), 80 and 240 kg ha yr⁻¹ of mineral P and K, respectively (PK) and PK plus 75 (NPK) or 150 kg N ha yr⁻¹ (NNPK). Soil DNA was extracted, with the bacterial 16S rRNA gene being PCR amplified and an amplicon-based Illumina Miseq sequence analysis conducted. Genes involved in soil nitrogen (*chiA*) and phosphorus mineralization (*phoD*) were also quantified.

Results:

There was a significant difference between Cont and all three fertilized treatments in terms of soil bacterial community structure (all P ≤ 0.05). There were also significant (P ≤ 0.05) differences between the fertilized treatments, with the exception of PK~NPK. The Shannon diversity index was significantly higher in PK (6.76) compared to Cont (6.56, P = 0.02), though this response was not seen in NPK or NNPK. Lastly, there was significantly higher abundance of the mineralization genes *chiA* and *phoD* in NNPK (4.75 × 10⁴ and 1.27 × 10⁵ gene copies g⁻¹ dw, respectively) compared to Cont (2.10 × 10⁴ and 6.91 × 10⁴ gene copies g⁻¹ dw, respectively).

Conclusions:

Long-term mineral fertilizer application strongly influenced soil bacterial community structure, with significant differences even being seen between different fertilized treatments. Soil bacterial diversity and potential activity for soil nutrient turnover also significantly increased.

Assessing soil microbial community changes to address agricultural sustainable management

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Aim: We assayed changes in genetic bacterial diversity together with microbial activity and biomass as indicators of soil quality in agricultural soils. Two studies were performed to evaluate the effects on microbial variables of disturbance factors (in-field long-term exposition to varying concentrations of trace elements As, Cd, Co, Cr, Cu, Ni, Pb, V, Zn) or possible sustainable pest management (in-microcosm addition of the potential natural herbicide coumarin, derived by *Melilotus neapolitana*), respectively.

Method: In Southern Italy agricultural soils, genetic bacterial diversity (as richness, Shannon index, evenness) was assayed by the 16S rDNA PCR-DGGE technique, widely applied to evaluate microbial response to disturbances. Microbial activity (as potential respiration by titration procedure), total microbial biomass (C_{mic} , by fumigation-extraction method) and fungal mycelium (by microscope counting) were determined and fungal fraction of microbial biomass ($C_{fung}\%C_{mic}$) was calculated.

Results: No negative effect of long-term exposition to varying trace element concentrations on microbial variables was generally observed and bacterial diversity and C_{mic} were even favoured by high Cr concentration. However, a change in the microbial community structure occurred being $C_{fung}\%C_{mic}$ negatively affected by high Cr concentration. Coumarin addition to soil (100-300 mg kg⁻¹) had a positive effect on soil respiration and no effect on C_{mic} , but caused a bacterial richness decrease, suggesting that further studies are necessary to better define coumarin doses to avoid any negative effects on microbial community.

Conclusions: This study suggests that microbial diversity together with biomass and activity may clarify the overall microbial response to ecological factor changes.

Soil Mesofauna Community Structure 20 Years after Distinct Restoration Efforts

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Aim:

After centuries of severe land degradation, Iceland has developed various restoration methods to promote succession from deserts into well-developed vegetated ecosystems during the last decade. We took advantage of a long-term restoration field experiment to study the effect of distinct restoration efforts on soil mesofauna assemblages.

Method:

In 1999, the Landbót restoration experiment was established in a severely degraded area in southern Iceland. We made use of four treatments (1 ha each, two replications); i) lupine sowing, ii) grass and fertilizer, iii) birch seedlings, iv) willow cuttings and a control (desert). We sampled eight soil cores per treatment, four times during July-October 2019, to a depth of five cm. Mesofauna were extracted in a MacFadyen high gradient apparatus during 9 days. Collembola were identified to species and mites to order.

Results:

20 years after revegetation efforts, all treatments had resulted in higher mesofauna abundances, richness and diversity than untreated plots. Collembola abundance and species richness was highest in lupine, whereas the willow islands hosted highest species diversity. Birch, willow and lupine plots hosted higher mite abundances than grass and control plots, and the highest mean number of mite orders was found in lupine.

Conclusions:

Revegetation of severely degraded areas has led to an increase in mesofauna densities and taxonomic richness. Different restoration efforts may steer mesofauna community structures in distinct directions. Further research is needed to disentangle the effect of vegetation (resource) and improved abiotic conditions on mesofauna community structure development during ecosystem restoration in harsh sub-arctic environments.

Assessing Soil Conservation of the Madrid Drove Roads Network, within the Life Cañadas Project.

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Aim:

To evaluate the state of soil conservation and its functionality, within the Madrid network of drove roads (DRs), which are the traditional routes used by shepherds and livestock for seasonal movements in search of the most productive pastures. Spanish DRs have suffered a progressive abandonment and degradation, threatening their role as ecological corridors. For this reason, some of them were selected in the LIFE CAÑADAS project, which aims at restoring and recovering its functionality.

Method:

Three categories of DRs were established: (i) reference (adequately grazed and maintained) (ii) abandoned (no livestock use, with biomass accumulation) and (iii) eroded drove roads. In this contribution, we present a previous diagnosis using edaphic indicators before the development of the restoration strategy. Samples were taken in summer 2020 and processed to obtain several parameters like physical-chemical properties (pH, EC, %C, TN, P, K) or enzyme activity, which was determined using a fluorometric method. We also developed the Tea Bag Index methodology, to estimate plant litter decomposition.

Results:

Our preliminary results show that reference plots have higher mean values of enzyme activity than abandoned and eroded DRs. Regarding the physical-chemical parameters determined, plots suffering from erosion are significantly different than reference and overgrown plots. Data from the TBI experiment are still being processed.

Conclusions:

These results indicate that two processes that are to some extent antagonistic, namely the loss of vegetation cover through erosion and the excessive accumulation of biomass due to the cessation of grazing, lead to a similar loss of soil functionality.

Nematode Diversity and Community Response to the Application of Recycling Derived Fertilisers in Irish Grassland

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¹*South East Technological University, Carlow , Ireland*

Aim: The aim of this study was to investigate the effects of struvite and ash products, termed as recycling derived fertilisers (RDFs), on soil nematode diversity and communities, and to conclude on the ecological safety of RDF utilisation in Irish grassland.

Method: The RDF products have been recovered from phosphate-rich sources as part of the INTERREG_NWE Project called ReNu2Farm. A three-year field experiment was conducted in Teagasc, Johnstown Castle, Wexford, Ireland. For diversity and community analyses, nematode DNA was extracted from soil samples, the 18S rRNA gene was sequenced and further bioinformatic analysis were employed to reveal any significant differences between the treatments.

Results: In 2019, ash derived from sewage sludge showed the lowest number of observed nematode species when compared with those in the unfertilised control. In 2020, the relative abundance of sensitive to environmental disturbance dorylaimids was decreased when compared with that in the unfertilised and mineral control treatment groups. In 2019 and 2020, order Dorylaimida was the dominant taxon across the treatment groups, whereas in 2021, plant parasitic and fungal feeding nematodes belonging to order Tylenchida, dominated across the treatments that received phosphorous in the mineral or recycled form.

Conclusions: Neither struvite nor ash derived from poultry litter reduced the number of observed nematode species, thus, maintained soil nematode biodiversity. The sewage sludge ash product requires further investigation before recommending its regular application as fertiliser. Overall, RDFs were identified as a valid source of recycled nutrients and a sustainable alternative to mineral fertilisers.

The microbial diversity and heterogeneity hidden in the progenitors of major crops

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Aim: During evolution under domestication, the microbial diversity in the rhizosphere of crops has been reduced, constraining our ability to select microbes with beneficial traits to increase crop performance. The microbial diversity hidden in the rhizosphere of crop wild progenitors can be explored to develop tools that improve crop yield and climate change resilience. Thus, we aim to explore the microbial diversity and heterogeneity of the microbiota associated to the wild progenitors of major crops.

Method: We explored the microbial community assembly (16S, ITS and 18S rRNA phylogenetic markers) in the rhizosphere of ten species of crop wild progenitors in their centres of origin. We sampled three plant individuals across 10-15 populations per wild progenitors following a soil-climate gradient.

Results: We compared the influence of environmental factors in the rhizosphere community assembly of bacteria, fungi and protists, and the cross-effects that may occur between them. We also characterized the intra-specific rhizosphere diversity within each wild progenitor and found that environmental and biotic factors drive ample variation in the ancestral microbiome of crops.

Conclusions: This work highlights the importance of several soil-climatic variables, and the effect of different microbial groups, in the rhizosphere diversity of crop wild progenitors. Together with the identification of key parameters that determine the heterogeneity of microbial communities along environmental gradients, it provides a necessary starting point for the selection of microbial phylotypes to improve crop performance worldwide.

Impacts of Solubilizing Microorganisms in a Three-year Crop Rotation System Under a Mediterranean Climate

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Aim:

Intensive agricultural systems including the use of chemical fertilizers and pesticides may have detrimental effects on soil productivity and health leading to soil nutrients depletion, loss of organic matter and soil biodiversity and affect the delivery of ecosystem services. Soil microorganisms are crucial for maintaining soil health, playing an essential role in nutrient cycling, degradation of contaminants and suppression of soil-borne diseases. In the present study, a three-year crop rotation system was tested with the aim to improve soil biodiversity, soil nutrient availability, soil water retention as well as reducing external inputs, productions costs, soil- borne pests and increasing crop production.

Method:

The experimental layout consisted of a randomized block design with the following treatments: conventional fertilization; reduced fertilization with nutrient solubilizing bacteria; reduced fertilization plus free-living fungi and bacteria; and just reduced fertilization. The crop rotation system consisted of four cycles: potato (*Solanum tuberosum*. L. var. Spunta), broccoli (*Brassica oleracea* L. var. *italica*), melon 'Piel de Sapo' (*Cucumis melo* L. var. *saccharinus* Chaud), and potato (*Solanum tuberosum*. L. var. Spunta).

Results:

In order to monitor the effects of the addition of solubilizing biological agents on soil biodiversity and other ecosystem services, soil physical-chemical properties, crop yield and quality, microbial communities, and functional genes of the carbon and nitrogen cycles were assessed. This work was funded by the H2020 SoildiverAgro-project (grant agreement 817819) which overarching goal is the enhancement of soil biodiversity in European agroecosystems to promote their stability and resilience together with the reduction of external inputs and crop performance increase.

Relationships of Acute and Chronic oak decline with soil biology and nutrient dynamics

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Aim:

Acute oak decline (AOD) widely impacts oak woodlands across Europe. AOD is known to cause rapid decline in tree health in a short span of 3-5 years. However, the interactions between such oak decline and tree rhizosphere and associated soil nutrient dynamics are not fully explored, despite indications that soil biotic and abiotic conditions are closely linked to cause-effect interactions with oak tree health. We aim to explore those complex interactions through this research.

Methods:

We have selected 3 oak trees each for 3 different treatments, consisting of trees that have 1. No symptoms, 2. Acute oak decline symptoms and 3. Chronic oak decline symptoms, in Writtle woodlands, Essex, UK. The selected trees will be the focus for quarterly rhizosphere soil sampling (cores to depth of 50 cm). Soil samples will be characterised for their physico-chemical properties and total nutrient contents. Soil nematodes and micro-arthropods will be measured using Baermann funnel and Tullgren funnel methods respectively. Rhizosphere microbial communities will be characterised using Phospholipid and Neutral lipid fatty acid analyses. Newly developed state-of-the-art microdialysis instrumentation will be field-deployed to measure continuous real-time changes in soil nitrate levels. Well established lab-based techniques will be used to validate the nitrate level measured by the instrument, and to analyse ammonium and phosphate levels in the rhizosphere. Nutrient addition through litterfall, and nutrient loss through N₂O and leaching will be measured bi-weekly. TreeTalkers will be used for continuous measurement of tree physiology.

Results and Conclusions:

We expect this research to provide insights into belowground dynamics of soil organisms and nutrients in temperate woodlands and their interaction with symptoms of oak decline that are manifested aboveground.

Challenges Below the Ground: Morphological and Genetic Species BoundariesIna Schaefer¹, Stefan Scheu¹¹*University of Goettingen, Goettingen, Germany***Aim:**

Metabarcoding and metagenomics are the up-and-coming tools to assess and monitor biodiversity of soil animal communities. This is for a good reason: communities can be analysed from bulk samples, time-intensive sorting and determination can be automated and processed in comparatively short time. Current drawbacks for a general application of HTS methods arise from choosing standardized barcoding regions and primers, and the completeness of databases to assess taxonomic diversity, but methodological shortcomings will disappear with time. However, awareness to the intrinsic challenges of genetic diversity of soil fauna still needs to be raised while establishing high-throughput sequencing technologies for screening soil animal diversity.

Method:

Sequences of the COI barcoding region were collected from morphotypes of Collembola and oribatid mite species across different habitats and at large geographic scale and analysed for the presence of a barcoding gap. Secondary barcoding genes were also sequenced for some species.

Results:

Genetic variance of morphotypes covered a continuum across habitats and space that corresponded with multiple species, in several cases without clear barcoding boundaries.

Conclusions:

The investigated morphotypes covered a range of COI haplotypes that did not necessarily cluster in distinct genetic groups. Accordingly, the identification of species based on genetic data was often equivocal, which likely will result in a large fraction of ambiguous OTUs in metabarcoding studies. For database build up, it is essential to include secondary barcode regions and collect samples from different habitats and across large geographic ranges, in order to include all soil animal diversity, instead of discarding unknown sequence reads.

Earthworms' and Gut Microbiome Diversity under Microplastics, Extreme Environmental Conditions and Different Types of Soil

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Aim: To observe how earthworms from agricultural areas and their gut microbiome diversity is affected with microplastics under extreme conditions of moisture, temperature at different soil types. **Method:** Multifactor experiments were established with epigeic, endogeic and anecic earthworms at laboratory conditions with 3 types of plastics, 3 types of soils, 2 moisture and 2 temperature conditions. Microplastics were applied at 0.2% simulating hotspots inside the soil. The experiment duration varied according to the sub-questions from 7, 14, and 55 days. Gut microbiome was extracted and identified. **Results:** as preliminary results indicate how *Eisenia hortensis* resist well extreme conditions of temperature with presence of microplastics, while *E. fetida* expired faster. Endogeic earthworms support high moisture conditions, while anecic earthworms as *Lumbricus terrestris* are the most sensitive to microplastics and environmental extreme situations. Positive growth rates were observed in those experiments of 7 days when the earthworms are adapting to the new/extreme conditions, while after a decrease in weight was observed. Earthworms' gut microbiome changed among extreme conditions. **Conclusions:** Earthworms are influenced by soil, moisture, and temperature conditions, and when microplastics are present different adapting procedures take place.

Soil microbial community composition and N₂O emissions as a function of tillage and fertilization practices

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Aim:

The aim of this study was to determine the effects of tillage and fertilization on the soil microbial community, particularly on the abundance of N cycling guilds, and to link them with measured N₂O emissions.

Method:

The study was conducted during the maize vegetation period on long-term combined tillage (no-till (NT) vs. plough tillage (CT)) and fertilization (unfertilized, mineral and compost) field trial, established in 1999. Gas samples were collected throughout the growing season using a static chamber approach, and a composite soil sample was collected at 10 cm depth to perform physicochemical analyses and quantification of microbial genes by qPCR (16S, ITS, *nirS*, *nirK*, *nosZI*, *nosZII*, *nrfA*, *amoA*).

Results:

After 21 years, the data showed a clear increase of soil organic carbon in NT compared to CT at 0-10 cm depth, depending on fertilization. Soil temperature conditions were comparable among tillage treatments, while NT showed higher soil saturation with water. Rain events following fertilization were the main triggers of N₂O emission peaks. N₂O emissions were the highest in mineral fertilization, followed by compost and nonfertilized plots. In general, the genetic potential for N₂O emissions was increased in no-till (*nosZ/nosZII* ratio) and mineral fertilization (bacterial *amoA*/16S ratio) and decreased in compost fertilization ($((nirK+nirS)/(nosZ+nosZII))$ ratio).

Conclusions:

Both tillage and fertilization influenced the composition of the N-cycling community. The genetic potential for N₂O emissions was higher in NT and under mineral fertilization and lower in compost amended soil. However, measured N₂O emissions were the highest under mineral fertilization, regardless of tillage.

The Potential of Biostimulant Use for Enhanced Nutrient Use Efficiency in Agricultural Grasslands

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Agricultural grasslands are of great economic, environmental and cultural importance across the globe. Rising intensification of these systems has led to large increases in fertiliser use, resulting in adverse environmental impacts. Practices that reduce the reliance on fertiliser are therefore greatly needed. One potential solution is the use of biostimulants, products which promote plant processes, often reporting reduced fertiliser requirements. However, research thus far has focused on horticultural and arable crops with little consensus on how they could best be used in grassland systems.

Aim: This project aims to assess the current state of biostimulant literature, identify biostimulant products which have evidence supporting their application to grasslands, and test selected products through greenhouse and field experiments.

Method: A systematic scoping review of the available literature on biostimulant use on grasses and grassland plant species has been performed, biostimulant products of interest identified during this review are currently being tested in greenhouse experiments.

Results: Microbial biostimulants were tested in 59 out of the 115 publications included in the scoping review, with certain microbial species appearing in several of these publications. This includes the N-fixing bacterium *Azospirillum brasilense* and the arbuscular mycorrhizal fungus *Rhizophagus irregularis* which have been reported to have positive effects on grass nutrient use, shoot and root growth.

These microbial biostimulants, along with two non-microbial biostimulants are currently being tested for grass-growth promoting effects under reduced fertilisation.

Conclusions: The results of this study will hopefully provide insight into the potential applications of soil microbes for more sustainable grassland agriculture.

Soil Biodiversity and Ecosystem Functioning (BEF) in Stone Coastal Terraced Vineyards

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Aim: The terraced steep slopes to obtain strips of arable land, supported by kilometers of dry stone walls became World Heritage Site in the Cinque Terre (North-Western Italy). In terms of soil biodiversity, the evaluation of soil functionality in terraced vineyards is not usually considered.

Method: In the National Park area, 6 sites were selected at different altitudes and distances from the sea. In 2020-2021, for each terraced plot (3-6 replicates/plot), soil samples were carried out in inter-rows. Soil quality assessment was performed by chemical analysis (C_{org} , N_{tot} , CEC), soil enzymatic analysis (12 enzyme activities), assessment of microbial biomass (dsDNA) and ecological survey of edaphic arthropods. The arthropod communities were evaluated by abundance and soil biological quality (QBSar index)

Results: Over all sites, soils exhibited high content of OM (53.6-72.2 g OM/kg soil) and microbial biomass (60-123 mg dsDNA g^{-1} soil). Concerning biogeochemical processes, enzymes linked to P cycle were abundant in vineyards at 200 m ASL x 300 m far from sea. In contrast, enzymes involved in the decomposition process were particularly high in one site with undisturbed interrow vineyard: here, microarthropod densities were highest too. The Acarofauna community represented the 80% of soil microarthropods, followed by Collembola (14%) and other groups (Arachnida, Crustacea, Myriapoda, Enthognata, Insecta). Topography did not affect arthropod abundances; however, the higher vineyards showed low QBSar values and simplification of structure community.

Conclusions: Vineyards in altitude should increase the effort to maintain the soil biodiversity and functionality.

Soil Microbial Diversity and Function along the Soil Depth Gradient in Multi Species Swards.

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Aim: To investigate whether the presence of known deep rooting plant species in intensively managed agricultural grasslands influenced microbial community composition, abundance and function along the soil depth gradient.

Methods: Microbial diversity and functional analyses were performed on soil samples taken from four soil horizons: A (0-15 cm), B (15-30 cm), C (30-60 cm) and D (60-90cm) in intensively managed grasslands with manipulated plant diversity. Microbial functional capacity was measured through enzymatic assays and substrate induced respiration assays. Microbial abundance was quantified using qPCR and diversity was measured through sequencing of 16S and ITS genes.

Results: Soil microbial phylogenetic gene abundance and carbon cycling function was found to decrease, and community composition was found to change, along the soil depth gradient, regardless of plant identity. Soil microbial phylogenetic gene abundance was not significantly influenced by plant identity along the soil depth gradient; however, 16S microbial community composition was significantly influenced by plant identity in the top 15cm of soil and fungal community composition was significantly influenced by plant identity between 15-30 cm in soil. Selected carbon cycling enzymes were found to be significantly more active at depth when deep rooting plant species were present.

Conclusions: Plant communities mediate the rate at which microbial carbon cycling, as measured through enzymatic assays, decreases along the soil depth gradient. Plant communities influence fungal community composition along the soil depth gradient.

Disturbed and Diverse - Management Practices Impact Urban Soil Microbial Communities in Green-Wood Cemetery

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Aim: A better understanding of urban soil microbial communities will allow for effective management practices that can support essential ecosystem services, such as nutrient cycling, handling of stormwater runoff, and promoting plant and tree health in urban spaces. The managers at Green-Wood Cemetery (Brooklyn, NY) have three levels of landscape management, intensive turf management, minimally managed meadows, and unmanaged woodlands. We hypothesize that there will be an inverse relationship between the level of management intensity and soil microbial diversity.

Methods: We tested this hypothesis by collecting total soil DNA for 16S amplicon sequencing and samples for community-level metabolic profiling using BioLog Ecoplates. We analyzed a total of 36 soil samples. The 16S amplicon DNA was sequenced on an Illumina MiSeq at Wright Labs, LLC. The DNA sequence data were analyzed using QIIME2 and Nephele. Using the Ecoplates we determined the utilization of 31 different carbon sources.

Results: Our preliminary data from the Ecoplates, and a subset of 16S amplicon samples, show that there are distinct microbial communities at the two soil depths tested and from the three management regimes. Consistent with results from other studies, we see greater soil biodiversity in the shallow samples. However, we see lower levels of microbial diversity in the unmanaged sites relative to the intensive and moderately managed sites.

Conclusions: Our work demonstrates that landscape management practices can impact soil microbial communities. We found that urban soils have microbial diversity that is equivalent to soils that experience lower levels of impact from human activity.

Early changes of several biological properties of vineyard soils managed with straw or gorse mulching

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Aim: The study compares the microbial activity and bacterial functional diversity in vineyard soils, rich in organic matter, under conventional management with herbicides to control weeds, or under management without herbicides and the application of straw or gorse biomass mulching.

Method: Soils receiving mulching in winter or herbicide in early spring were sampled at the beginning of July, and characterised for their general physic-chemical properties. The evaluation of biological properties included the analysis of the dehydrogenase activity, following standard methods, and the determination of the bacterial functional diversity, using Biolog EcoPlates

Results: The application of straw or gorse mulching did not significantly affect the soil dehydrogenase activity; however, the average degradation of the C substrates evaluated (AWCD) as well as the Shannon (H') and evenness (J') diversity indexes increased in soils receiving gorse mulching. Evenness also tended to increase in soils mulched with straw. The mulching with gorse increased the degradation activity of soil bacteria of several carboxylic acids, phenylalanine, phenylethylamine and glycogen, while the increases observed in soils receiving straw were restricted to malic acid, phenylethylamine and glycogen. The degradation of glycy-L-glutamic acid was inhibited in mulched soils.

Conclusions: Mulching affected the bacterial functional diversity of the vineyard soils analysed, although it did not significantly modify dehydrogenase activity. More detailed and long-lasting research is needed to properly assess the impact of mulching with different materials on these soils rich in organic C.

Legacy Effects of Drought on Grassland Microbial Communities Across the North American Great Plains

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Aim: We seek to assess the legacy effects of drought on plant-associated microbial communities in grasslands.

Method: Four North American grassland sites spanning a broad precipitation gradient were subjected to experimental growing season drought treatments for four years (2013-2017). The two treatments included chronic (removal of 66% of each growing season precipitation event) and intense (full precipitation exclusion throughout growing season) drought. Following a four-year recovery period, we sampled the bulk soil and dominant species at each site. We conducted 16S & ITS amplicon sequencing to assess bacterial and fungal communities in the bulk soil, rhizosphere, endosphere, and phyllosphere compartments.

Results: We have data from two years into the experiment, the completion of the experiment, and four years into recovery, allowing us to generate temporal insight regarding microbial response to severe field drought and ambient recovery. Our results suggest that bacterial community composition is highly responsive to drought, driven by alterations in Actinobacteria, Proteobacteria, Acidobacteria, and Bacteroidetes. Increased levels of glycosyltransferase and B-glucanase were found under both drought treatments. Fungal assessment was hindered by a lack of assigned genomes, though we noted an increase in Glomeromycetes in droughted plots. Dominant plant species' rhizosphere and endosphere communities differed amongst sites and species.

Conclusions: Functional genes related to stress resistance increased in prevalence, suggesting soil microbial communities will be primed for future drought events. Our results suggest that dominant plant species recruit microbes that may enhance drought tolerance, with a legacy of altered microbial composition.

Evolution and Assembly of Microbial Communities in Biochar-Amended SoilsNikolaos Paranychianakis¹, Rafaila - Nikola Mourgela¹¹*Technical University Of Crete, Chania, Greece***Aim:**

The overarching objective of this study was to evaluate the effect of biochar addition to the microbiomes of organic farming greenhouse soils. Specifically, we tackled the evolution of basic attributes of microbial communities in soils amended with biochar, a commonly used amendment for soil health restoration of degraded soils.

Method:

Different rates of biochar (0, 2.5, 5, 10%), produced by municipal solid wastes, were applied in soil microcosms collected from a greenhouse poor in SOM (0.9%). Following biochar incorporation, soils were wetted and maintained to 70% of water holding capacity and were sampled at weekly intervals. The last week a drying/rewetting step was applied to test the stability and resilience of microbial communities. Bioinformatic analysis of microbial communities was performed with dada2 pipeline in the R environment.

Results:

Data analysis revealed that biochar dose had no effect on α and β diversity of soil microbial communities. By contrast, the drying and rewetting cycle induced strong shifts on soil microbial community composition and α and β diversity. Contrary to our expectations, the deviation of microbial communities was stronger in soils treated with the highest biochar dose implying a higher contribution of stochastic process in microbial community assembly, a finding that was confirmed by the observed differences in the β NRI metric. Differences were also found in the properties of microbial networks and keystone taxa.

Conclusions:

These findings indicate that biochar may induce significant shifts in soil microbial communities following disturbance events posing barriers on the maintenance of engineered communities.

Facilitative Interactions in Soil Microbial Systems at the Polar RegionsJesse Jorna¹, Byron Adams¹¹*Brigham Young University, Provo, United States***Aim:**

Facilitative interactions are widespread in natural systems, yet the focus of community ecologists has been primarily on the quantification of competitive and trophic drivers of diversity. The belowground biodiversity of the polar regions offers an excellent toolbox to study the facilitative interactions of microbial communities at small, heterogeneous scales to understand how these interactions drive community diversity and function. We compare experiments and observations from the Arctic and Antarctic to temperate dryland systems to understand the relative importance of facilitative interactions across environmental gradients.

Method:

Active layer soil samples are collected above permafrost in the McMurdo Dry Valleys of Antarctica and in the Canadian Arctic at Cambridge Bay. Whole soil communities are characterized by 16S metabarcoding inventories. Co-occurrence methods are combined with phylogenetic measurements to describe the relative proportion of positive interactions across a simplified gradient of environmental stress in the form of water limitation. Other environmental drivers such as organic matter, salinity and micronutrients are measured at each site to create a null-model to which relative co-occurrence is compared.

Results:

Results for these experiments are pending – metabarcoding inventories will be compared to datasets from the Seville National Wildlife Refuge. Our expectations are that microbial interactions broadly follow a stress-gradient type distribution, with positive interactions becoming more frequent in ecosystems under increased environmental stress in the form of higher water limitation. Moreover, in the absence of plants facilitating belowground growth we expect facilitative interactions between bacteria to be more important drivers of community structure in the Antarctic.

Diversity-function relationship in soil microbial community in *Eucalyptus grandis* plantation from surface to deep horizons

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Tree plantations play a key role in carbon (C) sequestration. Yet, the mechanisms that underpin the C cycling in these tree systems are poorly understood. Although *Eucalyptus* is the most widely planted tree genus in the tropics, we miss estimates of its contribution to the soil C dynamics, its variability and determinants. Here we characterized the heterogeneity of soil physico-chemical and microbial (molecular and metabolic) parameters at 51 locations on surface (0-10 cm) and at 9 locations on 6 depths (at down to 4 meters) in a stand of *E. grandis* plantation installed 20 years ago. We used Illumina sequencing and the MicroResp™ microplate-based respiration system for the molecular and functional characterization, respectively, of the soil microbial community. We found substantial variations in the soil physico-chemical and microbial parameters at the plot scale. In the surface soil, the metabolic parameters (substrates used by the microbial community and their respiration rates) were explained by both the soil abiotic parameters and the bacterial and fungal community structure, but with a predominant role of bacterial composition. We also recorded variation of microbial parameters with soil depth, with increasing metabolic diversity in deeper soil layers. Collectively, our data suggest a strong heterogeneity of the soil respiration process across the plantation, which has to be considered for future sampling strategies when studying the role of tree plantations in the global C balance.

Comparative diversity patterns of vascular plants and testate amoebae along elevation gradients in Hawaii

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Aim:

Soil protists respond to changes in abiotic conditions and vegetation type from plot to continental scale. However comparative studies of plant and protist diversity are rare and the importance of native and endemic plant diversity has not been assessed.

Method:

We recorded testate amoeba (TA) and plant species data along four elevation gradients in forests (coast to treeline) and in the alpine zone (6 elevation each), on Maui and Big Island, Hawaii. We compared TA vs. overall, native and introduced plant diversity patterns with elevation.

Results:

Species richness of native plants and TA generally increased from the coast to treeline. Above treeline, TA richness declined with elevation. The diversity of introduced plants decreased with elevation in forests and alpine plots. TA species richness was positively correlated to plant richness, due entirely to the native and endemic component of plant diversity. TA community composition was best explained by native plant richness, moss or rock cover, pH and C and N content. Plant and TA communities showed highest and significant correlation in Mantel tests for the two upper forest elevations.

Conclusions:

The observed patterns suggest a strong impact of vegetation type and native diversity on soil microbial diversity. This patterns may however partly be due to the more favourable conditions for testate amoebae and soil life in general, especially higher organic matter content and soil moisture. The possible role of plant identity e.g. through litter chemistry effects should be further explored.

Plant Microbiome to Soil Microbiome: Soil Microbial Diversity and Function in Multi Species Swards

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Aim: To quantify how plant diversity in intensively managed multi-species agricultural grasslands affect soil microbial diversity and function.

Method: Microbial diversity and functional analyses were performed on soil samples taken from systematically varying plant community combinations within a six-species experimental trial (1-6 species), at four time points throughout the growing season. We quantified the effect of different plant species on microbial responses, and whether mixing the plant species resulted in antagonistic, neutral or positive effects on microbial responses. Further, the effect of additional nitrogen (N) fertiliser application on the soil microbiome of *Lolium perenne* monocultures was measured.

Results: Plant species identity effects were the main drivers of microbial composition, diversity and function in the soil, while effects of interspecific interactions among the plant species or functional groups were rarely significant. Bacterial abundance, crenarchaeal abundance and substrate induced respiration rates were lower on average in the *L. perenne* monocultures with 300 kg ha⁻¹ yr⁻¹ N (300N) compared to the other plant communities with 300 kg ha⁻¹ yr⁻¹ N, suggesting that high nitrogen treatments reduce microbial abundance and active microbial biomass. The 300N *L. perenne* monoculture generally had significantly different soil microbial community composition compared to all other plant monocultures.

Conclusions: Plant species identity effects, particularly those of legumes and herbs, affected the community composition and function of the soil microbiome. Thus, diverse plant mixtures in agricultural grasslands, compared to less diverse grasslands, can have a significant effect on the soil microbiome. High levels of N fertilisation can negatively affect soil microbial communities.

The Impact of Management on Soil-borne Biodiversity in Austrian Agriculture

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Aim:

We were interested in the impact of agricultural management practices on soil properties, plant performance and the soil-borne microbiome in Eastern Austria for a better understanding of the connection between land management, belowground microbial biodiversity and ecosystem services.

Method:

A set of experimental fields mainly run by Agricultural schools in Eastern Austria was established. Soil properties were measured by standard procedures. Fungal and bacterial communities from the topsoil were investigated by high-throughput sequencing of ITS2 and partial 16S amplicons, respectively.

Results:

In a series of experiments carried out mainly in eastern Austria the effects of management practices on soil properties, plant performance and the microbiome were investigated. Site, which integrates soil type, cropping history and climate, together with season were the major factors driving community composition. Intensively cropped arable land has distinct communities of fungi and bacteria compared to adjacent wildflower strips. Intensity of tillage induces a gradient in the microbiome from no-till with direct sowing to conventional ploughing. Some of the observed changes can be related to changes in soil properties. A single addition of biostimulants, on the other hand, does not induce any changes in properties of soil, plant or the microbiome.

Conclusions:

The findings are mostly in good agreement with results from other studies and help to predict management effects on soil-borne diversity and should help in an improvement of ecosystem services from agricultural sites through appropriate crop management.

SOILGUARD: Linking Soil Biodiversity and Agricultural Soil Management

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Aim: SOILGUARD is a European project that aims to improve and standardise methods for measuring soil biodiversity across different European regions. Soil microorganisms control a wide range of ecosystem services, such as nitrogen and carbon cycling that are essential to agricultural systems and are strongly influenced by land management. Therefore, it is important to understand how soil biodiversity differs between land management practices so we can better maintain and improve it.

Methods: Ireland is one of 17 countries participating in the SOILGUARD project. Soil biodiversity was compared between high N input perennial ryegrass grasslands and low N input multispecies grasslands farms in the south of Ireland. This was achieved by identifying and collaborating with farming stakeholders, visiting their farms, and taking soil samples for biodiversity analyses. The physical-chemical properties of the soil, such as pH and total carbon levels, were measured. Species and communities of nematodes and micro-arthropods in the soil were identified and quantified. Molecular assays were performed to investigate bacterial, archaeal, fungal and viral community structure and diversity in the soil.

Results: Samples are currently being processed

Conclusions: SOILGUARD will increase understanding of the effects of farm management on soil biodiversity and ecosystem services in intensively managed agricultural grasslands. This will also help us better understand and develop standard ways to measure soil biodiversity.

Tillage systems reflected in communities quantified by metabarcoding and abundance of earthworms and collembolans

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Aim:

Investigating the capacity of eDNA and metagenomics to detect different soil communities as observed for contrasting farming systems.

Method: An experimental long-term field design with tillage vs. no-tillage farming systems on a loamy soil location and a sandy soil location was subject to sampling for earthworms and collembolans. We employed two sets of primers to address minibarcodes of earthworms, 16S, and microarthropods, COI, (mites and springtails). For the earthworms we employed a soil DNA approach extracting a 1.5 kg composite soil sample with phosphate buffer and subsequent NucleoSpin Soil Kit[®] extraction. For collembolans we employed a community DNA approach creating a DNA soup of the animals using the NucleoSpin Soil Kit[®] for DNA extraction.

Results:

The well-established difference in soil biodiversity abundances between tillage systems was confirmed. The large anecic earthworms *Lumbricus herculeus* and *Aporrectodea longa* and the epigeic earthworms were most abundant in no-till systems. The microarthropods were positively influenced with no-tillage, but the extreme weather conditions during the sampling occasions have hidden some of the effects of the cultivation practices.

Conclusions: Although we cannot claim metabarcoding to be quantitative it reflected the structural community differences between the tillage and no-tillage farming systems.

A novel method to assess nematode anhydrobiosis reveals ecologically relevant differences across functional guilds

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Aim:

Soil nematodes are among the most abundant soil fauna. Their high taxonomic and functional diversity make them excellent indicators of soil health, and a number of nematode-based ecological indices have been developed to assess soil fertility, soil food web complexity, soil suppressiveness, and other relevant soil food web attributes and ecosystem services. However, some basic aspects of nematode ecology remain understudied. Anhydrobiosis, the ability to survive extremely dry soil conditions for long periods of time is a functional trait that influences nematode ability to survive dry spells, and which might be especially important in future climate conditions and affect the role of nematodes in soil processes. Although explored for specific nematode taxa, the extent of anhydrobiotic abilities across taxa, trophic, and colonizer-persister (c-p) groups of free-living nematodes remain unknown and deserve further attention.

Method: (heading must be in bold)

In this study, we developed a novel and efficient method to calculate anhydrobiotic rates across nematode taxa and functional guilds in laboratory conditions.

Results:

Inducing an experimental drought, we found that total soil nematode abundances were reduced, but the number of anhydrobiotic nematodes significantly increased. Nematodes across all trophic and c-p groups entered anhydrobiosis, and while nematodes in lower trophic and c-p groups responded quickly to water availability recovering mobility after drought, higher trophic and c-p groups were slower to recover from anhydrobiosis.

Conclusions:

Such different abilities may determine the dynamics of soil nematode communities after drought periods, thereby affecting all the associated ecosystem processes. Ecological implications of such findings are discussed.

Innovative Spent Coffee Ground-Based Biofertilizer: Effects on Soil Microbiome and Crop Health

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Aim:

Crop health is strictly related to soil biodiversity. The transition from chemical fertilizers to biofertilizers may represent a sustainable way to restore soil biodiversity, improve crop health and productivity.

Spent coffee ground (SCG) is a waste material with a high potential for the development of innovative biofertilizers. However, previous research showed that the use of SCG as fertilizer inhibits plants growth, mainly due to the presence of phytotoxic compounds. On the contrary, SCG-treated plants showed high nutritional values with an increased content in antioxidants and mineral elements.

The aim of this research was to test the effects of an innovative SCG-based biofertilizer (BF) on salad crops (*Lactuca sativa*), and on their rhizosphere microbial communities. And thus, to evaluate its potential in mitigating SCG's negative effects.

Method:

A randomized block design experiment was carried to compare the effects of BF and SCG at 3 different concentrations, each with 5 replicates. Plants functional traits and nutritional values were evaluated. 16S rRNA gene metabarcoding was used to assess the effects on rhizosphere communities.

Results:

BF-treated plants showed a higher polyphenols level and less stress signs compared to the SCG-treated and control ones. At the highest concentrations, BF modify bacterial communities with an increase of plant growth-promoting rhizobacteria (e.g., *Azospirillum*, *Arachidicoccus*) and other beneficial bacterial taxa, such as those involved in disease suppression, aromatic compounds degradation, nutrients cycling.

Conclusions:

BF resulted capable of reducing SCG negative effects on plant health, promoting the growth of plants beneficial microbial taxa and, therefore, favouring a healthier growth of crops.

MiRA FruiT-Microbial Resources for Agriculture, a FruiTful collaboration with a smallholder fruit trees farmer

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Background: Tree crops are fundamental for human nutrition and warrant food security and stability of many farms including smallholder ones. Being present on a time scale of years, and having a persistent, deeper root system, the impacts of tree crops (e.g., on nutrients mobilization, organic matter accumulation, beneficials, parasites...) largely differ from annual crops and thus cannot be considered as comparable. Moreover, due to the absence of annual rotation and lack of soil tillage, perennial tree crops also represent a stable food source not only for building up consortia of beneficial microbial communities but also for some root pathogens or parasites.

We hypothesized that plant rhizosphere is strongly influenced by plant species/genotype which is able to select and recruit microbes that will then colonize the aboveground organs influencing plant nutrition, development and fruit quality and exerting a strong influence on soil functionality.

In this context, we investigate whether two different fruit tree species: *Mangifera indica*, (mango) and *Punica granatum* (pomegranate), cultivated in a family-run farm at Chandrika lake, district of Ratnapura, Sri Lanka, influence differently the microbial recruitment from the surrounding soil. Both interrow bulk soil (10-20 cm) and rhizosphere soil (10-20 cm) were analyzed in order to understand the possible impact on plants nutrition, growth, pathogens tolerance, and healthy fruits productions.

Results: Metabarcoding analyses associated with soil physico-chemical characterization and evaluation of microbial biomass, presence of pathogen and microbial phytohormone production, have provided an exhaustive reference database on the biodiversity of bacteria and fungi thriving in the farm soil, cultivated with Mango and Pomegranate, and their relative functions. Among them, microbial markers of healthy productive plant species soils will be identified.

Conclusion: The results on the diversity and functional roles of this microbiota will be highly relevant for soil conservation and they will represent an added value for the commercial product and may provide farmers of this agriculture district with new tools (e.g. tailored microbial consortium) for agronomic innovation.

Soil Bacterial and Fungal Community Response to Nitrogen Fertilising Materials Recovered from Manure

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Aim: Soil bacteria and fungi provide a multitude of key ecosystem services and are central to the successful production of agricultural crops. Using diversity as an indicator, the research aimed to evaluate the response of soil bacterial and fungal communities to the application of sustainably sourced nitrogen (N) recycling-derived fertilising materials (RDFs) recovered from animal manure, as substitutes to synthetic N fertilisers.

Method: Soil samples were obtained from a one-year trial on field-scale application of N RDFs. Total DNA was extracted and amplicon sequencing of bacterial 16S V4-V5, and fungal ITS1 regions, was performed on Illumina paired-end platform. Sequenced data was processed and analysed using QIIME2 and R software.

Results: Soil with N RDFs applied displayed significantly higher levels of bacterial alpha diversity and significantly different community structures (beta diversity) compared to reference treatments. This liquid nature of the RDFs may have allowed microbial populations to flourish due to the provision of rapidly available nutrients. Furthermore, the additional moisture may have influenced communities due to a drought period experienced during the trial. Less variation was observed among fungal communities, with diversity increases observed appearing to be a response to N application in general, rather than specific forms.

Conclusions: The response of both bacterial and fungal communities to the application of RDFs suggest that soil health and quality would be maintained, and possibly even improved (bacteria) by utilisation of these sustainable alternatives to traditional synthetic N fertiliser. Further analysis after longer periods would provide more insight into long-term effects.

Plants and Microbes Respond Differently to Fertilization and Environmental Factors in a Kenyan Rice Field

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Aim:

In sub-Saharan Africa, rice is an important food crop and its demand is rising. Yields are, however, well below the average in other countries. Intensification is necessary to secure domestic production, but negative environmental impacts must be minimized.

Method:

At the KALRO station in Mwea, Kenya, an agronomic trial was conducted in a paddy rice field, where manure and NPK fertilization were compared. Yield, soil properties and microbial communities were investigated. Different groups of microbes were quantified by ddPCR and their community composition was determined by high-throughput amplicon sequencing of appropriate phylogenetic markers.

Results:

NPK fertilization gave rise to significantly higher grain and straw yield. SOC and TN decreased with soil depth, but no fertilizer effect was obvious. Similarly, no fertilizer effects were observed on concentrations of N_{min}. For all investigated microbial groups, a significant decrease in abundance was observed with soil depth at the reproductive plant stage. Microbial community compositions responded in different ways to the environmental factors soil depth, plant stage or fertilization. Additionally, an unintended spatial effect was observed which could have potentially masked more subtle influences on microbial community composition.

Conclusions:

Increased NPK fertilization can substantially booster rice production in SSA, but costs are often too high for local farmers. No negative environmental impacts of NPK fertilization at the applied dose could be observed on soil properties, microbial abundances and belowground biodiversity. Manure is of low quality and cannot provide the nutrients necessary for good yields, but a combination of both could be promising option for rice yield increase at an affordable price.

From Roots to Pollinators: Do Above- and Below-ground Organisms Interact Through Plants?

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Aim: This study investigates how soil biodiversity might alter plant traits and in turn affect pollinator behaviour. It is one of the first to investigate soil-plant-pollinator interactions (i) in a multispecies setting and (ii) incorporate the plant root system.

Method: A soil biodiversity gradient was created using the dilution-to-extinction approach, and experimental microcosms created using the annual plant *Phacelia tanacetifolia* Benth. The effects of soil biodiversity loss were explored by measuring above and below-ground plant traits, floral signals and rewards. A pollinator choice experiment was carried out to investigate the preference of a key group of pollinators, bumblebees (*Bombus terrestris* L.), for one plant treatment over another in a semi-field setting.

Results: Soil biodiversity loss did not affect most plant traits such as biomass, plant height, as well as floral signals such as total flower number and biomass. Bumblebees showed no preference for what plant was chosen to be visited first. Floral reward such as nectar also appears to remain unaltered in sugar concentration and chemical composition. Some biologically active secondary compounds were detected in nectar across the differing soil biodiversity treatments.

Conclusions: Although soil biodiversity is crucial for functioning of terrestrial ecosystems, this study shows that there were no measurable knock-on effects on floral choice by bumblebees. That said, bee visitation rate will shed better light on any direct or indirect effects. These findings and more are discussed in light of the effects on below-ground root biomass and the presence of a key taxa, arbuscular mycorrhizal fungi (AMF).

Higher Spatial Than Temporal Variation In Soil Protist Beta-Diversity Along Elevation Gradients

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Aim:

Biodiversity patterns along elevation gradients have long been studied for plants and animals, but only quite recently for soil microorganisms, especially protists (i.e., Eukaryotes excluding plant, animal or fungi). Micro-organisms have shorter generation times than macro-organisms and their communities were shown to vary rapidly in response to abiotic factors. This represents a potential bias for the study of elevation gradients if seasonal patterns are larger than spatial ones. To address this, we investigated the relative importance of spatial versus temporal turnover of soil protist community along elevation gradients.

Method:

We collected soil samples in forests and grasslands below the treeline along five elevation gradients in the Spanish Sierra Nevada and the Swiss Alps for two consecutive seasons (spring and summer). Using general eukaryotic primers and amplicon sequencing of soil eDNA, we decomposed total protist diversity into local alpha- and beta-diversity components and identified climatic and edaphic drivers of biodiversity patterns.

Results:

Soil protist communities varied spatially within and among transects but temporal variation was comparatively low. Best edaphic drivers of community turnover were the same between spring and summer, but their explanatory power varied among season.

Conclusions:

Altogether, our data showed a dominant spatial component of beta-diversity and suggest that patterns of soil protist communities along elevation gradients are more driven by spatial heterogeneity than inter-seasonal turnover. Such knowledge is pertinent for designing sampling for microbial macroecology and biogeography, but also to better document the diversity patterns of protists, one of the least known components of soil biodiversity.

Drivers of the composition of root-associated microbial communities in garrigue ecosystems

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Aim:

Plants dominating garrigue (phryganic) ecosystems of the Mediterranean are exposed to low-soil fertility and seasonal high temperatures and drought-stress. Diversity and structure of root-associated microbial communities of two typical plants was investigated. We aimed to identify ecological drivers that determine community assembly processes of host-associated microbial communities. We hypothesized soil properties, plant taxon and season as major drivers.

Method:

The roots, rhizosphere and adjacent bulk soil of early colonizer *Hyparrhenia hirta* (Poaceae) and climax shrub *Sarcopoterium spinosum* (Rosaceae), both naturally occurring in undisturbed sites nearby bentonite and perlite quarrying complexes in Milos island (Greece), were sampled after the dry (autumn) and the rain (spring) period. Microbial communities were analysed by NGS of PCR-amplified 16S and 18S rDNA genes. Extracellular enzyme activities, major soil functions and community level catabolic profiles were analysed.

Results:

Initial results show that dry periods significantly constrain enzyme activities in the perlite bulk soil, but not in the bentonite soil. Within the plant rhizosphere of the perlite soil, however, major enzyme activities are not constrained by drought. Results will shed light on whether distinct microbial community configurations are related to plant species (taxon), and how soil type and season potentially shape these patterns. Final, results will be presented in the conference.

Conclusions:

Plants are expected to develop strong interactions with their associated rhizosphere/root microbiota in multi-stressed ecosystems. In this work, we unravel the role of location/soil, plant taxon and season as potentially major drivers of the assembly of microbial communities associated with typical phryganic plants.

Relationship between Soil Microbial Community Composition and Soil Organic Carbon Pools in Agricultural Grasslands

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Aim:

To assess the relationship between soil microbial community composition and functionally-different soil organic carbon (SOC) pools.

Method:

The study was carried out in a grassland experiment established in Dowth, County Meath, Republic of Ireland. The grassland swards studied are: six-species mixture, twelve-species mixture, highly species-rich permanent pasture. A monoculture of perennial ryegrass was also included in the treatment as reference. All the four grasslands communities were established on four replicated blocks ($n = 16$) in a randomized complete block design. At the end of the first growing season, composite soil samples in the 0–10 cm layer was collected and analysed to determine the soil microbial community composition and biomass using phospholipid fatty acid (PLFA) analysis. Physical fractionation of soil samples was performed to determine the concentrations of particulate organic matter carbon (POMC) and mineral-associated organic matter carbon (MAOMC).

Results:

Particulate organic matter carbon was positively related to total microbial biomass as well as gram negative and gram positive bacterial biomass ($p < 0.05$) but not significantly related to the fungal biomass. However, there was no significant relationship between MAOMC and the biomass of any of the soil microbial groups.

Conclusions:

Particulate organic matter carbon – a labile carbon pool that is plant-derived, relates to most of the soil microbial groups identified in the PLFA analysis including gram positive and negative bacteria. This further demonstrates that gram negative and gram positive bacteria have preference for labile carbon sources emanating from plant origin.

'Digging a little deeper: a comparison of mycorrhizal communities between rewilded and intensive agricultural soils.'

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Mycorrhizal fungi have been recognised for their inter and intra-species role in facilitating communication and resource sharing, forming symbiotic relationships with vegetation through strands of mycelium. These belowground connections allow for nutrient transfers, kin recognition, and defence signalling which ultimately impact ecosystem processes and vegetation structure. Rewilding is a novel approach to ecological restoration, prioritising functionalism and ecosystem autonomy, to return land to nature through low-impact interventions. In the UK, rewilding projects often take place on degraded or low productivity farmland such as on the Knepp Castle Estate. Whilst much research has focused on above-ground rewilding and reintroductions of charismatic species, little attention has thus far been paid to rewilding's impacts on soil biota, and specifically mycorrhizal fungi. Through soil and vegetation analyses, this study looks to identify differences in mycorrhizal communities between rewilded and intensive agricultural sites in the south east U.K. Through comparison at different sites, the association between rewilding efforts and altered mycorrhizal community structure can be ascertained, with potential consequences for ecosystem functioning and recovery. Increased mycorrhizal diversity under rewilding conditions could indicate improved ecosystem resiliency through increased functional redundancy. Therefore, this project aims to understand if an association exists between rewilding and increased mycorrhizal diversity.

Does Plant Biostimulants Application Stimulate Soil Microbial Activities in Organic Potato Production under Field Conditions?

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Aim:

To investigate the efficacy of commercially available biostimulants on soil microbial activities in organic potato production under field conditions.

Method:

A factorial experimental design was set up under field conditions for two years at two locations characterized by sandy clay (2021) and sandy (2022) soil texture at the experimental stations of Aarhus University in Denmark. The two factors were nitrogen levels (100% and 50% of recommended nitrogen) and biostimulants of different origins, namely, microbial origin (Proradix and Vesta), plant extracts (Crop-set and Combi-set), seaweed extract (Acadian), humic and fulvic acids (Humifirst). The biostimulants were applied at recommended rates, time, and methods of application per the guidelines indicated on the product's label. Soil samples were collected to 0-25 cm depth before harvest and after removing the upper ground biomass. Two soil enzymes, dehydrogenase (DHA) and β -glucosidase (BGA), were selected as indicators of soil microbial activities.

Results:

There was no significant interaction effect of the biostimulants and nitrogen levels on both enzymes and at the two locations. The 100% nitrogen level resulted in a significantly ($p < 0.05$) higher DHA than the 50% nitrogen level only in the sandy soil. The biostimulants did not significantly change the DHA and BGA in sandy clay and sandy soil.

Conclusions:

In the current experiment, applying six different biostimulants to organic potato production did not significantly change the dehydrogenase and β -glucosidase enzyme activities regardless of the biostimulant origin and the soil texture. Additional parameters should be further determined to understand the impacts of biostimulants on soil microorganisms.

Microarthropod Communities in Switchgrass Cropping Systems and Their Effects on Soil Nitrogen

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Soil invertebrates has long been understood to have important influences on nitrogen (N) dynamics, with their activity increasing N mineralization by an estimated ~30% globally (Verhoef & Brussard, 1990). Their contributions to N mineralization are expected to be especially important in N-limited, marginal soils such as those targeted for bioenergy crop production. As the amount of land used for bioenergy crop production is expected to increase to help mitigate global climate change, it will become increasingly necessary to understand the soil invertebrate communities supported within these systems as well as their effects on N availability. To begin to address this in the context of switchgrass (*Panicum virgatum*) cropping systems, we first surveyed litter- and soil-dwelling microarthropods from switchgrass monocultures at the Kellogg Biological Station (Hickory Corners, Michigan) in 2018 and 2019. Microarthropod sampling in 2018 focused on peak growing season whereas sampling in 2019 occurred once in spring, peak growing season, and fall. To investigate the community level effects of microarthropods under switchgrass, as well as those of nematodes, on N dynamics, we then conducted a stable isotope tracing study using greenhouse mesocosms to assess their effects, either individually or in combination, on N mineralization and uptake by switchgrass. Field-collected microarthropods and/or nematodes were added to mesocosms containing ¹⁵N-labeled litter with controls receiving no fauna. Mesocosms were then harvested to assess ¹⁵N enrichment in switchgrass, microbial, and invertebrate biomass to trace the flow of litter-derived N across pools in the presence or absence of microarthropods and nematodes.

Phylogeographic Analysis of Nematodes in the Dry Valleys of Antarctica

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Aim

The aim of this study is to examine the extent and distribution of genetic diversity within nematode species in the Antarctic Dry Valleys and the Transantarctic Mountains. Glacial cycles since the Pleistocene glaciations have isolated populations of the four soil-dwelling nematode species in the Dry Valleys, resulting in genetic divergences. A phylogeographic analysis can show the locations where nematode populations were isolated and where gene flow could occur during glacial movement.

Method

The phylogeographic analysis used a shotgun metagenomic approach. Six locations were selected in the Dry Valleys based on their location within a lake basin. Nematodes were extracted from 100g of soil from each location using the sugar centrifugation method, then DNA was extracted from all nematodes using the Qiagen DNeasy PowerSoil Kit. Each sample was sequenced using Illumina NextSeq 2x150. The first set of samples were selected within a tight geographic range. Future samples will be sequenced that extend into the Transantarctic Mountains and potential refugia sites that were isolated by glacial movement.

Results

18S and mitochondrial COI sequences will be used to determine haplotype groups within the populations of each species.

Conclusions

The distribution of haplotype groups can give evidence for the degree of connectivity between previously isolated areas in Antarctica. Large-scale geologic disturbances, such as glacial cycles, have been the driver of Antarctic nematode genetic diversity in the past. However, climate change may increase connectivity in the Dry Valleys in the future, driving homogenization and subsequent loss of genetic diversity.

Collembola diversity in agroecosystems in South Africa

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Aim:

To determine the taxonomic diversity of Collembola in agroecosystems in South Africa.

Method:

We sampled various agroecosystems such as orchards, maize, and canola under different agricultural management practices, such as mulch and cover crops, to explore the Collembola diversity.

Results:

Overall, Collembola diversity was high, with several introduced species widely distributed. However, indigenous species from genera such as *Capbrya* and *Parisotoma* was also surprisingly abundant. Collembola communities differ in sites using mulch compared to sites not using mulch.

Conclusions:

Mulch play an important role in buffering and maintaining Collembola populations throughout the year. In addition to other soil biota indicators, Collembola are useful biological indicators of ecosystem health in South African ecosystems.

Soil Fauna Bioturbation in Northern Hemisphere in Relation to Climate and Litter QualityJan Frouz¹¹*Charles university, Praha, Czech Republic*

Soil fauna bioturbation may affect various processes related to decomposition and stabilization of organic matter, soil water retention, formation of habitat for soil biota and so on. In this contribution we summarized in field mesocosm experiment in which mesocosms containing litter and mineral soil in two separate compartments were exposed in soil. These mesocosms were either accessible to soil fauna or not which allow to measure removal of litter from soil surface as well as accumulation of litter in mineral soil as well as overall loss of litter from the mesocosm. Mesocosms were supplied in local litter and located in eighteen locations in all major biomes of northern hemisphere from tundra to tropical rain forest. Overall fauna significantly increased litter removal from litter surface and its accumulation in mineral soil the effect on overall loss was insignificant. The effect was higher in temperate and tropical climate and lower in cold and dry biomes.

Soil Functional Diversity Related to Aboveground Plant Biodiversity in a Grazed Island Ecosystem in Denmark

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Aim:

In this study, we will establish links between aboveground plant biodiversity and soil microbial functional diversity on a summer grazed Danish island.

Method:

By connecting the geo- and biodiversity of the island with organic matter decomposition functionalities of the soil community we identify links to soil carbon and nitrogen storage. Specifically, thirty plots were marked out on the ca. 140 ha island at which plant biodiversity analyses were conducted. The plots cover the island's main habitats: salt meadows, meadows, and developing dry grasslands. At each plot we sampled topsoils at 4 positions to represent local variability. Soils were analysed for OC, total N, pH, and community level physiological profiles (CLPP). The CLPPs were measured using the Microresp technique to make inferences about soil microbial functional diversity and activities.

Results:

Preliminary assessments suggest that the more plant biodiverse plots also contained greater SOC concentrations. We expect this will also correlate with increased soil microbial functional diversity and activities, as some degree of coupling between aboveground diversity and belowground functionality is often seen in grassland ecosystems, partly due to increased amounts and diversity of rhizodeposits. Microbial activity is important for mediating the turnover of plant derived organic matter into more stable soil OM pools, which is pertinent for soil carbon persistence.

Conclusions:

Linking plant biodiversity in a summer grazed pastures with belowground processes and the fate of soil organic matter points to functionally important interactions between above- and below-ground components of the ecosystem.

Multi-City Comparisons Belowground: Lessons Learned from GLUSEEN

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Aim:

In the first Global Soil Biodiversity Conference, we held a workshop to discuss the establishment of a network focusing on urban soil ecology. GLUSEEN aimed to bring together scientists, educators, and practitioners to 1) examine how soil communities in the urban are similar or different across the globe and 2) develop an experimental design and unified methods to study urban soils.

Method:

First, we defined a matrix of urban habitat types based upon disturbance and management intensity. In a pilot study, we conducted a "natural experiment" using three of the six types to compare soil characteristics, microbial and earthworm community structure and decomposition in five cities. Each habitat type was replicated five times, resulting in a total of 100 sites. The sixth city, Melbourne contributed teabag decomposition data later.

Results:

While some soil characteristics, such as SOM, and pH supported the Urban Ecosystem Converge Hypothesis, others, such as plant available nutrients, did not. Edaphic properties were important drivers in microbial and mesofauna communities, but not for earthworms. Earthworm assemblages were remarkably similar among the studies cities, but the mechanisms leading to this similarity differed. The level of soil disturbance significantly reduced microarthropod diversity, but for archaea, the trend was reverse.

Conclusions:

Despite limited funding, we produced a set of thought-provoking results and generated interest in urban soil ecology. We also learned about the challenges when working in many countries representing different cultures. To maintain and expand such a network requires both adequate funding and the enthusiasm of local scientists.

Soil microbiomes biodiversity in agroecosystems

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Aim:

The soil microbiome is a complex structure, but with the advent of developments in the molecular and bioinformatic fields, deeper insights into the importance, roles, and shifts under different conditions and over time are becoming possible. The aim of the study was to determine the biodiversity, structure and functionality of soil microbiomes in different agroecosystems on various soil type and under biotic and abiotic stressors and other natural, environmental, or anthropogenic factors including different compartments of soil and plants.

Method:

DNA extracted from collected soil and plant compartments was analysed via next generation sequencing using ITS1 or ITS2 molecular marker to determine fungal community composition and its trophic modes and guilds. Moreover 16S rDNA molecular marker was used for determination of bacterial community structure.

Results:

We indicated different composition of bacterial and fungal community under various crops, stress conditions (diseased plantations), soil type and tested compartments (bulk soil, rhizosphere, roots, plants, fruits).

Conclusions:

The microbiome shifted under stress conditions caused by phytopathogens. The healthy samples create more stable networks and are more resistant to stress conditions than networks observed in unhealthy samples with dysbiosis state. The microbiome research can be useful for developing agricultural crop strategy for sustainable agriculture.

This paper was financed by The National Centre for Research and Development in frame of the project BIOSTRATEG, contract number BIOSTRATEG3/344433/16/NCBR /2018; BIOSTRATEG3/347464/5/NCBR/2017; SUSCROP/I/POTATOMETABIOME/01/2019 and National Science Center in frame of the project Opus 15, UMO-2018/29/B/NZ9/00982.

Investigation of the Microbial Composition of Organic and Conventional managed Agricultural Soils across Europe.

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Aim:

Residues of plant protection products (PPPs) as well as their mixtures are rather the rule than the exception in European agricultural soils. The effects of these on ecosystem health are scrutinized in the H2020 SPRINT project. In this study general differences in the microbial composition of soils from both, organic and conventional managed farms from 11 case study sites (CSS) are investigated. As an approach to assess soil health the abundances of plant pathogens are examined.

Method:

Composite soil samples have been taken from approximately 20 fields (10 conventional and 10 organic managed) in all CSS. DNA was extracted with a lab made protocol. Subsequently, metagenomic sequencing was performed by an external service provider. Illumina reads were analysed with kraken 2 and bracken. The compositional data was examined for the abundance of plant pathogens, common in the respective cropping systems.

Results:

Preliminary results show that the CSS is the main driver for differences found in the soil microbial community. This indicates that the cropping system, abiotic factors and climate have a greater influence on soil microbiome than the farm management system. When zooming in at individual CSS, organic and conventional managed soils were distinct in their microbiome. But, no significant differences in the abundances of plant pathogens have been observed.

Conclusions:

Using the abundance of soil pathogens as indicator for soil health, we do not see a negative effect in organic managed farms. Suggesting that organic managed soils are in general able to avert crop specific pathogens. Further data analysis is necessary.

Perchlorate reducing microbes in the McMurdo Dry Valleys drive soil ecosystem biodiversityColin Robinson¹, Byron Adams¹*Brigham Young University, Provo, United States*

Perchlorate reducing microbes (PRM) have been shown to inhabit soils throughout the McMurdo Dry Valleys. To the best of our knowledge, these PRMs represent the first such microbes isolated from soil containing naturally occurring perchlorate. Perchlorate (ClO_4^-), a toxic anion that blocks iodine uptake by the mammalian thyroid gland and prevents seed germination, is present in abundance in Antarctic soil. In soils where PRMs are more abundant, we show that soil biodiversity is bolstered as PRMs work to detoxify soils. These findings could be applied to bioremediate contaminated waste sites where anthropogenically formed perchlorate salts have decimated ecosystems and reduced biodiversity.

Opportunities to Assess Drivers of Soil Biodiversity via U.S. National Cooperative Soil Survey Emerging Products

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Aim:

Traditional soil survey maps provide information on soil properties that change over millenia (i.e. inherent characteristics). However, soil survey users are interested in drivers of more dynamic soil properties (DSPs) that may change on a shorter time scale according to land use and management, including soil macro- and microbiota. The aim of this presentation is to share an overview of the U.S. Natural Resources Conservation Service (NRCS) Dynamic Soil Properties program to link DSPs to pedologic characteristics, land use and management information, and ecological states.

Method:

The Soil and Plant Science Division of USDA-NRCS has amended its technical guidance to include the collection and measurement of DSPs as part of standard soil survey procedures. To assist NRCS in selecting DSPs and scaffolding data collection efforts, soil survey has implemented the Dynamic Soil Properties for Soil Health (#DSP4SH) project. Standard methods were used by sixteen cooperators across the U.S. to measure soil carbon, soil enzymes, phospholipid fatty acids, and more. Each cooperator identified local fields that represented a “business-as-usual” agricultural system, a soil health management system, and a reference ecosystem within unique soil map units.

Results:

Results will be used to investigate the impact of pedologic, vegetative, and management effects on soil biodiversity that can then be used to inform and refine broader soil survey products.

Conclusions:

Simultaneously collecting pedologic, vegetative, and land management information as a routine part of soil survey activities can provide integrated opportunities to assess drivers of soil biodiversity through emerging national data products.

Long-term effect of crop management practices on clay soil properties and microbial diversity.

Richard Hogue¹, Thomas Jeanne¹

¹*Irda, Quebec, Canada*

Aim:

The impact on soil properties and microbial diversity have been studied after 10 years of conventional tillage (CT) vs no-till (NT) and of corn monoculture (Mon) vs soybean-wheat-corn rotation (Rot) in unfertilized (UF) or mineral fertilized (F) replicated plots.

Methods:

Soil physical, chemical and biological indicators were determined by standard methods. Amplicons sequence variants (ASV) were obtained by rRNA amplicon sequencing. Bacterial and eukaryotic diversity were assessed using Shannon Index, ordinations of the compositions of ASV and by the multivariate permutational analysis of variance on the Aitchison distance matrix.

Results:

The NT vs CT plots showed higher average values of soil gravimetric water content (+135%), mean weight diameter of water-stable aggregates (MWDWAS) (+36%), total nitrogen (+42%), total carbon (+26%), SR rates (+43%) and lower values of pH (-5%) while the NT-Rot plots showed the highest corn yield. The treatments had no long-term effect on the Shannon Diversity Index. The compositions of bacterial and eukaryotic communities in NT soils showed a strong correlation with MWDWAS, total N, total C, active carbon and extractables P and K, while in CT soils, such strong correlation was observed with the pH and the extractables elements Ca, Mg and Al. Specific ASVs in 6 among 10 bacterial phyla and 5 among 12 eukaryotic phyla were impacted by tillage management.

Conclusion:

Tillage management had major impact on soil physicochemical and biological properties, while the magnitude of the tillage effect was influenced by whether or not mineral fertilizers were applied.

Responses of Soil Microbes to Whole Orchard Recycling: Microbial Community Composition and N Cycling

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As soil degradation drives the transfer of carbon (C) to the atmospheric pool, implementation of organic management practices in agricultural ecosystems has increased in popularity worldwide. Addition of organic amendments, such as wood chips from whole orchard recycling (WOR), may favour the assimilation of nitrogen (N) into microbial biomass and induce changes in the microbial community composition. Aim: Here, the soil microbial community was characterized over two years, following WOR and applications of N-fertilizer. We hypothesize that WOR will shift the relative abundances of N cycling microbial groups, such as archaeal ammonia oxidizers, fungal nitrate/nitrite reducers, and bacterial N₂O reducers. Method: Soil microbial community composition and structure was characterized by 16S rRNA gene and fungal ITS amplicon sequencing on an Illumina MiSeq platform. The sequences were processed via DADA2, classified using Silva (16S rRNA genes) and UNITE (ITS), and analysed using vegan in R. Results: The most abundant bacterial and archaeal families observed in the soils include Nitrosomonadaceae, Nitrososphaeraceae, and Chitinophagaceae, while the most abundant fungal families were Phanerochaetaceae, Filobasidiaceae, and Glomeraceae. Principal coordinate analysis (PCoA) shows that the wood chip amended soil microbial communities are compositionally different from the unamended control communities. Conclusions: Organic amendment by WOR induced shifts in the soil microbial community composition, such that relative abundances of saprotrophs appear to increase and ammonia-oxidizing bacteria and archaea appear to decrease. These microbial data will be related to soil physicochemical data and placed in the context of other studies of woody organic amendments in soils.

Driving factors of the archaeal communities in sediments and soils of Brazilian soda lakes

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An extreme environment is a habitat characterized by harsh abiotic conditions that are hostile or even lethal to most life forms. Soda lakes are extreme environments found worldwide that contain high concentrations of sodium (Na⁺) and carbonate species (HCO³⁻ + CO₃²⁻) as dominant ions, leading to elevated and stable pH levels. These environments provide a unique habitat for a diverse haloalkaliphilic community and offer new research opportunities associated with extremophile life and biotechnology. At the same time, tropical soda lakes are sources of greenhouse gas emissions. Most known extremophiles belong to the Archaea domain and many of them thrive under environmental extremes of pH and salinity. Archaea also play crucial roles in the global carbon and nitrogen cycles and influence methane and nitrous oxide emissions. In this context, we selected six soda lakes with contrasting characteristics to explore part of the vast environmental variability found in this ecosystem and evaluated the archaeal diversity in both dry and wet seasons, using 16S rRNA amplicon sequencing. As these lakes are surrounded by sandy shorelines and forests, samples of lake sediment and soil under adjacent forest were collected, in order to investigate the interactions between archaeal groups inside and outside the lakes. Our first results showed signatures from 11 archaeal phyla (Crenarchaeota, Euryarchaeota, Halobacterota, Thermoplasmatota, Nanoarchaeota, Micrarchaeota, Asgardarchaeota, Hadarchaeota, Aenigmarchaeota, Altiarchaeota and Iainarchaeota). Seasonality appears to have no effect on archaeal communities and we observed higher richness of archaeal genera in sediment samples compared to forest soil samples. In general, pH, salinity and N-total were significantly correlated to the overall community structure. Ongoing investigations are exploring more deeply the interactions between the microbiota, abiotic factors and greenhouse gas fluxes.

This research was supported by the São Paulo Research Foundation (FAPESP) and Coordination for the Improvement of Higher Education Personnel (CAPES).

Effects of Microalgae-based Biofertilizers on Soil Microbiota

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Microalgae used in wastewater treatment may be applied to soil as a biofertilizer - this is a novel strategy for recycling of nutrients in the circular economy. There is little information about how the application of large concentrations of unicellular algae to soil will affect soil biochemistry, particularly when they are living algal cells with the potential to form a soil biofilm, whereas soil biofilms are expected to influence plant-microbe interactions.

Chlorophyte unicellular algae of the *Chlorella* genera are widely employed in algae-based water treatment systems, and *Chlorella sorokiniana* has proven to be highly adaptable for this purpose. We applied three filtrates of a *Chlorella sorokiniana* culture to soil microcosms, separating the microalgae from other microorganisms, as well as a sterile control filtrate without biological activity. Bacterial biomass in soils receiving the non-filtered (NF) slurry with viable algal cells was increased by 25% in the soil surface (0–8 mm), and heterotrophic activity in those treatments increased as measured by CO₂-C evolution. Total soil carbon concentrations were increased in the treatment with living algal cells (NF) by 0.4%, but no differences in organic carbon were measured; instead, it was found that inorganic carbon (CaCO₃) concentrations increased by 0.6% in the NF treatment only. Soil phosphorus availability was also reduced in the surface of the NF treatment, indicating an increased biological demand.

The results show that, when applied to soil, microalgae and associated biofilms will have relevant direct and indirect effects on soil quality and nutrients of agricultural importance.

Active microalgae biomass from wastewater treatment may be given added value as a biofertilizer, but little is known about how this may affect soil nutrient dynamics and biology. If the goal is to recycle waste nutrients and matter. However, the potential persistence of unicellular green algae after such an application is not known, nor the influence of their photosynthetic activity on soil organic carbon - the aim of the present study was to probe these basic questions. In a controlled laboratory microcosm experiment, suspensions of *Chlorella* sp. microalga culture and sterile filtrates were applied to an agricultural soil and incubated for 42 days, whereas the effect of darkness was also tested to understand the importance of photosynthetic activity of the algae. Autotrophic microorganism development was 3.5 times higher in treatments with algae application as measured by chlorophyll pigment concentration. Against expectations that increased photosynthetic activity would decrease the CO₂-C flux, the algal suspension with a photoperiod significantly increased soil respiration compared to culture filtrates without algal cells, with accumulated quantities of 1.8 and 0.7 g CO₂-C m⁻², respectively. Also, phospholipid fatty acid (PLFA) analyses showed that the suspension accelerated the development of a stable community of eukaryotic and prokaryotic microorganisms in the soil surface, whereas bacterial PLFA biomarkers were significantly associated with eukaryote biomarkers on the study level.

Microalgae can be used in wastewater treatment to recover nutrients that can be thereafter applied to soil as a biofertilizer, which constitutes a novel strategy in circular economy. Microalgae based fertilizers are well known as nutrient suppliers to plant with important effect in trace element and phytostimulation, live algae applied in a liquid slurry to soil may add both organic carbon and

nutrients while providing other benefits such as biological carbon fixation, but little is known about how this may affect soil nutrient dynamics and biology. We applied three filtrates of a *Chlorella sorokiniana* culture to soil microcosms, separating the microalgae from other microorganisms, as well as a sterile control filtrate without biological activity. Bacterial biomass in soils receiving the non-filtered (NF) slurry with viable algal cells was increased by 25% in the soil surface (0–8 mm), and heterotrophic activity in those treatments increased as measured by CO₂-C evolution. Total soil carbon concentrations were increased in the treatment with living algal cells (NF) by 0.4%, but no differences in organic carbon were measured; instead, it was found that inorganic carbon (CaCO₃) concentrations increased by 0.6% in the NF treatment only. Soil phosphorus availability was also reduced in the surface of the NF treatment, indicating an increased biological demand.

monitorizando su efecto sobre su microbiota edáfica mediante secuenciación de fragmentos de los genes 16S y 18S rRNA. La aplicación del cultivo de microalgas (NF) y sus correspondientes filtrados sin algas ($\varnothing < 2.5 \mu\text{m}$) y estéril ($\varnothing < 0.22 \mu\text{m}$) a los microcosmos de suelo modifica notablemente la microbiota del suelo, estableciendo una mayor predominancia no sólo de microflora autótrofa, sino que también estimulando los géneros asociados al filo Cyanobacteria, con capacidad de fijación de N, lo que supone la capacidad de incrementar los contenidos de C y N en la superficie del suelo y la formación de biocostras con un efecto en la estabilización del suelo.

The results show that, when applied to soil, microalgae and associated biofilms will have relevant direct and indirect effects on soil quality and nutrients of agricultural importance

LIFE SySTEMiC: Soil microbiome in three different forest management systems of *Fagus sylvatica* forests

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Aim:

Assessing the sustainability of different types of forestry practices on soil biodiversity is complicated because of variation both in the nature of the forest resource and in the impacts of different management measures. The informed choice of a silvicultural system is a crucial step that can have consequences for sustainability and forest ecosystem biodiversity. The project "LIFE SySTEMiC" examines best close-to-nature forest managements regarding genetic resources of forest trees and related soil biodiversity aiming to support stability and connectivity of forests in changing climates, and their adaptability to future environments.

Method:

The study was performed in three different forest managements systems (unmanaged forest nature reserve, low close-to-nature forestry, and medium combined system) across *Fagus sylvatica* dominated forests in Slovenia, Italy, and Croatia. Soil microbiomes were analysed in mixed soil cores using Illumina sequencing with fungal, bacterial, and archaeal rRNA specific primers.

Results:

We will present the influence of forest management system on soil microbiome. The data will be correlated with soil factors and genetic variability of *F. sylvatica*. We expect to observe a change towards more stable, less diverse, and more specialised communities of analysed taxonomic groups with decreasing the forest management intensity.

Conclusions:

The results will help to understand the importance of belowground processes when choosing the best silvicultural practices for sustainable forest management. Currently, the implementation of the soil biodiversity knowledge into forest practices rarely considers soil biota as a decision factor in forest management.

Microbial Indicators of Soil Health in a Perennial Grain Crop

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Aim:

Kernza (*Thinopyrum intermedium*), the first ever developed perennial grain crop, supports a robust soil microbiome and can help build agricultural systems that are both resilient to and mitigate climate change. However, there are gaps in our understanding of how soil microbial properties should be interpreted, especially in semiarid regions. We aim to determine if and how soil microbial properties can indicate changes in soil health and carbon sequestration in an annual wheat field transitioning to a perennial grain crop.

Method:

Soil samples were collected from dryland wheat, Kernza, and perennial grassland fields in southeastern Wyoming, USA. Samples were collected before Kernza planting (spring 2021) and one year after (spring 2022), and were analysed for a range of soil health parameters, including microbial community composition (phospholipid fatty acids) and function (enzyme activities) and eleven different carbon and nitrogen pools.

Results:

We found key differences between perennial grassland and annual wheat systems, including higher surface (0-5cm) enzyme activity and labile organic matter pools, more stratification between depths (0-5 and 5-15cm), and a higher proportion of fungi in the perennial grassland. In the field transitioning to Kernza, several soil properties became more similar to the perennial system, such as depth stratification of enzyme activity and labile organic matter pools.

Conclusions:

Transition to a perennial crop resulted in soil health changes, even in the first year. Going forward, fast-responding soil microbial properties could provide sensitive indicators of changing soil health in similar systems, and guide farmers and researchers in sustaining agricultural lands.

Resilience of ectomycorrhizal fungal communities of *Quercus pubescens* to drought and wildfire

Tanja Mrak¹, Nataša Šibanc¹, Philip Brailey-Jones², Ines Štraus¹, Jožica Gričar¹, Hojka Kraigher¹

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Aim:

Temporal studies that would offer insight into resilience of ectomycorrhizal (ECM) communities in stress prone climates are scarce. Our study investigated vitality, community composition, diversity, and function of *Quercus pubescens* ECM fungi in relation to environmental parameters in Sub-Mediterranean Slovenia for two years (June 2016-May 2018), including two summer droughts (2016, 2017) and a wildfire (August 2016).

Method:

ECM community was sampled every two months on three plots. Vital ECM root tips were morpho-anatomically characterized and representative root tips sequenced. The ratio of vital to non-vital ECM root tips was calculated. Vital ECM fungi were assigned to exploration types.

Results:

Altogether we identified 93 taxa of ECM fungi. The ratio of vital to non-vital ECM root tips dropped below one in August 2016 after drought and wildfire and remained below one until January 2018. ECM communities were varying significantly among the plots but were relatively stable in time. Species richness and dominance varied with environmental variables. The most abundant exploration type was short distance which was related to precipitation.

Conclusions:

Different lineages and functional groups of fungi may be important in this stress-prone environment to maintain the nutritional status of *Q. pubescens*. High variability in vitality of ECM root tips over time could be explained by the long-term decrease of carbohydrate flux belowground due to sequence of droughts and wildfire. Temporal stability of ECM community is indicating relative stress resilience of the fungal communities at the investigated site.

Nitrification Communities in Silage Corn Agroecosystems

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Several long-term experiments were performed on agricultural sites in Northern Utah, USA and in Watkinsville, Georgia USA over the last 20 years. The Utah soils are highly calcareous silt loams with a pH of approximately 8.0. The Georgia soils are Cecil sandy loams with initial pH 5.3. We compared the effects of contrasting nitrogen sources of varying quality and quantities on the nitrification process and communities of the ammonia oxidizing bacteria (AOB), ammonia oxidizing archaea (AOA) and nitrite oxidizing bacteria (NOB). Both the abundance and diversity of the AOB were the most changed by fertilization with ammonium sulfate. Process rates and kinetics were also changed by ammonium sulfate applications especially for the AOB while AOA were more responsive to compost amendments. Kinetics of substrate availability and temperature were also investigated. Modeling of nitrification needs to integrate both organism abundance and the kinetic response to be applicable to realistic soil conditions. Metagenomic analysis organic amendments of steer waste compost and poultry litter compost are compared to the soil communities at the respective sites.

Use of X-ray microtomography images to support the teaching and research of the soil arthropods

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Aim:

Use images of X-ray microtomography in order to improve the knowledge of different arthropods of soil fauna

Method:

Specimens of springtail, ricinulids, and ants were mounted in micropipette tips of 10 ul and processed in an Xradia Versa 510 X-Ray microcomputerized Tomography System at the University Laboratory of X-Ray Microtomography (LUMIR), Centro de Geociencias (CGEO) of the UNAM. Images and videos were performed to improve the teaching methods to the students and the research of soil biology, and also to reach the soil fauna to general public.

Results:

The specimens were processed and generated images and videos of springtail, ricinulid and ant that can use in teaching. Also, the files can be used to print 3D models and as well visualize in immersion 3D device. This material shows structures that can be difficult to see with other techniques but with the use of X-ray microtomography images morphology and anatomy can give important information in the study of soil fauna.

Conclusions:

This technique innovation is useful to study some anatomic structures of the micro and mesofauna of soil, that can be difficult to see and can innovate the teaching and research of soil fauna.

Belowground functional traits in dryland ecological restorationAlbert Barberán¹¹*University Of Arizona, Tucson, United States*

10–20% of drylands worldwide already defined as degraded, the United Nations has declared restoring degraded drylands as a top priority for supporting human life in the coming decades. Despite time-consuming and expensive efforts, dryland restoration success remains low. Although soil microorganisms and plants are inextricably linked, researchers and restoration practitioners rarely consider the soil microbiome in the design and deployment of management strategies, under the assumption that aboveground restoration can trigger concomitant belowground restoration. I will present my research group's strategy of integrating the conceptual framework of functional ecology (community-level traits, trade-offs, and life-history strategies) with tools of metagenomics to harness the ecosystem-level role and applied potential of the soil microbiome for restoration.

How does Stoichiometric Imbalance in Foliage impacts Oribatid Mite Reproduction Success?

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Aim: Linking changed N:P ratios in foliage due to nitrogen deposition to reproduction success of oribatid mites. Are oribatid mites impacted by quality of food regarding stoichiometric imbalance? If so, to which extent?

Method: Three common and representative oribatid mite species of forest stands are bred under controlled lab-conditions in petri dishes. They are given food with varying N:P ratios to link egg-production directly to food source. The control group does not receive any food to correct for eggs laid from stored energy. Eggs in batches are counted, collected, and separated for monitoring. Hatching-success gives information about egg quality and further future population sizes of oribatid mites. Nutritional content of the given food is analysed and processed statistically to link certain nutrients to number of laid eggs.

Results: In process of data analysis – It is possible to breed oribatid soil mites in captivity and to collect eggs. Phosphorus is suspected to be a limiting factor in food for successful reproduction.

Conclusions: Shifted N:P ratios due to Nitrogen deposition impacts reproduction success and therefore population size of oribatid mites. Since these group or microarthropods are the most important secondary decomposers, effects are wide-ranging through terrestrial eco systems.

Environmental Impact of Two Planting Techniques on Edaphic Microarthropod Communities in Tuscan Vineyards (Italy)

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Aim: The effects on soil ecosystem of two vineyards plantation techniques for soil preparation were monitored and compared with old vineyards.

Method:

In Tuscany region (Central Italy), two hilly areas were selected based on different approaches of vineyard plantation: site 1) soil levelling and deep ploughing after uprooting ancient vineyard, monitored for 6 years (2011-2016); site 2) local trench for minimizing soil disturb and maintaining the most of soil biological heritage of the antecedent meadow, monitored for 3 years (2014-2016). In each site, the new vineyard was compared with an old one, by sampling 3 plots/new vs 3 plots/old vineyard. Soil samples were taken from the upper 10 centimetres in spring/autumn and analysed for physical - chemical and microarthropod features (abundance, taxa richness, QBSar index) and evaluated by vineyard age, time evolution and plot location.

Results: In site 1, after three years from the plantation, the abundance and biological soil quality showed lower values in the new than in the old vineyard. Over time, the community structure resulted more complex; biological soil quality, basing on microarthropods, increased significantly only after four years. In site 2, after few months from plantation, QBSar values were high (>100) in all plots and similar in the old and new vineyard (Mann-Whitney test, P=0.334).

Conclusions: the top layer conservation is essential for soil biota and agricultural productive capacity in Mediterranean regions, highly suffering from susceptibility to degradation. Planting a new vineyard involves technical choices which are crucial for ecosystem services.

Soil microarthropod communities in the Western Alps: application of QBS-ar index to assess soil quality

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Aim: Aim of this study was to assess soil quality using edaphic arthropod communities in different areas of Alpi Marittime and Marguareis Natural Parks. Areas under forest management were compared with areas of high naturalness, and differences between woodlands and open areas such as grasslands and peatlands were evaluated. In addition, the impact of a forest fire occurred in 2003 in Andonno (CN) on edaphic communities was assessed.

Method: Soil quality was calculated by analyzing microarthropod communities using the soil biological quality index (QBS-ar). Soil samples were taken from 11 sites and then placed in a Berlese- Tullgren funnel for extraction of microarthropods, which were then sorted, divided into functional groups and each was assigned an EMI (eco-morphological index) score.

Results: The results confirmed that woodlands show higher QBS-ar values and microarthropod communities typical of stable ecosystems, grasslands have variable, but significantly lower values than forests. Peatlands showed the lowest QBS-ar values, but not significantly different compared to grasslands. Forest management and forest type do not seem to influence QBS-ar values. Interestingly, the fire-affected Andonno site showed high QBS-ar values, with no significant difference between burned and unburned areas, indicating excellent soil quality.

Conclusions: Silvicultural management does not have an impact on the QBS-ar index or on soil invertebrates. Results obtained at the Andonno site show that the soil can recover several years after a fire to an optimal state of health. QBS-ar index is ideal for long-term monitoring and assessing the impact of certain management practices and disturbances in different soils.

A global panorama on the uses of soil microorganisms

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Aim:

We aimed to determine the leading global players publishing in key topics related to the application and use of soil microorganisms.

Method:

We searched the Web of Science and Patenscope for papers and patents, respectively, published between 2011 and 2021 with a combination of queries including terms such as “Soil,” “Diversity,” and words referring to major microbial groups. We built a database and implemented science data tools to search for eleven uses of microbial biodiversity. The patent search was implemented in the R software through the patentsview package.

Results:

China, the USA, Brazil, and India are among the top five countries in most of the evaluated uses. Brazil was first on BNF and bioindicator research. India was first on PGPR and phosphate and potassium solubilization. The USA stood on biological control and antibiotic resistance research, and China on bioremediation, industry, antibiotics, and biodiversity. The other countries are most countries from Europe and Asia.

Most Bacteria patents were deposited by institutions in North America, Europe, and Asia. Exceptions were patents developed by Chile, Brazil, Australia, and New Zealand institutions. For Archaea, most patents were concentrated in the USA, with a few distributed among Canada, Chile, and Japan. Fungi-related patents were concentrated mainly in the United States and Europe.

Conclusions:

Developing countries are big players in soil microbiology-related research. Nevertheless, patents are concentrated in institutions from North America, Europe, China, and Japan, pointing to a potential asymmetrical translation of scientific research into patentable technologies.

Distribution and Ecological Preference of Complete Ammonia Oxidizers in Terrestrial Ecosystems

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The discovery of complete ammonia oxidizers, comammox *Nitrospira*, represents a breakthrough in the history of nitrification research. Phylogenetic analyses demonstrate that the functionally dominant comammox *Nitrospira* in terrestrial ecosystems are separated from most sequences obtained from aquatic systems where nitrogen nutrients are low as oligotrophic environments. This study was aimed to examine the ecological preference of comammox *Nitrospira* in terrestrial ecosystems.

We collected soil samples from large scale environmental settings in Australia and determined the abundances and community compositions of comammox *Nitrospira* and ammonia-oxidizing bacteria (AOB) and archaea (AOA) by using real-time PCR and sequencing approaches. It was found that comammox *Nitrospira* were more abundant than AOA and AOB in about one-quarter of the soil samples. The analyses of soil variables and the abundance, diversity and composition of comammox *Nitrospira* revealed the niche specialization and ecological preference of comammox *Nitrospira* in the soils. Among all the tested soil properties, $\text{NH}_4^+\text{-N}$ and C/N are the most important factors in shaping the abundance and community composition of comammox *Nitrospira*. An investigation of 130 forest soil samples with $\text{NH}_4^+\text{-N}$ concentrations ranging from 0.30-59.62 mg kg^{-1} across eastern Australia revealed that clade A abundance was significantly and positively correlated with NH_4^+ , total N and pH, with NH_4^+ as the most important contributor. Our findings suggest that comammox *Nitrospira* are not strictly oligotrophic but both oligotrophic and copiotrophic with a broader ecological niche breadth. The different comammox *Nitrospira* phylotypes may have evolved to thrive under different environmental conditions, including nitrogen-rich agricultural ecosystems.

Designing a Nature-inspired Engineering Tool to Address Soil Pollution

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Aim:

Chlorinated volatile organic compounds (CVOCs) form one of the most wide-spread forms of soil pollution on our planet. On industrial sites they can present as dense non-aqueous phase liquids (DNAPLs) and spread in the soil and groundwater. This is why we propose to build a vertical flow barrier by injecting metal – dissolved organic matter (DOM) flocs that will isolate the source zone and limit the spread. These flocs should also react with the contaminants to stimulate their microbial degradation through a dechlorination process, and remediate the soil pollution on the long term.

Method:

In order to create the most efficient method, we have to understand the floc formation process and identify which parameters influence their stability. Three types of metal combinations - based on aluminum and iron (Al and Fe), that will serve as coagulants in the precipitation process - will be tested at different pH values and molar metal/Carbon ratios in solution to measure the CO₂ production and microbial decomposition under aerobic and anaerobic conditions over time.

Results:

These biodegradability experiments will help us unravel key chemical soil parameters and identify the molecular interactions between coagulants and DOM that are critical for our nature-inspired remediation tool.

Conclusions:

We will gain fundamental insights into flocculation and floc stability, that will support the design of future applications to isolate and degrade CVOC contamination in soils.

Saline Soil Microbial Community Assessment Towards Improving Coastal Agriculture in Cabusao, Camarines Sur, Philippines

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Aim:

The main objective of this study was to quantify, characterize, and evaluate the soil halophilic bacterial communities at Cabusao, Camarines Sur, Philippines.

Method:

Twenty (20) sampling points were determined, with five (5) points per salinity level (non-saline, slight, moderate and severe). The sampling periods were July (dry season) and October (wet season), 2019. From each point, composite surface soil samples (0-30-cm depth) were obtained from nine (9) equidistant holes forming a square-shaped 1-ha area. The following parameters were obtained: field EC and pH (1:1 soil-deionized H₂O ratio), soil texture, Heterotrophic Plate Count (HPC) in R2A agar supplemented with 3%, 5%, 9%, 15%, 20%, and 30%, and Shannon Diversity (H) from sequenced 16S Metagenomic Data.

Results:

Seventeen (17) soil samples were classified as Clay, while the remaining were Silty Clay. Higher pH was also observed during the wet season sampling, with the Severe Category being substantially higher than the other categories. H values were found to be similar across seasons and within salinity categories, regardless of obtained HPC counts. Some bacteria of interest identified include *Actinoallomorus luridus*, *Bellilinea caldifistulae*, *Ectothiorhodospira haloalkaliphila*, *Flavobacterium weaverense*, *Planococcus maritimus*, *Pseudomonas azotoformans*, and *Pseudomonas fluorescens*.

Conclusions:

Cabusao soils appear to host a very diverse microbial community that can be potentially tapped as inoculants to remediate saline soils. Such diversity was found to not be solely dependent on the just the pH and EC of the soil and the season, but on certain other environmental factors (e.g. salt concentration).

Screening for Crop and Cover Plant Traits with Potential to Restore Degraded SoilsCsilla Hudek¹, John Quinton¹, Ian Dodd¹, Nick Ostle¹¹*Lancaster Environment Centre, Lancaster University, Lancaster, United Kingdom*

Aim: Within the international TUDI project we seek to identify characteristics of crop and cover vegetation to mitigate and restore degraded agricultural soils, improve soil health and confer resilience to future perturbations. Plant-soil feedback theory provides an important framework to test the effect of plant types and their traits on soil properties which underpin sustainable yields. Better understanding plant-soil feedbacks across degraded land will enhance trait selection to mitigate damage and recover soil functionality.

Method: We used the plant functional trait approach to determine and combine plants for restoration purposes. Plant functional traits and their associated soil impacts help us use ecological strategies to overcome soil degradation issues. In this work, above/below-ground traits (biomass, cover percentage, rooting depth, branching, root length, root diameter, rhizosphere) to restore agricultural soils were determined using locally relevant crop and cover vegetation from different food systems (grassland, orchard, vineyard and arable). Their traits were used to test and predict effects on soil health. To test our hypotheses, we capitalised on long term datasets from different cropping systems, and new data from sites across different climatic gradients.

Results: Data on soil degradation threats, their level and effect on yield as well as data on soil properties and crop cover were provided. There is a need to collect data on some readily measured root traits to further validate our findings.

Conclusions: Meaningful trait-based plant selection can improve farm scale resource use efficiency by reducing the need for excessive use of external inputs and protecting soils.

Does context matter? The influence of surrounding land use type on key soil biology.

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Aim: Land use conversion from one management type to another is known to effect various soil biota groups. However, little is known about the potential influence of soil biota inhabiting surrounding land use types on communities inhabiting newly converted land parcels. In addition, most studies investigating effects of land use change only consider one component of the soil community. To address these knowledge gaps, we test the hypothesis that there is no influence of surrounding land use type on soil biota.

Methodology: Barcode metagenomics and taxonomic techniques will be employed to quantify four biological components: bacteria, fungi, nematodes and microarthropods, each representing a key component of the soil food web.

Results: Our transect-based field experiment quantifies how communities in surrounding land use types contribute to the diversity and structure of communities inhabiting land in the early stages of rewilding. We have compared the biology of rewilded sites that are either surrounded by woodland or land with a history of agriculture. We also evaluated the effects of surrounding land use on agricultural soil biodiversity health, and here compared soils from conventional arable agricultural sites that are either surrounded by woodland(s), grass-leys, or conventional agriculture.

Conclusions: The primary goal of our experiment is to provide scientific evidence on whether biota in surrounding land use types influence the type or restructuring and/or recovery of soil communities, thus allowing land managers to make better informed decisions on which land parcels to convert within a mosaic of land use types to maximise soil biodiversity.

Nitrogen Preference and Manipulation of Rhizosphere Nitrogen Cycling, an Aid to Agricultural Sustainability.

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¹University Of Sheffield, Sheffield, United Kingdom, ²The James Hutton Institute, Dundee, United Kingdom

Nitrogen is crucial for plant survival and commonly applied as synthetic fertiliser in the form of NH_4NO_3 or urea in conventional agriculture. In soil, ammonium is rapidly converted to nitrate through nitrification making the applied N more susceptible to loss. These losses typically occur via leaching, runoff or emissions of the potent greenhouse gas nitrous oxide usually via denitrification. Obviously, these losses reduce efficiency and increase costs to the farmer as well as causing significant damage to the environment. Plants interact with the soil microbial community to generate bespoke rhizosphere microbiomes with downstream effects on function. Previously, on a limited number of cultivars, we observed variation in rates of both nitrification and denitrification between different cultivars of a major arable crop, barley. This was associated with variation in the relevant functional microbial communities associated with these processes. We have assessed if this may be linked to the preference of cultivars to uptake ammonium or nitrate and performed a screen of c200 cultivars, under different conditions, identifying significant variation across cultivars in these two key processes. We are in the process of assessing if this variation in function is linked to altered functional gene dynamics. Downstream these results will be used to assess if breeding for altered preference or manipulation of nitrification and/or denitrification represent routes to improve the sustainability of conventional agriculture.

Influence of different amendments on microbial communities in a soil with organic and inorganic contamination.

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Soil contamination is a problem with serious consequences that influences both ecological aspects (including biodiversity conservation) and soil use. Anthropogenic activities cause the releases diverse pollutants into the environmental compartments; for instance, the strong dependence on fossil fuels generates significant spillage risks associated with notable environmental impacts and substantial hazards for human health. In turn, soil contamination by heavy metals and metalloids is also a cause for concern due to their persistence in the environment and their non-biodegradable nature, which leads to their accumulation to toxic levels. The type and availability of contaminants is strongly related with the biodiversity of the ecosystems, where microorganisms play an important role, and this is especially relevant if soils are affected by mixtures of contaminants. Concurrent contamination is indeed a challenge for the sustainable remediation of contaminated soils. In this context, the objective of this work was to study the changes in the microbial population structure when different amendments are used for the bioremediation of a multi-polluted soil (simultaneous presence of hydrocarbons, heavy metal(loid)s, polychlorinated biphenyls, micro plastics, etc). The experiment was conducted in field conditions on a pilot scale and monitored for 150 days. Together with microbial diversity, the chemical degradation or immobilization of the contaminants was also evaluated.

About Time: Temporal Dynamics of the Soil Microbiome in Agricultural Soil

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Aim:

Soil biodiversity is under threat due to intensive land use and climate change. Soil microorganisms might benefit from the use of compost or biochar. Numerous studies have investigated the potential impact of these amendments, but often only a snapshot have been investigated whereby temporal variability was neglected. Therefore, within this research we aim (1) to understand how rapid the soil microbiome responds to amendments and/or seasonal changes, (2) to evaluate the dynamics at different soil depths (3) to determine the representativeness of samples taken on a given time point.

Method:

Two Flemish fields have been sampled on a monthly basis for one year at varying depth (Field 1: 0-10cm, 10-30cm and Field 2: 0-25cm). The soils were subjected to either compost (Field 1: 0 vs 2 000 kg C ha⁻¹y⁻¹) or biochar (Field 2: 0 vs 10 900 C ha⁻¹). The bacterial and fungal communities were analysed using PLFA or and soil chemicals were characterized.

Results:

Certain bacterial and fungal species exhibited distinct temporal patterns. Compost effects were time-dependent, while treatment effects caused by biochar affected the soil microbiome less. We also found that the soil microbiome was less affected when deeper layers of the soil were studied. Samples taken in a shorter time frame can be representative of the global soil microbiome, taking into account potential field heterogeneity. However, large seasonal effects causing temperature or soil moisture changes might hamper a representative sample.

Conclusions:

Time was the strongest driver of certain microbial groups, followed by the compost treatment.

An updated Key to UK Pauropoda

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Aim: Pauropoda, the smallest myriapods, remain a neglected group, especially in the UK where most experts have retired or passed away. Current attempts at a UK key are composed of diagrams found in papers from the late 1900s. To raise interest and contribute to a future recording scheme, we aimed at creating updated dichotomic and character matrix keys to species.

Method: Individuals were collected at the University of Reading via brush or Tullgren funnel from rotting wood and soil, and their habitat information was recorded. Photographs of the live specimens were taken with a Laowa 25mm F2.8 Macro lens and slide mounted individuals were photographed via the Olympus BX63 compound microscope at 200x and 1000x magnification. Electron micrographs of relevant structures for identification were also taken. Our new key was composed in the style of the keys presented in *Mangfotingar 2005*.

Results: The University of Reading campus yielded seven species of pauropod, only one specimen was acquired for each of two species, so not all structures could be imaged. We complemented 3 diagrams from *Mangfotingar 2005* for structures we missed. The dichotomic key was saved as an OpenOffice Writer document (ODT) and the Matrix keys as a tab-separated values (TSV) file.

Conclusions: This detailed but user-friendly key will serve as a useful resource for individuals wishing to identify UK specimens. We recommend that specimens that do not fit our key be sent to us, allowing us to add more species to our key, and eventually include all UK pauropod species.

Evaluating Grazing Pressure on Soil Springtail Community Composition and Diversity in Canadian Garry Oak Meadows

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Aim: The focus of my work is to evaluate grazing pressure on soil springtail community composition, richness, and evenness in shallow-soil Garry oak meadows in British Columbia, Canada.

Method: Two research sites on Salt Spring Island were used. There were established deer exclosures at both sites, one with a 7-month-old fence enclosing a large area, and the other with multiple 13-year-old 5 m² exclosures. Both sites had six each of fenced and unfenced plots (5 m², 24 total plots). I collected four soil cores (including the litter layer) from every plot at both sites (96 total) in October. Springtails were extracted using a high-efficiency Tullgren-type extractor. To account for site-specific variation, the four soil cores were bulked for chemical analyses after extraction and tested for pH, total carbon and nitrogen, available phosphorus, and potassium. Prior to collecting soil cores, soil compaction, moisture, and temperature were measured using a penetrometer and soil probe, respectively. The following spring, plant percent cover in a 0.5 m² plot at each sampling location (96) was determined.

Results: Since excess deer herbivory alters litter inputs through changes to the plant community, it is expected to alter springtail communities. I will compare and discuss the influence of exclosures on composition, richness, and evenness of soil springtail communities at each site.

Conclusions: Deer exclosures are common management tools to protect sensitive Garry oak ecosystems at risk from excessive deer grazing. My research evaluates the influence of this tool on belowground ecosystem diversity and community composition.

Diversity and Ecological Preference of Tardigrades from Selected Australia Soils

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Aim: Tardigrades, also known as 'water bear', a monophyletic group of microscopic ecdysozoans best known for their ability to withstand extreme environmental conditions. They are widespread in terrestrial or semi-terrestrial environments. However, due to the methodological challenges to characterize their identity and diversity, the ecological preference, and their interaction with soil microbiomes are poorly understood. This study aimed to investigate the diversity of and ecological preference of tardigrades in selected Australian soils.

Method: We collected 195 soil samples along Australia south-east coastal and some inland areas. Soil physiochemical characteristics, including soil pH, total organic carbon (TOC), total carbon (TC), total nitrogen (TN), ammonium, and nitrate were determined. Soil DNAs were extracted and sequenced by targeting the 16S SSU rRNA, 18S SSU rRNA and ITS region to obtain the information of bacteria, eukaryotes, and fungi communities respectively.

Results: After the genes sequencing, quality control and removal of plant and fungal sequences, tardigrade sequences accounted for 5.99% of all sequences however no tardigrades sequences were found in two-thirds of the samples. At least 14 types of tardigrade species were detected from those samples and *Eremobiotus alicatai* were the most common species. The relative abundance of tardigrades was significantly correlated with soil TC, TN. The tardigrades were most affected by bacterial and fungal communities, and some precipitation index.

Conclusions: The findings from this study provides novel insights into the ecological characteristics of tardigrades, bridge the gaps between soil microorganisms and soil micro-fauna, and call a need of the new methodology in tardigrades research.

Soil nematode biodiversity as an indicator of soil functioning under municipal sewage application

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Aim:

Disposal of municipal sewage to land is a common practice, particularly in small communities where other options are not available. This study aimed to understand the impact of sewage application on soil nematode biodiversity and the implications for soil functioning.

Method:

Soil samples from a municipal sewage application (treated) and a control site with similar slope and aspect were collected from transects sampled during (2017) and 6 (2019) and 29 months (2021) after sewage applications had ceased on the treated area. There were six replicate samples from both transects. Nematodes were extracted from soil using trays and community composition determined by microscopy.

Results:

During sewage application total nematode abundance was greater under the control than disposal site but this effect disappeared once application had ceased. The disposal site during application was characterised by having a higher nematode channel ratio (ratio of bacterial to fungal feeding nematodes) with more bacterial feeders and predators. This effect persisted 6 months after application had ceased (more bacterial feeders and fewer fungal feeders) but had disappeared by 29 months after application.

The proportion of predatory nematodes was significantly greater at the disposal site during application but declined with time since application.

Conclusions:

The long-term application of sewage onto the land disposal site created a food web dominated by bacterial feeding nematodes, reflecting faster nutrient cycling and potentially with greater losses of nutrients to the environment. These differences declined with time since application reflecting recovery of soil functioning at the disposal site towards untreated levels.

Soil Biodiversity, Soil Bioindication and Soil Policies

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Aim:

Soils and soil organisms form complex systems and therefore are obstructive to an analytic approach that usually seeks to reduce a system to its elementary components and to direct interactions among these components. Not surprisingly, so far soil policies have failed to capture the complexity of soil and soil biodiversity. Despite the inherent difficulties of complexity, designing simple effective policies and operative solutions is required for soil protection.

Method:

Soils and soil organisms are main drivers in organization and functioning of natural and anthropic ecosystems as they shape the aboveground communities. In addition, soil organisms interact directly and indirectly with each other through modifications of their environment and through soil food webs. The simplification that is required to obtain relevant (bio)indicators must be developed in a cooperative manner among the relevant stakeholders.

Results:

In Switzerland, the creation of a network of scientists and policymakers has enabled direct exchange of strategical information (balance between policy needs and possible scientific results) and the design of several applied research projects. The experts were also able to contribute to the (ongoing) process of revising the current law on soil protection and advocate for the inclusion of soil organisms' direct protection and setting specific reference value for soil biodiversity.

Conclusions:

Cooperation carried out for over 30 years by a working group "Soil Biology Implementation" that includes representatives of federal and cantonal administrations and research institutions has proven to be an effective approach in designing soil biodiversity policies.

First Application of the SBVJS Method used for the Integrated Assessment of a Hazelnut Orchard

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Aim:

Mycological components, soil nature, vegetation, humus forms, soil microfauna and human activities drive the evolutionary dynamics of the terrestrial environment. Various indicators from the study of these components make it possible to assess the trends of habitat successions.

Method:

The method presented for the first time at the Global Symposium on Soil Biodiversity organized in 2021 by FAO in Rome, Italy, now called SBVJS (Synergic Biotic eValuation Joint System), allows to expand the criteria for integrated assessment of soil and environmental quality, facilitating the use of environmental data from different disciplines with the aim of their rationalization and practical use for land managers.

Results:

In this first study using the SBVJS method, the biological quality of a 1.2 ha stand in the Vico Lake Valley (Latium Region, Italy) cultivated with *Corylus avellana* L. in Cultivars: *Tonda Gentile Romana* 50% and *Nocchione* 50% is analysed.

Particular attention was paid to the agronomic management of the hazelnut grove and to the number and type of pesticides used.

The results obtained confirm how useful the indicators used are to arrive at an integrated assessment that allows a thorough estimate of the analysed territory without incurring in erroneous interpretations derived from partial and incomplete data.

Conclusions:

The health status of a territory and its possible soil degradation can be monitored by integrating the pre-existing soil quality indicators with the SBVJS Method, which, thanks to the study of five key components of any terrestrial ecosystem, allows a complete and comprehensive assessment of environmental quality.

Soil Health Improvement in Intensive Agrotechnologies by Use of Microbial Fertilizers in Ukraine and Europe

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Restoring microbial biocenoses can solve two major issues: the soil fertility decline and the increase amount of carbon in the atmosphere. Reduction in the diversity of saprophytic microorganisms is the result of excessive use of mineral fertilizers, pesticides and soil-depleting tillage. This occurs in the context of carbon cycle disruption when plant residues returned to the soil are insufficient to feed beneficial microorganisms. The unique complex of saprotrophic fungi and PGPR bacteria in the microbial preparation Ecostern has a positive effect on the composition of the soil microbiota. The restored balance of microorganisms allows you to stop the loss of humus compounds and even start their accumulation.

Nowadays the problem of accumulation of P and K inaccessible to plants in soils is acute for the farmers' community along with increasing application rates of nitrogen fertilizers. A drop in the use of mineral fertilizers that is one of the key points of the European Green Deal requires alternative ways to provide plants with macronutrients. The PGPR bacteria are always companions of the plant's root system in resilient ecosystems, so they are the first candidates for improving the efficiency of the plant's nutrition system in intensive but environmentally neutral farming. The complex of bacteria developed by BTU-CENTER allows reducing the application of mineral fertilizers by up to 30% without reduction in the yield due to prolongation of the bioavailability of the nutrients used. Long-term studies show a positive aftereffect on agrocenoses even with a single colonization of the soil.

Stimulating the Soil Microbiome in a Reconstructed Soil

Katy Jo Stanton¹, Emma Duley¹, Tim Pettitt¹, Mark Nason¹, Alexandra Wagstaffe¹, Joseph Jones¹, Rachel Thompson¹, George Littlejohn², Michele Kiernan²

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Aim:

By comparing microbial communities in an established and newly formed reconstructed soil, with 'traditional' soil preparation methods, we hope to understand how a soil microbiome is formed over time. The botanic gardens at the Eden Project, UK were created from reconstructed soils 20 years ago, thus providing an ideal comparison against newly created soils.

Method:

Reconstructed soil created from composted green waste, china clay sand, and composted bark, was compared with double digging, mulch application, and no tillage treatments. Baseline eDNA samples taken from each treatment and compared with samples taken 3 months later. These samples were compared with an established reconstructed soil (20 years old), originally the same recipe but with the addition of mulch applied every 2 years.

DNA analysis will be used to compare microbial community composition.

Results:

This is an ongoing experiment. Results are expected to show different communities at baseline becoming more similar over time.

Conclusions:

By comparing microbial communities from an established and newly formed reconstructed soil, with 'existing' soil will increase our understanding of microbial community relationships in soil formation.

Seedling Emergence Bioassay to Determine Natural Disease Suppression of Reconstructed Soils Against *Pythium* Damping Off.

Tim Pettitt¹, Katy Jo Stanton¹, Emma Duley¹, Mark Nason¹, Joseph Jones¹, Rachel Thompson¹, Alexandra Wagstaffe¹

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Aim:

Use measurements of reconstructed soils' capability to suppress phytopathogen growth and pathogenicity as an indicator of soil wellbeing and fitness.

Method:

Seedling modules filled with reconstructed soil consisting of varying fractions of green waste, bark and sand, were placed in sand oatmeal. In each experiment each treatment was set up in three replicate inoculated and 3 replicate uninoculated control modules and these were arranged in three randomised blocks. Inoculum was a *Pythium* isolate, 2000 cfu/g. Seeds of spinach were sown 5 per module at depth of 10 mm. Germination and post emergence damping off, up to first true leaf were measured in each replicate.

Results:

Additions of biologically active material, such as composted green waste, had a significant impact on pathogen development and pathogenicity, resulting in reduced disease. The implications for this phenomenon in the assessments of soil health are discussed. This is tempered by the potentially negative impact of high microbially active materials on plant growth.

Conclusions:

The green waste fraction in reconstructed soils appears to drive resistance to *Pythium*. Further research is recommended to understand the reasons behind this.

The best recipe for earthworms and plant crops in vermicomposting

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Aim:

Vermicomposting can be an environmental-friendly way to treat organic wastes and nurture the soils in sustainable agriculture. The purpose of the study is to investigate how the composition of domestic food wastes and Chinese herbal medicine residues affects the rate of production and quality of vermicomposting on plant growth and earthworm fertility.

Method:

The study was conducted by 18 setting-up microcosms with six treatments of substance compositions, which were: C-rich substance only, high C:N ratio, N-rich substance only, low C:N ratio, residues of Chinese herbal medicine and the control. After 60 days of incubation, the quality of vermicompost was examined through physicochemical properties analysis, Cress seed germination test, planting growth test, and the body weight and mortality rate of earthworms.

Results:

All types of vermicasts are safe for planting crops as the germination indexes were over 80% except the control. Vermicomposts with C- and N- substances were less acidic, increased in nitrate and decreased in ammonium, while Chinese herbal medicine residue was more acidic but with a higher concentration of nitrate. Treatment with low C:N not only shows the highest and most significant increases in the number of earthworm and their cocoons, but also showed a significant increase in shoot dry weight of crops. Treatment with high-N substances and Chinese herbal medicine residue also shows beneficial impacts on earthworm growth and crop growth.

Conclusions:

To conclude, vermicompost with low C:N is more suitable for plant growth. It also provides good environmental conditions for earthworms' survival and reproduction, which confirms the sustainability of vermicomposting.

Soil amendment on contaminated soils and impact on mesofauna in an agricultural contextCéline Pernin¹, Sylvain Demuynck¹, Fabien Grumiaux¹¹*Université de Lille - LGCgE, Villeneuve d'Ascq, France*

Aim: The north of France is rich of a flourishing industrial past which left traces at the level of the quality of the grounds. Many agricultural areas are contaminated by metals and remediation solutions must be found. The objective of the present work is to evaluate the effects of a biochar elaborated from *Miscanthus x giganteus* cultivated on soils contaminated by the activities of the former foundry Metaleurop Nord (Noyelles-Godault). The interest of miscanthus biochar was evaluated in comparison with wheat and industrial hemp.

Method: Three agricultural plots located on a gradient of metallic contamination were monitored for 2 years. The plant biochar was amended at a dose of 2% m/m. The faunal communities, meso (collembola) and macrofaunal (woodlice, carabid beetles and earthworms) were monitored annually. The mesofauna was sampled by soil cores, the macrofauna by interception jar and the worms by using a chemical extraction (AITC).

Results: Regarding collembola, no difference between the amended and unamended plots was found regardless of the site considered. As expected on agricultural plots, epiphytic and hemiphytic species were found, with or without biochar. Similarly, the macrofauna is not impacted by the presence of biochar. Finally, although worm densities appear to be higher in plots without biochar than in plots with biochar, no significant difference appears.

Conclusion: If the monitored fauna communities do not seem to be impacted by the plant biochar amendments, the latter does not represent a hindrance to the recolonization of the soils, to the presence and maintenance of these communities.

The Interplay of Biotic- and Abiotic Processes that Stabilizes Soil Organic Carbon During Water Erosion

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Soil erosion is a major threat for soil biodiversity. Especially, loess soils in hilly landscapes under intensive agriculture practices face the risk to lose top-soil and valuable soil biodiversity. Currently, we lack fundamental understanding how/if we can protect soil biodiversity from soil erosion by stimulating a healthy soil community which will lead to increase in soil carbon stocks.

Aim:

Our research aims to unravel the interplay between biological components and inorganic phases in stabilizing soil organic carbon(SOC) during water erosion in loess soil-grassland. We study: i) under which circumstances erosion processes and SOC loss is minimized; ii) which biotic components(plants, microbes) stabilize OC; iii) in which molecular form SOC is occluded in aggregates.

Method:

We set up plant-soil systems with *Trifolium pratense* and *Lolium perenne* in loess soil of a low and high SOC content. We grew the plants with mycorrhizal inoculum versus no-inoculum added in soil of low SOC content to test if mycorrhiza is able to prevent soil erosion. The plants grew 8 weeks on a slope followed by simulated rainfall. Runoff, root- and soil samples are collected; the related the biological parameters: soil microbial biomass, extracellular polymeric substances, fungal biomass, root AMF colonisation; and abiotic parameters: aggregate stability, SOC occluded in aggregates and the molecular components (will) be measured.

Results:

We expect the two plant species could reduce soil erosion, and there could be a positive relationship between microbes steered by plant exudates and aggregate stability. Especially, we hope to reveal the fungal pathway to SOC stabilization.

Effects of Urban Park Management Practices on Mesofauna Communities

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Aim: The increasing urbanisation of territories is at the heart of many societal and environmental issues. In cities, green spaces and especially parks appear to be essential places for the conservation of biodiversity. However, questions arise about how to manage urban parks in order to satisfy the needs of citizens and above all to conserve biodiversity. Urban soils and their biodiversity provide important ecosystem services, although they are still understudied. The objective here was to compare the mesofauna communities, in terms of structure and composition, according to three management practices in a Parisian urban park.

Method: The mesofauna was sampled in spring 2021 in Suzanne Lenglen Park (Paris, France) in areas of lawn, heavily mown grassland, and lightly mown grassland. Mesofauna was extracted with a MacFadyen extractor. Soil physico-chemical analyses were also carried out.

Results: The average springtails density values obtained are broadly in the same range as those found in the literature. Springtails density did not differ significantly between the three management practices, although there was a trend towards lower density in the heavily mown grassland. Mesofauna community composition is still being processed. The management method did not affect moisture in this study.

Conclusions: This preliminary study provides an overview of management methods' impact on mesofauna communities. In order to verify these conclusions, we repeated the measurements in 2022 whose results are currently being analysed. In 2023 we will extend our sampling to more Parisian parks with the same management practices.

Soil Community Changes Accompanying Semi-Natural Grassland Restoration

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Aim:

European dry calcareous grasslands are rare, species-rich habitats of semi-natural origin. Significant changes in land use during the last century, including the abandonment of traditional management, have caused profound changes in these plant communities. Following abandonment, spontaneous succession leads to shrub and tree encroachment and the extinction of grassland species. Attempts to restore semi-natural grassland involve the removal of woody vegetation and reinstating mowing or grazing regimes. The importance of microbes in ecosystem restoration has become increasingly appreciated in recent years. Owing to the fundamental link that soil microbiota shares with plant community structure and wider ecosystem function and dynamics, characterising these communities promises to inform our understanding of ecological progress towards reference states.

Method:

We used environmental DNA (eDNA) from the soil of dry calcareous 'alvar' grasslands in western Estonia to characterise soil communities in ecosystems experiencing restoration management. Sampling was conducted at 36 sites. Each site comprised plots that had reached different stages of abandonment (open vegetation, scrub encroachment, young forest) prior to restoration several years previously; as well as a reference state control that had experienced continuous traditional management. From each plot, a topsoil sample was collected for molecular analysis. High throughput sequencing of eDNA (metabarcoding) was performed using different molecular markers to characterise communities of prokaryotes, eukaryotes (general) and plants.

Results:

We measure alpha and beta diversity and the representation of different guilds and functional groups among soil communities.

Conclusions:

The effects of grassland restoration on different soil biotic groups will be discussed.

Global survey and bibliometric analysis of economic valuation of ecosystem services provided by soil biodiversity

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Aim:

Identify the main global players publishing in topics related to economic valuation of ecosystem services provided by soil biodiversity.

Method:

In March 2022 we conducted an online global survey (GS) and a bibliometric analysis (BA) on soil biodiversity. The BA embraced the period 2011-2021, using Web of Science database. We used a combination of queries including terms related to ESSB and economic valuation. The bibliometric package from software R and a SQL protocol were used to analyze the data.

Results:

Of the 1791 GS respondents 52% work with ES. Of those, 69% work with nutrient cycling, while 52% with biodiversity conservation. About the organisms, 65% work with soil microbes. Diversity indexes based on species richness and abundance are used by 46% of respondents. The BA revealed a trend of increasing scientific production. A total of 2311 authors published 538 articles in 267 sources. Average citations per document were 16.5. Among the most 10 productive countries, USA and Chinese authors participated in 85% of publications and Indian and Brazilian authors in 20%. The values obtained of ES are quite varied and both the GS and the BA showed that their capture are associated with the method used.

Conclusions:

The research groups involved in economic valuation on ES are pioneers and indicate that further studies are needed to bridge existing gaps. Economic valuation data are essential in order to subsidize efforts for management and conservation of soils and their biodiversity.

Linear transport infrastructure as a relay for soil biodiversity

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Aim: Several studies have highlighted the impact of linear transportation infrastructures on the flows of certain animal populations. These infrastructures have important ecological impacts on the environment, as they contribute to the parcelling out of habitats of organisms. However, they can also represent refuges in uniform landscapes, particularly for the soil fauna. This study is particularly interested in the infrastructure of energy transport via the electric pylons.

Method: Three management modalities under pylons were studied: conventional agriculture, grazed meadows and unmanaged. Five pylons distributed on 2 sites in the north of France, Rhumingham and Bailleul, were monitored. This monitoring focused on the meso (springtails) and macrofaunal (woodlice, ground beetles and earthworms) communities of the soil. The sampling was done under the pylon and at 5 and 15 m from the pylon.

Results: No significant refuge effect is visible for carabid beetles, which prefer open environments, adapted to their way of life. The distribution of carabid beetles is little affected and seems to be homogeneous on the cultivated plots. Similarly, the vegetation under the pylons does not seem to influence their presence either. The only evidence in favor of this refuge effect is the greater abundance of woolouse and worms under pylons in fallow areas compared to adjacent cultivated plots.

Conclusion: The pylons monitored did not show an overall positive effect on the abundance and composition of edaphic communities. The effects are punctual and limited to 1 or 2 taxa (collembola, woodlouse). No influence on the most mobile taxa was observed.

Evolution of Fauna Communities on Newly Installed Rooftop Gardens

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Aim: Over the past ten years, urban agriculture has developed considerably around the world. The increasing urban population and the demand for fresh local produce are among the drivers of this trend. Rooftop gardens, developed on Technosols, are one of the urban agriculture forms that are rapidly expanding. Soils, which are at the heart of the functioning of these rooftop gardens, are likely to provide a wide range of ecosystem services to the city, other than food production, although these services are not really evaluated. Our project aims to conduct a combined study of the evolution over time of soil quality, percolating water and biodiversity. Here we will focus on the study of soil biodiversity.

Method: The monitoring was carried out the first year following the installation of three Technosols with varying levels of organic matter. Samples of the macrofauna, mesofauna and microfauna were collected once a month for one year between May 2021 and May 2022.

Results: A change in soil fauna density was observed, with a strong increase in the density of mesofauna and microfauna during the first few months of Technosols installation. A change in macrofaunal community composition was also observed between the beginning and end of the experiment. Although some results remain to be analysed, no differences are currently observed between the three modalities.

Conclusions: A fast dynamic of the faunal communities was observed during the first year of Technosols installation. These results will also be compared to all the other measurements carried out.

Soil fertility and corn plant productivity in a simulated Amazonian dark earth (Terra Preta Nova)

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Aim:

Evaluate the impact of Terra Preta Nova practices on soil fertility and plant production in a nutrient poor Latosol.

Method:

A fractional factorial experiment was installed using 160 pots with 4 kg soil (dry wt) each. In each pot, each of the five components of ADEs (earthworms *Pontoscolex corethrurus*, OM horse manure, Brazil nut biochar, ground fish bones and ceramics) were added or not, generating 32 treatments, and after 60 days plant height, above and below-ground (root) biomass, root length, and soil fertility levels were assessed.

Results:

All of the ADE components used to create the Terra Preta Nova had significant impacts on maize production. Surprisingly, biochar had a slightly negative impact and ceramics had a major positive impact on shoot mass, while highest positive impacts overall on plant parameters (up to 26% increase in shoot mass) were observed with addition of organic matter and fish bone meal, in particular. Earthworms positively impacted both shoot and root mass. Several important two-way as well as three-way interactions were detected.

Conclusions:

These results show the potential for wider use of household and farm refuses, such as bones, manures and broken pottery in soil improvement, and the importance of interactive effects in affecting plant growth, factors that need further attention in future soil fertility and management schemes such as Terra Preta Nova technologies, based on the Amazonian Dark Earth concept.

Soil microbiota and arbuscular mycorrhizal fungi buffer negative effects of drought on *Trifolium pratense* productivity

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Aim: Plant rhizosphere is a biodiversity hot-spot with a multitude of intricated interactions. Many studies focus on specific rhizosphere inhabitants only, but a more comprehensive overview is required for recognizing key players and their functioning. We therefore investigated the effect of drought and soil steam-sterilization on both the aboveground biomass productivity of red clover (*Trifolium pratense*) and on the soil bacterial and fungal community.

Method: A greenhouse experiment with 24 pots and five *T. pratense* individuals, each, was set up for investigating three fixed factors: water regime (moist vs. drought), soil treatment (steam-sterilized vs. native soil), and inoculation with arbuscular mycorrhizal fungi (AMF) (inoculated vs. non-inoculated). Plant biomass, *Rhizobium* root nodules, and AMF spore counts were assessed for each pot. Quantitative real-time PCR (qRT-PCR) was used for a monitoring of fungal, rhizobial and AMF biomass. The structure of soil microbiomes (fungi, AMF, bacteria) was addressed by separate community-specific Illumina analyses.

Results: Plant biomass productivity increased in steam-sterilized soil, even under drought, compared to native soil. Drought induced higher abundances and diversity of AMF, regardless of the soil treatment, while root nodules decreased in steam-sterilized, drought affected soil only. Steam-sterilization alleviated plant stress, and enhanced their performance due to lower nutrient competition and pathogen pressure, and caused an increased of plant beneficial microbes, especially AMF.

Conclusions: Our results clearly show that changes in plant performance are accompanied by changes in the diversity and community composition of the soil microbiota. Responses to stressors are regulated by both, plant and interacting microbes.

EMERGE Biology Integration Institute: Integrating Research and Education to Illuminate EMergent Ecosystem Response to ChanGE

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Aim: Understanding how biological systems – human and natural – interact with and influence each other over time is a Grand Challenge of Biology. Resolving this challenge is essential to predicting ecosystem response to change, to inform human action and policy in areas such as climate change and land use. Yet it has been hampered because the Biological research community spans many sub-fields, each with its own perspectives, approaches, and with little exposure to one another. **Method:** The EMergent Ecosystem Responses to ChanGE (EMERGE) Biology Integration Institute (BII) integrates 15 disciplines across 14 organizations, to integrate research and training, and field observations and laboratory experiments, to understand a climate-critical case study: how a rapidly warming Arctic is transforming some permafrost into wetlands, accelerating cycling of carbon, and further affecting earth's climate. The EMERGE BII leverages a decade of system characterization of a thawing permafrost peatland at Stordalen Mire, Sweden to produce a framework for evaluating multi-level responses to changes in natural and engineered ecosystems. **Results:** By mapping the diversity and carbon cycling roles of microbes, viruses, and mobile elements; uncovering the interactions among them, plants, and soil organic matter; and connecting these to the consequences for carbon gas emissions, under changing conditions; we are forging a framework for understanding emergent ecosystem responses to change. **Conclusions:** This project is improving the understanding of how thawing permafrost systems respond to and cause changes, with a focus on carbon cycling, and laying a groundwork for a more generalizable model.

Land-use Influence on Belowground Plant-Parasitic Nematode Communities at the Regional Scale

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Aim:

Plant parasites are among the biggest threats to food security worldwide. While there are several studies on the topic, the distribution and main drivers of soilborne plant parasites are still unknown. We aimed to assess effects of land use and the contribution of environmental factors in shaping belowground herbivore communities at a regional scale.

Method:

We conducted a wide soil sampling campaign of the North of Portugal, using a 20-km grid design that ensured coverage of the highly variable land-use, geography and climate. Six areas with differing land use intensity were sampled per square: annual and perennial agriculture, pasture, urban areas and exotic and native forests, in a total of 406 soil samples. Edaphoclimatic data was obtained through European datasets (Lucas soils initiative, Copernicus, others). Plant-parasitic nematodes (PPN) were extracted and identified to genus level, and their community analysed through the NINJA software, followed by multivariate analysis to assess effects of land-use and environmental factors.

Results:

Pastures supported significantly more diverse PPN communities, with higher alpha diversity, biomass and herbivory footprint. Forests had the lowest diversity, although more heterogeneous communities within sites. The influence of environmental factors such as soil properties, land cover and climate on the distribution of PPN communities could not be established.

Conclusions:

The established relationship between land-use and the PPN communities has implications for the management of below-ground herbivory pressure and soil conservation. Finer studies incorporating local abiotic conditions rather than broader estimates will allow further inferences on the impacts of specific edaphoclimatic conditions on the PPN communities.

Temporal dynamics of soil microbiome in a Majorcan vineyard

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Aim: The microbial composition of the soil is an important factor to consider in viticulture. It can influence on the "terroir" and on the organoleptic properties of wine. Knowing the soil microbiome composition can help to adjust treatments in the vineyard. However, microbial communities can change over time. The aim of this work was to study the soil microbiome at different phenological states of the vines in order to know its temporal variation.

Method: The study has been carried out in a vineyard in Binissalem, Mallorca, Spain. Soil samples from rhizospheric zone of 18 vines were taken in January, June and September of 2021. We analysed the soil microbial communities using the data obtained from NGS of soil DNA from the 16S (bacteria) and ITS (fungi) regions using BeCrop® technology. Sequences obtained from Illumina amplification were used to calculate α diversity index and analysed by nonmetric multidimensional scaling method.

Results: The results reveal that the microbiota is unstable over a full growing season. Edaphic microbial diversity associated with the rhizosphere increases during the seasonal period, being lower in January and higher in September. On the other hand, it can be observed that community composition varies with species that appear only in one moment.

Conclusions: In conclusion, for integrated management based on the rhizospheric soil microbiome, the seasonal changes must be taken into account. It's important to sampling at different vine phenological stages and study the impact of soil management on microbiota over the season to ensure beneficial effects on the agroecosystem.

Analysis of the interaction between arbuscular mycorrhiza and potato nematodes using X-ray Computed Tomography technique

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Plants are typically the central component of multipartite associations in the field. Roots are often colonized simultaneously by pathogenic and mutualist symbionts that compete for plant resources, potentially impacting plant root development. Understanding how plants interact with both symbionts is important to unravel the network strategies and potential influence on plant performance and ecosystem evolution and function. The latest X-ray Computed Tomography (CT) techniques make it possible to visualize plant roots and soil organisms in situ in 3-dimensions, enabling the impact of the interaction of microorganisms on plants to be observed.

Potato cyst nematodes (PCN) establish parasitic interactions with potato roots causing significant impacts on plant physiology. Potatoes are also highly mycorrhizal, benefitting from associations with arbuscular mycorrhizal fungi (AMF). Using X-ray CT techniques, I determined the impact of the interaction of both microorganisms on potato root development and architecture. A positive impact caused by AMF was observed, resulting in a significantly improved root development and volume ($p < 0.01$) suggesting increased resource allocation to roots. Conversely, PCN had a negative effect, resulting in a less dense root architecture ($p < 0.01$). However, in the presence of both symbionts at same time, the decrease density and root volume was less accentuated ($p < 0.05$) than in PCN-only colonised plants.

These results provide important insights into the belowground dynamics of plant–AMF-PCN interactions through their effects on root architecture. The imaging technique provides a framework to study root architecture which can be used to improve our understanding of plant resource allocation to each competing symbiont.

Conservation Agriculture Enhances Soil Fauna Richness and Abundance in Low Input Systems: Examples From Kenya

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Conservation agriculture (CA) (zero tillage + organic inputs as surface residue) is believed to improve soil nutrient status, soil structure, control soil erosion, and also enhance soil fauna diversity. Despite the widespread interest in CA, empirical evidence of the benefits of CA on soil fauna diversity is limited, especially in low-input systems of sub-Saharan Africa (SSA). Consequently, the magnitude and effect by CA on soil fauna remains unquantified. The aim of this study was to evaluate the effect of CA and associated management practices on soil fauna richness and abundance. We hypothesized that CA and mixed cropping would positively influence soil fauna richness and abundance. We compared CA with conventional till (CT; with or without residues) in sole maize and maize-bean cropping systems. Soil macrofauna and mesofauna were sampled across the treatments in medium-term (6 years) trials in Embu, Central Kenya, and Kakamega (6 years) and a long-term trial in Nyabeda (15 years) using soil monoliths and core samplers, respectively. In agreement with our hypothesis, higher macrofauna taxonomic richness and mesofauna was recorded in CA than in CT without residues. This study demonstrated that: (1) medium to long-term addition of organic residues enhances soil fauna richness and abundance, (2) CA increases soil fauna taxonomic richness and abundance compared with CT, and (3) CA under maize-bean intercropping, rotation and sole maize cropping systems promote soil fauna richness and abundance compared with sole legume (common beans). We conclude that adoption of CA is important in enhancing richness of soil fauna. Given the numerous challenges faced by smallholder farmers of SSA in the adoption of CA, who in most cases rarely practice all the three CA principles simultaneously, we propose a further study that will determine the effects and interactions between each of the CA components on soil fauna richness and abundance.

Keywords: tillage, organic resources, soil fauna, richness, abundance

Cover crop mixtures assemble a soil microbiota similar to that of monocultures

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Aim:

Cover crops are used in cropping systems to enhance ecosystem services such as soil protection against erosion or soil microbial activity. Different cover crops are selected to steer specific processes, but whether cover crop mixtures have added value over monocultures remains debated. Here, we tested the hypothesis that cover crop mixtures accumulate a distinct soil microbiota than monocultures, which could promote more varied microbially-driven soil functions.

Method:

We performed a field experiment at three locations in The Netherlands with distinct soil types. At each location, we grew nine monocultures of different cover crop species, two mixtures of five and eight species, and a fallow control using a block design with four replicated 6x2 m plots. After three months, we measured crop biomass and profiled the soil bacterial and fungal communities via high-throughput amplicon sequencing.

Results:

Distinct cover crop species had similar biomass production patterns in monoculture across locations, and mixtures had an average productivity as compared to monocultures. The diversity, community structure, and composition of soil microbial communities was primarily determined by the geographical location, and then by cover crop treatment within each site. In all cases, fungal communities more readily responded to cover crop treatments than bacterial communities, but cover crop mixtures did not increase microbial diversity nor assembled distinct microbial communities as compared to monocultures.

Conclusions:

Although distinct cover crop species had disparate effects on the soil microbiome, cover crop mixtures did not assemble a markedly distinct soil microbiota as compared to monocultures.

Long-term Management Practices Promoting Plant Species Richness May Improve Stability of Ecosystem Functions to Drought

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Aim: Drivers such as land use change and increased climate extreme frequency have led to a reduction in grassland biodiversity globally. Experimental evidence suggests a positive impact of biodiversity on the stability of numerous ecosystem functions but there is little research describing this relationship under field conditions, especially for long term experiments. If this relationship holds true for real world environments it would have huge implications for the protection and management of future grasslands. Here, I use a long-term (30 year) grassland study site applying treatments to promote plant species richness to determine if they lead to an increase in stability of ecosystem functions as measured by temporal stability as well as resistance to and recovery from drought. **Method:** Using treatments which produced the largest difference in plant species richness over 30 years (addition of seed and cessation of fertiliser), I measure pools of plant available and microbial carbon, nitrogen and phosphorus as well as greenhouse gas fluxes and enzyme activity fortnightly for a period of 5 months to assess temporal stability. Further, an imposed 6-week drought event in summer also allowed for analysis of resistance and recovery. **Results:** Preliminary analysis of CO₂ fluxes indicates that treatments with low species richness suffered a reduction in temporal stability under drought, measured as the inverse coefficient of variation, when compared high species richness control treatments which remained stable. **Conclusions:** Long-term management strategies targeting the improvement of plant species richness may promote stability of ecosystem processes and therefore resilience to future environmental perturbations.

Soil-borne fungal pathogen diversity and host selectivity in a grassland community

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Aim:

Soil-borne pathogens are thought to drive plant community dynamics, controlling dominant plant populations and promoting plant diversity. Despite this important function, there's little knowledge about the diversity of pathogens in natural habitats and the factors that determine their effects on plant performance. We aimed to characterize the soil-borne fungal pathogens in a grassland community and reveal how their colonization of, and impacts on different plant species depend upon the plant diversity context.

Method:

We planted forb and grass phytometers in 105 experimental 70×70 cm grassland plots with varying levels of plant species and functional richness, in the context of a long-term biodiversity experiment. After three months, we measured the specific plant biomass in each plot and profiled fungal communities in roots of phytometer and resident plants, as well as in bulk soil. We investigated the relationship between the occurrence of putative fungal pathogens and measures of plant richness, composition, and productivity.

Results:

Fungal communities in roots of phytometer and resident plants were primarily determined by host plant identity, with forbs and grasses assembling distinct communities, and were comparably little affected by plant richness. Likewise, host identity drove the occurrence of selected, dominant fungal pathogens in phytometers, but in this case the composition of resident plant communities also significantly predicted pathogen abundance.

Conclusions:

Our results show that plant community composition is an important determinant of the local distribution of soil-borne fungal pathogens in grassland communities. The links between the occurrence of such pathogens and grassland primary productivity will be discussed.

Understanding the role of the soil microbiome on soil health in a young almond orchardKelsey Fenn¹, Joshua Garcia¹, Cristina Lazcano¹, Mallika Nocco¹¹*University of California, Davis, Davis, United States*

Aim: In California, 660,000 hectares of soil are occupied by almond orchards, giving almond growers substantial opportunities to achieve long term soil health and biodiversity throughout the state. Biological soil indicators, such as microbial respiration and active carbon, have increasingly been included in assessing soil health. However, a knowledge gap still exists in understanding how the diversity and potential function of the microbiome can be related to soil health indicators. We hypothesize that the soil microbiome is linked to soil health in perennial orchard systems by providing nutrition, drought resilience and carbon storage throughout the lifetime of an orchard. The objective of our study was to determine how soil health corresponds to the microbiome in the surface and subsurface soil layers of a young almond orchard.

Method: We collected soil cores from 24 locations throughout the orchard in depth layers at 0-15 cm, 15-46 cm, 46-76 cm, and 76-122 cm. A comprehensive assessment of soil health was performed for physical, chemical, and biological indicators. The microbiome was characterized by using fungal and bacterial gene markers and measuring extracellular enzyme activity.

Results We suggest biological soil health indicators illuminate how biotic communities affect soil function in an orchard system throughout the soil profile.

Conclusions: Few studies examine biological soil properties deeper than 30 cm where roots systems are present. Assessing these parameters up to 76 cm provides an often understudied opportunity to assess how microbial communities impact subsoil layers and what influence they have on the biogeochemistry of achieving healthy soils.

Impact of Long-term Phytomanagement of Cu/Pb Mine Tailings on Soil Biochemical Functionality

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Aim: The study evaluates the long-term effects on soil functionality of different phytomanagement options in a former Pb/Zn mine (Rubiais) established in the frame of the PhytoSUDOE and Phy2SUDOE (SOE4/P5/E1021) projects in the temperate-humid zone of Spain.

Methods: The long-term influence of willow (*Salix smithiana* Willd) plants, either as monoculture or intercropped with alder (*Alnus* sp.), and soil amendments based on organic residues (green compost) or inorganic fertilization (NPK) on several soil enzyme activities was evaluated in samples collected in 2021 from field trials established in 2011 in a Pb/Zn/Cd contaminated site. Results from phytomanaged soils are compared with those obtained in unplanted soils, untreated or treated with compost.

Results: In the absence of compost amendment, the soil enzymatic activities in the willow monoculture plots (with near neutral pH) tended to be even lower than in the unplanted plots. The addition of compost led to an increase in soil organic matter and in all enzyme activities. The highest values were observed in compost amended plots cultivated with willow in co-cropping with alder. When activity values are expressed per carbon unit, the positive effect of compost tended to disappear, except in intercropped plots.

Conclusions: The addition of green compost combined with intercropping of willow (*S. smithiana*) with alder (*Alnus* sp.), appears to be a suitable management to increase and maintain in the long term the functionality of mine tailings soils contaminated with Pb, Zn and Cd and with pH close to neutrality.

Nematode Biodiversity and Community Structure under Heavy Metal Stress in an Irish Mining Site

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Aim:

The aim of this study was to observe the effects of heavy metal (cadmium, lead and zinc) contamination on terrestrial nematode biodiversity and community structure in Silvermines, Co. Tipperary, in Ireland.

Method:

Four contaminated sites were sampled in the area over three years (2008, 2009, 2010) and the nematode biodiversity and community were analysed from the upper soil layer (0-20 cm); a non-contaminated site was also sampled, approximately 5 miles away from the core contamination area. Nematodes were identified morphologically and various ecological indices were calculated.

Results:

Significant differences in soil variables (soil moisture, organic matter content, pH and heavy metal levels) were detected between the contaminated and non-polluted sites. Similarly, there were significant changes in nematode community in correspondence to the levels of contamination and the soil conditions. Nematode biodiversity in Silvermines was detrimentally affected by high levels of cadmium and zinc (compared to that at the non-contaminated site), but not by lead. In total 57 species of 56 genera were identified, belonging to 27 families of nine orders. Changes in the structure of functional groups did not relate to the heavy metal contaminants under investigation.

Conclusions:

The total maturity index (\square MI), the total maturity index 2-5 (\square MI2-5), the fungivore/bacterivore ratio (f/b), and the % c-p groups were found to be good indicators for temporal soil recovery from heavy metal contamination in the investigated area. These findings are significant, especially in the context of the Silvermines Rehabilitation Project.

Long Term Tillage Changes Size and Structure of Prokaryote Communities in a Chernozem Soil

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Aim:

Assess the effects of tillage upon size and structure of soil prokaryote communities in the context of a temperate climate agroecosystem under maize monocrop.

Method:

We investigated a long term tillage experiment located in the Eastern Romanian Danube plain. The experiment was established in 1976 and comprises three treatments: no till, disk and mouldboard plough. Microbial biomass carbon measured through fumigation direct extraction was used as an indicator for community size. Diversity and composition of Archaea and Bacteria communities were measured through 16S rRNA gene amplification followed by Illumina MiSeq sequencing.

Results:

Our findings show that in the case of topsoil (0-20 cm) there is significantly less microbial biomass carbon across the tillage disturbance gradient. Furthermore, the increase in microbial biomass that characterizes no till treatment can be observed even in the case of subsoil (20-50 cm), way below the ploughed layer.

We also found that there were no differences across treatments when diversity indexes (Richness, Shannon Diversity and Evenness) were calculated at the ASV level. However, when indexes were calculated at phylum level, we noticed higher richness coupled with lower Shannon evenness in the case of no till. NMDS ordination followed by PERMANOVA test revealed distinct prokaryotic communities among all three tillage systems.

Conclusions:

Community size and composition differ among various tillage treatments. Contrary to findings of other scholars, in our experiment Shannon evenness at phylum level was found to be lower for no till.

Soil eDNA shows promise as a method for terrestrial mammal surveys

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Aim: A wide variety of methods for surveying terrestrial mammals have been developed, including conventional live traps, line transects, thermal imaging, camera traps and track and sign surveys. However, these methods can be invasive and are typically time-intensive, leading to high associated costs per unit sample effort. In recent years, water bodies have proved to be a good source of environmental DNA (eDNA) to detect terrestrial mammals inhabiting a watershed using metabarcoding. This method has been found to detect more species at lower costs compared to conventional methods, but is only useful in areas where there is a suitable water body present. **Method:** In this study we collected both woodland soil and pond water samples for eDNA analysis from open and closed canopy woodland habitats at each of three sites at six timepoints. Cameras were installed to provide a complementary method of woodland mammal detection. **Results:** The overall number of taxa detected was the same in water and soil samples, but there were some differences in what taxa were detected, and fewer water samples were needed to detect that number of species. **Conclusions:** This demonstrates the potential for using soil DNA for mammal surveys in areas where water sources are not present. Further research is required to optimise sampling strategies.

Global diversity of viruses in legume nodules is driven by dominant nitrogen fixing symbiont

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Environmental phages have been shown to heavily affect biogeochemical cycles and to use laterally transferred genes to control host metabolism in aquatic environments. Based on surveys of phage genomes in other environments, the current paradigm is that phages may have a similar role in soil, rhizosphere, hydrothermal vents etc., and are therefore important players which may affect and be affected by microbial diversity and environmental parameters.

Here we present a surprising discovery of phage communities in nitrogen-fixation nodules of the legume chickpea (*Cicer spp.*), which display a biogeographic signal across eight countries in four continents. This signal is likely related to the dominant nitrogen-fixing bacterial phylotype which is at least in part determined by agricultural management practices, and is recruited from the surrounding soil or inoculated during sowing. Roughly a third of the nodules contained phage communities. The low diversity of those communities likely reflects the microbial diversity of potential hosts within the nodule.

The diversity of phage communities identified in a single country or in two or more countries ranged from a single phage to almost 40. The highest phage richness was identified in Ethiopia and India, where agricultural management is minimal. Three phages were identified in every country sampled, implying potential vertical transmission. Roughly one third of the phages identified were lysogenic.

Although nodules often contain a microbial community, these phages likely infect *Mesorhizobium*, the nitrogen-fixing bacteria associated with chickpea, as the dominant strain of *Mesorhizobium* has a significant effect on the phage community composition within a nodule. While the exact role phages play in the structure and function of the nodule microbial community, their consistent presence, seemingly counterproductive to the symbiosis of nitrogen fixing bacteria and plant, implies that they are not destructive to the nodule.

Soil Mesofauna Biodiversity State of Knowledge in Last Decade Revealed by a Bibliographic Study

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Aim: Evaluate the research effort dedicated to soil mesofauna in the last decade in the world.

Method: A bibliographic study was carried out based on the search in the Web of Science database for soil mesofauna, Collembola, soil mites, Enchytraeidae and Symphyla and possible similar terms, between 2011 and February, 2022. A database was built in PostgreSQL, and connected with the R statistical program enabling customized queries with keywords of interest and elimination of redundant articles. The Microsoft Excel version 2019 was used to build graphs and maps based on analysis of 1812 article records of authors from 65 different countries. **Results:** The top 20 countries with the highest number of publications account for 82% of the scientific production on the subject. USA leads the ranking with 174 publications, with almost 10% of the records, followed by Brazil, China, Spain, Germany, France, Italy, Poland, Australia and the United Kingdom. Collembola is the most studied soil mesofauna group with 56% of the studies, followed by soil mites with 38% and Enchytraeidae with 5.6%. The main objectives of the studies were related to bioindication, soil quality assessment and ecotoxicology. **Conclusions:** Large geographic gaps in knowledge of soil mesofauna biodiversity were observed, as well as a large disparity in the number of publications between the groups surveyed.

Effect of Nitrogen Source, Rate and Timing on Soil Bacterial and Fungal Communities in Soybean

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Although soybeans (*Glycine max* [L.]) form a symbiotic relationship with *Rhizobium japonicum* bacteria, enabling N fixation, additional N fertilizer is routinely applied to increase yield and protein content in seed. The aim of this study was to determine the effects of N source, rate and timing on soil microbial communities in a soybean crop and identify potential feedback on plant and soil health. Method: Trials were conducted in 2017-2019 to evaluate different N fertilizer sources (ammonium nitrate AN, ammonia sulphate AS, urea), rates (0, 30, 50 or 70 kg N ha⁻¹) and timing (R1 beginning bloom or R3 beginning pod). Soils were analysed for NH₄/NO₃, total C and N, and Mehlich extractable nutrients at seeding, R5 (beginning seed) and harvest. Bacterial and fungal communities were assessed using 16S and ITS1 amplicon sequencing. Results: The N source and rate had a significant effect on soil NH₄, NO₃, total N, pH at 0-15 cm at the R5 sampling stage. The application timing also had an effect on NH₄ at R5 and NH₄ and NO₃ at harvest. For the microbial communities, there was a significant effect of N source on 16S Shannon diversity with urea treatments having higher diversity than AN and AS. For the fungal communities, timing and N source had a significant effect on the number of ITS OTUs observed, Chao and ACE estimates, but not on Shannon diversity indices. Microbial community data is being further explored for effects on predicted bacterial and fungal functional groups using FAPROTAX and FUNGuild.

Monitoring the Soil Microbial Diversity in Young Florests

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: Characterize and monitoring the soil microbiome of a reforested area from planting up to five years. Test whether there is an association between tree species and microbiome diversity and its contribution for the sequestration of carbon.

Method: A total of 80 soil samples from 64 reforest locations (experimental group) and 16 non-reforest locations (control group) from Mangualde (Viseu) were collected. The species of the reforest locations differentiate between Pine and Quercus and only Pine, and all sampled sites were examined at two different depths (10-20 and 20-30 centimeters). The DNA was extracted with Qiagen DNeasy PowerSoil following manufacturer's instructions, and the taxonomical profile of each sample was assessed through metagenomics sequencing of 16S, 18S and ITS rRNA gene, using a standard library preparation protocol with subsequent analysis through QIIME v.2-2022.2 pipeline.

Results: In control samples a total of 257 archaea and bacteria, 88 eukaryota and 195 fungi were identified, and the most abundant bacteria, eukaryota and fungi were Conexibacteraceae and Solibacteraceae; *Magnoliophyta* and Alphaproteobacteria; *Penicilium* and *Martierella*, respectively. The analysis of microbial diversity among samples and depths was performed, indicating a significative difference in the fungal microbiome between samples, and a higher microbiome diversity in the samples collected from 10 to 20 centimetres of depth.

Conclusions: This study was able to characterize the non-reforest soil microbiome and found differences in the microbiome diversity between depths. However, more samples need to be processed to compare these results with reforested soil samples and see if there is correlation with replanted species.

Bacterial colonization shaped by soil texture and OM type during early-stage soil structure formation

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Aim: The interactions among microorganisms, organic matter (OM) and minerals in soil play important roles in aggregate formation. However, little is known about these interactions because of the inherent complexity of soil. We aimed to test the effects of soil texture and OM type on the development of the bacterial community during soil aggregation.

Method: An artificial soil incubation experiment was conducted with different mineral compositions to simulate different soil textures (clay loam, loam and sandy loam) and OM types, including bacterial necromass (*Bacillus subtilis*) or milled hay litter as particulate organic matter (POM) of different size (POM: 0.63–2 mm, sPOM: < 63 µm). The bacterial community abundance and structure were determined after 30 days of incubation by real time PCR and Illumina sequencing of the 16S rRNA gene.

Results: The abundance of the bacterial community in the clay loam was significantly lower than in the loam and sandy loam, indicating a weaker bacterial proliferation in clay loam. No effects of soil texture on the structure of the bacterial communities were determined. Adding necromass resulted in a bacterial community with high abundance and low diversity; adding POM resulted in a community with low abundance and high diversity; adding sPOM supported an intermediately sized and composed community.

Conclusions: OM types exerted stronger effects on bacterial 16S rRNA gene abundance and diversity compared to soil texture. The species and complexity of OM was the main determinant of bacterial development in soil, which in turn can influence aggregate formation.

Can Mathematical Corrections Compensate Differences of Earthworm Biodiversity Estimations Issued from Different Sampling Methods?

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Assessing earthworm biodiversity at wide geographical scales relies on meta analysis of existing data and new large scale surveys. But those sources often rely on different sampling methods which may not give comparable results. Previous studies have already explored differences on abundance, biomass or functions of communities sampled with different methods and how they respond to different cultural practices. In this study we focus on the ability of two sampling methods based on ISO standard (ISO 23611-1:2018) to characterize biodiversity. We explore if mathematical corrections developed to overcome sampling bias in biodiversity estimations allow for a better comparison between them. We open perspectives for future earthworms biodiversity surveys. We used data which were recorded during previous projects and we compared i) hand sorting (HS method) of soil monoliths and ii) chemical extraction (formaldehyde) followed by hand sorting of soil monoliths (CE method). Both methods were applied simultaneously on the same plots, The dataset comes from different studies covering 31 plots distributed on 7 different sites in France. They were sampled in 2013, 2014 and 2017. The plots cover different soil uses: grassland, crop field, agroforestry, orchard and forest. Our study showed that chemical extraction associated with hand sorting (CE) better captures rare species (low abundance) and observed richness value is close to the asymptotical one: CE seems to provide a good estimation of true richness. Our results highlight that merging data issued from different sampling methods may induce bias in data analysis. Standardization to a fix sample size improves the concordance of species richness estimation. Despite the fact that Shannon and Simpson diversity are more consistent between methods even without correction, we should have expected a better correlation because these metrics are considered as not very sensitive to sampling effort. Simpson diversity index, especially, shows an overestimation in HS compared to CE for the most diverse communities. This ends to different community structure evaluation by the two sampling methods. Anecic species as well as *Octolasion cyaneum* are the most frequently missing taxa in HS as compared to CE. Considering those results, chemical extraction (AITC replacing formaldehyde) followed by hand sorting should be favoured in surveys aiming at measuring earthworm biodiversity.

Recovery of Ectomycorrhizal Fungi Community during Natural Forest Regeneration after Barkbeetle Induced Dieback

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Aim:

Between 2004 and 2008, a forest dieback in the Plešné lake watershed (National Park Šumava, Czech Republic) caused by barkbeetle outbreak resulted in >90% loss of Norway spruce trees accompanied by a decrease of abundance of ectomycorrhizal fungi (EMF). The advance of natural forest regeneration is variable due to the legacy of pre-disturbance forest structure and microsite heterogeneity. Thus, a gradient from open sites with retarded regeneration, through places with high density of young trees to fragmented remnants of survived mature forests occurs within the catchment. We asked whether is the forest succession mirrored in EMF community composition.

Method:

In 2019, we sampled soil DNA at 41 sites within the catchment and identified soil fungal community composition.

Results:

The relative representation of EMF within the fungal community ranged from ~2% in the plots with the least successful regeneration to >70% in the survived forest fragments. The EMF proportion was positively related to amount of survived (or grown-up) mature trees and/or regeneration density. While species richness was positively related to density of mature trees, the EMF species composition was not substantially and unequivocally driven by the grown trees and regeneration counts.

Conclusions:

Within this highly heterogeneous catchment ecosystem, EMF community composition is probably determined by micro-site specific properties including pre-disturbance state and history rather than sole stand progression within the forest-life cycle. The heterogeneous forest resulting from natural regeneration ensured by non-intervention regime provides wide variety of microhabitats that allows maintaining diverse EMF community even after stand replacing disturbance.

The German National Center for Biodiversity Monitoring: Ongoing Work on Soil Biodiversity

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Aim:

The German National Center for Biodiversity Monitoring exists since spring 2021 and is affiliated with the Federal Agency for Nature Conservation. The German Monitoring Center was commissioned by the German government with the advancement of the nationwide biodiversity monitoring. For this purpose, it is developing an overall concept in interagency coordination and close cooperation with the stakeholders involved from monitoring practice, science, nature conservation associations, state and federal authorities. In the future, this will allow for more comprehensive and nationwide statements on the status and trends of biodiversity in Germany and create the data basis for researching the causes of biodiversity changes as well as developing measures for conservation and monitoring their success.

Method:

The German National Center for Biodiversity Monitoring has convened an expert committee "Monitoring of Soil Biodiversity and its Functions" that is currently developing basic principles and criteria as well as initial proposals for the establishment of nationwide basic monitoring modules of soil biodiversity.

Results:

The results from the two-year work of the expert panel will be published at the end of 2023, when the establishment phase of the Monitoring Center is completed. The results will be incorporated into the overall concept for a nationwide biodiversity monitoring.

Conclusions:

In Germany, the monitoring of soil biodiversity and its functions has not yet been integrated into a systematic cross-national environmental monitoring and the identification of synergy potentials of existing monitoring programs is a field of work of the expert panel.

COI Metabarcoding of Soil Oomycetes Associated with Industrial Hemp Production in Southcentral Pennsylvania, USA

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Aim:

The reemergence of industrial hemp cultivation in Pennsylvania after a roughly 80-year absence poses novel challenges for disease management under modern, sustainable agricultural conditions. While hemp is susceptible to multiple root and foliar diseases, this project focuses on soilborne oomycetes, which are associated with pre- and post-emergent damping off of seeds and seedlings. The aim of this study is to establish a baseline assessment of oomycete biodiversity associated with industrial hemp production utilizing culture-based and environmental DNA sequencing methods.

Method:

Six production areas were selected for study and included both fiber and CBD hemp cultivars. Soil samples were collected prior to planting and approximately mid-season; soil nutrient levels were determined for pre-planting samples. Oomycetes were directly baited from soil samples, grown on selective agar, and identified using mitochondrial COI sequencing. In addition, bulk environmental DNA was extracted in duplicate from all soil samples for high-throughput Illumina sequencing of the COI barcode utilizing optimized oomycete-specific primers.

Results:

Culture-based identifications revealed an abundance of common soil *Pythium* species, such as *P. heterothallicum* and *Phytophthium vexans*, which are not known to cause significant disease. Other abundant species such as *P. ultimum* and *P. irregulare* are known to cause root rot in other hosts and may be important potential pathogens to monitor in hemp. COI metabarcoding analysis is ongoing and will be analyzed in conjunction with soil chemical data.

Conclusions:

Given the growing interest in industrial hemp production, this study provides crucial baseline data on soilborne oomycetes and their potential impacts on yield.

Effects of pristine and UV-aged polyethylene microplastics on the survival and reproduction of soil mesofauna

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Aim:

The persistent residence of microplastics (MiPs) in soils is of increasing concern, yet little is known about their impacts on soil fauna. In this study we explored the impacts of pristine and UV-aged polyethylene (PE) particles at environmentally relevant concentrations on soil mesofauna (enchytraeids and collembolans) in a microcosm incubation experiment.

Method:

We exposed 10 individuals of *Enchytraeus crypticus*, 10 *Folsomia candida* and 20 *Proisotoma minuta* to pristine and UV-aged PE (40–48 µm) added to an organic farm soil at concentrations of 0, 0.2, 2, 20, 200 and 2000 mg/kg to assess their survival and reproduction rates.

Results:

We observed a general decrease in survival but an increase in reproduction of *E. crypticus* when exposed to both pristine and UV-aged PE. In contrast, *F. candida* showed the opposite response, with increased survival and decreased reproduction rates when growing in the MiP contaminated soils. Despite these trends, significant effects of MiPs exposure were observed for *P. minuta* only, with 34% and 31% survival rates at 20 mg/kg UV-aged PE and 2000 mg/kg pristine PE, respectively, and reproduction rates of 39% at 200 mg/kg UV-aged PE, respectively. After 28d incubation, we found significant differences in survival and reproduction was found when comparing the endpoints between each species across all of the species and for both PE types.

Conclusions:

Our results suggest that MiPs have contrasting effects on individual species of soil mesofauna, which need to be taken into account for understanding the effects of plastic pollution on soil population dynamics and community structure.

Which bacteria from soil and earthworm microbiomes are producers of phytohormone-like molecules under coffee?

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Earthworms are known to stimulate plant growth. This stimulation is the result of their interactions with soil microorganisms. The aim of this work is to determine which bacteria are producers of phytohormone-like molecules, using data that were generated from the study of the bacterial and metabolic diversity in different soil compartments with and without earthworms (*Pontoscolex corethrurus*) under two coffee species (*Coffea arabica* and *C. canephora*). The bacterial and metabolome diversity were studied in the bulk and rhizosphere soils and in the earthworm gut content and casts. The bacteria were identified through 16S rDNA amplicon sequencing on a MiSeq Illumina platform. The bioinformatic analysis of sequences was performed in QIIME2. The presence and abundance of phytohormone-like compounds were determined by untargeted metabolomic analysis based on accurate mass spectrometry (UPLC-MS-QTOF) of soil samples from the four sites. The identification of bacterial taxa producing phytohormone-like molecules will be done with the review of libraries that refer to bacteria and their respective phytohormone-like molecules production. Up to now we have the database of the bacteria diversity in the different soil compartments as well as the metabolic profile. From this we have notice already the presence of these bacteria *Bacillus*, *Pseudomonas*, *Sphingomonas* which are hormone-like producers. In the metabolic profile we putatively identified phytohormone-like compounds as dioxindole-3-acetic acid, hydroxyindole-3-acetic acid (E)-ribosylzeatin 5' - phosphate and dihydrojasmonic acid in the gut content. The review of the libraries is in process, and we expect to make the relation between these compounds and the bacterial taxa present that should produce them. These results will bring more clarity to explain how the presence of earthworms promote the plant growth.

Effect of Bioinoculants and Biochar on Grapevine-Associated Soil Microbial Communities

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Aim:

To assess the effect of microbial inoculants and biochar on the structure and diversity of fungal and bacterial communities colonizing the rhizosphere of grapevines planted in a new vineyard in the North of Portugal.

Method:

Alvarinho grapevines grafted onto R110 rootstocks were planted in pots containing 8L of substrate and 10% of biochar. Grapevines were inoculated with a mixture of the plant growth promoting rhizobacteria (PGPR) *Pseudomonas fluorescens* S3X and *Pseudomonas* sp. EAV and the arbuscular mycorrhizal fungi (AMF) *Rhizophagus irregularis* (INOQ Agri, Germany) according to the following scheme (5 replicates): C - control (without inoculation and/or biochar); B – PGPR; F - AMF; MIX – PGPR+AMF; Ch – biochar; ChB – biochar+PGPR; ChF – biochar+AMF; ChMIX – biochar+PGPR+AMF. Pots were maintained under greenhouse conditions for 1 yr and transplanted to the field. After 2 years, composite soil samples were collected from the rhizosphere of each grapevine and the fungal and bacterial communities analysed using Illumina MiSeq sequencing.

Results: The most abundant phyla were Ascomycota and Basidiomycota, for fungi and Proteobacteria, Actinobacteria, Planctomycetes and Bacteroidetes for bacteria. The inoculation of AMF decreased both the diversity and the equitability of rhizospheric fungal communities. Biochar and the Mix bacterial inocula influenced the diversity of the fungal communities, however no effect was observed for bacteria. The structure of both microbial communities was significantly influenced by biochar addition and bioinoculation.

Conclusions: Grapevine-associated microbial communities showed high genera diversity. In general, the applied microbial inocula and/or the supplementation with biochar influenced the structure and diversity of the microbial communities colonizing the rhizosphere of grapevines grown under field conditions.

Diversity and ecology of the *Dendrobaena* genus (Oligochaeta: Megadrili) from IranRobabeh Latif², Atabak Roohi Aminjan³, Maria J I Briones¹¹University Of Vigo, Vigo, Spain, ²Semnan University, Semnan, Iran, ³Bu-Ali Sina University, Hamedan,**Aim:**

To date, seven species belonging to the *Dendrobaena* genus have been described in Iran, which show high intraspecific variability. Therefore, the aim of this study is to gain ecological knowledge about this lumbricid genus, with the widest geographical distribution in Iran.

Method:

The georeferenced information of all sampling sites was obtained using the global positioning system (GPS). The distribution models were constructed based on five bioclimatic variables from Worldclim (<http://www.worldclim.org>).

Results:

Mean Temperature and Mean Temperature of Coldest Quarter were the best predictors of species occurrence. Accordingly, the most suitable habitats for the Iranian *Dendrobaena* species are limited in Northwest regions of the country and restricted to Mountainous areas.

Conclusions:

Low temperature oscillations may have promoted population sizes in those areas with more precipitation in. Probably another reason for the higher abundance of these species in these regions is their low active dispersal capabilities and the effect of mountains as physical barriers.

Two distinct ecological behaviours within anecic earthworm species in temperate climates

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Aim: We present a comprehensive review of the scientific literature and synthesize the relationships between anecic earthworms and plant-derived materials in temperate climates, focusing on the distinctions between *Lumbricus centralis* (Bouché, 1972), *Lumbricus terrestris* (Linnaeus, 1758), *Aporrectodea longa longa* (Ude, 1885) and *Aporrectodea giardi* (Ribaucourt, 1901), four of the most widespread and studied anecic species.

Method: The following combinations of keywords were used in the ISI-Web of Science research database: (“lumbricus centralis” OR “lumbricus terrestris” OR “aporrectodea longa” OR “aporrectodea giardi”) AND (feed* OR plant* OR organic matter* OR mass* OR weight* OR growth* OR burrow* OR gallery*) which returned 1272 publications. After carefully checking all generated results, 102 references published between 1963 and 2022 were selected.

Results: In this review we highlight that within anecic earthworms, *Lumbricus* anecic species (here after “LAS”) mainly consume fresh plant-derived materials on the soil surface modifying the quantity and spatial organisation of said materials. By contrast, *Aporrectodea* anecic species (here after “AAS”) consume mainly aged plant-derived materials already incorporated into the soil and only a small proportion of surface-available plant-derived materials. Linked to this contrasting feeding behaviour, we highlighted that AAS have a denser and more complex burrow network than LAS. This burrowing behaviour suggest that AAS burrow into the soil to search for soil organic matter incorporated in the soil whereas the LAS essentially focus on burying the surface litter into their burrow. Consequently, LAS seem to benefit from easily assimilated elements, grow faster and reach maturity in a shorter time span than AAS species.

Bacterial and Macro/mesofauna Diversity of a Portuguese Mine Tailing

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Aim:

- Assess the culturable metallophyte-associated bacterial strains and macro and mesofauna diversity in a Portuguese mine tailing
- Characterize the plant-growth promoting traits of the most metal- tolerant bacterial strains

Method:

Culturable bacteria were isolated from the rhizosphere of the five most abundant metallophytes (*Agrostis capillaris*, *Cytisus striatus*, *Erica arborea*, *Pinus pinaster*, *Rubus ulmifolius*, and *Salix caprea*) of the mine tailings. Thirty-seven strains were identified by 16S rRNA sequencing and their tolerance to Cu, Cd, and Zn was assessed. The most tolerant strains were screened for various growth-promoting traits, such as the production of siderophores and indoleacetic acid (IAA), ACC-deaminase activity, and phosphate solubilization capacity. For the best-performing strains, GenIII Microplates™-Biolog were used to complete their characterization. To evaluate the effect of metal contamination on the mesofauna and macrofauna diversity, pitfalls traps were set up in the mine tailing and in a reference zone near the mine.

Results:

Over 80% of the bacterial strains were Gram-positive, with 45% being Bacilli. Along with *Bacillus*, the most predominant genera were *Pristea* sp., *Arthrobacter* sp., *Rhodococcus* sp. and *Burkholderia* sp. All bacterial strains were able to produce IAA and siderophores, but only 50% showed ability to solubilize P. A higher macro and mesofauna diversity was obtained in the reference zone when compared with the tailing, although the number of individuals was higher in the latter.

Conclusions:

Mine tailings harbor a high bacterial diversity, with most of the strains presenting plant-growth-promoting traits. These strains can be used for bioaugmentation under phytoremediation approaches. Macro and mesofauna diversity was affected by metal contamination, with the tailing presenting the most tolerant species.

Temporal response of organic matter indices in semi-arid biomes in Benfontein Nature Reserve, South Africa

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Aim:

The aim of the study was to investigate temporal changes of the selected soil organic matter (SOM) indices *viz* soil carbon (C), nitrogen (N), C:N ratio and microbial biomass (MB) in the Benfontein Nature Reserve which hosts a wide range of ecological diversity.

Method:

Benfontein Nature Reserve has three major biomes namely Nama-Karoo, Savanna, and Grassland. These biomes have unique different ecological systems with similar climatic conditions. Soil samples were taken in 2022 in all three biomes during autumn and winter of 2022, within two soil layers (0-10 and 10-20 cm) to investigate the selected SOM indices namely SOM, soil C and N and MB.

Results:

Generally, the Grassland biome had higher values for SOM, total C and N, and C:N ratio in both soil layers when compared to the other two biomes for both seasons. This can be attributed to grasses with a significant root system in this biome. Lower values for MB were found in the Grassland biome for both seasons due to elevated C:N ratio values. Conversely, elevated values for MB were found in the Savanna biome probably due to N from the seed pods of the *Acacia erioloba* trees stimulating microbial activity. Lower values for all SOM indices were found in the deeper soil layers, particularly in the Savanna biome.

Conclusions:

The Grass biome had higher values of the SOM, total C and N as well as higher C:N ratios. Higher MB were found in the Savanna biome. This study is still under further investigation.

How to model and map soil biodiversity patterns and functions across Europe with Minotaur project

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Aim:

This work reports first results of Minotaur project (within European Joint Program SOIL) that aims to provide models, maps and policy-relevant indicators with validated reference values for monitoring soil biodiversity and associated functions in relation to climate change. In particular the selected harmonized indicators were described with referred data and metadata, sampling and first results from 11 long term (at least 10 years) cereal experiments (LTE) across Europe were reported, to relate climate and soil types with soil cultivation practices and fertilization types.

Method:

Validation of selected indicators with targeted measurement was assessed by experimental design with randomized parcels in LTE. The protocol provides samples to assess microbiota, -micro -meso and -macrofauna with indicators related to ecosystem functions, as regulation of SOC, nutrients and water, and disease suppression, by soil C and nutrients content, enzymatic activities, aggregate stability, soil infiltration and soil pathogens.

Results:

Sampling and soil fauna and flora extraction carried out in autumn 2022 were described. First results regarding effect of different tillage methods on abundance and community structure of microarthropods (QBS-ar) and density of earthworms, related to infiltration and aggregate stability, were reported. This results will be implemented in Minotaur inventory of soil biodiversity data sources, by a template with standardized metadata, compliant with Eudaphobase structure.

Conclusions:

This interdisciplinary approach, comparing selected indicators in LTE seems interesting to provide information for mapping and modelling soil biodiversity in Europe. Data are still in elaboration, promising to increase existing databases, using common metadata.

Rhizobacterial Isolates from the Metal Hyperaccumulator *Noccaea caerulescens* Growing in a Ni Enriched Soil

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Aim: The study is dedicated to analysing the diversity of cultivable bacteria in the rhizosphere of the metal hyperaccumulating plant *Noccaea caerulescens* growing in ultramafic soil. The aim of the work is contributing to the valorisation of the endemic biodiversity in metal enriched environments and was carried out in the frame of the project Phy2SUDOE (SOE4/P5/E1021).

Methods: Bacterial strains were isolated from the rhizosphere of individuals of the metal hyperaccumulating *Noccaea caerulescens* (J.Presl & C.Presl) F.K. Mey. collected in an environment naturally enriched in Ni (ultramafic substrate). The isolates were identified by partial sequencing of the 16S rRNA gene and the Ni tolerance and several plant growth promotion properties (PGP) were evaluated.

Results: The collection of isolates was dominated by members of the *Actinobacteria*, namely of the families *Micrococcaceae*, *Microbacteriaceae*, *Streptomyetaceae* and *Nocardiaceae* and *Alphaproteobacteria* of the family *Phyllobacteriaceae*. The genera more represented among the cultivated rhizobacteria were *Paenarthrobacter*, *Streptomyces* and *Mesorhizobium*. The PGP properties evaluated included the analysis of P solubilisation, the production of siderophores and ACC deaminase.

Conclusions: The analysis of the diversity of cultivable bacteria in the rhizosphere of a metal hyperaccumulating plant allowed to identify isolates with potential application in the phytomanagement of metal enriched or contaminated substrates.

The global fungal biodiversity, biogeography and ecology viewed through the high-throughput sequencing results

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Several areas of biodiversity research have been changed dramatically with the advance of high-throughput sequencing. Despite limitations, high-throughput sequencing is nowadays the most frequently chosen method to characterize fungal communities. Until late 2021, the papers utilizing high-throughput sequencing approaches to study natural habitats in terrestrial ecosystems worldwide, in total >500 studies, have yielded over 1.1 billion sequences of the primary mycological molecular marker, the ribosomal internal transcribed spacer contained in the GlobalFungi database <https://globalfungi.com>. With a conservative threshold for fungal species delimitation at 97% ITS sequence similarity, the total estimated fungal richness is 6.3 million taxa, mostly Ascomycota (57%) and Basidiomycota (37%). The highest alpha diversity of fungi is associated with soil and litter habitats followed by air, plant shoots, plant roots and deadwood. Based on the high-throughput sequencing data, the highest proportion of unknown fungal species is associated with samples of lichen and plant tissues. The meta-study of fungal communities in soil identified climate as the most important driver of different aspects of fungal biogeography. Climate not only was the primary constraint on the global distribution of vast majority of the most common fungi but also shaped fungal communities and their diversity. In contrast to plants and most other taxa, tropical diversity of soil fungi was found low, and most of their diversity is concentrated at high latitudes. Climate change may significantly affect ecosystem functioning because the climatic tolerances of mycorrhizal fungi, important for plant nutrition, appear to be significantly more constrained by climatic variables than plant pathogenic fungi.

How Divers are Enchytraeid Assemblages and What Does Drive Their Species-richness?

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Aim:

Enchytraeids play an important functional role, in particular, in acidic soils, where major groups of soil fauna, e.g. earthworms, are less dominant or even lacking. The aim is to give an overview about our knowledge on enchytraeid species richness and assemblage structure in soils and the environmental drivers responsible.

Method:

Own as well as literature data were used for a metanalysis providing an up-to-date overview of species richness, community structure, vertical distribution and densities in different types of terrestrial ecosystems. The effect of environmental variables available for sufficient numbers of sites was explored by statistical methods (ordination).

Results:

Whereas enchytraeids reach particularly high densities in acidic soils, their most diverse assemblages are found in soils with close to neutral pH. Soil moisture is clearly important, but relevant data for sampling sites (being more than mere snapshots for the time of sampling) are scarce. Rarely available but not to be neglected are salinity and soil texture. Land use is particularly important when connected to heavy disturbance (arable soils), where several disturbance-tolerant species dominate. Molecular barcoding has confirmed or revealed a number of cases of cryptic species, making the assessment of true species diversity difficult based on older literature data difficult.

Conclusions:

Enchytraeid diversity is higher than assumed and understudied in large parts of the world. The stress put on their importance in acidic soils has led to the false impression that they “prefer” these soils. Assemblages have rarely more than 30 species and their bioindication potential is rather high.

Author Index

A

<u>A. Harvey, J</u>	<u>286</u>	<u>ANGELI, N</u>	<u>579</u>
<u>Aagaard</u>	<u>465</u>	<u>Angulo-Pérez, D</u>	<u>395</u>
<u>Kristensen, J</u>			
<u>Aalders, L</u>	<u>249, 468, 531</u>	<u>Anne-Laure, P</u>	<u>413</u>
<u>Aares, K</u>	<u>204</u>	<u>Anslan, S</u>	<u>272</u>
<u>Abdala-Roberts,</u>	<u>395</u>	<u>Antoniello, L</u>	<u>418</u>
<u>L</u>			
<u>Abraham, L</u>	<u>242</u>	<u>Antoninka, A</u>	<u>261, 478</u>
<u>Abrahão, A</u>	<u>100</u>	<u>Antonio Gallardo</u>	<u>104</u>
<u>Abram, F</u>	<u>93</u>	<u>Antunes, A</u>	<u>338</u>
<u>Acedo, A</u>	<u>346</u>	<u>Antunes, L</u>	<u>247, 590, 246</u>
<u>Acin-Albiac, M</u>	<u>346</u>	<u>Anza, M</u>	<u>54</u>
<u>Adams, B</u>	<u>360, 412, 462,</u> <u>471</u>	<u>Aponte, C</u>	<u>620</u>
<u>Afkhami, M</u>	<u>430</u>	<u>Araqao, O</u>	<u>250</u>
<u>Aquirre-</u>	<u>448</u>	<u>Arassus, R</u>	<u>562</u>
<u>Gutiérrez, J</u>			
<u>Ah-Peng, C</u>	<u>416</u>	<u>Arcenequi, V</u>	<u>103</u>
<u>Aigle, A</u>	<u>140</u>	<u>Archidona-Yuste,</u>	<u>423</u>
		<u>A</u>	
<u>Akanwari, J</u>	<u>68</u>	<u>Ardichvili, A</u>	<u>344</u>
<u>Albracht, C</u>	<u>165, 488</u>	<u>Arellano, E</u>	<u>155</u>
<u>Aleihela</u>	<u>551</u>	<u>Armesto, J</u>	<u>618</u>
<u>Yamannalage, A</u>			
<u>Alfaro, F</u>	<u>395</u>	<u>Arnedo, M</u>	<u>105</u>
<u>Alifriqui, M</u>	<u>204</u>	<u>Arrebola Díez, E</u>	<u>353</u>
<u>Allag, D</u>	<u>513</u>	<u>Arthikala, M</u>	<u>395</u>
<u>Allen, P</u>	<u>430</u>	<u>Ascher-Jenull, J</u>	<u>127, 545</u>
<u>Alteio, L</u>	<u>300</u>	<u>Ashton, L</u>	<u>116</u>
<u>Alvarez, D</u>	<u>482</u>	<u>Ashwood, F</u>	<u>184, 236, 277</u>
<u>Alvarez-Segura,</u>	<u>133</u>	<u>Asselberg, W</u>	<u>524</u>
<u>N</u>			
<u>Alves, D</u>	<u>315, 617</u>	<u>Astorga, M</u>	<u>155</u>
<u>Alves, M</u>	<u>611</u>	<u>Aubry, C</u>	<u>358</u>

<u>Amanor, Y</u>	<u>316</u>	<u>Auclerc, A</u>	<u>126, 344</u>
<u>Aminjan, A</u>	<u>613</u>	<u>Aupic-Samain, A</u>	<u>76</u>
<u>Amouroux, P</u>	<u>155</u>	<u>Averill, C</u>	<u>88</u>
<u>Ampt, E</u>	<u>574</u>	<u>Ayaga, G</u>	<u>568</u>
<u>Andrews, T</u>	<u>85</u>	<u>Ayuke, F</u>	<u>568</u>
<u>Angel, R</u>	<u>359</u>		

Á

<u>Álvarez-Jiménez, M</u>	<u>609</u>
---------------------------	------------

B

<u>Babczenko, P</u>	<u>208</u>	<u>Bever, J</u>	<u>528</u>
<u>Babin, D</u>	<u>414</u>	<u>Bezemer, T</u>	<u>210</u>
<u>Bače, R</u>	<u>601</u>	<u>Bharti, D</u>	<u>145</u>
<u>Bach, A</u>	<u>135, 136, 213, 169</u>	<u>Biancofiore, G</u>	<u>113</u>
<u>Bach, E</u>	<u>122</u>	<u>Biasioli, F</u>	<u>517</u>
<u>Baciarelli Falini, L</u>	<u>271</u>	<u>Bidartondo, M</u>	<u>537</u>
<u>Baeten, L</u>	<u>203</u>	<u>Bieluczyk, W</u>	<u>132</u>
<u>Baggs, E</u>	<u>133</u>	<u>Bigaran, F</u>	<u>535</u>
<u>Bagnara, G</u>	<u>247</u>	<u>Billings, S</u>	<u>528</u>
<u>Bahn, M</u>	<u>308</u>	<u>Bilton, A</u>	<u>571</u>
<u>Bajc, M</u>	<u>486, 584</u>	<u>Bird, S</u>	<u>529</u>
<u>Baker, K</u>	<u>122</u>	<u>Biryol, C</u>	<u>218</u>
<u>Baldoni, N</u>	<u>271</u>	<u>Bisot, C</u>	<u>187</u>
<u>Baldrian, P</u>	<u>225</u>	<u>Blair, J</u>	<u>605</u>
<u>Baldrian, P</u>	<u>88, 210, 627</u>	<u>Blanco-Romero, E</u>	<u>324</u>
<u>Baldy, V</u>	<u>76, 262</u>	<u>Blasbichler, H</u>	<u>158</u>
<u>Baldy, V</u>	<u>218</u>	<u>Blatrix, R</u>	<u>343</u>
<u>Balint, M</u>	<u>455</u>	<u>Blazewicz, S</u>	<u>512</u>
<u>Bálint, M</u>	<u>375</u>	<u>Blazewicz, S</u>	<u>474</u>
<u>Bálint, M</u>	<u>378</u>	<u>Bluhm, S</u>	<u>99</u>
<u>Ballabio, C</u>	<u>483, 281</u>	<u>Blum, J</u>	<u>171, 172</u>

<u>Ballasus, H</u>	<u>604</u>	<u>Bluoin, M</u>	<u>609</u>
<u>Balog, A</u>	<u>84</u>	<u>Bodelier, P</u>	<u>170</u>
<u>Bandian, D</u>	<u>418</u>	<u>Bodner, G</u>	<u>418</u>
<u>Banfield, J</u>	<u>474</u>	<u>Boekhorst, J</u>	<u>469</u>
<u>Baragaño, D</u>	<u>222</u>	<u>Bolger, T</u>	<u>137</u>
<u>Barantal, S</u>	<u>344</u>	<u>Bolton, E</u>	<u>238</u>
<u>Baratova, L</u>	<u>72</u>	<u>Bonato Asato, A</u>	<u>338</u>
<u>Baraza, E</u>	<u>560, 541</u>	<u>Bonfanti, J</u>	<u>240</u>
<u>Barber, N</u>	<u>122</u>	<u>Bonin, A</u>	<u>303</u>
<u>Barberán, A</u>	<u>502</u>	<u>Bonin, A</u>	<u>320, 307</u>
<u>Barcelo, M</u>	<u>181</u>	<u>Bonkowski, M</u>	<u>489, 488</u>
<u>Barclay, A</u>	<u>347</u>	<u>Bonomelli, C</u>	<u>155</u>
<u>Bardgett, R</u>	<u>262, 571</u>	<u>Booth, O</u>	<u>391</u>
<u>Bardgett, R</u>	<u>133</u>	<u>Borges, B</u>	<u>250</u>
<u>Bardgett, R</u>	<u>308</u>	<u>Borgmeier, A</u>	<u>462</u>
<u>Bardgett, R</u>	<u>564</u>	<u>Borruso, L</u>	<u>434, 350</u>
<u>Barel, J</u>	<u>319</u>	<u>Borsanelli, A</u>	<u>254</u>
<u>Baretto, C</u>	<u>277</u>	<u>Bosch, J</u>	<u>194</u>
<u>Barger, N</u>	<u>261</u>	<u>Bota, J</u>	<u>560</u>
<u>Barile, R</u>	<u>298</u>	<u>Botez, F</u>	<u>583</u>
<u>Barnes, A</u>	<u>211</u>	<u>Boulangé, A</u>	<u>125</u>
<u>Barois, I</u>	<u>609</u>	<u>Boulogne, I</u>	<u>389</u>
<u>Baronti, S</u>	<u>117</u>	<u>Bouraoui, D</u>	<u>384</u>
<u>Barot, S</u>	<u>344</u>	<u>Bourgault, P</u>	<u>501</u>
<u>Barré, P</u>	<u>102</u>	<u>Bourlat, S</u>	<u>323</u>
<u>Barreto, C</u>	<u>184</u>	<u>Bowker, M</u>	<u>261</u>
<u>Barros, R</u>	<u>484, 342</u>	<u>Bradford, M</u>	<u>390</u>
<u>Barsoum, N</u>	<u>585</u>	<u>Bradley, R</u>	<u>501</u>
<u>Bartrons, M</u>	<u>105</u>	<u>Bragato, G</u>	<u>271</u>
<u>Bartz, M</u>	<u>338</u>	<u>Brailey-Jones, P</u>	<u>493</u>
<u>Bashkir, D</u>	<u>399</u>	<u>Brajesh, S</u>	<u>395</u>
<u>Bässler, C</u>	<u>334</u>	<u>Brajesh K. Singh</u>	<u>104</u>
<u>Bastida, F</u>	<u>139, 342</u>	<u>Brand, M</u>	<u>344</u>
<u>Bastrakov, A</u>	<u>72</u>	<u>Branqarí, A</u>	<u>293</u>
<u>Battigelli, J</u>	<u>247, 529</u>	<u>Bråthen, K</u>	<u>204</u>
<u>Bautista, K</u>	<u>513</u>	<u>Brennan, F</u>	<u>65, 200, 93, 376, 112, 308, 403,</u>

			<u>402, 411, 417, 419</u>
<u>Beaumelle, L</u>	<u>333, 332, 217</u>	<u>Brennan, F</u>	<u>316</u>
<u>Becker, R</u>	<u>125</u>	<u>Brennan, F</u>	<u>405</u>
<u>Beenaerts, N</u>	<u>220</u>	<u>Brenzinger, K</u>	<u>170</u>
<u>Behr, J</u>	<u>414</u>	<u>Breuil, M</u>	<u>540</u>
<u>Beier, C</u>	<u>105</u>	<u>Breznikar, A</u>	<u>486</u>
<u>Beja, P</u>	<u>597</u>	<u>Briones, M</u>	<u>613, 607</u>
<u>Beja-Pereira, A</u>	<u>597</u>	<u>Brondani, M</u>	<u>562</u>
<u>Belda, I</u>	<u>395, 386</u>	<u>Brophy, C</u>	<u>411, 417</u>
<u>Belgrove, O</u>	<u>595</u>	<u>Brown, G</u>	<u>338, 555, 552, 247, 507, 590, 246</u>
<u>Belin, M</u>	<u>344</u>	<u>Brown, S</u>	<u>122</u>
<u>Bell, C</u>	<u>561, 547, 537</u>	<u>Bru, D</u>	<u>540</u>
<u>Bell, C</u>	<u>556</u>	<u>Brubaker, M</u>	<u>180</u>
<u>Bell, J</u>	<u>149, 175</u>	<u>Bruggink, J</u>	<u>162</u>
<u>Bell, N</u>	<u>249, 468, 531</u>	<u>Bruni, E</u>	<u>416</u>
<u>Bello Currás, D</u>	<u>573</u>	<u>Bruni, E</u>	<u>439</u>
<u>Benavente-Hidalgo, L</u>	<u>523</u>	<u>Bruni, E</u>	<u>415</u>
<u>Bender, L</u>	<u>610</u>	<u>Buck, R</u>	<u>122</u>
<u>Bender, S</u>	<u>458</u>	<u>Bucka, F</u>	<u>598</u>
<u>Bending, G</u>	<u>573</u>	<u>Bucur, D</u>	<u>282</u>
<u>Benoiston, A</u>	<u>333</u>	<u>Buée, M</u>	<u>579</u>
<u>Berard, C</u>	<u>389</u>	<u>Burslem, D</u>	<u>497</u>
<u>Berendonk, C</u>	<u>185</u>	<u>Burton, V</u>	<u>377</u>
<u>Berg, M</u>	<u>240</u>	<u>Buscot, F</u>	<u>304, 165, 334, 488</u>
<u>Berger, H</u>	<u>418</u>	<u>Buswell, V</u>	<u>347</u>
<u>Berry, L</u>	<u>123</u>	<u>Butt, K</u>	<u>184, 614</u>
<u>Bestion, E</u>	<u>333</u>	<u>Byrne, L</u>	<u>411, 417</u>
<u>Betta, E</u>	<u>517</u>	<u>Byrne, L</u>	<u>364</u>

C

<u>C. Pereira, E</u>	<u>561</u>	<u>Christian, N</u>	<u>367</u>
<u>Cabebe, G</u>	<u>242</u>	<u>Chuckran, P</u>	<u>261</u>

<u>Cabral Michel, D</u>	<u>593</u>	<u>Cilliers, S</u>	<u>466</u>
<u>Calderon Sanou, I</u>	<u>341</u>	<u>Clark, M</u>	<u>238</u>
<u>Calderon-Sanou, I</u>	<u>338</u>	<u>Clement, L</u>	<u>524</u>
<u>Calusinska, M</u>	<u>453</u>	<u>Cluzeau, D</u>	<u>102, 589, 599, 614, 284</u>
<u>Calzolari, C</u>	<u>113</u>	<u>Cocchiararo, B</u>	<u>378</u>
<u>Cameron, D</u>	<u>522</u>	<u>Coe, K</u>	<u>261</u>
<u>Cameron, E</u>	<u>217</u>	<u>Coelho, M</u>	<u>254, 507</u>
<u>Candia, P</u>	<u>155</u>	<u>Coelho, M</u>	<u>247</u>
<u>Canfora, L</u>	<u>256</u>	<u>Coelho, M</u>	<u>250</u>
<u>Cannavacciuolo, M</u>	<u>102</u>	<u>Coelho, M</u>	<u>250</u>
<u>Cannavo, P</u>	<u>344</u>	<u>Coimbra, S</u>	<u>597</u>
<u>Cantera, I</u>	<u>320, 307, 295, 303</u>	<u>Colby, S</u>	<u>522</u>
<u>Caprioli, G</u>	<u>425</u>	<u>Cole, J</u>	<u>254</u>
<u>Caries, A</u>	<u>343</u>	<u>Coletta, M</u>	<u>425, 145, 369</u>
<u>Carmignac, D</u>	<u>344</u>	<u>Colla, F</u>	<u>275</u>
<u>Carreira, C</u>	<u>314</u>	<u>Colla, F</u>	<u>224</u>
<u>Carrijo, T</u>	<u>63</u>	<u>Colleran, K</u>	<u>347</u>
<u>Carrillo Rincon, A</u>	<u>242</u>	<u>Collins, G</u>	<u>455</u>
<u>Carter, T</u>	<u>370</u>	<u>Collins, G</u>	<u>375</u>
<u>Carteron, A</u>	<u>320, 307, 295, 303</u>	<u>Collins, J</u>	<u>97</u>
<u>Caruso, T</u>	<u>133, 137, 336</u>	<u>Colombi, T</u>	<u>279</u>
<u>Carvalho, R</u>	<u>559</u>	<u>Concha Cano Díaz</u>	<u>104</u>
<u>Casale, F</u>	<u>506</u>	<u>Conlon, R</u>	<u>357, 342, 324</u>
<u>Castaño-Meneses, G</u>	<u>499</u>	<u>Conz, R</u>	<u>87</u>
<u>Castillo, D</u>	<u>362</u>	<u>Cook, D</u>	<u>586</u>
<u>Castro, D</u>	<u>63</u>	<u>Corbett, L</u>	<u>391</u>
<u>Castro, P</u>	<u>611, 617</u>	<u>Corcimarú, S</u>	<u>225</u>
<u>Castro, P</u>	<u>621</u>	<u>Cordell, S</u>	<u>416</u>
<u>Castro, P</u>	<u>283</u>	<u>Cordell, S</u>	<u>415</u>
<u>Cazorla, F</u>	<u>349</u>	<u>Cordes, P</u>	<u>602</u>

<u>Cazorla López, F</u>	<u>353</u>	<u>Cordovez, G</u>	<u>155</u>
<u>Cazzaniga, S</u>	<u>570</u>	<u>Corilo, Y</u>	<u>624</u>
<u>CEBRON, A</u>	<u>579</u>	<u>Corona Cuevas,</u>	<u>247</u>
		<u>R</u>	
<u>Ceja-navarro, J</u>	<u>479</u>	<u>Correia, M</u>	<u>247, 590, 246</u>
<u>Ceja-Navarro, J</u>	<u>474</u>	<u>Corstanie, R</u>	<u>573</u>
<u>Celniker, S</u>	<u>479</u>	<u>Cortet, J</u>	<u>276</u>
<u>César Plaza</u>	<u>104</u>	<u>Cortet, J</u>	<u>283, 344, 240</u>
<u>Cesco, S</u>	<u>350</u>	<u>Cortez, L</u>	<u>513</u>
<u>Cespi, M</u>	<u>425</u>	<u>Corwin, J</u>	<u>395</u>
<u>Chaer, G</u>	<u>247, 507</u>	<u>Cosby, J</u>	<u>236</u>
<u>Chalasani, D</u>	<u>395</u>	<u>Costa, S</u>	<u>559</u>
<u>Chandra Nayaka,</u>	<u>395</u>	<u>Costantini, E</u>	<u>505</u>
<u>S</u>			
<u>Chao, H</u>	<u>198</u>	<u>Cote, J</u>	<u>333</u>
<u>Chao, J</u>	<u>321</u>	<u>Cottin, A</u>	<u>96, 102</u>
<u>Chardon, I</u>	<u>170</u>	<u>Cottis, T</u>	<u>98</u>
<u>Chauvat, M</u>	<u>389</u>	<u>Coulibaly, S</u>	<u>550</u>
<u>Chauvin, C</u>	<u>102, 344</u>	<u>Coulibaly, S</u>	<u>358</u>
<u>Chelinho, S</u>	<u>607</u>	<u>Couradeau, E</u>	<u>179</u>
<u>Chemidlin</u>	<u>96</u>	<u>Cowan, D</u>	<u>125, 194</u>
<u>Prévost-Bouré, N</u>			
<u>Chemimdlin</u>	<u>396</u>	<u>Craig, H</u>	<u>585</u>
<u>Prévost-bouré, N</u>			
<u>Chen, T</u>	<u>168, 240, 321,</u>	<u>Crandall, S</u>	<u>179</u>
	<u>239</u>		
<u>Chen, T</u>	<u>225</u>	<u>Crotty, F</u>	<u>226</u>
<u>Cheng, L</u>	<u>257</u>	<u>Crowther, T</u>	<u>88</u>
<u>Chenu, C</u>	<u>554</u>	<u>Croy, R</u>	<u>248</u>
<u>Cho, K</u>	<u>152, 253</u>	<u>Culumber, M</u>	<u>481</u>
<u>Chodak, M</u>	<u>525</u>	<u>Cunha, J</u>	<u>611, 617</u>
<u>Choma, M</u>	<u>601</u>	<u>Cunha, L</u>	<u>555</u>
<u>Chomel, M</u>	<u>133, 262</u>		

Č

<u>Čapek, P</u>	<u>601</u>
-----------------	------------

d

<u>da Silva, O</u>	<u>507</u>	<u>de Nascimento, L</u>	<u>416</u>
<u>de Angelis, P</u>	<u>105</u>	<u>de Oliveira, A</u>	<u>254</u>
<u>de Boer, W</u>	<u>170</u>	<u>de Oliveira, A</u>	<u>250</u>
<u>de Castro, F</u>	<u>133</u>	<u>de Ruiten, P</u>	<u>247</u>
<u>de Celis, M</u>	<u>395</u>	<u>de _____ Vicente Moreno, A</u>	<u>353</u>
<u>de Goede, R</u>	<u>446</u>	<u>de Vries, F</u>	<u>133, 305</u>
<u>de Groot, A</u>	<u>183</u>	<u>di Gesu, L</u>	<u>333</u>

D

<u>Dadzie, F</u>	<u>441</u>	<u>Dhandapani, S</u>	<u>391</u>
<u>Daquis, R</u>	<u>344</u>	<u>Di Giulio, A</u>	<u>506</u>
<u>Dahl, G</u>	<u>416</u>	<u>Dignam, B</u>	<u>249</u>
<u>D'alessandro, A</u>	<u>425</u>	<u>Dimaano, V</u>	<u>513</u>
<u>D'Alessandro, A</u>	<u>145</u>	<u>Dingkuhn, R</u>	<u>284</u>
<u>D'Alessandro, A</u>	<u>369</u>	<u>Diniz, P</u>	<u>250</u>
<u>Damien, B</u>	<u>190</u>	<u>Dippold, M</u>	<u>331</u>
<u>Damien, D</u>	<u>413</u>	<u>Dirilgen, T</u>	<u>437</u>
<u>Damjanić, R</u>	<u>486</u>	<u>Dittrich, F</u>	<u>256</u>
<u>DANGER, M</u>	<u>579</u>	<u>Djemiel, C</u>	<u>96</u>
<u>Daniel, T</u>	<u>543</u>	<u>Dobarco, M</u>	<u>252</u>
<u>Daniell, T</u>	<u>347, 522, 556</u>	<u>Dodd, I</u>	<u>515</u>
<u>Darcy, S</u>	<u>297</u>	<u>Doick, K</u>	<u>184</u>
<u>Darcy, S</u>	<u>300</u>	<u>Dolnik, C</u>	<u>309</u>
<u>Darnet, E</u>	<u>333</u>	<u>Domnariu, H</u>	<u>583</u>
<u>D'Astous-Pagé, J</u>	<u>476</u>	<u>Donhauser, J</u>	<u>278</u>
<u>Dauchel, H</u>	<u>389</u>	<u>Donne, C</u>	<u>409</u>
<u>David, A</u>	<u>430</u>	<u>Donnini, D</u>	<u>271</u>
<u>D'Avino, L</u>	<u>620</u>	<u>Döring, T</u>	<u>71</u>
<u>Davison, J</u>	<u>551</u>	<u>Döring, T</u>	<u>323</u>
<u>De Almeida, T</u>	<u>554, 550</u>	<u>Dörsch, P</u>	<u>98</u>
<u>De Celis, M</u>	<u>386</u>	<u>Dougherty, A</u>	<u>398</u>
<u>De Goede, S</u>	<u>156</u>	<u>Dovč, N</u>	<u>486</u>

<u>De Menezes, A</u>	<u>411, 405, 417</u>	<u>Dowling, D</u>	<u>357, 342, 431, 324</u>
<u>De Neve, S</u>	<u>129, 215</u>	<u>Doyle, E</u>	<u>112</u>
<u>De Smedt, P</u>	<u>203</u>	<u>Dozières, A</u>	<u>344</u>
<u>De Souza</u> <u>Moreira, F</u>	<u>593</u>	<u>Drury, C</u>	<u>182</u>
<u>De Swaef, T</u>	<u>215</u>	<u>Du, Z</u>	<u>168</u>
<u>De Tender, C</u>	<u>524</u>	<u>Duan, G</u>	<u>395</u>
<u>De Vries, F</u>	<u>147</u>	<u>Duckert, C</u>	<u>415</u>
<u>Debode, J</u>	<u>524</u>	<u>Ducommun, C</u>	<u>344</u>
<u>Decaëns, T</u>	<u>166</u>	<u>Duff, A</u>	<u>65</u>
<u>Decker, P</u>	<u>455</u>	<u>Duley, E</u>	<u>313, 542, 544</u>
<u>Degrune, F</u>	<u>278</u>	<u>Dumack, K</u>	<u>488</u>
<u>Degtyarev, M</u>	<u>72</u>	<u>Dumack, K</u>	<u>215</u>
<u>Deharveng, L</u>	<u>240</u>	<u>Dumortier, A</u>	<u>208</u>
<u>Delcourt, N</u>	<u>283</u>	<u>Dunfield, K</u>	<u>622</u>
<u>Delgado</u> <u>Baquerizo, M</u>	<u>173</u>	<u>Dunn, L</u>	<u>396</u>
<u>Delgado-</u> <u>Baquerizo, M</u>	<u>395, 95, 232, 161, 386</u>	<u>Duquesne, É</u>	<u>208</u>
<u>Deltedesco, E</u>	<u>434</u>	<u>Duran, D</u>	<u>324</u>
<u>Demchenko, E</u>	<u>309</u>	<u>Durán-Wendt, D</u>	<u>342</u>
<u>Demuynck, S</u>	<u>548, 553</u>	<u>Dutra, I</u>	<u>254</u>
<u>Dequiedt, S</u>	<u>96, 102</u>	<u>Duvivier, J</u>	<u>553</u>

E

<u>Ebeling, A</u>	<u>488</u>	<u>Emmerson, M</u>	<u>133</u>
<u>Ebersberger, I</u>	<u>455</u>	<u>Emmett, B</u>	<u>105</u>
<u>Echaiz, C</u>	<u>155</u>	<u>Emsens, W</u>	<u>86</u>
<u>Eckardt, F</u>	<u>125</u>	<u>Enderle, E</u>	<u>147</u>
<u>Edelenbos, M</u>	<u>452</u>	<u>Engelbart, L</u>	<u>354</u>
<u>Eder, E</u>	<u>509</u>	<u>Engell, I</u>	<u>365</u>
<u>Eggleton, P</u>	<u>116</u>	<u>Enkerli, J</u>	<u>278</u>
<u>Ehaliotis, C</u>	<u>442</u>	<u>Epelde, L</u>	<u>54, 283</u>
<u>Eichenberg, D</u>	<u>604</u>	<u>Erick, D</u>	<u>413</u>

<u>Eisenhauer, N</u>	<u>332, 338, 166, 220, 293, 206, 211, 219, 488</u>	<u>Erickson, T</u>	<u>441</u>
<u>Ekelund, F</u>	<u>348</u>	<u>Erséus, C</u>	<u>610</u>
<u>Eler, K</u>	<u>400</u>	<u>Espinosa, H</u>	<u>325</u>
<u>Eloe-Fadrosh, E</u>	<u>624</u>	<u>Estera-Molina, K</u>	<u>474</u>
<u>Elzes, G</u>	<u>570</u>	<u>Estera-Molina, K</u>	<u>479</u>
<u>Emerson, J</u>	<u>586</u>	<u>Estiarte, M</u>	<u>105</u>
<u>Emery, S</u>	<u>367</u>	<u>Evans, B</u>	<u>230</u>
<u>Emilio Guirado</u>	<u>104</u>	<u>Eydoux, L</u>	<u>344</u>
<u>Emily, M</u>	<u>594</u>	<u>Eze, S</u>	<u>519</u>
<u>Emmerling, C</u>	<u>84, 83</u>		

E

<u>Fabiani, A</u>	<u>505</u>	<u>Firestone, M</u>	<u>479</u>
<u>Falaschi, M</u>	<u>295</u>	<u>Fisher, K</u>	<u>261</u>
<u>Faraloni, C</u>	<u>117</u>	<u>Fliessbach, A</u>	<u>533</u>
<u>Farfan, M</u>	<u>422</u>	<u>Flintham, H</u>	<u>585</u>
<u>Färkkilä, S</u>	<u>272</u>	<u>Fløjgaard, C</u>	<u>465</u>
<u>Farny, N</u>	<u>242</u>	<u>Florionová, A</u>	<u>101</u>
<u>Feitosa, Y</u>	<u>482</u>	<u>Foley, M</u>	<u>474</u>
<u>Felföldi, T</u>	<u>610</u>	<u>Fonner, B</u>	<u>558</u>
<u>Feng, L</u>	<u>168</u>	<u>Fontaneto, D</u>	<u>303</u>
<u>Fenn, K</u>	<u>255, 576</u>	<u>Fonte, S</u>	<u>338</u>
<u>Feola Conz, R</u>	<u>229</u>	<u>Fontes, N</u>	<u>611</u>
<u>Feola Conz, R</u>	<u>237</u>	<u>Forestieri, B</u>	<u>178</u>
<u>Ferlian, O</u>	<u>219</u>	<u>Forey, E</u>	<u>389</u>
<u>Fernández, J</u>	<u>388</u>	<u>Fornasier, F</u>	<u>404</u>
<u>Fernández Alonso, M</u>	<u>395</u>	<u>Forrestal, P</u>	<u>65</u>
<u>Fernández Calviño, D</u>	<u>388</u>	<u>Forster, J</u>	<u>585</u>
<u>Fernández- Alonso, M</u>	<u>386</u>	<u>Forster, L</u>	<u>347</u>
<u>Fernández- Bravo, M</u>	<u>278</u>	<u>Förster, A</u>	<u>84</u>
<u>Fernandez- Galliano, A</u>	<u>449</u>	<u>Fortini, L</u>	<u>506</u>

<u>Fernández-Palacios, J</u>	<u>416</u>	<u>Fountain, L</u>	<u>522</u>
<u>Fernando T. Maestre</u>	<u>104</u>	<u>Fournier, B</u>	<u>439</u>
<u>Ferreira, T</u>	<u>555, 552, 247, 590, 246</u>	<u>Fox, A</u>	<u>92, 376</u>
<u>Ferrin, M</u>	<u>105</u>	<u>Frac, M</u>	<u>467</u>
<u>Ficetola, F</u>	<u>307, 295, 303</u>	<u>Fraser, F</u>	<u>573</u>
<u>Ficetola, G</u>	<u>320</u>	<u>Fraser, T</u>	<u>591</u>
<u>Field, K</u>	<u>543, 547, 556, 537</u>	<u>Frazão, J</u>	<u>614</u>
<u>Fiera, C</u>	<u>225</u>	<u>Frédéric, M</u>	<u>413</u>
<u>Figueroa, F</u>	<u>618</u>	<u>Frédérique, C</u>	<u>413</u>
<u>Figueroa, R</u>	<u>155</u>	<u>Freudhofmaier, M</u>	<u>418</u>
<u>Fillmore, S</u>	<u>591</u>	<u>Frey, B</u>	<u>278, 225</u>
<u>Finn, J</u>	<u>200, 411, 417, 419</u>	<u>Fritze, H</u>	<u>368</u>
<u>Finn, J</u>	<u>405</u>	<u>Frouz, J</u>	<u>464, 86</u>
<u>Finzgar, D</u>	<u>584</u>	<u>Fujinuma, J</u>	<u>416</u>
<u>Fiore, M</u>	<u>482</u>	<u>Fung, O</u>	<u>546</u>
<u>Fiore-Donno, A</u>	<u>489</u>	<u>Fusco, T</u>	<u>506</u>
<u>Firestone, M</u>	<u>474, 512, 459</u>		

G

<u>G.F. Veen, C</u>	<u>286, 317</u>	<u>Giovannoni, J</u>	<u>257</u>
<u>Gabriel, R</u>	<u>416</u>	<u>Giuliano, E</u>	<u>237</u>
<u>Gagnarli, E</u>	<u>505, 404</u>	<u>Glaser, K</u>	<u>309</u>
<u>Galindo-Castañeda, T</u>	<u>237</u>	<u>Glen, M</u>	<u>260</u>
<u>Galla, G</u>	<u>275</u>	<u>Gliesch Silva, M</u>	<u>305</u>
<u>Galla, G</u>	<u>224</u>	<u>Goddard, M</u>	<u>519</u>
<u>Gallego, J</u>	<u>327</u>	<u>Godoy, L</u>	<u>155</u>
<u>Gallego, J</u>	<u>222</u>	<u>Goggioli, D</u>	<u>404</u>
<u>Gambra, D</u>	<u>541</u>	<u>Goggioli, D</u>	<u>505</u>
<u>Ganault, P</u>	<u>338, 166, 276</u>	<u>Goldmann, K</u>	<u>304, 334</u>
<u>Gannett, M</u>	<u>257</u>	<u>Gomes, S</u>	<u>574</u>
<u>Gao, C</u>	<u>269</u>	<u>Gomez, A</u>	<u>452</u>

<u>Gao, C</u>	<u>210</u>	<u>Gómez, E</u>	<u>271</u>
<u>Gao, S</u>	<u>481</u>	<u>Gomez-Brandon, M</u>	<u>287</u>
<u>Garbeva, P</u>	<u>399</u>	<u>Gongalsky, K</u>	<u>72</u>
<u>Garbisu, C</u>	<u>54</u>	<u>Gongalsky, K</u>	<u>338</u>
<u>Garces, K</u>	<u>367</u>	<u>Gonzalez, O</u>	<u>245</u>
<u>Garcia, J</u>	<u>257, 255, 475, 576</u>	<u>González, M</u>	<u>388</u>
<u>Garcia, R</u>	<u>327</u>	<u>González, R</u>	<u>247</u>
<u>García, C</u>	<u>139</u>	<u>Gonzalez-Maldonado, N</u>	<u>255, 475</u>
<u>García Barreda, S</u>	<u>271</u>	<u>González-Prieto, S</u>	<u>407</u>
<u>García Carmona, M</u>	<u>103</u>	<u>Gorbunova, A</u>	<u>72</u>
<u>García-Díaz, C</u>	<u>139</u>	<u>Gorfer, M</u>	<u>434, 418</u>
<u>Garcia-Jimenez, B</u>	<u>346</u>	<u>Gostinčar, C</u>	<u>302</u>
<u>García-Orenes, F</u>	<u>103</u>	<u>Gould, I</u>	<u>519</u>
<u>Garcia-Palacios, P</u>	<u>386</u>	<u>Govednik, A</u>	<u>400</u>
<u>García-Palacios, P</u>	<u>395</u>	<u>Gowers, G</u>	<u>238</u>
<u>Garcia-Verde, F</u>	<u>346</u>	<u>Graça, A</u>	<u>611</u>
<u>Garrido-Sanz, D</u>	<u>324</u>	<u>Grace, C</u>	<u>446</u>
<u>Garrizo-Sanz, D</u>	<u>342</u>	<u>Grandy, A</u>	<u>317</u>
<u>Gatti, F</u>	<u>153</u>	<u>Grange, G</u>	<u>200</u>
<u>Gattini, F</u>	<u>155</u>	<u>Gray, J</u>	<u>522</u>
<u>Gauzens, B</u>	<u>338</u>	<u>Grebenc, T</u>	<u>302, 486</u>
<u>Gavín-Centol, P</u>	<u>423</u>	<u>Greenlon, A</u>	<u>474, 586</u>
<u>Gaxiola, A</u>	<u>618</u>	<u>Greve, M</u>	<u>125</u>
<u>Gayan, A</u>	<u>163</u>	<u>Gričar, J</u>	<u>493</u>
<u>Gebremikael, M</u>	<u>452</u>	<u>Griffiths, H</u>	<u>116</u>
<u>Gebremikael, M</u>	<u>215</u>	<u>Grina, V</u>	<u>251</u>
<u>Geedey, A</u>	<u>149</u>	<u>Grogan, H</u>	<u>197</u>
<u>Gehring, C</u>	<u>478</u>	<u>Grosch, R</u>	<u>414</u>
<u>Geisen, S</u>	<u>132, 335, 348</u>	<u>Grumiaux, F</u>	<u>548, 553</u>
<u>Geisen, S</u>	<u>185</u>	<u>Gryta, A</u>	<u>467</u>

<u>Geissen, V</u>	<u>469</u>	<u>Gschwend, F</u>	<u>278</u>
<u>Geistlinger, J</u>	<u>414</u>	<u>Guariento, E</u>	<u>158, 288</u>
<u>Gendreau, E</u>	<u>344</u>	<u>Gubry-Rangin, C</u>	<u>140</u>
<u>Genevet,</u>	<u>343</u>	<u>Guénon, R</u>	<u>344</u>
<u>Genova, G</u>	<u>350</u>	<u>Guerra, C</u>	<u>95, 338, 247</u>
<u>Gerard, E</u>	<u>248, 468</u>	<u>Guerra, C</u>	<u>559</u>
<u>Gerard, E</u>	<u>249</u>	<u>Guerrero-Analco,</u>	<u>609</u>
		<u>J</u>	
<u>Gérard, S</u>	<u>166</u>	<u>Guerrieri, A</u>	<u>320, 307, 295</u>
<u>Gerber, S</u>	<u>451</u>	<u>Guerrieri, A</u>	<u>303</u>
<u>Germaine, K</u>	<u>357, 342, 431,</u>	<u>Guevara , R</u>	<u>609</u>
	<u>324</u>		
<u>Gernon, D</u>	<u>197</u>	<u>Gugger, R</u>	<u>163</u>
<u>Ghignone, S</u>	<u>426, 114</u>	<u>Guidi, S</u>	<u>505, 404</u>
<u>Ghosh, D</u>	<u>188</u>	<u>Guillaume, L</u>	<u>269</u>
<u>Giachello, S</u>	<u>295, 303</u>	<u>Guillocheau, S</u>	<u>599, 284</u>
<u>Gibson, K</u>	<u>478</u>	<u>Gupta, S</u>	<u>359</u>
<u>Gichuhi, E</u>	<u>434</u>	<u>Gura, I</u>	<u>619</u>
<u>Gignoux, J</u>	<u>344</u>	<u>Guseva, K</u>	<u>297</u>
<u>Giles, M</u>	<u>347</u>	<u>Guseva, K</u>	<u>300</u>
<u>Gill, R</u>	<u>585</u>	<u>Gutiérrez</u>	<u>353</u>
		<u>Barranquero , J</u>	

H

<u>H. van der</u>	<u>286</u>	<u>Hilpold, A</u>	<u>350</u>
<u>Putten, W</u>			
<u>Haapalainen, M</u>	<u>366</u>	<u>Hilton, S</u>	<u>573</u>
<u>Haase, P</u>	<u>378</u>	<u>Hines, J</u>	<u>332</u>
<u>Habteselassie, M</u>	<u>495</u>	<u>Hinojosa, L</u>	<u>147</u>
<u>Halldórsson, G</u>	<u>381</u>	<u>Hinojosa</u>	<u>305</u>
		<u>Sanchez, L</u>	
<u>Hallet Sánchez, J</u>	<u>347</u>	<u>Hipp, A</u>	<u>149, 175</u>
<u>Hamberg, L</u>	<u>363</u>	<u>Hoagland, L</u>	<u>123</u>
<u>Han, X</u>	<u>318</u>	<u>Hoar, K</u>	<u>242</u>
<u>Hanner, R</u>	<u>482</u>	<u>Hodson, M</u>	<u>230</u>
<u>Hannula, E</u>	<u>156, 373</u>	<u>Hoeffner, K</u>	<u>102, 614, 284</u>
<u>Hannula, E</u>	<u>131</u>	<u>Hoeffner, K</u>	<u>599</u>

<u>Hao, C</u>	<u>321</u>	<u>Hoffland, E</u>	<u>446</u>
<u>Hardie, M</u>	<u>260</u>	<u>Hoffman, T</u>	<u>231</u>
<u>Harings, M</u>	<u>269</u>	<u>Hogue, R</u>	<u>476, 477</u>
<u>Harkes, P</u>	<u>469</u>	<u>Hohberg, K</u>	<u>84, 455</u>
<u>Harper, L</u>	<u>585</u>	<u>Hokka, H</u>	<u>368</u>
<u>Harris, J</u>	<u>573</u>	<u>Holmes, G</u>	<u>245</u>
<u>Hart, M</u>	<u>180</u>	<u>Holtz, B</u>	<u>481</u>
<u>Hartmann, M</u>	<u>174, 87, 229, 237</u>	<u>Hoover, D</u>	<u>370</u>
<u>Hartmann, M</u>	<u>279</u>	<u>Hopkins, D</u>	<u>125</u>
<u>Hasler, R</u>	<u>77</u>	<u>Hoppe, B</u>	<u>334</u>
<u>Hassani, M</u>	<u>245</u>	<u>Hornung, E</u>	<u>466</u>
<u>Hassi, U</u>	<u>129, 215</u>	<u>Horrique, W</u>	<u>96</u>
<u>Hauffe, H</u>	<u>275</u>	<u>Horváthová, T</u>	<u>359</u>
<u>Hauffe, H</u>	<u>224</u>	<u>HOSSANN, C</u>	<u>579</u>
<u>Haus, W</u>	<u>415</u>	<u>Hou, F</u>	<u>147</u>
<u>Havlicek, E</u>	<u>533</u>	<u>Hou, X</u>	<u>564</u>
<u>He, J</u>	<u>508</u>	<u>Houston, K</u>	<u>522</u>
<u>He, J</u>	<u>530</u>	<u>Howard, N</u>	<u>543</u>
<u>He, Z</u>	<u>530</u>	<u>Howe, A</u>	<u>254</u>
<u>Hedde, M</u>	<u>166</u>	<u>Howe, A</u>	<u>250</u>
<u>Hedde, M</u>	<u>562</u>	<u>Hoysted, G</u>	<u>537</u>
<u>Heger, T</u>	<u>278</u>	<u>Hu, H</u>	<u>530</u>
<u>Heimovaara, T</u>	<u>509</u>	<u>Hu, J</u>	<u>129, 215</u>
<u>Heintz-Buschart, A</u>	<u>165, 488</u>	<u>Hu, S</u>	<u>257</u>
<u>Heinze, S</u>	<u>185</u>	<u>Hu, Y</u>	<u>305</u>
<u>Helder, J</u>	<u>570</u>	<u>Huang, S</u>	<u>416</u>
<u>Hemkemeyer, M</u>	<u>185</u>	<u>Huber, S</u>	<u>418</u>
<u>Hernandez-Lopez, A</u>	<u>395</u>	<u>Hudek, C</u>	<u>515</u>
<u>Hernández-Tirado, A</u>	<u>499</u>	<u>Huerta Lwanga, E</u>	<u>399</u>
<u>Herrera-Alsina, L</u>	<u>140</u>	<u>Hug, A</u>	<u>533</u>
<u>Herrera-Estrella, L</u>	<u>121</u>	<u>Hug, A</u>	<u>278</u>
<u>Hetman, Y</u>	<u>429</u>	<u>Huguenin-Elie, O</u>	<u>376</u>
<u>Heuer, H</u>	<u>348</u>	<u>Huhn, C</u>	<u>354</u>

Hevia, V 383
Hicks, L 293
HILAIRE, E 579
Hilpold, A 288

Hultman, J 368
Hume, D 248, 468
Hungate, B 474
Hunt, I 260

I

Ibáñez Huerta, A 499
Ibarra-Garibay, L 499
Ikoyi, I 65, 200
Illmer, P 275, 232, 224,
290, 308
INCREMENTO-
Consortium 541
Indjic, D 339

Ingrisch, J 308
Insam, H 545
Ipinza, B 155
Iribar, A 333
Ivors, K 245

i

in 't Zandt, D 101

in 't Zandt, M 101

J

J. Field, K 561
J.I. Briones, M 483

Jacomini, C 535
Jacomini, C 506
Jaeger, A 87

James, J 122
James, S 371
Janeiro-Tato, I 327
Janion-
Scheepers, C 463
Jänsch, S 315, 610
Jansen, B 509
Jassey, V 319
Javal, M 343
Jean-Baptiste, V 102

Joergensen, R 185
Johnson, D 133, 262, 497,
571
Johnson, E 219
Johnson, N 478
Joimel, S 240, 358, 554,
550
Jones, A 483, 281
Jones, J 313, 542, 544
Jones, L 301
Jongenelen, P 570

Jongepier, E 305
Joos, L 524
Jorna, J 412
Józefowska, A 521, 525
Jucevica, E 251

<u>Jeanbille, M</u>	<u>540</u>	<u>Juilleret, J</u>	<u>453</u>
<u>Jeanne, T</u>	<u>476, 477</u>	<u>Julie, M</u>	<u>413</u>
<u>Jech, S</u>	<u>261</u>	<u>Julliard, R</u>	<u>344</u>
<u>Jeffery, S</u>	<u>97</u>	<u>Jumpponen, A</u>	<u>528</u>
<u>Jehmlich, N</u>	<u>188</u>	<u>Jung, M</u>	<u>253</u>
<u>Jenab, K</u>	<u>300</u>	<u>Junggebauer, A</u>	<u>99, 157</u>
<u>Jesus, E</u>	<u>247, 254, 250,</u> <u>507</u>	<u>Juntao Wang</u>	<u>104</u>
<u>Joannès, G</u>	<u>413</u>	<u>Jurburg, S</u>	<u>128</u>
<u>Jochum, M</u>	<u>219</u>		

K

<u>Kadir, S</u>	<u>198</u>	<u>Kirk, M</u>	<u>528</u>
<u>Kagainis, U</u>	<u>251</u>	<u>Kirse, A</u>	<u>323</u>
<u>Kahout, P</u>	<u>88</u>	<u>Kivijärvi, P</u>	<u>366</u>
<u>Kaiser, C</u>	<u>297</u>	<u>Klamerus- Iwan,</u> <u>A</u>	<u>525</u>
<u>Kaiser, C</u>	<u>300</u>	<u>Klarner, B</u>	<u>219</u>
<u>Kakouli-Duarte, T</u>	<u>581</u>	<u>Klein, T</u>	<u>285</u>
<u>Kakouli-Duarte ,</u> <u>I</u>	<u>385</u>	<u>Klinth, M</u>	<u>610</u>
<u>Kakouridis, A</u>	<u>512, 459</u>	<u>Knief, C</u>	<u>598</u>
<u>Kammann, S</u>	<u>309</u>	<u>Knuth, D</u>	<u>469</u>
<u>Kaňa, J</u>	<u>601</u>	<u>Kochar, M</u>	<u>107</u>
<u>Kandeler, E</u>	<u>171, 100, 172,</u> <u>269, 354</u>	<u>Kögel-Knabner, I</u>	<u>598</u>
<u>Kao-Kniffin, J</u>	<u>257</u>	<u>KOHLER, A</u>	<u>579</u>
<u>Kapinga, E</u>	<u>381</u>	<u>Kohout, P</u>	<u>210, 220, 627</u>
<u>Karimi, B</u>	<u>96</u>	<u>Kompała-Baba, A</u>	<u>525</u>
<u>Karisto, P</u>	<u>366</u>	<u>Königer, J</u>	<u>483</u>
<u>Karpinska, A</u>	<u>385</u>	<u>Konstantinidis, K</u>	<u>593</u>
<u>Karst, J</u>	<u>265</u>	<u>Kontunen-</u> <u>Soppela, S</u>	<u>272</u>
<u>Karsten, U</u>	<u>309</u>	<u>Kopáček, J</u>	<u>601</u>
<u>Kastelec, D</u>	<u>274</u>	<u>Korobushkin, D</u>	<u>72</u>
<u>Kaštovská, E</u>	<u>601</u>	<u>Korthals, G</u>	<u>170</u>
<u>Kato, R</u>	<u>214</u>	<u>Kosina, P</u>	<u>479</u>

<u>Kattilakoski, M</u>	<u>368</u>	<u>Kost, E</u>	<u>229</u>
<u>Kaufmann, B</u>	<u>343</u>	<u>Kotze, E</u>	<u>619</u>
<u>Kay, P</u>	<u>260</u>	<u>Kotze, J</u>	<u>466</u>
<u>Keiblinger, K</u>	<u>418</u>	<u>Koul, V</u>	<u>534, 107</u>
<u>Keith, A</u>	<u>236, 277, 301</u>	<u>Kováč, I'</u>	<u>240</u>
<u>Keller, T</u>	<u>279</u>	<u>Kovács-Láng, E</u>	<u>105</u>
<u>Kelliher, J</u>	<u>624</u>	<u>Kraigher, H</u>	<u>486, 493</u>
<u>Kellner, H</u>	<u>334</u>	<u>Kraigher, H</u>	<u>584</u>
<u>Kennedy, J</u>	<u>446</u>	<u>Krause, H</u>	<u>174</u>
<u>Kennedy, N</u>	<u>316</u>	<u>Krehenwinkel, H</u>	<u>375</u>
<u>Khomenko, I</u>	<u>517</u>	<u>Kristensen, H</u>	<u>452</u>
<u>Kidd, P</u>	<u>621</u>	<u>Kröel-Dulay, G</u>	<u>105</u>
<u>Kiernan, M</u>	<u>542</u>	<u>Krogh, P</u>	<u>315, 225, 421, 276</u>
<u>Kiers, T</u>	<u>88, 187</u>	<u>Krumins, J</u>	<u>541</u>
<u>Kihara, J</u>	<u>568</u>	<u>Krüß, A</u>	<u>604</u>
<u>Kilian, I</u>	<u>323</u>	<u>Krzywoszynska, A</u>	<u>70</u>
<u>Kim, S</u>	<u>111</u>	<u>Ksenofontov, A</u>	<u>72</u>
<u>Kim, T</u>	<u>152, 253</u>	<u>Kubota, Y</u>	<u>416</u>
<u>Kim, Y</u>	<u>152</u>	<u>Kumar, S</u>	<u>145</u>
<u>Kim, Y</u>	<u>253</u>	<u>Kumar Basuri, C</u>	<u>145</u>
<u>Kimbrel, J</u>	<u>512</u>	<u>Kundel, D</u>	<u>229</u>
<u>Kimbrel, J</u>	<u>474</u>		

L

<u>La Terza, A</u>	<u>425, 145, 369</u>	<u>Li, R</u>	<u>185</u>
<u>Labouyrie, M</u>	<u>281</u>	<u>Liberati, D</u>	<u>105</u>
<u>Laganière, J</u>	<u>265</u>	<u>Lindbo, D</u>	<u>370</u>
<u>Laiho, R</u>	<u>368</u>	<u>Lindo, Z</u>	<u>247, 137</u>
<u>Lammel, D</u>	<u>111</u>	<u>Lindo, Z</u>	<u>75</u>
<u>Lampert, M</u>	<u>184</u>	<u>Linnyk, V</u>	<u>268</u>
<u>Landis, D</u>	<u>457</u>	<u>Linsler, D</u>	<u>365</u>
<u>Lanfranci, Q</u>	<u>344</u>	<u>Littlejohn, G</u>	<u>542</u>
<u>Lapa, S</u>	<u>72</u>	<u>Liu, B</u>	<u>256</u>
<u>Lastovetsky, O</u>	<u>112</u>	<u>Liu, S</u>	<u>293</u>

<u>Lata, J</u>	<u>344</u>	<u>Liu, X</u>	<u>497</u>
<u>Latif, R</u>	<u>613</u>	<u>Livne-Luzon, S</u>	<u>285</u>
<u>Lattacher, A</u>	<u>269</u>	<u>Lloret, E</u>	<u>388</u>
<u>Latvala, S</u>	<u>366</u>	<u>Llusia, J</u>	<u>516</u>
<u>Laumer, C</u>	<u>595</u>	<u>Loades, K</u>	<u>347</u>
<u>Lavallee, J</u>	<u>133</u>	<u>Loeke, T</u>	<u>528</u>
<u>Law, M</u>	<u>546</u>	<u>Lombaers, C</u>	<u>570</u>
<u>Lazcano, C</u>	<u>245, 255, 475, 576</u>	<u>Longepierre, M</u>	<u>279</u>
<u>Le Gall, S</u>	<u>269</u>	<u>López, M</u>	<u>349</u>
<u>Leavens, E</u>	<u>149, 175</u>	<u>Lopez Valdivia, I</u>	<u>237</u>
<u>Lebedev, I</u>	<u>72</u>	<u>Lopez-Anton, M</u>	<u>327</u>
<u>Lebre, P</u>	<u>194</u>	<u>Lorenzen Elberg, C</u>	<u>306</u>
<u>Lebre, P</u>	<u>125</u>	<u>Lorenzetti, R</u>	<u>113</u>
<u>Lebrija-Trejos, E</u>	<u>325</u>	<u>Lori, M</u>	<u>174</u>
<u>Lecoq, B</u>	<u>343</u>	<u>Lorite, J</u>	<u>416, 439</u>
<u>Lee, D</u>	<u>253</u>	<u>Lövenich, P</u>	<u>185</u>
<u>Lee, Y</u>	<u>253</u>	<u>Lozano, A</u>	<u>347</u>
<u>Lee, Y</u>	<u>152</u>	<u>Lozano Fondón, C</u>	<u>154</u>
<u>Lehmitz, R</u>	<u>455</u>	<u>Lu, B</u>	<u>391</u>
<u>Leigh, E</u>	<u>223</u>	<u>Lu, J</u>	<u>90</u>
<u>Leinweber, P</u>	<u>309</u>	<u>Lu, J</u>	<u>67</u>
<u>Leitinger, G</u>	<u>557</u>	<u>Lucas, A</u>	<u>344, 343</u>
<u>Leitner, S</u>	<u>434</u>	<u>Ludwig, A</u>	<u>166</u>
<u>Lejoly, J</u>	<u>265</u>	<u>Luescher, A</u>	<u>92, 376</u>
<u>Lénack, E</u>	<u>284</u>	<u>Lugato, E</u>	<u>281</u>
<u>Lentendu, G</u>	<u>416, 415, 439</u>	<u>Lumini, E</u>	<u>426, 114</u>
<u>Leprisé, A</u>	<u>284</u>	<u>Lunn, J</u>	<u>391</u>
<u>Lesch, S</u>	<u>225</u>	<u>Luo, C</u>	<u>564</u>
<u>Leštan, D</u>	<u>274</u>	<u>Luo, S</u>	<u>564</u>
<u>Leventis, G</u>	<u>442</u>	<u>Lux, J</u>	<u>134</u>
<u>Leviana, L</u>	<u>198</u>	<u>Lynch, J</u>	<u>237</u>
<u>Li, C</u>	<u>508</u>		

M

<u>M. Suz, L</u>	<u>448</u>	<u>Mendanha, T</u>	<u>452</u>
<u>Maaß, S</u>	<u>111</u>	<u>Mendes, I</u>	<u>247, 507</u>
<u>Macagnano, A</u>	<u>117</u>	<u>Mendes, L</u>	<u>132</u>
<u>MacColl, K</u>	<u>622</u>	<u>Meng, Q</u>	<u>168</u>
<u>MacDougall, A</u>	<u>622</u>	<u>Menge, D</u>	<u>434</u>
<u>MacEachern, D</u>	<u>591</u>	<u>Mengoni, A</u>	<u>311</u>
<u>Maček, I</u>	<u>274</u>	<u>Ménival, C</u>	<u>218</u>
<u>Machado de Lima, N</u>	<u>441</u>	<u>Menta, C</u>	<u>154, 153, 268</u>
<u>Macia-Vicente, J</u>	<u>570, 574</u>	<u>Merbold, L</u>	<u>434</u>
<u>Maćik, M</u>	<u>467</u>	<u>Mercer, T</u>	<u>519</u>
<u>Mackenzie, R</u>	<u>262</u>	<u>Merloti, L</u>	<u>132</u>
<u>Mäder, P</u>	<u>174, 229</u>	<u>Merrit, D</u>	<u>441</u>
<u>Mäder, P</u>	<u>354</u>	<u>Mescher, M</u>	<u>237</u>
<u>Maggs-Kölling, G</u>	<u>194</u>	<u>Meuli, R</u>	<u>384</u>
<u>Magilton, M</u>	<u>133, 519</u>	<u>Micheni, A</u>	<u>568</u>
<u>Magkourilou, E</u>	<u>547, 556</u>	<u>Midgley, M</u>	<u>149, 175</u>
<u>Magkourilou, E</u>	<u>561</u>	<u>Mihelič, R</u>	<u>400</u>
<u>Magnone, D</u>	<u>519</u>	<u>Mikhailyuk, T</u>	<u>309</u>
<u>Maherali, H</u>	<u>622</u>	<u>Miko, L</u>	<u>86</u>
<u>Maienza, A</u>	<u>114, 117, 113</u>	<u>Milla, R</u>	<u>395</u>
<u>Maillard, F</u>	<u>579</u>	<u>Milla, R</u>	<u>386</u>
<u>Maiolino, P</u>	<u>178</u>	<u>Miller, M</u>	<u>624</u>
<u>Maisto, G</u>	<u>287, 298</u>	<u>Millett, J</u>	<u>301</u>
<u>Makihara, D</u>	<u>434</u>	<u>Mimee, B</u>	<u>124</u>
<u>Malamud, N</u>	<u>325</u>	<u>Mimmo, T</u>	<u>350</u>
<u>Malaquias, J</u>	<u>247, 507, 590</u>	<u>Minasny, B</u>	<u>252</u>
<u>Malaquias, J</u>	<u>246</u>	<u>Minasny, B</u>	<u>241</u>
<u>Malas, M</u>	<u>64</u>	<u>Mishler, B</u>	<u>261</u>
<u>Malhi, Y</u>	<u>448</u>	<u>Mitchell, E</u>	<u>415</u>
<u>Mancinelli, R</u>	<u>210, 181</u>	<u>Mitchell, E</u>	<u>416</u>
<u>Mandolini, E</u>	<u>518</u>	<u>Mitchell, E</u>	<u>439</u>
<u>Mandolini, E</u>	<u>514, 557</u>	<u>Mitterer, M</u>	<u>350</u>
<u>Mani, D</u>	<u>207</u>	<u>Mo, L</u>	<u>268</u>
<u>Mann, D</u>	<u>453</u>	<u>Mocali, S</u>	<u>620</u>
<u>Manrique, E</u>	<u>204</u>	<u>Moeskjaer, S</u>	<u>522</u>

<u>Manuel Delgado Baquerizo</u>	<u>104</u>	<u>Mohammed, C</u>	<u>260</u>
<u>Marais, E</u>	<u>194</u>	<u>Molendijk, L</u>	<u>570</u>
<u>Maraun, M</u>	<u>602</u>	<u>Molins, A</u>	<u>560</u>
<u>Marcangeli, Y</u>	<u>344</u>	<u>Moll, J</u>	<u>334</u>
<u>Marchán, D</u>	<u>166</u>	<u>Mollier, A</u>	<u>562</u>
<u>Margot, B</u>	<u>413</u>	<u>Moll-Mielewczik, J</u>	<u>278</u>
<u>Marhan, S</u>	<u>171, 100, 172</u>	<u>Mommer, L</u>	<u>574</u>
<u>Marichal, R</u>	<u>338</u>	<u>Mommer, L</u>	<u>570</u>
<u>Marié, X</u>	<u>284</u>	<u>Monard, C</u>	<u>614</u>
<u>Marjanovic, Z</u>	<u>271, 225</u>	<u>Monribot, J</u>	<u>609</u>
<u>Markkola, A</u>	<u>272</u>	<u>Monson, F</u>	<u>277</u>
<u>Marks, E</u>	<u>484</u>	<u>Montanarella, L</u>	<u>247</u>
<u>Maron, P</u>	<u>96, 102, 344, 396</u>	<u>Montero, O</u>	<u>484</u>
<u>Marshall, S</u>	<u>249</u>	<u>Monterroso, C</u>	<u>577</u>
<u>Marsi, M</u>	<u>198</u>	<u>Montgomery, I</u>	<u>336</u>
<u>Marta, S</u>	<u>320, 307, 295, 303</u>	<u>Moon, J</u>	<u>374</u>
<u>Martin, C</u>	<u>305</u>	<u>Moora, M</u>	<u>551</u>
<u>Martin, K</u>	<u>403, 402</u>	<u>Moradtalab, N</u>	<u>414</u>
<u>Martin, K</u>	<u>84</u>	<u>Moreau, L</u>	<u>333</u>
<u>Martin, M</u>	<u>324</u>	<u>Moreira, F</u>	<u>597</u>
<u>MARTIN, F</u>	<u>579</u>	<u>Moreira, H</u>	<u>54, 283, 621, 617</u>
<u>Martín, M</u>	<u>342</u>	<u>Moreira, H</u>	<u>611</u>
<u>Martín-Azcárate, F</u>	<u>383</u>	<u>Moreno, D</u>	<u>346</u>
<u>Martineau, C</u>	<u>265</u>	<u>Moreno, J</u>	<u>139</u>
<u>Martinez-Chavez, L</u>	<u>97</u>	<u>Miralles-Ferrer, A</u>	<u>560</u>
<u>Martinez-Cuesta, R</u>	<u>324</u>	<u>Morillo, J</u>	<u>618</u>
<u>Martínez-Martínez, S</u>	<u>388</u>	<u>Moro, I</u>	<u>303</u>
<u>Martinovic, T</u>	<u>584</u>	<u>Morriën, E</u>	<u>131</u>
<u>Martinsson, S</u>	<u>610</u>	<u>Morriën, E</u>	<u>549</u>
		<u>Motta, A</u>	<u>555</u>

<u>Martyniuk, D</u>	<u>527</u>	<u>Mounier, A</u>	<u>540</u>
<u>Marzaioli, R</u>	<u>379</u>	<u>Mourgela, R</u>	<u>410</u>
<u>Mas-Claret, E</u>	<u>437</u>	<u>Mousavi, H</u>	<u>98</u>
<u>Mason, K</u>	<u>236</u>	<u>Mousquer, J</u>	<u>247</u>
<u>Masse, J</u>	<u>124</u>	<u>Moya-Laraño, J</u>	<u>423</u>
<u>Mataix-Solera, J</u>	<u>103</u>	<u>Mozzicafreddo, M</u>	<u>425</u>
<u>Mathieu, J</u>	<u>338</u>	<u>Mrak, T</u>	<u>486, 493</u>
<u>Matsumoto, B</u>	<u>586</u>	<u>Mtandavari, F</u>	<u>249</u>
<u>Matus, I</u>	<u>362</u>	<u>Mtandavari, Y</u>	<u>468</u>
<u>Matus Acuna, V</u>	<u>457</u>	<u>Mülbaier, H</u>	<u>455</u>
<u>Mau, R</u>	<u>261</u>	<u>Müller, C</u>	<u>465</u>
<u>Mautuit, A</u>	<u>344</u>	<u>Müller, J</u>	<u>188</u>
<u>Mayer, J</u>	<u>174, 229</u>	<u>Müller, P</u>	<u>71</u>
<u>Mayerhofer, J</u>	<u>384</u>	<u>Müller, R</u>	<u>174</u>
<u>McBratney, A</u>	<u>252</u>	<u>Mulliez, P</u>	<u>102</u>
<u>McBratney, A</u>	<u>241</u>	<u>Mulot, M</u>	<u>439</u>
<u>McCay, T</u>	<u>191</u>	<u>Mungall, C</u>	<u>624</u>
<u>McCue, L</u>	<u>624</u>	<u>Münkemüller, T</u>	<u>341</u>
<u>McDaniel, M</u>	<u>317</u>	<u>Muñoz, M</u>	<u>441</u>
<u>McGuire, K</u>	<u>325</u>	<u>Münzbergová, Z</u>	<u>101</u>
<u>McHugh, D</u>	<u>371</u>	<u>Murchie, A</u>	<u>328</u>
<u>Medina-Sauza, R</u>	<u>609</u>	<u>Murphy, B</u>	<u>58</u>
<u>Meehan, M</u>	<u>262</u>	<u>Murphy, J</u>	<u>65</u>
<u>Mehring, H</u>	<u>338</u>	<u>Murúa, J</u>	<u>618</u>
<u>Melecis, V</u>	<u>251</u>	<u>Murugan, R</u>	<u>620</u>
<u>Memoli, V</u>	<u>298</u>	<u>Muth, T</u>	<u>406</u>
<u>Menasserri, S</u>	<u>589</u>	<u>Mutschlechner, M</u>	<u>232</u>
<u>Mench, M</u>	<u>54</u>		

N

<u>Nabel, M</u>	<u>135, 136, 71, 213, 169, 323</u>	<u>Nicolas, A</u>	<u>474</u>
<u>Nagler, M</u>	<u>127, 545</u>	<u>Niedrist, G</u>	<u>350</u>
<u>Naidonova, O</u>	<u>429</u>	<u>Nightingale, A</u>	<u>391</u>
<u>Nason, M</u>	<u>542, 544</u>	<u>Nigmann, U</u>	<u>604</u>
<u>Nason, M</u>	<u>313</u>	<u>Ning, D</u>	<u>479</u>

<u>Natal da Luz, T</u>	<u>315</u>
<u>Natal-Luz, T</u>	<u>617</u>
<u>Nathalie, F</u>	<u>413</u>
<u>Nathani, K</u>	<u>374</u>
<u>Negri, I</u>	<u>178</u>
<u>Neher, D</u>	<u>85, 478</u>
<u>Neilson, R</u>	<u>347, 230</u>
<u>Neuhauser, S</u>	<u>232</u>
<u>Neuhoff, D</u>	<u>71</u>
<u>Neuhoff, D</u>	<u>323</u>
<u>Neumann, G</u>	<u>414</u>
<u>Nguyen, V</u>	<u>581</u>
<u>Nico Eisenhauer</u>	<u>104</u>

<u>Niro, E</u>	<u>379</u>
<u>Niu, X</u>	<u>391</u>
<u>Niva, C</u>	<u>247, 590, 246</u>
<u>Nocco, M</u>	<u>255, 475, 576</u>
<u>Noll, M</u>	<u>334</u>
<u>Norris, C</u>	<u>265</u>
<u>Norton, J</u>	<u>495</u>
<u>Nouwen, O</u>	<u>220</u>
<u>Novotny, V</u>	<u>416</u>
<u>Nowell-Bampton, V</u>	<u>449</u>
<u>Nuccio, E</u>	<u>512, 459</u>
<u>Nweze, J</u>	<u>359</u>

O

<u>Obregón, D</u>	<u>622</u>
<u>Ochoa-Hueso, R</u>	<u>317</u>
<u>Ochoa-Hueso, R</u>	<u>383</u>
<u>Odetayo, O</u>	<u>446</u>
<u>Oehl, F</u>	<u>225</u>
<u>Oellers, J</u>	<u>135, 136, 213, 169</u>
<u>Ohlmann, M</u>	<u>341</u>
<u>Ojanen, P</u>	<u>368</u>
<u>O'Keefe, J</u>	<u>465</u>
<u>Oldach, P</u>	<u>238</u>
<u>Oliveira, M</u>	<u>247</u>
<u>Oliver, M</u>	<u>261</u>
<u>Ollio, I</u>	<u>388</u>
<u>Ommeslag, S</u>	<u>524</u>

<u>Ooi, M</u>	<u>441</u>
<u>Oram, N</u>	<u>308</u>
<u>Orgiazzi, A</u>	<u>483, 281</u>
<u>Orrù, L</u>	<u>256</u>
<u>Ossola, A</u>	<u>466</u>
<u>Ostertag, R</u>	<u>416, 415</u>
<u>Ostle, N</u>	<u>564</u>
<u>Ostle, N</u>	<u>515</u>
<u>O'Sullivan, O</u>	<u>93</u>
<u>Oszust, K</u>	<u>467</u>
<u>Ouyang, Y</u>	<u>495</u>
<u>Ovaskainen, O</u>	<u>378</u>
<u>Oyarte Galvez, L</u>	<u>187</u>

Ó

<u>Óskarsson, H</u>	<u>381</u>
---------------------	------------

P

<u>Pablo García-Palacios</u>	<u>104</u>	<u>Petrová, E</u>	<u>359</u>
<u>Paetsch, J</u>	<u>375</u>	<u>Pettitt, T</u>	<u>313, 544</u>
<u>Paffetti, D</u>	<u>486</u>	<u>Pettitt, T</u>	<u>542</u>
<u>Pajak, M</u>	<u>525</u>	<u>Pett-Ridge, J</u>	<u>474, 512, 459</u>
<u>Palacios-Vargas, J</u>	<u>499</u>	<u>Pett-Ridge, J</u>	<u>479</u>
<u>Palomino, J</u>	<u>395</u>	<u>Philippot, L</u>	<u>540</u>
<u>Panaqos, P</u>	<u>483, 281</u>	<u>Phillips, H</u>	<u>217</u>
<u>Panek, J</u>	<u>467</u>	<u>Phillips, H</u>	<u>166</u>
<u>Papa, G</u>	<u>178</u>	<u>Phillips, H</u>	<u>332</u>
<u>Paranychianakis, N</u>	<u>410</u>	<u>Phillips, L</u>	<u>449</u>
<u>Parnell, J</u>	<u>346</u>	<u>Pietrzykowski, M</u>	<u>525</u>
<u>Parr, K</u>	<u>116</u>	<u>Pintarič, S</u>	<u>274</u>
<u>Parron, L</u>	<u>247</u>	<u>Pirhonen, M</u>	<u>366</u>
<u>Parron Vargas, L</u>	<u>552</u>	<u>Piveteau, P</u>	<u>102</u>
<u>Pasari, B</u>	<u>395</u>	<u>Pjevac, P</u>	<u>300</u>
<u>Paschke, K</u>	<u>206</u>	<u>Plaas, E</u>	<u>365</u>
<u>Patil, S</u>	<u>624</u>	<u>Planchais, S</u>	<u>344</u>
<u>Patro, T</u>	<u>395</u>	<u>Plantegenest, M</u>	<u>594</u>
<u>Patwary, R</u>	<u>522</u>	<u>Plassard, C</u>	<u>562</u>
<u>Paul Chowdhury, S</u>	<u>414</u>	<u>Plavsic, M</u>	<u>339</u>
<u>Paula, F</u>	<u>482</u>	<u>Plunger, J</u>	<u>158, 288</u>
<u>Paz, P</u>	<u>362</u>	<u>Png, K</u>	<u>564</u>
<u>Peay, K</u>	<u>192</u>	<u>Poch, R</u>	<u>247</u>
<u>Pedro, B</u>	<u>413</u>	<u>Podile, A</u>	<u>395</u>
<u>Pedzich, S</u>	<u>191</u>	<u>Podmirseg, S</u>	<u>127, 545</u>
<u>Peguero, G</u>	<u>105</u>	<u>Poll, C</u>	<u>269, 354</u>
<u>Peintner, U</u>	<u>517, 518, 557</u>	<u>Pollierer, M</u>	<u>151, 157</u>
<u>Peintner, U</u>	<u>514</u>	<u>Pollierer, M</u>	<u>99</u>
<u>Pelaez, A</u>	<u>327</u>	<u>Pommeresche, R</u>	<u>98</u>
<u>Peláez, A</u>	<u>222</u>	<u>Ponge, J</u>	<u>105</u>

<u>Peláez, A</u>	<u>523</u>	<u>Poret-Peterson, A</u>	<u>481</u>
<u>Pellegrinetti, T</u>	<u>482</u>	<u>Porto, J</u>	<u>611</u>
<u>Pellerin, F</u>	<u>333</u>	<u>Porto, M</u>	<u>597</u>
<u>Pellitier, P</u>	<u>192</u>	<u>Postma, J</u>	<u>570</u>
<u>Pelosi, C</u>	<u>332</u>	<u>Postolache, C</u>	<u>583</u>
<u>Peltoniemi, K</u>	<u>368</u>	<u>Potapov, A</u>	<u>108, 109, 67, 338, 276</u>
<u>Peña-Álvarez, V</u>	<u>222, 523</u>	<u>Potapov, A</u>	<u>240</u>
<u>Peñas, J</u>	<u>416, 439</u>	<u>Potapov, M</u>	<u>240</u>
<u>Peña-Venegas, C</u>	<u>63</u>	<u>Pothula, S</u>	<u>360</u>
<u>Peña-Venegas, C</u>	<u>338</u>	<u>Potthoff, M</u>	<u>365</u>
<u>Penev, P</u>	<u>474</u>	<u>Poulenard, J</u>	<u>295</u>
<u>Pennanen, T</u>	<u>366, 363, 368</u>	<u>Pouyat, R</u>	<u>466</u>
<u>Peñuelas, J</u>	<u>516</u>	<u>Power, K</u>	<u>178</u>
<u>Peñuelas, J</u>	<u>105</u>	<u>Poydras, T</u>	<u>528</u>
<u>Perea, R</u>	<u>541</u>	<u>Praeg, N</u>	<u>275, 232, 224, 290, 308, 434</u>
<u>Pereira, S</u>	<u>611</u>	<u>Pravia, A</u>	<u>277</u>
<u>Pereira, S</u>	<u>617</u>	<u>Preece, C</u>	<u>516</u>
<u>Pereira, S</u>	<u>621</u>	<u>Preedy, K</u>	<u>347</u>
<u>Pereira, S</u>	<u>283</u>	<u>Preiser, J</u>	<u>67</u>
<u>Peres, G</u>	<u>620</u>	<u>Pressel, S</u>	<u>537</u>
<u>Pérès, G</u>	<u>589, 594, 599, 614, 284</u>	<u>Prevosto, B</u>	<u>218</u>
<u>Perez, A</u>	<u>155</u>	<u>Prieto-Fernandez, Á</u>	<u>621, 577, 407, 283</u>
<u>Pérez-Pardal, L</u>	<u>597</u>	<u>Probst, M</u>	<u>287, 517, 514, 518, 557</u>
<u>Perilla Henao, L</u>	<u>586</u>	<u>Prosenkov, A</u>	<u>327, 523</u>
<u>Peris, J</u>	<u>349</u>	<u>Prosenkov, A</u>	<u>222</u>
<u>Peris-Felipo, F</u>	<u>346</u>	<u>Prosser, J</u>	<u>140</u>
<u>Peris-Felipo, F</u>	<u>155, 163</u>	<u>Prout, B</u>	<u>468</u>
<u>Pernin, C</u>	<u>548, 553</u>	<u>Provent, F</u>	<u>358</u>
<u>Perrone, M</u>	<u>404</u>	<u>Pruschitzki, U</u>	<u>219</u>
<u>Perrone, S</u>	<u>473</u>	<u>Prylutskyi, O</u>	<u>88</u>
<u>Pertile, G</u>	<u>467</u>	<u>Pugnaire, F</u>	<u>204</u>
<u>Pestana, K</u>	<u>415</u>		

<u>Petchey, O</u>	<u>319</u>
<u>Petersdorf, M</u>	<u>504</u>
<u>Petersdorf, M</u>	<u>162</u>
<u>Petersen, H</u>	<u>105</u>
<u>Petrakis, G</u>	<u>442</u>

<u>Purvis, A</u>	<u>377</u>
<u>Putten, W</u>	<u>318</u>
<u>Pylak, M</u>	<u>467</u>
<u>Pylni, S</u>	<u>112</u>

Q

<u>Qin, C</u>	<u>192</u>
<u>Qin, J</u>	<u>421</u>
<u>Quideau, S</u>	<u>265</u>
<u>Quigley, E</u>	<u>607</u>

<u>Quijano-Medina, I</u>	<u>395</u>
<u>Quinton, J</u>	<u>515</u>
<u>Quinton, J</u>	<u>564</u>
<u>Quist, C</u>	<u>131</u>

R

<u>R. Gallego2, J</u>	<u>523</u>
<u>Rad, C</u>	<u>484</u>
<u>Rad, C</u>	<u>342</u>
<u>Rajniš, T</u>	<u>274</u>
<u>Ramond, J</u>	<u>125</u>
<u>Ramsay, L</u>	<u>522</u>
<u>Ranits, C</u>	<u>300</u>
<u>Ranjard, L</u>	<u>96, 102, 344, 396</u>
<u>Rasche, F</u>	<u>84</u>
<u>Readyhough, T</u>	<u>85</u>
<u>Redmond, C</u>	<u>416</u>
<u>Redondo-Nieto, M</u>	<u>342, 324</u>
<u>Reed, S</u>	<u>261</u>
<u>Remelli, S</u>	<u>154, 153, 268</u>
<u>Reverchon, F</u>	<u>609</u>
<u>Revillini, D</u>	<u>430</u>
<u>Reynolds, D</u>	<u>182</u>

<u>Robles, L</u>	<u>255</u>
<u>Robles, L</u>	<u>475</u>
<u>Rocha, F</u>	<u>254</u>
<u>Rock, A</u>	<u>242</u>
<u>Rodgers, H</u>	<u>492</u>
<u>Rodrigues, R</u>	<u>132</u>
<u>Rodríguez Eugenio, N</u>	<u>247</u>
<u>Rodriguez-Garrido, B</u>	<u>54, 407</u>
<u>Rodríguez-Garrido, B</u>	<u>621, 577</u>
<u>Rodriguez-Rojas, L</u>	<u>518</u>
<u>Rodriguez-Sanchez, A</u>	<u>123</u>
<u>Rodríguez-Valdés, E</u>	<u>523</u>
<u>Rog, I</u>	<u>285</u>
<u>Roisin, Y</u>	<u>208</u>
<u>Rojales, J</u>	<u>513</u>
<u>Rojo, V</u>	<u>315, 610</u>
<u>Romahn, J</u>	<u>378, 375</u>

<u>Rhein, R</u>	<u>604</u>	<u>Römbke, J</u>	<u>315, 455, 610</u>
<u>Rhymes, J</u>	<u>133</u>	<u>Romdhane, S</u>	<u>540</u>
<u>Ribeiro, T</u>	<u>250</u>	<u>Romero, F</u>	<u>281</u>
<u>Rice, C</u>	<u>528</u>	<u>Rondolini, M</u>	<u>271</u>
<u>Rich, V</u>	<u>558</u>	<u>Roose, T</u>	<u>391</u>
<u>Richard, C</u>	<u>589</u>	<u>Rose Edwin, N</u>	<u>93</u>
<u>Rief, A</u>	<u>288</u>	<u>Roß-Nickoll, M</u>	<u>135, 136, 213, 169</u>
<u>Riesgo-Mazaira, M</u>	<u>327</u>	<u>Roth, T</u>	<u>384</u>
<u>Rillig, M</u>	<u>111</u>	<u>Rothfuss, Y</u>	<u>269</u>
<u>Rimet, F</u>	<u>453</u>	<u>Roucaute, M</u>	<u>599</u>
<u>Rineau, F</u>	<u>220</u>	<u>Rousk, J</u>	<u>293</u>
<u>Ristok, C</u>	<u>206</u>	<u>Rousseau, M</u>	<u>183</u>
<u>Ritz, K</u>	<u>573</u>	<u>Rousset-Rouvière, S</u>	<u>358</u>
<u>Rivera, D</u>	<u>395</u>	<u>Ruiz, J</u>	<u>349</u>
<u>Rivilla, R</u>	<u>324</u>	<u>Russel, D</u>	<u>276</u>
<u>Rivilla, R</u>	<u>342</u>	<u>Russell, D</u>	<u>225</u>
<u>Rixen, C</u>	<u>489</u>	<u>Rutigliano, F</u>	<u>379</u>
<u>Roberts, D</u>	<u>347</u>	<u>Rutrough, A</u>	<u>374</u>
<u>Robin, A</u>	<u>413</u>	<u>Ryan, D</u>	<u>431</u>
<u>Robinson, C</u>	<u>471</u>	<u>Ryan, K</u>	<u>411, 405, 417, 419</u>
<u>Robles, D</u>	<u>481</u>	<u>Rzehak, T</u>	<u>275, 232, 224</u>

S

<u>Sadet-bourgeteau, S</u>	<u>102</u>	<u>Sierka, E</u>	<u>525</u>
<u>Saez Sandino, T</u>	<u>104</u>	<u>Siewert, B</u>	<u>517</u>
<u>Sage, H</u>	<u>367</u>	<u>Siggers, J</u>	<u>409</u>
<u>Sahdra, A</u>	<u>449</u>	<u>Signorini, M</u>	<u>350</u>
<u>SAINT-ANDRE, L</u>	<u>579</u>	<u>Sikes, B</u>	<u>528</u>
<u>Salazar-Fillippo, A</u>	<u>86</u>	<u>Siles, J</u>	<u>139</u>
<u>Salinas, C</u>	<u>123</u>	<u>Siles Asaff, I</u>	<u>121</u>
<u>Salmane, I</u>	<u>251</u>	<u>Silva, O</u>	<u>247, 590, 246</u>

<u>Salmela, M</u>	<u>363</u>	<u>Silva, P</u>	<u>607</u>
<u>Salmon, S</u>	<u>240</u>	<u>Sim, C</u>	<u>253</u>
<u>Salmon, S</u>	<u>105</u>	<u>Simon, E</u>	<u>300</u>
<u>Samad, A</u>	<u>265</u>	<u>Simoni, S</u>	<u>505, 404</u>
<u>Samar, E</u>	<u>513</u>	<u>Sinanaj, B</u>	<u>537</u>
<u>Sanchez, A</u>	<u>344</u>	<u>Singer, S</u>	<u>479</u>
<u>Sánchez Durán, S</u>	<u>271</u>	<u>Singh, B</u>	<u>258, 386</u>
<u>Sánchez-Moreno, S</u>	<u>423</u>	<u>Singh Sidhu, J</u>	<u>237</u>
<u>Sánchez-Navarro, V</u>	<u>388</u>	<u>Siniscalco, C</u>	<u>535</u>
<u>Sanchis, A</u>	<u>103</u>	<u>Six, J</u>	<u>87, 229, 237</u>
<u>Sanczuk, P</u>	<u>203</u>	<u>Six, J</u>	<u>279</u>
<u>San-Jose, L</u>	<u>333</u>	<u>Skidmore, A</u>	<u>183</u>
<u>Santini, G</u>	<u>287</u>	<u>Slate, M</u>	<u>261</u>
<u>Santini, G</u>	<u>298</u>	<u>Sleutel, S</u>	<u>215</u>
<u>Santonja, M</u>	<u>76, 218</u>	<u>Sleutel, S</u>	<u>129</u>
<u>Santorufó, L</u>	<u>287, 298</u>	<u>Smalla, K</u>	<u>414</u>
<u>Sapkota, R</u>	<u>306, 314</u>	<u>Smith, M</u>	<u>409</u>
<u>Saravesi, K</u>	<u>272</u>	<u>Smith, M</u>	<u>624</u>
<u>Sarma, P</u>	<u>395</u>	<u>Snethlage, M</u>	<u>290</u>
<u>Sarto, M</u>	<u>528</u>	<u>Sniegocki, R</u>	<u>374</u>
<u>Sartori, G</u>	<u>535</u>	<u>Soares de Carvalho, T</u>	<u>593</u>
<u>Sathiya Seelan, J</u>	<u>374</u>	<u>Soares Filho, C</u>	<u>254</u>
<u>Savage, J</u>	<u>415</u>	<u>Sokol, N</u>	<u>474</u>
<u>Schade, M</u>	<u>163</u>	<u>Solascasas, P</u>	<u>383</u>
<u>Schaefer, I</u>	<u>392, 602</u>	<u>Solbach, M</u>	<u>165, 488</u>
<u>Schaffner, U</u>	<u>564</u>	<u>Solberg, S</u>	<u>98</u>
<u>Scheffczyk, A</u>	<u>315</u>	<u>Soleiman, J</u>	<u>448</u>
<u>Scheu, S</u>	<u>67, 99, 151, 157, 392</u>	<u>Solís García, I</u>	<u>609</u>
<u>Schiefelbein, U</u>	<u>309</u>	<u>Solly, E</u>	<u>87</u>
<u>Schiffers, K</u>	<u>71</u>	<u>Sommermann, L</u>	<u>414</u>
<u>Schlaghamersky, J</u>	<u>629</u>	<u>Soto, D</u>	<u>388</u>
<u>Schlöter, M</u>	<u>376</u>	<u>Soto, M</u>	<u>54</u>

<u>Schmalenberger, A</u>	<u>225</u>	<u>Soudzilovskaia, N</u>	<u>210, 220, 181</u>
<u>Schmelz, R</u>	<u>455, 610</u>	<u>Sousa, Á</u>	<u>617</u>
<u>Schmelz, R</u>	<u>315</u>	<u>Sousa, A</u>	<u>617</u>
<u>Schmidt, I</u>	<u>105</u>	<u>Sousa, J</u>	<u>315</u>
<u>Schmidt, O</u>	<u>521, 236, 403, 402, 446</u>	<u>Sousa, P</u>	<u>607</u>
<u>Schmidt, O</u>	<u>197</u>	<u>Spaans, F</u>	<u>328, 336</u>
<u>Schneider, C</u>	<u>451, 455</u>	<u>Sparks, J</u>	<u>257</u>
<u>Schöb, C</u>	<u>204</u>	<u>Spence, S</u>	<u>180</u>
<u>Schoebitz, M</u>	<u>362</u>	<u>Spielvogel, S</u>	<u>331</u>
<u>Schon, N</u>	<u>531</u>	<u>Spor, A</u>	<u>540</u>
<u>Schöpfer, L</u>	<u>171</u>	<u>Stache, F</u>	<u>354</u>
<u>Schröer, L</u>	<u>135, 136, 213, 169</u>	<u>Stanley, D</u>	<u>437</u>
<u>Schulz, S</u>	<u>376</u>	<u>Stanton, K</u>	<u>542, 544</u>
<u>Schuster, R</u>	<u>172</u>	<u>Stanton, K</u>	<u>313</u>
<u>Schwab, S</u>	<u>254</u>	<u>Stark, L</u>	<u>261</u>
<u>Schwalb, S</u>	<u>185</u>	<u>Stathopoulou, D</u>	<u>442</u>
<u>Schwartz, C</u>	<u>344</u>	<u>Steenwerth, K</u>	<u>475, 481</u>
<u>Schwarzfeld, M</u>	<u>449</u>	<u>Steinwandter, M</u>	<u>127, 158, 290, 288</u>
<u>Schweigkofler, W</u>	<u>179</u>	<u>Sterck, F</u>	<u>156</u>
<u>Schwelm, A</u>	<u>335</u>	<u>Stevenson, P</u>	<u>437</u>
<u>Schwilch, G</u>	<u>533</u>	<u>Stewart, J</u>	<u>88</u>
<u>Scott, T</u>	<u>501</u>	<u>Strasberg, D</u>	<u>416</u>
<u>Searcy, C</u>	<u>430</u>	<u>Stratemann, L</u>	<u>135, 136, 213</u>
<u>Seeber, J</u>	<u>275, 127, 224, 158, 290, 288</u>	<u>Stratemann, L</u>	<u>169</u>
<u>Serrano Grijalva, L</u>	<u>317</u>	<u>Strigens, A</u>	<u>237</u>
<u>Sessitsch, A</u>	<u>418</u>	<u>Strobl, S</u>	<u>127</u>
<u>Setälä, , H</u>	<u>466</u>	<u>Strobl, S</u>	<u>545</u>
<u>Shaaf, S</u>	<u>395</u>	<u>Struik, P</u>	<u>318</u>
<u>Shackelford, N</u>	<u>529</u>	<u>Strybos, S</u>	<u>86</u>
<u>Shahrtash, M</u>	<u>122</u>	<u>Stucke, A</u>	<u>267</u>
<u>Shaw, L</u>	<u>391</u>	<u>Sturludóttir, E</u>	<u>381</u>
<u>Shelton, B</u>	<u>180</u>	<u>Suescun, U</u>	<u>333</u>

<u>Shepherd, M</u>	<u>277</u>	<u>Suhadolc, M</u>	<u>400, 274</u>
<u>Shi, S</u>	<u>249, 248, 468</u>	<u>Sultana, T</u>	<u>68</u>
<u>Shi, Y</u>	<u>331</u>	<u>Sun, X</u>	<u>240</u>
<u>Shimizu, T</u>	<u>187</u>	<u>Sünnemann, M</u>	<u>211</u>
<u>Shiono, T</u>	<u>416</u>	<u>Suojala-Ahlfors, I</u>	<u>366</u>
<u>Siegenthaler, A</u>	<u>183</u>	<u>Swallow, M</u>	<u>265</u>
<u>Siegieda, D</u>	<u>467</u>	<u>Swart, G</u>	<u>349, 163</u>
<u>Siepel, H</u>	<u>504, 592</u>	<u>Sweeney, C</u>	<u>564</u>
<u>Siepel, H</u>	<u>162</u>	<u>Swingley, W</u>	<u>149</u>
<u>Sieradzki, E</u>	<u>474</u>	<u>Sys, S</u>	<u>451</u>
<u>Sieradzki, E</u>	<u>586</u>	<u>Szlavec, K</u>	<u>203, 466</u>

Š

<u>Šibanc, N</u>	<u>274, 302, 486, 493</u>	<u>Šurinová, M</u>	<u>101</u>
<u>Štraus, I</u>	<u>493</u>	<u>Šustr, V</u>	<u>359</u>

T

<u>Taberlet, P</u>	<u>295</u>	<u>Tiemann, L</u>	<u>317</u>
<u>Tahovská, K</u>	<u>601</u>	<u>Tiemann, L</u>	<u>457</u>
<u>Tajovský, K</u>	<u>168</u>	<u>Tienda Serrano, S</u>	<u>349</u>
<u>Talavera, M</u>	<u>423</u>	<u>Tienda Serrano, S</u>	<u>353</u>
<u>Tamayo-Ramos, J</u>	<u>342</u>	<u>Tietema, A</u>	<u>305</u>
<u>Tang, J</u>	<u>191</u>	<u>Tietema, A</u>	<u>105</u>
<u>Tang, Y</u>	<u>374</u>	<u>Tison, L</u>	<u>332</u>
<u>Tang, Y</u>	<u>241</u>	<u>Todman, L</u>	<u>573</u>
<u>Tanka, F</u>	<u>301</u>	<u>Topalovic, O</u>	<u>348</u>
<u>Tappeiner, U</u>	<u>288, 350</u>	<u>Torro-Galiana, A</u>	<u>347</u>
<u>Tarchi, F</u>	<u>505, 404</u>	<u>Toschki, A</u>	<u>135, 136, 213</u>
<u>Tardif, A</u>	<u>550</u>	<u>Toschki, A</u>	<u>169</u>
<u>Tasser, E</u>	<u>557</u>	<u>Tosi, M</u>	<u>622</u>

<u>Täufer, F</u>	<u>323</u>	<u>Toth, Z</u>	<u>466</u>
<u>Tayaban, K</u>	<u>180</u>	<u>Toyota, K</u>	<u>214</u>
<u>Tebbe, C</u>	<u>256</u>	<u>Tracy, S</u>	<u>403, 402, 561</u>
<u>Tedersoo, L</u>	<u>88, 281</u>	<u>Tracy, S</u>	<u>197</u>
<u>Tejedor Calvo, E</u>	<u>271</u>	<u>Tracy, S</u>	<u>437</u>
<u>Telagathoti, A</u>	<u>517, 514, 518</u>	<u>Trap, J</u>	<u>218, 562</u>
<u>Tella Garcia, E</u>	<u>557</u>	<u>Trasar-Cepeda, C</u>	<u>407, 577</u>
<u>Tentugal, R</u>	<u>617</u>	<u>Trautmann, S</u>	<u>232</u>
<u>Terrat, S</u>	<u>96</u>	<u>Trifuoggi, M</u>	<u>379</u>
<u>Terrat, S</u>	<u>396</u>	<u>Triped, J</u>	<u>102</u>
<u>The SBF Team</u>	<u>108</u>	<u>Trivedi, P</u>	<u>395, 409</u>
<u>Thébaut, E</u>	<u>338</u>	<u>Tsai, S</u>	<u>482</u>
<u>Theissinger, K</u>	<u>375</u>	<u>Tsai, S</u>	<u>132</u>
<u>Thiele-Bruhn, S</u>	<u>256</u>	<u>Tsai, S</u>	<u>250</u>
<u>Thijs, S</u>	<u>220</u>	<u>Tsegaye Gebremikael, M</u>	<u>129</u>
<u>Thompson, R</u>	<u>542, 544</u>	<u>Tsiafouli, M</u>	<u>276</u>
<u>Thomson, R</u>	<u>313</u>	<u>Tsiknia, M</u>	<u>442</u>
<u>Thouvenot, L</u>	<u>332, 219</u>	<u>Tucker, C</u>	<u>261</u>
<u>Thuiller, F</u>	<u>295</u>	<u>Turcati, L</u>	<u>344</u>
<u>Thuiller, W</u>	<u>338, 341</u>	<u>Turillazzi, F</u>	<u>404</u>

U

<u>Ugolini, F</u>	<u>117</u>	<u>Urionabarrenetxea, E</u>	<u>54</u>
<u>Unuk Nahberger, I</u>	<u>486</u>	<u>Urwin, P</u>	<u>547</u>
<u>Urbach, D</u>	<u>290</u>	<u>Urwin, P</u>	<u>561</u>
<u>Urbina, I</u>	<u>346</u>	<u>Urwin, P</u>	<u>556</u>
<u>Urich, T</u>	<u>489</u>		

V

<u>Väänänen, P</u>	<u>368</u>	<u>Verbeke, I</u>	<u>247</u>
<u>Vaccari, F</u>	<u>113</u>	<u>Verbruggen, E</u>	<u>86</u>
<u>Vaccaro, F</u>	<u>311</u>	<u>Verbruggen, E</u>	<u>516</u>

<u>Vahter, T</u>	<u>551</u>	<u>VERGNES, A</u>	<u>344, 343</u>
<u>Valboa, G</u>	<u>505</u>	<u>Verheyen, K</u>	<u>203</u>
<u>Valdes, H</u>	<u>155</u>	<u>Verlingue, K</u>	<u>343</u>
<u>Valtonen, A</u>	<u>272</u>	<u>Vestergård, M</u>	<u>348</u>
<u>Van der Putten,</u>	<u>132</u>	<u>Vestrovsky, T</u>	<u>627</u>
<u>W</u>			
<u>Van Nuland, M</u>	<u>88, 192</u>	<u>Vettori, C</u>	<u>486</u>
<u>Van Rijssel, S</u>	<u>282</u>	<u>Vidal-Beaudet, L</u>	<u>344</u>
<u>Van Tol, J</u>	<u>619</u>	<u>Vierna, J</u>	<u>315, 610</u>
<u>Vandecasteele, B</u>	<u>524</u>	<u>Vieublé, L</u>	<u>554</u>
<u>Vandvik, V</u>	<u>101</u>	<u>Vignozzi, N</u>	<u>505</u>
<u>Vangronsveld, J</u>	<u>220</u>	<u>Vigo, C</u>	<u>430</u>
<u>Vanquellova, E</u>	<u>184</u>	<u>Vilela, J</u>	<u>54</u>
<u>Varah, A</u>	<u>230</u>	<u>Vilkij, Z</u>	<u>262</u>
<u>Varga, S</u>	<u>519</u>	<u>Villar-Moreno, R</u>	<u>353</u>
<u>Vargas, R</u>	<u>247</u>	<u>Villenave, C</u>	<u>102, 344</u>
<u>Varner, R</u>	<u>558</u>	<u>Visentin, F</u>	<u>268</u>
<u>Varone, L</u>	<u>535</u>	<u>Visser, J</u>	<u>570</u>
<u>Vasconcelos-</u>	<u>223</u>	<u>Vittadini, E</u>	<u>369</u>
<u>Brogioni, L</u>			
<u>Vautrin, F</u>	<u>102</u>	<u>Vittoz, P</u>	<u>416, 439</u>
<u>Vaz, B</u>	<u>255</u>	<u>Vizcaíno, A</u>	<u>315, 610</u>
<u>Vázquez</u>	<u>499</u>	<u>Volkering, F</u>	<u>509</u>
<u>González, M</u>			
<u>Veen, C</u>	<u>156, 282, 286</u>	<u>Voyron, S</u>	<u>426</u>
<u>Vega, A</u>	<u>611</u>	<u>Vrignaud, G</u>	<u>102</u>
<u>Velmala, S</u>	<u>366, 363</u>		

V

<u>van Bodegom, P</u>	<u>210, 181</u>	<u>van der Zanden, I</u>	<u>195</u>
<u>van den Bergh, S</u>	<u>170</u>	<u>van Diepen, L</u>	<u>398, 492</u>
<u>van den Hoogen,</u>	<u>88</u>	<u>van Diepen, L</u>	<u>231</u>
<u>J</u>			
<u>van der Hagen, H</u>	<u>210</u>	<u>van Diggelen, C</u>	<u>86</u>
<u>van der Heijden,</u>	<u>458</u>	<u>van Diggelen, R</u>	<u>86</u>
<u>M</u>			

van der Heijden, M 281
van der Putten, W 156, 282, 217

van der Putten, W 317
van der Vinne, A 570

van Ruijven, J 574

van Straalen, N 60
Velmala, S 368
von Rohr, G 533
von Spinn, J 158

W

Wadoux, A 252
Wagstaffe, A 313, 542, 544
Wall, D 200, 112
Wall, D 316
Wall, D 125, 247, 422
Wall, D 423
Walsh, L 197

Walter, C 594
Wang, D 564
Wang, J 395, 386
Wang, M 322, 342, 324
Weatherley, A 530
Weber, B 290
Wee, J 152, 253
Wei, L 257
Weicht, T 85
Weigelt, A 488
Weiß, L 604
Weißbach, S 451
Weißbecker, C 604
Weisskopf, P 279
Welton, P 415

Wesemael, W 129, 215
West, J 189
Wetzel, C 453
Whitman, T 189
Whitmore, A 573
Wichern, F 185
Widmer, F 174, 384, 278, 92, 376, 533

Widmer, F 279
Widyastuti, R 67
Williams, J 585
Wills, S 473, 370
Winandy, L 333
Winding, A 306, 314
Winterfeldt, S 293
Witjes, M 338
Wong, C 255
Woś, B 525
Wu, D 321
Wu, J 564
Wu, W 605
Wu, X 185
Wu, Y 564

X

Xie, C 191

Xue, P 252

Xu, G 268

Y

Yagi, R 415

Yakovenko, D 538

Yang, Q 395

Yang, X 182

Yao, E 475

Yao, T 598

Yarwood, S 466

Yesilonis, I 466

Young, G 197

Young, M 449

Young, S 248, 468

Yuan, M 474, 459

Yuan, M 479, 512

Z

Zaady, E 395

Zahorec, A 457

Zaitsev, A 72

Zanella, A 268

Zapf, K 123

Zaviezo, T 155

Zawadka, J 573

Zaytsev, A 276

Zeiss, R 219

ZELLER, B 579

Zervas, A 306

Zeze, A 125

Zhang, C 338

Zhang, N 549

Zhong, L 151

Zhou, G 161

Zhou, H 564

Zhou, J 52

Zhou, Z 67

Zhu, K 192

Zhu, Y 395

Ziadi, N 124

Zimmermann, I 331

Zinger, L 333

Zobel, M 551

Zornoza, R 388