3rd Global Soil Biodiversity Conference 2023

Late Breaking Poster Abstracts

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Deadwood as a hotspot for biodiversity, better revealed by sequential DNA extraction

Maraike Probst[1], Judith Ascher-Jenull[1], Sabine Podmirseg[1], Sophia Strobl[1], Magdalena Nagler[2], **Heribert Insam[1]**, Maria Gòmez-Brandòn[3]

[1]Dept of Microbiology, University of Innsbruck, Innsbruck, Austria, [2]EURAC, Bozen, Italy, [3]Grupo de Ecoloxía Animal (GEA), Universidade de Vigo , Vigo, Spain

Aim: Studies on the microbiota of various habitats mostly rely on total DNA extracts obtained directly from environmental samples. The total DNA consists of both intra- and extracellular DNA, which differ in terms of their ecological interpretation. In the present study, we have investigated for the first time the differences among the three DNA types using microbiome sequencing of *Picea abies* deadwood logs.
Method: We differentiated among the microbiome derived from three different extraction procedures, yielding total, eDNA, Intra- and extracellular DNA.
Results: While the bacterial compositions of all DNA types were comparable in terms of more abundant organisms and mainly depended on the decay class, we found substantial differences between DNA types with regard to less abundant amplicon sequence variants (ASVs). The analysis of the sequentially extracted intra- and extracellular DNA fraction, respectively, increased the ecological depth of analysis compared to the directly extracted total DNA pool. Both DNA fractions were comparable in proportions and the extracellular DNA appeared to persist in the *P. abies* deadwood logs, thereby causing its masking effect. Indeed, the extracellular DNA masked the compositional dynamics of intact cells in the total DNA pool.
Conclusions: Our results provide evidence that the choice of DNA type for analysis might benefit a study's answer to its respective ecological question, and it may offer a better picture of the contribution of minor taxa.

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Explore rhizobiomes in crop rotation system

Shunran Hu[1], Stefan Geisen[1]

[1]*Wageningen University and Research, Wageningen, the Netherlands*

Aim:
Crop rotation systems increase the biodiversity aboveground, change soil physicochemical properties, and thus stimulate the diversity belowground. Conversely, rhizobiomes may enhance plant performance regarding health and growth. However, most studies in the field of rhizobiome have only focused on the community composition. What is not yet clear is the temporal change of rhizobiome functioning and multitrophic interactions. We will investigate the rhizobiomes across crop growth stages in diversified rotation systems, which may contribute to linking the distinct rhizobiomes to rhizobiome functioning in terms of crop performance.

Method:
We collected soil samples from four rotation systems across four growth stages of wheat. The rhizobiomes (bacteria, fungi, nematodes and protists) in the soil samples were added as inocula in a pot experiment. Within 60 days, we determined the roles of rhizobiomes and their interactions in contributing to crop performance by measuring the growth of maize and nutrient cycling.

Results:
We expect that increased crop diversity promotes rhizobiome diversity. The diversified rotation systems harbour higher abundances of plant beneficial rhizospheric microorganisms (PBRMs) in all growth stages. So far, we found that the rhizobiomes in diversified crop rotation systems had positive effect on plant growth in first harvest (after 15 days). However, the influences of rhizobiomes were not significant in second harvest (after 30 days).

Conclusions:
The results showed that increased rhizobiomes diversity stimulate plant growth and nutrient cycling in early stage, but the differences disappear after some time as the rhizobiomes in soil might be controlled by the new host plant.

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Does intercropping promote soil Mesofauna resilience to stress?

Deaa Alwanney[1], Thomas Döring[1]

[1]*Agroecology and Organic Farming Group, University of Bonn, Auf dem Hügel 6, Bonn, Germany*

Aim:

Global climate change implies threats to soil biodiversity. Yet, the impact of dry periods and robust precipitation is still poorly understood. Whereas many environmental avails of intercropping has been established, field-based research on the interaction with soil inhabitants under stress is lacking.

Method:

The response of oat, Faba bean and their mixture to 2-levels of water stress were tested. For continues 10 days, plots either received 12 ml daily (Fld) or deprived from water (Dry). Soil samples were collected before treatment (T0) and 5 times afterwards at 10-day intervals for Berlese traps.

Results:

Mesofaunal density was more vulnerable to dry than wet conditions. The highest density observed at T0 in the beans have shifted to oat at T1.

Under (Fld), sole crops harbored more individuals than the mixture at T1, and more diversified community at T5 witnessed by Shannon-index as following; Oat>Bean>Mixture. Crop did not alter the community under (Dry).

Unlike beetles, springtails correlated negativity to soil temperature and positively to water content. Both were more abundant in bean than oat at T2 and T4.

Detritivores as well as Acari:Collembola are promising indicators for resilience estimation, while rapid increase in fungivorous post to (Fld) does not necessarily indicate recovery.

Contrary to expected, Phytophagous forms did not vary among cropping systems and they recovered faster in sole crops suggesting a rethinking in legume-cereal combination as a resilience promoting measure against weather extremes.

Conclusions:

Soil mesofauna sensitivity and dependence on multiple factors provide a promising but yet a limited tool to forecast climate change effects.

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Influence of islands of natural vegetation on the diversity of arbuscular mycorrhizal fungi in vineyards

Josefina Bota[1]**,** Elena Baraza[1], Arantxa Molins[1], Alvaro López-García[2]

[1]Grup de Recerca en Biologia de les Plantes en Condicions Mediterranies, INAGEA, Departament de Biologia, Universitat de les Illes Balears, Palma, Spain, [2]Instituto Interuniversitario de Investigación del Sistema Tierra en Andalucía (IISTA); Universidad de Jaén, Campus Las Lagunillas, s/n. 23071 , Jaén, Spain

Aim: In recent years, numerous studies have demonstrated the importance of arbuscular mycorrhizae fungi (AMF) in the healthy maintenance of multiple crops, including vineyards. The diversity of AMF in the crops is largely determined by the management of the soil of the crop itself. However, it is possible that the presence of natural vegetation serves as a reservoir to increase the diversity of AMF species in nearby crops. The general objective of this proposal is to investigate to what extent the microbial communities present in natural areas disperse towards vineyards distributed throughout the island of Menorca.

Method: The study has been carried out at 6 vineyards of Menorca Spain. In each plot, a 60 m transect was carried out that included 30 m in the natural vegetation and 30 in the vine plantation. A combined sample of roots was taken at every 5 m of the transect. We analysed the root AMF communities using the data obtained from NGS of soil DNA from 18S rRNA gene using the Glomeromycota-specific primers. Sequences obtained from Illumina amplification were used to calculate α diversity index and analysed by PERMANOVA and nonmetric multidimensional scaling method (NMDS).

Results: The phylogenetic diversity of AMF is higher in vineyards than in natural areas. Moreover, the NMDS ordination obtained from the abundance of families of AMF shows how the natural samples appear closely linked to the abundance of Glomeraceae while the vineyard samples include a greater diversity of families of AMF. The PERMANOVA analysis shows a significant influence of land use on the composition of families, but this effect was modulated by the sample vineyard. Contrary, the distance to the edge was not significant.

Conclusions: The transformation from natural vegetation to a vineyard has meant a meaningful change in the biological properties of the soils of Menorca. However, the results reveal a greater phylogenetic diversity of AMF within the vineyards and a low influence of the surrounding vegetation on AMF community composition. The current management of Menorcan vineyards allows the maintaining of a diverse community of AMF that ensures its function in the soil.

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Method and Technique of Soil Animal Knowledge Graph Construction: A Case Study of Soil Mites

Meixiang Gao[1,2], Jiaqi Zhu[1,2], Shuang Liu[3], Xin Cheng[4], Dong Liu[5], Yanshegn Li[4]

[1]Ningbo University, Ningbo, China, [2]Ningbo Universities Collaborative Innovation Center for land and marine spatial utilization and governance research at Ningbo University, Ningbo, China, [3]Miyun Experimental Middle School Attached to Beijing Normal University, Beijing, China, [4]School of Remote Sensing and Information Engineering, Wuhan University, Wuhan, China, [5]Key laboratory of Wetland Ecology and Environment, Northeast Institute of Geography and Agroecology Chinese Academy of Sciences, Changchun, China

Aim:
Soil zoology is undergoing a period of development with a knowledge system at its core and data-driven. The current widely used data processing and analysis methods based on databases are facing the contradiction between the rapid growth of data and the lack of data processing capacity.

Method:
Data mining methods based on rapidly developing big data science and AI techniques have outstanding advantages in solving the contradictions, but they need to rely on a strong domain knowledge base, yet there is a paucity of research on knowledge graph in the soil animal domain. The soil animal knowledge graph (SAKG) is proposed, which is a knowledge base with a directed graph structure, where the nodes of the graph represent entities or concepts related to soil animals, and the edges of the graph represent various semantic relationships between the entities or concepts.

Results:
This study introduced the concept, connotation and construction method of SAKG, demonstrated the method and process of constructing a mountain SAKG with the example of soil mite diversity in Tianmu Mountain, China, and explored the scientific questions that can be solved by a mountain SAKG with the three questions of where the distribution of soil animal diversity concerns, which species coexist together and how environmental conditions affect species distribution.

Conclusions:
This study shows that SAKG has unique potential and advantages in addressing important scientific questions about biodiversity, and has promoted the development of soil animal informatics at the intersection of soil zoology, information science and data science.

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Higher earthworm abundance in conventionally managed agricultural fields than ecologically managed fields

Sachin Bhattarai[1,2], Daniela Sauer[1], Juergen Friedel[3], Martin Potthoff[1], Stephen Asabere[1]

[1]University of Göttingen, Goettingen, Germany, [2]University of Hildesheim , Hildesheim, Germany , [3]University of Natural Resources and Life Sciences, Vienna, Austria

Aim: (i) To quantify the effect of ploughing activity on earthworm abundance in an experimental farm of the University of Göttingen, Reinshof.
(ii) to compare the earthworm abundance between an ecologically managed field vs conventionally managed fields.
Method: Earthworm sampling, using the mustard method, was done between the 22nd of April and the 3rd of May 2021. Three differently managed fields were sampled: ecologically managed with ploughing, conventionally managed with ploughing and conventionally managed without ploughing. Earthworms were collected at 30 locations per field. Soil organic matter contents, penetrometer resistance, and soil moisture were also measured.
Results: The conventionally managed ploughed field exhibited a mean earthworm abundance of 98.9 individuals per square metre, which was more earthworms than the ecologically managed field which showed a mean earthworm abundance of only 7.86 individuals per square metre. The highest mean earthworm abundance of 160.8 individuals per square metre was observed in the conventionally managed non-ploughed field along with highest species richness, organic matter content, soil moisture, nitrogen content, and penetrometer resistance. The ecological ploughed field, in contrast, showed the lowest values for all these parameters.
Conclusions: The non-ploughed fields provide a suitable environment for earthworm communities, as perturbation of earthworms is avoided and soil organic matter levels are maintained: a key requirement for earthworms, increasing their abundance. A very low abundance of earthworms in the ecologically managed field may be explained by the combination of frequent ploughing, low soil moisture and low soil organic matter content.

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Waste management in Nepal .

Sabina Devkota [1], Geeta Bhattrai Bastakoti [2] and Shree Prasad Vista [1]

[1]Nepal Agricultural Research Council, (NARC), Khumaltar, Lalitpur

[2]Community of Evaluators, Nepal (CoE-Nepal)

**Corresponding Author: Sabina.devkota@gmail.com*

Agro waste management in Nepal remains important issue which still needs to be given more importance considering its policy gaps and management mechanism. Kathmandu Metropolitan city has focused in bio waste management in their annual policy and program (2075/76) but management ways is still unclear. Despite its promotion there remains a less understanding how this bio decomposers are being promoted by the actors involved in the value chain. In this context, waste decomposers may be the option to decompose bio-waste materials quickly. Incomplete or immature composts cause many deleterious effects to soil, which in turn affects plant growth and ecosystem function. This study basically tries to understand what kind of waste decomposers are available in the market Nepal, what range of composition is being preferred by the users and the results of satisfaction by the users in terms of waste decomposer. Linking the findings with policy this paper explores and identifies the gaps in terms of waste decomposers that policy can address and the areas that needs to be addressed and considered for improvement at institution level for effective waste management.

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InteraCt: Predicting the impacts of rewired plant-soil biotic interactions on peatland carbon dynamics

Yvet Telgenkamp[1], Janna Barel[1]

[1]Radboud University Nijmegen, Nijmegen, Netherlands

Peatlands cover only 3% of the land worldwide but contain over 30% of all carbon stored in soils globally, which makes them one of the densest terrestrial carbon stores. Carbon dynamics in peatlands revolve primarily around production that largely surpasses decomposition. Both processes are regulated by plant and soil communities. However, climate change threatens to imbalance these processes, which could turn peatlands into major carbon sources. Here, we introduce the newly launched *InteraCt* project. In *InteraCt*, we study what role of plant-soil biotic interactions play in safeguarding the carbon sink function in natural peatlands and how changing environmental and climatic conditions influence that. To do so, we will embark on a cross-European field campaign in 2023. We will visit peatlands along an established enviro-climatic gradient to map above- and belowground interactions in (semi-)natural peatlands. This information will be used to construct plant-soil biota networks and assess whether these linkages affect the robustness of the C-sink function under enviro-climatic change. In the long term, we plan to experimentally investigate the role of plant-soil biotic networks in the resilience of peatland C-dynamics to drought by quantifying their C-cycle function using stable isotopes. In two related ongoing projects we are currently exploring how drought, nitrogen deposition and vascular plant community cover influence greenhouse gas fluxes, microbial community composition, *Sphagnum* (peat moss) functional traits and decomposition.

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Rebound of Soil Aggregation, Carbon Stocks, and Biodiversity Under Regenerative Agriculture Approaches

Sam Keenor[1], Brian J. Reid[1], Ezgi Özkurt[2,3], Falk Hildebrand[2,3], Rebekah Lee[1]

[1]University Of East Anglia, Norwich, United Kingdom, [2]Quadram Insitute of Biosciences, Norwich, United Kingdom, [3]Earlham Institute, Norwich, United Kingdom

Aim:
To determine the influence of a regeneratively managed perennial crop system on soil aggregation, carbon stability and soil biodiversity.

Method:
Soil was collected from regeneratively managed blackcurrant fields, established for 1-, 2-, 4- and 8-years. Soil samples were used to determine soil aggregate stability, pH, SOM/SOC content (loss on ignition), and aggregate fraction carbon stability (CHNO). Soil microbial (16S/ITS) and soil mesofauna analyses (pitfall traps) were conducted to assess soil biodiversity.

Results:
Soil aggregate stability and stable aggregate fractionation was observed to increase with time. Total SOM/SOC were observed to increase with duration of regenerative approaches. Soil pH not significantly altered over the 8-year period. Soil carbon recalcitrance (defined by H:C vs. O:C plots was observed to increase. Soil mesofauna and microbial biodiversity assessment is ongoing and will be completed by the meeting.

Conclusions:
Data acquired sustains regenerative agricultural methods as a means to rebuild soil carbon stocks and improve soil aggregate development. As such regenerative agriculture principals may hold promise for ecosystem rejuvenation and enhancement.
It is hypothesised that this observed soil carbon uplift will support biodiversity gains for mesofauna and microbial populations. These being supported by greater provision of carbon resources to sustain soil food webs. However, synergies and antagonisms between more resource and its chemical (reactance) and physical (greater aggregate stability) protection are expected to have additional shaping influences on the ultimate outcomes observed.

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GlobalAMFungi Database: World Atlas of Arbuscular Mycorrhizal Fungi

Tomáš Větrovský[1], Petr Baldrian[1], Petr Kohout[1], Clémentine Lepinay[1], Štěpánka Moulíková[1]

[1]*Institute Of Microbiology Of The Czech Academy Of Sciences, Prague, Czech Republic*

Aim:
Arbuscular mycorrhizal (AM) fungi belonging to the subphylum Glomeromycotina are key plant mutualistic symbionts that interact with more than 70% of plant species, including many agricultural crops. In this interaction with plants, they play an important role in nutrient and water uptake by plants and alleviate their biotic and abiotic stress, making them essential for human food security. Given that the presence of AM fungi is greatly underestimated in many studies describing fungal communities using high-throughput sequencing (HTS), in particular the low detection by generic fungal primers and the need for amplification by AM fungus-specific primers for their reliable determination, we decided to develop a specific database based on the collection of published data on the composition of AM fungal communities obtained by HTS methods.

Method:
We surveyed all available HTS studies from 2012 to 2021 targeting AM fungi using specific primers and collected and analyzed their data based on the three most used molecular markers such as ITS2, LLSU, SSU.

Results:
Based on our previous experience in developing the GlobalFungi database, we created the GlobalAMFungi database (https://globalamfungi.com/) including 100 studies with nearly 8500 samples from all over the world.

Conclusions:
The GlobalAMFungi Database follows the FAIR data initiative: make data Findable, Accessible, Interoperable and Reusable and provide a convenient access for users. The database includes data from all terrestrial habitats and contains information on fungal communities from soil, rhizosphere, roots and sediments.

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Trophic plasticity in microarthropods across soil depth and forest type

Jingzhong Lu[1], Junbo Yang[1], Peter Cordes[1], Mark Maraun[1], Stefan Scheu[1]

[1]University Of Göttingen, , Germany

Aim: Many traits including trophic niche parameters are attributed to species. However, generalist species may vary in trophic niches with environments, making species-based knowledge hard to extrapolate beyond local food webs. Here we test trophic consistency in oribatid mite and collembolan species, the most abundant arthropods that occupy all trophic levels in soil food webs.

Method: We used stable isotope analysis to compare trophic niches of 40 Oribatida species and 27 Collembola species that co-occur in litter (OL) and soil (0–5 cm, mainly OF/H, AH) of five forest types (native European beech, non-native Douglas fir, range-expanding Norway spruce, two beech–conifer mixed forests).

Results: Although stable isotope signatures of bulk material differed between litter and soil, 13C and 15N values of Oribatida species were remarkably stable irrespective of soil depth. By contrast, 15N values of Collembola species is higher in soil than in litter consistently across all forest types. Furthermore, both Oribatida and Collembola were more enriched in 13C in European beech than in coniferous forests, but forest type little affected 15N values of Oribatida and Collembola across a range of site conditions.

Conclusions: We conclude that trophic plasticity is higher in Collembola than that in Oribatida across microhabitats. Forest management including non-native tree species little affects trophic position (δ15N values) of soil microarthropod species, suggesting that trophic position can be used as a trait in community analysis of Oribatida across forest ecosystems.

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Global spatial patterns of testate amoebae diversity distribution and the forces behind it.

Valentyna Krashevska[1], Vincent Jassey[2], Romain Walcker[2], David Singer[3], Matthieu Mulot[3], Edward A. D. Mitchell[3], Yuri Mazei[4], Andrey N. Tsyganov[4], Stefan Geisen[5], David M. Wilkinson[6]

[1]University of Göttingen, Göttingen, Germany, [2]Laboratoire Ecologie Fonctionnelle et Environnement, CNRS, Toulouse, France, [3]Laboratory of soil biodiversity, University of Neuchâtel, Neuchâtel, Switzerland, [4]Department of General Ecology and Hydrobiology, Lomonosov Moscow State University, Moscow, Russia, [5]Wageningen University and Research, Wageningen, The Netherlands, [6]School of Life Science, University of Lincoln, Lincoln, UK

Aim:

Global data are fundamental to understanding general patterns in ecology and the environmental challenges. Soil biota are still poorly studied. Testate amoebae are a common group of shelled amoeboid protists that are widespread in terrestrial systems. However, their diversity and distribution have not yet been investigated and visualised on a global scale. Thus, the aims of our study are to understand spatial patterns of their diversity distribution and to evaluate the forces driving their biodiversity.

Method:

With extensive data collection effort involving testate amoebae community researchers, we compiled terrestrial data on testate amoebae from 9235 locations worldwide. We used available satellite data (WorldClim, SOilGrids, MODIS, etc.) obtained with the Google Earth engine to build an environmental matrix and applied random forest models to make our predictions.

Results:

In total, 1187 species were recorded, with the highest species number in Asia (699) and the lowest in Antarctica (151). Species richness is higher in the tropics, but relatively high in some temperate forests and even in the tundra. Preliminary analysis has shown that the main drivers of species richness are altitude, temperature, and precipitation seasonality.

Conclusions:

The richness is higher in the equatorial zone and decreases towards the poles, a clear trend in the southern hemisphere, but not in the northern. The data we have collected are the basis for identifying the fundamental ecological determinants of diversity and species composition of testate amoebae and for understanding patterns in microbial diversity. We will share the latest results of our ongoing analyses.

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The role of microclimate and below-ground biodiversity in driving soil processes in European forests.

Emily Bingham[1], Hannah Griffiths[1]

[1]*University Of Bristol, Bristol, United Kingdom*

Aim:

To deepen our understanding of the influence of microclimatic heterogeneity on soil biodiversity and consequences for carbon flow in European forests.

Method:

Six decomposition replicates are installed in 50 plots across a latitudinal gradient from Finland to Italy (n=300). Dataloggers in each replicate are positioned beneath open and closed canopies to encapsulate a range of microclimatic conditions. Replicates have 6 wood samples with contrasting traits (2x hard wood, 2x soft wood and 2x fresh wood with bark) and two leaf litter decomposition bags using region specific litter. Samples are subject to two treatments: accessible or inaccessible to invertebrates. Soil eDNA will be extracted and metabarcoding techniques used to amplify and sequence DNA across taxa to characterise the whole soil food-web. Taxon-specific approaches will provide supplementary data on species abundance and size.

Results:

Predicted results are that dataloggers under open canopy will record higher overall temperatures and soil moisture, with greater variation, than under closed canopy. Small-scale, within plot differences in microclimate will drive variation in soil biodiversity with consequences for decomposition rates and carbon cycling. Microclimate and soil biodiversity will have a greater influence on decomposition rates than latitudinal gradients in climate.

Conclusions:

There is a lack of spatial and temporally explicit data necessary to understand soil biodiversity and ecosystem function relationships worldwide. This research will highlight drivers of below-ground biodiversity and cascading consequences for rates of key processes, such as carbon cycling, that are key in mitigating the climate crisis.

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The Role of Soil Communities in Explaining BEF Relationship in European Forests.

Laís Maia[1], Olivier Bouriaud[2], Timo Domisch[3], Bogdan Jaroszewicz[4], Michael Scherer-Lorenzen[5], Federico Selvi[6], Hannah Griffiths[1]

[1]University of Bristol, Bristol, United Kingdom, [2]Universitatea Stefan cel Mare Suceava, , Romania, [3]Natural Resources Institute Finland, Joensuu, Finland, [4]University of Warsaw, Warsaw, Poland, [5]University of Freiburg, Freiburg, Germany, [6]Università di Firenze, Firenze, Italy

Tree species richness positively affects ecosystem functioning in European forests, but biodiversity effects are also context dependent. Belowground communities, which underpin many forest processes could explain some of the unexplained variability in forest BEF relationships. However, we lack large-scale, high-resolution data on the interaction between below and aboveground biodiversity to explain forest functioning (e.g carbon storage). **Aim:** Here, we will carry out sampling within the well-established plots from the FunDivEUROPE network to investigate if the diversity and community composition of soil organisms can predict forest diversity-productivity relationships and if soil diversity is positively related to C storage in trees and soil. **Method:** To establish the relationship between below-ground biodiversity we remeasured tree DBH of >15,000 trees to generate plot-level 5-yearly growth rate and we will sample soil eDNA in 166 forest sites (30x30m^2) across Europe (Finland, Poland, Germany, Romania and Italy). We will also collect data on soil bulk density, DON, DOC, N, P, pH, nitrate, ammonium, TC, TIC, soil organic matter content, soil moisture, physical structure, soil respiration, leaf litter fauna, soil compaction and PLFA. **Results:** Thus, we expect to access the importance of soil biotic and abiotic variables and vegetation composition to determine the relationship between below-ground diversity and C stocks in trees and soil. Additionally, in three plots within each country we would like to explore the contributions of soil **α**- and **β**- diversity in driving BEF relationships. For that, we will sample eDNA in a scale ranging from within-plot level to thousands of kilometres (distance between countries). **Conclusion:** This research will improve the understanding of how biotic communities could underpin the growth of trees and C storage across a continental scale.
For more project partners and institutions check the link: shorturl.at/yUY56

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Soil seed bank characteristics along a gradient of past human disturbances in a tropical forest

Christian Adjalla[1,2], Félicien Tosso[2,4], Kolawolé Valère Salako[3,5], Achille Ephrem Assogbadjo[2]

[1]Alliance of Bioversity International and CIAT, Cotonou, Benin, [2]Laboratoire d'Ecologie Appliquée, Faculté des Sciences Agronomiques, Université d'Abomey-Calavi, Cotonou, Benin, [3]Laboratoire de Biomathématiques et d'Estimations Forestières, Université d'Abomey-Calavi, Abomey-Calavi, Benin, [4]Université de Liège - Gembloux Agro-Bio Tech. Forest is life, Terra Teaching and Research Centre, Liège, Belgium, [5]Service d'Evolution Biologique et Ecologie, Université Libre de Bruxelles, Brussels, Belgium, Brussels, Belgium

Aim
This study aims to assess the characteristics of the soil seed bank (SSB) across a gradient of human disturbed vegetation types.

Method
Using the regeneration emergence method, we assessed the patterns of SSB (i) across four vegetation types with variable intensity of past human disturbances: typical dense forest - degraded dense forest - young preforest fallow - old preforest fallow, and (ii) in relationships to soil depth (0–5 cm, 5–10 cm, 10–15 cm, 15–20 cm) in a protected tropical semi-deciduous dense forest in Benin, West-Africa. The standing vegetation (adults and regeneration) data and soil samples were collected using a systematic sampling of 60 plots of 10 m × 10 m in the four vegetation types.

Results
Herbaceous plants dominated (67% -78%) the SSB. From the SSB, five tree species emerged: *Ceiba pentandra*, *Dialium guineense*, *Ficus sur*, *Leucaena leucocephala* and *Lonchocarpus sericeus*. Regarding tree species, the total densities of germinated seeds ($seeds.m^{-2}$) were higher in typical dense forest (28.00 ± 7.22) and young preforest fallow (16.67 ± 7.07) than in old preforest fallow (10.00 ± 6.75) and degraded dense forest (8.89 ± 3.81). The similarity of the species composition between the SSB and the surrounding vegetation was low (Jaccard's similarity index ranged from 0 to 17.64%), indicating that the majority of tree species in the surrounding vegetation were absent in the SSB.

Conclusions
This study highlighted a need of planting effort of native tree species to restore degraded areas.

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Mycoviruses in Saprotrophic Fungi and their roles in the Soil Ecological Processes

Ruiqi Wang[1], Emilia Hannula[1,2]

[1]Department of Environmental Biology, Institute of Environmental Sciences (CML), Leiden University, Einsteinweg 2, 2333 CC Leiden, the Netherlands, , , [2]Department of Terrestrial Ecology, Netherlands Institute of Ecology, PO Box 50, 6700 AB Wageningen, the Netherlands, ,

Aim:
The rapid development of sequencing technologies has revealed the wide existence of viruses in diverse fungal hosts. Viruses inside fungal hosts have the potential to mediate fungal phenotypes, such as regulation of metabolite production, hypervirulence, and drug resistance. Saprotrophic fungi are widely distributed in terrestrial ecosystems, governing soil carbon cycling and plant nutrition flow by degrading organic matter. Thus, mycovirus may affect saprotrophic fungi's functions in the soil ecosystem at the strain or community level. Therefore, this work will improve the understanding of mycoviruses' roles in the soil ecological processes by studying fungus-mycovirus-environmental interaction.

Method:
Mycoviruses screening and characterization are carried on with RNA visualization and sequence analysis. Virus-free fungal lines are generated by hyphal tipping and antibiotic treatment. Fungal phenotypes changes will be manifested by trait measurements. Soil carbon and aggregate-related properties will be evaluated.

Results:
From the total RNA size distribution comparison, there are potential virus-existing saprotrophic fungi. And some of them do have phenotypic traits change modulated by viruses.

Conclusions:
The understanding of mycovirus-saprotrophic fungal host interaction illustrates that there is significant potential for mycovirus in the soil ecological process. Further work will clarify by what traits change and to what extent will mycovirus affect soil carbon dynamics. And whether environmental abiotic and biotic factors play roles in its manifesting.

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Exploring the Fate and Impacts of Microplastics in Agricultural Soil: the PAPILLONS Project

Hannu Fritze[1], Salla Selonen[2], Paula Redondo Hasselerharm[3], Sylwia Adamczyk[1], Wulf Amelung[4], Matty P. Berg[5], Melanie Braun[4], Darina Dvorakova[6], Cornelis A.M. van Gestel[5], Jari Haimi[7], Rene Heyse[4], Rachel Hurley[8], Jacub Hofman[9], Sarmite Kernchen[10], Shin Woong Kim[11], Christian Laforsch[10], Martin G.J. Löder[10], Virtudes Martinez-Hernandez[3], Raffaella Meffe[3], Andreu Rico[3], Johanna Nikama[1], Matthias Rillig[11], Vili Saartama[2], Klara Šmidova[9], Helena Soinne[1], Jyri Tirroniemi[2], Aristeidis S Tsagkaris[6], Sannakajsa Velmala[1], Luca Nizzetto[8]

[1]Natural Resources Institute Finland (Luke), Helsinki, Finland, [2]Finnish Environment Institute (SYKE), Helsinki, Finland, [3]IMDEA Water Institute, , Spain, [4]University Bonn, Germany, Bonn, Germany, [5]Vrije Universiteit Amsterdam, Amsterdam, Netherlands, [6]University of Chemistry and Technology, Prague, Czech Republic, [7]University of Jyväskylä, , Jyväskylä, Finland, [8]Norwegian Institute for Water Research (NIVA) , Oslo, Norway, [9]RECETOX, Masaryk University , , Poland, [10]University of Bayreuth, Bayreuth, Germany, [11]Freie Universität Berlin, Berlin, Germany

Mulching films have been identified as a source of plastic additive chemicals and microplastics in agricultural soils. Biodegradable mulching films have been developed as alternatives. Biodegradable mulching films are intended to be left in the field after use but their impacts in soil are still unknown. Moreover, the impacts of microplastics are mostly studied in controlled laboratory conditions, whilst field studies with varying interactions and environmental conditions are scarce. In the field experiments of the H2020 funded project PAPILLONS (Plastics in agriculture: impacts, lifecycles and long-term sustainability), the fate and impacts of microplastics are studied in Finland, Germany and Spain. The experiments started in the beginning of the growth season in 2022, by introducing two types of microplastics in the study plots at two concentrations and five replicates. The two types of microplastics were produced by grinding recycled mulching film pellets: one from conventional polyethylene (PE) films and the other from biodegradable films composed of a blend of starch and polybutylene adipate co-terephthalate (starch-PBAT blend). Both experimental concentrations represent the range found in agricultural soils: 0.005% and 0.05% per dry weight of soil. Malted barley is grown in the experimental fields. Before seeding and at the end of the growing seasons 2022 and 2023 soil samples are taken to analyse physicochemical properties of the soil, microplastics, plastic additives, soil invertebrates and microbial community and activity. Barley growth, stress indicators and crop quality are also measured. In this presentation, this holistic field experiment of PAPILLONS project is introduced.

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Resistant Cities – connecting soil biodiversity of urban living environments with human health

Hannu Fritze[1], Taina Pennanen[1], Krista Peltoniemi[1], Sannakajsa Velmala[1], Leila Korpela[1], Oili Tarvainen[2], Marika Laurila[2], Marjo Neuvonen[2], Jouni Karhu[2], Katja Kangas[2]

[1]Natural Resources Institute Finland (luke), Helsinki, Finland, [2]Natural Resources Institute Finland (Luke), Oulu, Finland

Human contact with a diverse natural environment reduces inflammatory diseases like asthma. This is again in connection to a more diverse microflora inhabiting species rich environments which finally becomes reflected in the human microflora serving to protect from autoimmune diseases. This so called “Biodiversity / Old Friend Hypothesis” might protect humans also from non-inflammatory diseases. As urbanization is the main reason for lesser human contact with the environment, urban green spaces become the source of the microbiota serving to form the armor of human microflora.

Here we present a study design which is currently performed in two northern cities, Oulu and Helsinki, Finland, with 0,2 and 0,6 million inhabitants respectively. We have identified a characterization of urban green spaces including variations from built parks to urban forests. This survey provided a total of 150 urban green spaces which were 2022 sampled for their soil microbial diversity and analyzed for their plant community. The study sites were selected from residential areas of Northern Birth Cohort 1966 and 1986 members, who’s clinical records are known due to regular monitoring, as well as from popular nature recreation sites in urban areas. Collected biodiversity data will be combined with health data of Cohort members to investigate the possible impacts on immunological health and susceptibility to infections. Here we present the layout of our study design and the forthcoming analyses. The goal is to instruct future city planning and give value to diverse urban green areas.

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Towards smart soil-sensing: developing a proxy for soil health.

Rosa Boone[1,2], Bjorn Robroek[2], Hans Kroon, de[1]

[1]Experimental Plant Ecology Group, Radboud Institute for Biological and Environmental Sciences, Faculty of Science, Radboud University , Nijmegen, 6525 AJ Nijmegen, The Netherlands, [2]Aquatic Ecology & Environmental Biology Group, Radboud Institute for Biological and Environmental Sciences, Faculty of Science, Radboud University , Nijmegen, 6525 AJ Nijmegen, The Netherlands

Aim

The transition towards sustainable agriculture can be eased by improved knowledge on the trinity production-soil health-soil biodiversity. Soil conditions and health is largely underpinned by microbial community composition and its metabolic activity. Moreover, the rapid response of microbial communities to changing conditions makes the former an ideal proxy for soil health. Soil microorganisms are responsible for emitting volatile organic carbons (VOCs) in high quantity and diversity. Hence, soil volatiles could be promising to monitor soil biological health. This project aims to link VOC profiles to soil health parameters.

Method

To assess the VOC profile in agricultural soils, a field campaign has been conducted in spring and autumn of 2022. In total, 18 grasslands – varying in management (Conventional, Extensive and Semi-natural, n=6) – were selected. VOC moles were installed one day prior to sampling, at a depth from 0-25 cm. During sampling, VOCs were actively extracted and captured in thermal desorption tubes. These tubes were measured on the Gas Chromatograph, coupled with a Mass Spectrometer. In addition, soil samples were collected and analysed for soil chemical and physical parameters and microbial community composition.

Results

Early results suggest that VOC profiles were distinct for agricultural fields under different management. Notably, a PCA analysis shows a clear division between conventional and semi-natural grasslands.

Conclusion

The results indicate that VOC profiles may be a useful indicator that can help farmers to asses soil health. However, further analysis is necessary to determine which particular VOC’s are indicative of different management systems.

Biodiesel co-product decreased soil N losses, maintained the health and stability of soil microbial ecosystems

Qunli Shen[1,2], Paul Voroney[2], Meng Li[1], Philip C Brookes[3]

[1]Archaeal Biology Center, Shenzhen Key Laboratory of Marine Microbiome Engineering, Institute for Advanced Study, Shenzhen University, Shenzhen, P. R. China
[2] School of Environmental Sciences, University of Guelph, Guelph, ON, Canada
[3] Soil Science Department, Rothamsted Research, Harpenden, Herts, UK

Aim: Biodiesel co-product (BCP), a labile organic substrate C for soil microorganisms, is produced from the conversion of waste cooking oil to biodiesel. We investigated the impacts on biological N transformations, the composition and diversities of soil microbial communities following BCP amendment of soils at water contents ranging from 40 to 100% water holding capacity (WHC).
Method: We collected acidic soil samples from tea plantation fields in Hangzhou, Zhejiang, China. The soil water contents were altered to different contents (40, 60, 80, and 100% WHC) with BCP amendments (1.5 mg BCP-C g^{-1} soil) during 56 days of incubation. Quantitative PCR analysis and amplicon sequencing were used to detect functional gene copies and changes in soil microbial communities and diversities, respectively.
Results: The BCP amendments significantly promoted N immobilization and soil microbial biomass at all soil moistures. Also, the amendments increased the abundance of ammonia-oxidizing archaea (AOA) and ammonia-oxidizing bacteria (AOB) at 40% and 60% WHC on day 7. Amendment with BCP significantly decreased N_2O emissions by increasing *nosZ* gene copies and decreasing the gene copies ratios of (*nirS*+*nirK*)/*nosZ*. The amendment significantly decreased fungal diversities at all WHCs, but it only decreased bacterial diversity at 100% WHC. Of note, BCP amendments significantly increased the OTU numbers of beneficial microbes (e.g., *Trichoderma* spp.) in all water contents, with fewer OTU numbers of putative pathogenetic species (*Fusarium* spp. and *Aspergillus* spp.)
Conclusions: BCP amendment not only decreased soil N losses but also was conducive to the health and stability of soil ecosystems.

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Factors determining fungal communities associated with roots in plants from the páramo del Cumbal, Colombia

Elena Baraza[1], Wilmer Dajhan Navarrete[2], María Camila Enriquez[2], Josefina Bota[1], Arantxa Molins[1], Joshua Borrras[3], Maria Elena Solarte[2]

[1]Research Group on Plant Biology under Mediterranean Conditions, Departament de Biologia, Universitat de les Illes Balears (UIB) – Agro-Environmental and Water Economics Institute (INAGEA), Palma, Spain, [2]Laboratorio de Ecofisiología Vegetal, Grupo de investigación Biología de Páramos y Ecosistemas Andinos, Facultad de Ciencias Exactas y Naturales, Departamento de Biología, Universidad de Nariño, Pasto, Colombia , [3]Laboratory of Botany, Research Group on Plant Biology under Mediterranean Conditions, Department of Biology, University of Balearic Islands, Palma, Spain

Aim: The *páramos* are high-elevation mountain ecosystems found exclusively in the neotropics, located between about 3000 meters (m) and 5000 m of altitude. These ecosystems are threatened by agriculture and livestock activities, which often result in land abandonment once the areas are no longer profitable. This study aimed to compare the fungal communities associated with roots in plants from two areas of Páramo de Cumbal, (Nariño - Colombia) that are at different stages of recovery following disturbance.
Method: Two study sites with recovery time of 12 and 45 years after agriculture and livestock intervention were analyzed. At each site, we measured the physicochemical properties of the soil, the density of mycorrhizal spores (DEs) and the percentage of mycorrhization (%Mi) in roots of 15 individuals of *Calamagrostis effusa* and *Diplostephium glandulosum*. Additionally, DNA was extracted from roots and analyzed by Illumina sequencing of the internal transcribed spacer (ITS).
Results: DEs did not differ significantly between sites. %Mi differed between species but not between sites. Fungal α-diversity was not affected by the site. However, a PERMANOVA model indicated a significant effect of both plant species and site on the composition of the fungal community. An RDA analysis revealed that pH, cation exchange capacity, Calcium disposable, the site and plant species influenced the fungal community composition.
Conclusions: Our study shows that root fungal community was determinate not only by plant species but also by soil characteristics, which can vary between sites with different stages of recovery and vegetation composition.

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Perennial crops favour microarthropods well adapted to soil, contributing to the improvement of its quality

Lorenzo D'Avino[1], Gaia Bigiotti[1], Francesco Vitali[1], Stefano Mocali[1]

[1]*CREA Research Centre for Agriculture And Environment, Florence, Italy*

Aim:
Actions aimed at the improvement of soil quality are consolidated priorities for the European Union and the biodiversity of soil mesofauna is recognized as one of the best indicators of soil quality. Soil management of different crops could interfere with microarthropods, threatening soil biological quality. Thus, we compared the impact of different cropping systems, such as apple, tomato and strawberry, on biological soil quality in 17 agricultural sites, located across 5 European Member States.

Methods:
Mesofauna biodiversity was assessed by Berlese animal extraction and application of QBS-ar index (Soil Biological Quality focused on microarthropods). QBS-ar represents an appropriate tool to classify diversity of soil microarthropod community, grouping different biological forms (BFs) according to the morpho-type well adapted to epigeic, hemiedaphic or euedaphic soil conditions. In addition, abundance of different BFs in the three cropping systems were compared.

Results:
Tomato showed the lowest QBS-ar value, significantly different from apple, which had the highest values, whereas strawberry showed intermediate values. The same result was observed for BF richness: herbaceous annual crop > herbaceous perennial crop > perennial orchard. The frequency of euedaphic BFs was higher in the perennial crops than in tomato. However, the abundance of microarthropods belonging to euedaphic BFs collected in strawberry and apple differed as well.

Conclusion:
Despite different pedoclimatic conditions and management, apple orchards showed the highest frequency of euedaphic BFs, whilst tomatoes the lowest, confirming the hypothesis that crop persistency favours microarthropods well adapted to soil, contributing to the improvement of its quality.

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Does long-term microbial exposure to warmer/drier conditions alter soil carbon allocation dynamics during drought?

Vinzent Leyrer[1], Juliette Blum[1], Telse Zimmermann[2], Sven Marhan[1], Christian Poll[1]

[1]Soil Biology Department, Institute of Soil Science and Land Evaluation, University of Hohenheim, Stuttgart, Germany, [2]Department of Agronomy, Institute of Crop Science, University of Hohenheim, Stuttgart, Germany

Aim:

The assimilation of carbon (C) by plants and its subsequent allocation into different soil pools following root exudation depends on temperature conditions and water availability. Thus, increasing extreme events like drought as well as overall warmer and dryer conditions, will affect this dynamic. This has major implications on future C cycling between atmosphere, plant, soil and its living organisms. We used the *Hohenheim Climate Change* (HoCC) experiment as an agroecosystem research platform to explore, how microbial exposure to long-term (13 years) reduced water availability and soil warming (according to a realistic future climate scenario) modifies the allocation of recently assimilated carbon during drought and after rewetting.

Method:

The plots in the HoCC agroecosystem were exposed to a drought of eight weeks (May to June 2021) with subsequent rewetting. With ^{13}C enriched CO_2, we labelled Winter wheat at three timepoints, thus three growing stages: (1) at pre-drought, (2) peak drought conditions, and (3) shortly after rewetting. We then traced ^{13}C into roots, microbial biomass, PLFAs/NLFAs, labile carbon (EOC) and CO_2.

Results:

At all timepoints (1 to 3), we found an overall reduced allocation of assimilated C into all pools in the long-term warmer and dryer, compared to the wetter treatment. However the response pattern to drought and rewetting was almost identical between both.

Conclusion:

While overall less C got assimilated, future climate agroecosystems respond very similar to drought in terms of C allocation within the soil.

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Fungal Biodiversity and Microbial Metabolism in Plastic-polluted Soils

Lidia Nicola[1], Marta Elisabetta Eleonora Temporiti[1], Solveig Tosi[1]

[1]Department of Earth and Environmental Sciences, University Of Pavia, Pavia, Italy

Aim:
The aim of this work was to study soil fungal biodiversity and soil microbial metabolic profiles in three different sites in northern Italy, where different soil macro- and microplastic concentration was assessed.

Method:
The microplastic count of the soil samples was performed using the oil extraction method, while the number of macroplastic was assessed using a 5 mm sieve. The carbon metabolic profiling of soil microorganisms was performed using Biolog EcoPlates, which measure the use of different carbon substrates (amines, amino acids, carbohydrates, carboxylic acids, phenols, and polymers). The metabarcoding of fungal communities was performed on the ITS1 fragment of the 18S ribosomal cDNA, using the Illumina MiSeq System.

Results:
The results showed an intense and significant decrease of soil microbial metabolic ability concerning al the examined carbon substrates in the site with the highest concentration of microplastics. Moreover, the soil mycobiota composition was significantly different in the most pristine site, when compared with the other two sites. The metabarcoding of soil samples revealed a general dominance of *Mortierellomycota* followed by *Ascomycota* in all sampled soils.

Conclusions:
In conclusion, this study is an initial step towards the understanding of the complex effects of the increasing and compelling problem of plastic pollution on soil microbial communities and their activities directly in the environment.

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The Effect of Acacia Saligna Invasion on the Soil Nematode Population

Itaii Applebaum[1], Tirza Doniger[1], Chen Sherman[1], Yosef Steinberger[1]

[1]*Bar-Ilan University, Ramat Gan, Israel*

Aim: *Acacia saligna* is an Australian plant that has become invasive in several Mediterranean climate ecosystems. The goal of the present study was to determine the influence of *A. saligna* on the soil free living nematode community in the soil under its canopy in a Mediterranean sand dune area in Israel, across different seasons and soil depths.

Method: Nematodes were extracted using Baermann funnel, and the population structure was determined using meta sequencing. The trophic mode group and c-p index of each genus was determined using relevant literature.

Results: The nematode community changed in terms of dominant species, trophic composition, diversity and in terms of population maturity between the seasons, and to a lesser degree between the plants and depths.

Conclusions: The effect of *A. saligna* on the soil nematode population is complex, and changes according to the season and depth. This research highlights the need for multi seasonal studies regarding the soil nematode population.

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Utilising eDNA to monitor earthworm biodiversity and populations with different agricultural soil management techniques.

Yu Zhao[1], Penelope Watt[1], Tim Daniell[1]

[1]*University Of Sheffield School of Biosciences, Sheffield, United Kingdom*

Aim:
Earthworms play a key role in promoting soil health, structure, and turnover. Thus, an accurate understanding of the effect of agricultural soil management on earthworm populations and biodiversity can be directly linked to soil health. The aim of our work is to monitor earthworm populations through eDNA samples taken from soil samples in order to compare their diversity across multiple agricultural regimes.

Method:
In this study, 25 soil samples were collected from sites in the southwest and east of England with regenerative and conventional agricultural management techniques. Firstly we extracted earthworm DNA from soil samples and then We used eDNA amplification, purification and sequencing (NGS) to obtain earthworm sequence numbers and biodiversity.

Results:
Overall, it was found that there were differences in the diversity of earthworms in the different agricultural regimes. In addition, worm counts showed that abundance between sites with different management techniques varied and that regenerative fields had the greatest numbers of adults and juveniles.

Conclusion:
Our results indicate that earthworm diversity and abundance varies with management practices and that eDNA testing could be of significant benefit to assessing earthworm populations in the soil.

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Establish an Evaluation System for Soil Biodiversity in the Netherlands, to Promote Healthy Soils.

Merlijn Schram[1], Jasper Wubs[1], Wim van der Putten[1]

[1]*Nioo-knaw, Wageningen, Netherlands*

Aim:

Establish an evaluation system for soil biodiversity in the Netherlands, in terms of species composition and across major land use types, to promote healthy soils.

Method:

We set up a nation-wide soil biodiversity sampling strategy using stratification by soil abiotics, land use and management intensity. Currently, we have sampled >700 locations in grasslands and arable fields, and in the coming years we will expand these to include forests, urban soils and other natural habitats. For these soils we analyse the biodiversity in microbial communities, Annelids, Arthropods, Nematodes and Enchytraeidae using metabarcoding. In addition, we determine soil physio-chemical conditions and record site management with the local land managers. Furthermore, we installed large Soil Ecotrons to study how soil management practises impact soil biodiversity and functioning across soil types.

Results:

Our initial analysis shows that changes in management practices impact earthworm communities across all soil types. Furthermore, we find that more extensive management consistently promotes a higher fungal-to-bacterial ratio.

Conclusions:

We conclude that commonly used soil health indicators show the expected patterns in our nation-wide sampling campaign. This suggests that such indicators are robust and can be used across a wide ranges of soil types and environmental conditions. In the future, we aim to deepen our knowledge of soil biodiversity patterns, to help fine-tune sustainable management practise. Furthermore, we aim to connect our approach to other national and supra-national initiatives so as to harmonize and speed up meaningful soil biodiversity assessments.

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Composition and Complexity of Soil Microbial Communities Differ Across the Atlantic Forest-Brazilian Savanna Transition

Luis Felipe Guandalin Zagatto[1], Veridiana de Lara Weiser[2], Lucas William Mendes[1], Solange dos Santos Silva[1], Gabriel Silvestre Rocha[1], Anderson Santos de Freitas[1], Siu Mui Tsai[1]

[1]Center For Nuclear Energy In Agriculture, University Of São Paulo (CENA/USP), Piracicaba, Brazil, [2]São Paulo State University (UNESP), Bauru, Brazil

Aim:

The Atlantic Forest (AF) and the Brazilian Savanna (BS) are two global biodiversity hotspots. Little is known about the soil in the transition between those biomes; thus, we evaluated the soil microorganisms and abiotic properties in a gradient between those areas under the tropical regime, where savanna specialist plants are being naturally replaced by generalist species.

Methods:

Soil samples (10 replicates) from AF, BS, and an ecotonal area (EC) were DNA-extracted and evaluated through metagenomic sequencing and qPCR analysis. DNA sequences were annotated with the MG-RAST pipeline. Physicochemical properties and the activity of the soil enzymes acid phosphatase, β-glucosidase, and arylsulfatase were evaluated. All data were analyzed in R.

Results:

Although there was no difference in α-diversity, each soil presented a distinct microbial community that was correlated to parameters such as enzymatic activity and pH (PERMANOVA-p<0,001). Bacterial and fungal communities showed similar composition and abundance in all areas. In contrast, archaeal abundance increased in the AF-BS gradient, being higher in BS (respectively AF=1962, EC=10328, and BS=16614 gene copies). Also, in BS, Thaumarchaeota abundance was replaced by Euryarchaeota, and methanogenic were more abundant. Network analysis showed higher community complexity in EC and decreased in BS, for both taxonomic (2639 and 1011 interactions) and functional profiles (1085 and 533 interactions).

Conclusions:

Across the gradient, □-diversity modulates the microbial communities under distinct vegetation. EC presented a similar complexity to AF, indicating a more stable microbiome. In contrast, the results indicated a less complex and resilient environment for the microbial communities in BS.

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Soil biodiversity analysis for sustainable production systems (SoilProS)

Wim H. van der Putten, Ciska (G.F.) Veen, Paul L.E. Bodelier, Elly Morriën, L. Basten Snoek, Doina Bucur, Walter D.C. Schenkeveld, Judith E. van de Mortel, Marloes Hendriks, Freddy C. ten Hooven, Merlijn Schram, E.R. Jasper Wubs, Justine Lejoly, Kyle Mason-Jones

Netherlands Institute Of Ecology, Wageningen, the Netherlands

Current agricultural practices largely bypass the role of biota and biodiversity in soils and substrates. The result is that food production systems increasingly emit greenhouse gases and nutrients, while being poorly buffered against drought and rainfall events, and soil-borne diseases. Restoring these important functions of soils and substrates is currently less limited by what we can measure than by how to interpret the data. Here, we present a new research project where we solve this: ‘SoilProS (Soil biodiversity analysis for sustainable production systems)’. In this project we collect over 1000 field samples in grasslands and arable fields in the Netherlands and measure soil biodiversity and soil functioning. We use artificial intelligence-based machine learning to make soil/substrate biodiversity of food production systems predictable with respect to the effectiveness of practical measures in their capacity to enable food production with fewer emissions to atmosphere, ground and surface water, greater water buffer capacity and disease suppressiveness. The results of this 5-year project will contribute to enhanced soil health in food production systems.

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Soil Invertebrate Communities in Kauri-dominated Forests and the Impact of Tree Pathogens

Marijke Struijk[1], Andrew Barnes[1], Jamie Stavert[2]

[1]University Of Waikato, Hamilton, New Zealand, [2]Department of Conservation, Auckland, New Zealand

New Zealand kauri (*Agathis australis*), threatened by the root-borne pathogen *Phytophthora agathidicida*, are culturally significant trees and deemed ecological keystone species that likely exert great influence on belowground food webs.

Aim: To characterise soil food-web structure and functioning in kauri-dominated forests and the influence of *P. agathidicida* on the belowground ecosystem.

Method: At sets of kauri and broadleaf trees throughout the Waitākere Ranges, New Zealand, we (1) sampled litter macrofauna, soil mesofauna and nematodes, and identified specimens to functional feeding-group, and (2) assessed soil decomposition rates using the Teabag Index and soil micro-invertebrate feeding activities using bait-lamina strips, alongside (3) various environmental variables. We collated these data to characterise food webs under kauri versus broadleaf trees, determine impacts of *P. agathidicida* on food-web structure and functioning, and model food-web energy fluxes.

Results: Preliminary analyses reveal that mesofauna abundance was higher under broadleaf trees than under kauri. Similarly, micro-invertebrate activity was lower under kauri with similar soil types to broadleaf trees, although some kauri-specific soil types provided favourable high-activity habitat. *P. agathidicida* presence did not clearly affect mesofauna abundance and structure, but corresponded to higher decomposition rates.

Conclusions: Tree pathogens threaten the survival of many iconic tree species worldwide and climate change will likely enable further pathogen spread. Research on indirect and beyond-the-host impacts of tree pathogens on forest ecosystems is critically lacking. Our findings provide insights into the role of kauri trees for structuring soil food webs and the consequences of pathogen infection in a unique New Zealand forest ecosystem.

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Long-Term Effect of Wood Ash and Quicklime on Soil Microarthropods in an Acidic Grassland

Samira Terzenbach[1], Juliane Filser[1]

[1]*University of Bremen, FB02, UFT, Ecology, Bremen, Germany*

Aim:
Wood ash and quicklime are both used to increase soil pH, yet differ in their chemical composition. We investigated if repeated treatments with either wood ash or a combination of wood ash and quicklime exhibit differential long-term effects on the community composition of soil microarthropods.

Method:
In an acidic meadow in northwestern Germany seven plots have been repeatedly mown and treated since 2015: one half of each plot received pure wood ash, the other one a mixture of wood ash and quicklime. In May 2021, soil properties in the plots and surrounding soil (control) were measured, microarthropods were extracted from the upper 0-4 cm soil layer and identified to higher taxonomical groups.

Results:
The pH in the treated plots had risen to about 6.5 compared to the controls (pH = 3.9), accompanied by up to tenfold increases in contents of calcium, phosphorous and magnesium. In the control soil, average densities of Collembola and Acari were similar with 52,500 and 54,300 individuals per m^2, respectively. The number of taxa was similar in all treatments. There was weak evidence that quicklime caused a density decrease in Entomobryidae and that pure wood ash led to a density increase in (less dominant) Uropodina.

Conclusions:
This first sampling was limited to the uppermost soil layer and gave hints on a differential response of microarthropods to the treatments studied. For robust conclusions, repeated sampling and higher taxonomic resolution is required. Including deeper soil layers might render additional insight concerning less mobile taxa.

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Your Smartphone Can Measure Earthworm Stabilised Soil Aggregates

Pia Euteneuer[1], Vera Waschnig[1], Helmut Wagentristl[1], Reinhard, W. Neugschwandtner[1], Kevin, R. Butt[2]

[1]University of Natural Resources and Life Sciences, Vienna, Department of Crop Sciences, Vienna, Austria, [2]University of Central Lancashire, School of Natural Science, Preston, United Kingdom

Earthworms can support aggregate formation and stability during gut passage, burrowing activity and secretion of polysaccharides. *Lumbricus terrestris* were inoculated into two long-term soil tillage field experiments (10 yrs or 23 yrs) with ploughing, cultivator or no-till. In May, 14 earthworms m^{-2} were released into enclosures at both sites in Austria classified as chernozem soil. The aim was to investigate effects of enhanced vs ambient earthworm populations on soil parameters such as soil aggregate size and stability. After harvest in November, soil samples were collected to 10 cm depth (10 cm dia.) around burrows of *L. terrestris* (burrow) or away from burrows (control). Samples were hand-searched for earthworms or air-dried and sieved through a vibratory sieve shaker to determine mean-weight diameter. Five mm samples were then analysed with SLAKES a smartphone application devised by the University of Sydney (Australia). SLAKES measures the slaking index of soil aggregates immersed in deionized water by an image recognition algorithm within 10 min. Earthworms numbers of plough and cultivator plots (mostly endogeic) almost doubled around burrows compared with controls, but similar numbers were found for no-till. On both sampling sites, SLAKES distinguished between the three soil tillage systems and identified a more stable soil in middens than around burrows or control. In a next step, standard analyses such as wet sieving are planned, but SLAKES is a simple method and first results show that it has the potential to identify earthworm-processed soil.

Induced climate change in semi-arid Mediterranean environment: impact on biochemical properties linked to carbon cycle

Fernando Del Moral Torres[1]**,** Isabel Miralles[1], Natalia Rodríguez-Berbel[1], Rocío Soria[1], Rafael Hernández[1], Miguel Ángel Domene[2], Ángel Cortés[3], Isabel Delgado[3], Raúl Ortega[1]

[1]Department of Agronomy & Center for Intensive Mediterranean Agrosystems and Agri-food Biotechnology (CIAIMBITAL), University of Almeria, E-04120 Almería, Spain., Almería, Spain, [2]Health and food Department. Cajamar Experimental Station. E-4710. El Ejido, Spain., Almería, Spain, [3]Department of Biology & Geology. University of Almeria, E-04120 Almería, Spain., ,

*Corresponding autor: fmoral@ual.es

Aim: Evolution of soil biochemical properties linked to carbon cycle in a semi-arid Mediterranean scenario of climate change induced by using Open Top Chambers (OTCs).
Method: Following a completely randomised design, three OTCs were established around *Lavandula dentata* L. plants in February 2022. Three other equal area spots, including similarly developed *Lavandula* plants and without OTCs, were selected as controls. All the spots were located on a 657 m^2 flat plot with homogeneous soil and climatic characteristics. Soil samples were taken at the beginning of the experiment and seasonally in spring and summer with a 10 cm auger. Total organic carbon (TOC), oxidisable organic carbon (LOC), dehydrogenase (DH) and b-glucosidase (BG) enzymatic activities were determined. Temperatures affecting soil and plants were measured continuously using TOMST4 sensors.
Results: A mean induced heating of 1.07ºC at 8 cm soil depth and 3.04ºC at 30 cm above the surface were measured. A significant increase in DH ($p\text{-value}<0.05$), BG ($p\text{-value}<0.01$) and LOC ($p\text{-value}<0.1$) and a decrease in TOC ($p\text{-value}<0.1$) were observed. LOC/TOC ratio is therefore also increased. For TOC, differences are the highest in spring. For LOC, DH and BG, the differences increase consistently over time, which is indicative of a general increase in microbial activity and oxidative capacity of the studied soil.

Conclusions: Simulated climate change has led to increased microbial activity and altered carbon cycling in Mediterranean semi-arid soils with increments in b-glucosidase and dehydrogenase enzymatic activities and increased LOC/TOC ratio.
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Evolution of bacterial communities in a semi-arid Mediterranean soil under a climate change scenario

R. Ortega[1*], I. Miralles[1], N. Rodriguez-Berbel[1], R. Soria[1], R. Hernández[1], M.A. Domene[2], A. Fernández[3], I. Delgado[3], F. del Moral[1].

[1]Department of Agronomy & Center for Intensive Mediterranean Agrosystems and Agri-food Biotechnology (CIAIMBITAL), University of Almeria, E-04120 Almería, Spain.
[2]Health and food Department. Cajamar Experimental Station. E-4710. El Ejido, Spain.
[3]Department of Biology & Geology. University of Almeria, E-04120 Almería, Spain.
** Corresponding author: rortega@ual.es*

Aim: To study the evolution and activity of bacterial communities in a semi-arid Mediterranean soil under a climate change scenario induced by Open Top Chambers (OTCs)

Method:
Three OTCs (120 cm bottom diameter – 50 cm open top diameter) were established in February 2022 in a typical southeast Iberian soil (sandy loam, pH = 8.6, Total Organic Carbon = 0.7%, electrical conductivity = 0.3 mS/cm, calcium carbonate = 25%). Three other equal area spots and without OTCs, were selected as controls. Temperatures and humidity in soil were measured using TOMST4 sensors. Seasonally, variations in bacterial communities have been analyzed with NGS techniques (16S Full-length Amplicons PacBio Sequel2), and in the microbiological activity through measuring changes in soil CO_2 concentrations and iδ13CO2 isotopic ratios (Picarro G2201i).
Results:

Seasonal changes in bacterial communities have been observed, thus being exacerbated in many cases by the OTCs effect. In general terms, Proteobacteria and Firmicutes phyla increased, while Plantomycetota and Bacteroidota decreased notably. CO_2 levels in soils were controlled by humidity and OTCs. In spring, after several rain events, soil concentrations reached 1000 ppm, increasing 300 ppm more where the OTCs. After the dry season, CO_2 levels dropped to 500 ppm, although OTCs still favoured higher concentrations, with around 150 ppm more.
Conclusions:
Results can indicate bacterial taxa that can be benefited or disadvantaged by global warming and predict increases in CO_2 greenhouse gas emissions from semiarid Mediterranean soils.
Acknowledgement:
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Online Taxonomic Catalog of the Brazilian Oribatid Mite (Acari: Oribatida) Fauna: an open-source tool

Carlos Barreto[1,2]

[1]Algoma University, Sault Ste Marie, Canada, [2]Ontario Ministry of Natural Resources and Forestry, Sault Ste Marie, Canada

Aim: My aim was to create and update a taxonomic catalog of oribatid mites in Brazil using an online and dynamic open-source tool.

Method: The Taxonomic Catalog of the Brazilian Fauna (TCBF) is a project started in 2015 as a group effort of more than 500 zoologists to generate the first list of valid species for the country. A complete synonymic list, references, distributional data by region, state, biome, and hydrographic basin are also available. Here I used oribatid mites (Acari: Oribatida), my study group, to highlight the resources available in the TCBF. I also updated the number of species present in the country from the checklist published in 2017.

Results: Currently 583 species of oribatid mites are listed for Brazil. Species distribution by Brazilian biomes reveals that Atlantic Forest is the most diverse with 309 species, even though these results are biased due to intense historical sampling. In fact, 10 out of the 27 Brazilian states have no record for oribatid mites.

Conclusions: The oribatid mite fauna of Brazil is still partly unknown. I encourage sampling in ecosystems other than forests, as I showed there exists bias towards this ecosystem. Considering the catalog is dynamic, and allows corrections in real time, inclusion of newly discovered species, and expansion of species distribution, I believe its functions are powerful tools that can help protecting the biodiversity of Brazil through acting as a governmental base source for public policy decisions. This is paramount given Brazil is a global biodiversity hotspot.

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Contribution of Lumbricus terrestris in Crop Production in Three Soil Tillage Systems

Pia Euteneuer[1], Helmut Wagentristl[1], Rebecca Hood-Nowotny[1], Anna Hofer[1], Marion Windisch[1], Ernst Weiler[1], Stefan Widy[1], Gernot Bodner[1], Reinhard Neugschwandtner[1], Kevin Butt[2]

[1]University of Natural Resources and Life Sciences, Vienna, Department of Crop Sciences, Vienna, Austria, [2]University of Central Lancashire, School of Natural Science, Preston, United Kingdom

Soil tillage decreases earthworm numbers and soil aggregate stability. To examine possible reverse effects, additional *Lumbricus terrestris* were inoculated into two long-term soil tillage trials in Austria. The aim was to investigate impacts of enhanced vs ambient (control) earthworm populations on plant and soil parameters under field conditions in three soil tillage systems (plough, cultivator, no-till). *L. terrestris* (14 earthworms m^{-2}) were added in May 2019 (site 1) or 2020 (site 2) into 7 m^2 enclosures in maize (*Zea mays*) followed by winter wheat (*Triticum aestivum*). Overall, earthworm inoculation doubled midden abundance in enclosures of cultivator or plough (15 middens m^{-2}), and slightly increased abundance in no-till (34.7 middens m^{-2}) compared to respective controls. Earthworm enhancement had no effect on maize yield at site 1, but it was higher at site 2 in enhanced plots compared to control plough and cultivator. The wheat yield in the following year was similar between treatments at both sites. Principal components analyse including number of middens, precipitation, leaf area index, plant δC^{13} and aggregate stability showed that differences in yield at the two sites are related to plant available water and plant growth, whereas treatments were separated by numbers of middens and slaking of soil aggregates. Overall, earthworms showed their ability to manipulate some of the impacts of soil tillage under field conditions such as slaking within a season and support plant growth, but only with sufficient water supply.

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Australian research consortium for unravelling the role of soil fauna in nutrient transformations

Hangwei Hu[1], Brajesh Singh[2], Daniel Murphy[3], Qinglin Chen[1], Tony Weatherley[1], Eleonora Egidi[2], Wei Xu[3], Jizheng He[1]

[1]The University Of Melbourne, Melbourne, Australia, [2]Western Sydney University, Sydney, Australia, [3]Murdoch University, Perth, Australia

Aim:

Soil fauna are greatly diverse and abundant in soil, and support vital soil processes and functions. Soil faunal communities remain largely underrepresented in the studies of soil processes and functions, and this underlines the urgent need to better understand the driving forces and future changes of soil fauna, their interactions with microorganisms, and their contributions to key soil functions.

Method:

An Australian Research Consortium has been established to characterize the dynamics of the diversity and composition of widely distributed and globally important soil faunal groups in typical Australian agroecosystems. The selected soil faunal groups represent different body sizes, life-history strategies and trophic levels, and the selected ecosystems cover the major agricultural soil types in Australia.

Results:

Our Consortium will (i) identify the key environmental factors structuring the diversity and composition of six globally representative soil faunal groups (including nematodes, tardigrades, collembolans, mites, ants, and earthworms) in agricultural lands of key Australian crop systems (wheat, sugarcane, cotton and pastures); (ii) establish how soil faunal communities steer the compositions of soil microbial communities through predator-prey interactions, and to link soil faunal communities and food webs with soil functioning; (iii) explore the contributions of trophic interactions of soil faunal communities in regulating key biological processes of soil nitrogen and phosphorous cycles in agricultural lands.

Conclusions:

Our Consortium will create new frameworks to combine conventional morphological identification, advanced stable isotope tracing technique, and state-of-the-art molecular approaches, to renovate our understanding of the distribution patterns of soil faunal communities in Australian agricultural land.

How mutualistic are arbuscular mycorrhizal fungi from arable soils?

Martina Janoušková[1], Martin Rozmoš[2], Paula Buil[1,3], Petra Bukovská[2], Jan Jansa[2]

[1]*Institute of Botany of the Czech Academy of Sciences, Pruhonice, Czech Republic,*
[2]*Institute of Microbiology of the Czech Academy of Sciences, Prague, Czech Republic,*
[3]*Department of Botany, Faculty of Science, Charles University, Prague, Czech Republic*

Aim:

Agricultural practice is known to impact on the diversity and community composition of arbuscular mycorrhizal fungi (AMF), which are important symbionts of most crop species. Intensive agriculture has been also proposed to select for less mutualistic species or genotypes of AMF because the conditions or arable soils favour ruderal life strategy and decrease the plant needs for the nutritional benefits of mycorrhiza. The main aim of the presented research is to test this assumption.

Method:

A cross-inoculation experiment was established with *Plantago lanceolata* to compare four pairs of AMF communities, each from arable field and neighbouring grassland, in terms of community composition and mycorrhiza functioning. A range of plant parameters were collected to characterize the growth and nutrient uptake of the host plants as compared to non-mycorrhizal controls.

Results:

AMF communities from arable soils and grasslands consistently differed in composition, and induced overall similar responses in their host plants. However, the arable-field communities were significantly more efficient in providing phosphorus, while the grassland communities conferred significantly higher net benefits in terms of improved growth.

Conclusions:

Our results suggest that AMF communities from arable soils and grasslands are functionally different, but the former are not less efficient in providing nutrients to their host plants. In future research, it is important to address a broader range of mycorrhizal benefits in order to better understand both the selection pressures of agricultural practice on AMF as well as the role of AMF in plant production.

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Back to the Roots: The Bacterial Communities in the Rhizosphere of Grapevine

Leonie Dries[1], Stefan Ratering[2], Simone Bussotti[3], Otmar Löhnertz[1], Anne Vortkamp[4], Sylvia Schnell[2]

[1]Hochschule Geisenheim University, Geisenheim, Germany, [2]Justus-Liebig University Giessen, Giessen, Germany, [3]AGRION, Fondazione per la Ricerca l'Innovazione e lo Sviluppo Tecnologico dell'Agricoltura Piemontese, Manta, Italy, [4]REACH EUREGIO Start-up Center, University of Muenster, Muenster, Germany

Aim: The rhizosphere is the space where crucial processes for the productivity of viticultural systems take place. The composition of the bacterial communities associated with the rhizosphere of grapevines is known to depend on plant genotype. However, the genotype of grafted grape-vines differs between scion and rootstock; the role of each genotype is unclear.

Method: In order to dis-entangle the effect of scion and rootstock, the rRNA (V4–V5 region of 16S rRNA) extracted from the rhizosphere of the grape varieties Riesling and Mueller-Thurgau ungrafted vs. grafted on different rootstocks were sequenced in three experimental set-ups in two different years.

Results: The bioinformatic analysis with tools designed to be robust for compositional data showed, that the investigated rootstocks or scions or combinations, respectively, recruited bacterial communities with distinguishable traits. Statistical differences were revealed between ungrafted Riesling and Mueller-Thurgau, and between grafted Riesling and ungrafted Riesling, and ungrafted Mueller-Thurgau and grafted Mueller-Thurgau.

Conclusions: Thus, confirming the role of scion and rootstock genotype as a driver of the structure and composition of bacterial communities in the rhizosphere of grapevines.

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Colonization of Experimental Wadden Sea Salt Marshes by Soil Mesofauna

Md Ekramul Haque[1], Ting-Wen Chen[1], Maria Rinke[1], Mark Maraun[1], Stefan Scheu[1]

[1]J.F. Blumenbach Institute of Zoology and Anthropology, University Of Goettingen, Goettingen, Germany

Aim

Salt marshes are unique habitats characterized by heterogenous terrestrial-marine interfaces characterized by variations in inundation frequency. Soil animal communities therein are affected by stochastic processes such as colonization and extinction. We investigated colonization processes of experimental Wadden Sea salt marshes by soil mesofauna.

Method

Two experimental saltmarsh systems (consisting of mudflat sediment without terrestrial animals) were established in the Wadden Sea of Spiekeroog, Germany. The first system was established along the marine-terrestrial boundary from pioneer zone (PZ) to lower saltmarsh (LSM) to upper saltmarsh (USM) of the island of Spiekeroog. The second system was established on artificial islands (about 500 m from the seashore) at the same tidal height as the first one (i.e., PZ, LSM, and USM). After five years, soil mesofauna of each zone from both experimental systems as well as from respective natural saltmarsh zones of the island of Spiekeroog were sampled.

Results

A total of 18 Oribatida, 18 Collembola and 28 Mesostigmata species were found. Species compositions in the experimental saltmarsh systems differed from respective zones in the natural saltmarsh. In both experimental systems, soil mesofauna most intensively colonized the USM, less the PZ and least the LSM, with colonization being more pronounced in the island of Spiekeroog than the artificial island system.

Conclusions

Colonization of the USM and PZ was favoured by dispersal via wind and water, respectively, whereas both were less pronounced in the LSM. Faster colonization of the island of Spiekeroog than the artificial island system indicates that active dispersal is important for colonizing nearby terrestrial habitats.

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Global Oribatida Initiative (GO): synthesizing taxonomy, data and knowledge in soil mites

Dorothee Sandmann[1], Ina Schaefer[1], Stefan Scheu[1], Mark Maraun[1], Jing-Zhong Lu[1]

[1]University of Goettingen, Goettingen, Deutschland

Globally distributed oribatid mites are among the most abundant and diverse soil microarthropods. Worldwide about 11,500 species have been described over the past 260 years and about 150 are added every year. Despite an increase in understanding diversity and density of soil organisms and a growing awareness of their functional importance, a global assessment of the distribution of Oribatida communities in a spatial-explicit manner does not exist. Here, we present a road map to achieve this goal by (1) establishing one authoritative, consensual, global, up-to-date taxonomy of the world's oribatid mite species on a global biodiversity platform, (2) installing a GO team including taxonomists and ecologists to supervise the data collection, and (3) improving the global coverage of datasets by calling for collaborations via global and local platforms, especially to cover oribatid mite communities from underrepresented regions. With a global dataset of Oribatida communities, we want to study environmental drivers of oribatid density and diversity at a global scale. Another aim is to connect taxonomy and ecology more closely and, by bringing together scientific and literature data, to make oribatid research more widely recognized and impactful. This initiative also serves as a cornerstone to better understand the ecology and functional roles of oribatid mites in terrestrial ecosystems.

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Investigating the Influence of Soil Moisture on Aestivation in Green Earthworms (Allolobophora chlorotica)

Roberta Bray[1], Mark Hodson[2], Penelope Watt[1]

[1]School of Biosciences, University of Sheffield, Sheffield, United Kingdom, [2]Department of Environment and Geography, University of York, York, United Kingdom

Aim:
Given the increased frequency and severity of extreme climatic events, including droughts, predicted with climate change, I aimed to investigate the impact of decreasing soil moisture content on aestivation (diapause) in the most abundant UK earthworm, *Allolobophora chlorotica*.

Method:
Adult *A. chlorotica* of known mass were placed into soil substrates of 30% or 25% moisture and kept either under constant conditions or left to dry gradually. These substrates were destructively sampled once they reached moisture contents of 18%, 13%, 10%, 8% and 6%, and individual earthworms were identified as being either active, aestivating, or dead. Surviving earthworms were weighed and placed into soil with optimal moisture for a further period before being weighed again.

Results:
Soil moisture had a significant effect on the proportion of aestivating earthworms. At 18% moisture, all individuals remained active, but at 13%, most (83%) of the earthworms were aestivating. Survival decreased when moisture decreased below 13%, and mortality was 100% at levels below 10%. The initial change in mass earthworms experienced depended on the extent of drying they were exposed to and whether they had undergone aestivation. There were no significant differences in overall changes in mass between treatment groups as smaller increases in mass that occurred during drying conditions were compensated for by greater increases during optimal conditions.

Conclusions:
These results confirm that soil moisture is an important driver of aestivation in earthworms. Aestivation clearly influences earthworm mass, but this appears to be transient with greater increases during optimal conditions offsetting any losses.

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Interactions between Litter-feeders and Soil-feeders and Effect on Decomposition in a Microcosm Experiment

Camille D'hervilly[1], Jan Frouz[1]

[1]Biology Center CAS, České Budějovice, Czech Republic

Aim:

Soil fauna strongly affects the decomposition process. However, fauna with different feeding preferences may have a very different impact. The aim of the study was to investigate the effect of the interaction between litter-feeders and soil-feeders during decomposition on microbial biomass and the forms of soil organic carbon.

Method:

We performed a three-months microcosm experiment with the endogeic earthworm *Aporrectodea caliginosa* (soil-feeder) and litter-feeders (isopods and the epigeic earthworm *Dendrodrilus rubidus*), alone or in combination. We used soil from a young post-mining area and alder leaves, added at the surface or fragmented and mixed with the soil.

Results:

A. caliginosa directly consumed the leaves, at a similar rate than *D. rubidus*. Carbon loss through respiration and dissolved organic carbon content in the soil were the highest in presence of *D. rubidus*. Nitrate content in the soil was the highest when both earthworm species were present together. *A. caliginosa* had a positive effect on soil microbial biomass when litter was added at the surface, but a negative one when litter was mixed in small pieces with the soil.

Conclusions:

The endogeic earthworm *A. caliginosa* did not depend on the activity of litter-feeders to access the fresh litter, but the final impact on decomposition differs according to the earthworm species and the mode of leaf addition. A simultaneous presence of both earthworms could promote nitrate accumulation. Current analyses of the forms of the soil organic matter will provide additional information.

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Evolution of bacterial communities after restoring old degraded agricultural soils in semi-arid Mediterranean climate

Isabel Miralles Mellado[1], Natalia Rodríguez-Berbel[1], Rocío Soria Martínez[1], Raúl Ortega Perez[1]

[1]*Department of Agronomy & Center for Intensive Mediterranean Agrosystems and Agri-food Biotechnology (CIAIMBITAL), University of Almeria., ALMERIA , Spain*

Aim: Monitoring soil bacterial communities after application of different organic amendments to restore abandoned agricultural soils in semi-arid Mediterranean climate.
Method: Fifteen randomised experimental plots (7 × 5 m) were installed in an abandoned crop field in Sierra Alhamilla (Almería, SE Spain). Four organic amendments from different types of composted residues were applied (3 plot replicates/treatment), and other 3 untreated plots were used as control soils. Three natural non-degraded surrounding soils were set as quality reference. During 3 sampling campaigns (0, 3 and 12 months), samples were collected to study changes in bacterial communities at phylum and genus level associated with each treatment. Soil DNA was extracted and 16S rRNA gene sequenced with Illumina platform, obtaining taxonomical classification using QIIME2 software and SIVLA database. Finally, IndicSpecies analysis was performed to determine genus-level bacterial taxa associated with each treatment.
Results: In general, Proteobacteria and Bacteroidetes phyla proliferated at 3 months and decreased at 12 months, while Actinobacteria, Acidobacteria and Planctomycetes phyla had the opposite behaviour. All treatments (restored, control and natural soils) favoured the proliferation of different soil-specific indicator taxa.
Conclusions: Restoration with organic composted residues generated changes in the bacterial communities, favouring the initial proliferation of fast-growing phyla at 3 months, meanwhile they decreased after 12 months, proliferating them slower-growing phyla. In addition, organic amendments favoured the growth of soil bacterial genera involved in C, N and P cycling, as well as plant growth promoting and fungal antagonist bacteria.
Acknowledgements: BIOQUALIRES (PID2021-127591OB-I00).

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Agricultural expansion affects microbial properties differently depending on the agroecological zone

Dora Neina[1]

[1]*Department of Soil Science, University of Ghana, Accra, Ghana*

Aim: Agricultural expansion in Sub-Saharan Africa is characterized by different farm ages in smallholder communities. The study investigated changes in microbial and related properties in different farm types in Ghana's Forest (Dompem) and Forest–Savannah Transition (Adansam) zones as influenced by the duration of cultivation.

Method: Soils from the farms: One year (first cultivation of cleared forest/fallow), Three years, Five years, and Ten years were analyzed for pH, soil organic carbon (SOC), active C (POXC) using potentiometry, thermal combustion and permanganate oxidizable C, respectively. Microbial properties of moist soils were measured for basal respiration (BR) and microbial biomass (MB) by alkali trap and chloroform fumigation incubation, respectively.

Results: In the first three years, SOC and BR of the acidic, loamy Dompem soils declined by 1-23% and 6-25% ($p < 0.001$), respectively, whereas POXC and pH did not differ among farms. Positive correlations occurred between SOC and POXC ($r = 0.81$, $p < 0.001$), SOC and BR ($r = 0.42$, $p < 0.01$), whereas BR correlated negatively with dithionite Al ($r = -0.35$, $p < 0.01$). MBC measurements are ongoing.

Conversely, the SOC declined by 3-26% in the first five years but increased by 26% in the less acidic, arenic Adansam soils in year ten. POXC, BR, MBC and soil pH did not differ among the farms. SOC and POXC had a strong positive correlation ($r = 0.70$, $p < 0.01$).

Conclusions: Agricultural expansion influenced microbial properties differently in each agroecological zone due to varied effects of belowground factors.

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Alteration of microbiome and resistome during manure bioconversion into insect frass

María Gómez-Brandón[1], Dennis Beesigamukama[2], Maraike Probst[3], Thomas Klammsteiner[3], Yong-Guan Zhou[4], Chrysantus Tanga[2]

[1]Department of Ecology and Animal Biology, University of Vigo, Vigo, Spain, [2]International Centre of Insect Physiology and Ecology, Nairobi, Kenia, [3]Department of Microbiology, University of Innsbruck, Innsbruck, Austria, [4]Key Lab of Urban Environment and Health, Institute of Urban Environment , Xiamen, China

Aim: Beneficial effects of insect frass on soil and plant health are primarily ascribed to plant-accessible nutrients and moderated contents of chitin. Frass-associated microbes are also likely to play a role. The aim of the present study was to elucidate the variation in the microbiome and the resistome during bioconversion of cattle manure into insect frass by *Pachnoda sinuata* larvae known as African fruit beetle.

Method: The composition and diversity of bacterial and fungal communities were determined by Illumina amplicon sequencing. The characterization of the resistome was assessed by employing a high-throughput quantitative PCR (HT-qPCR) platform to target 384 ARG subtypes encoding resistance to all the major categories of antibiotics.

Results: The insect frass was characterized by an increased bacterial diversity and richness compared to the cattle dung, but this trend did not hold for fungi. This was accompanied by a decrease in the copy number of genes conferring resistance to aminoglycoside, diaminopyrimidine, multidrug, sulfonamide and tetracycline antibiotics. A reduced abundance of mobile genetic elements including transposase and integrase genes was also exhibited in the frass.

Conclusions: Our findings provide evidence about the attenuation of ARGs during manure bioconversion into insect frass by the beetle *P. sinuata*. This is essential to improve management strategies that support a sustainable balance between waste mitigation and reducing the risk of manure-borne pollutants like ARGs. In parallel, this points the usefulness of frass as a promising biofertilizer instead of conventional livestock manure.

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Effect of microplastic particles in microbial communities under environmental relevant conditions

Cecilia Díaz[1], Karsten Schlich[1], Martin Hoppe[2], Jan Köser[2]

[1]Fraunhofer-Institut für Molekularbiologie und Angewandte Ökologie, Schmallenberg, Germany, [2]Federal Institute for Geosciences and Natural Resources, Hannover, Germany

Aim: (heading must be in bold)
Our aim was to investigate the effect of polystyrene particles (PS-P) and polystyrene particles with a core of silver nanoparticles (Ag-PS-P) in a sewage treatment plant (STP) and a subsequent outdoor lysimeter study.

Method: (heading must be in bold)
Synthetically synthesized particles were added into single STPs according to OECD 303A. Samples were taken from sludge and effluent to determine the fate of the MPs. Additionally, the effect on the microorganisms was investigated by measurements of the DOC elimination.
After 12 days, PS-P and Ag-PS-P were added via sludge into soil to achieve three test concentrations. Replicates were incubated outdoor (lysimeter) and leachate samples were taken at regular intervals over a 4-month period. The effect on soil microorganisms (substrate induced respiration, potential ammonium oxidation (PAO) was examined. Changes in bacterial (16S-23S intergenic region) and fungal (ITS- 5.8S-ITS2 region) communities were studied by using ARISA-PCR (automated ribosomal intergenic spacer analysis).

Results: (heading must be in bold)
SEM analysis showed that PS-P particles are mainly retained (as non-aggregated) in the sewage sludge and soil.
No effect on the DOC elimination by any of the treatment was observed during the exposure time in the STP, however Ag-PS-P treatments (highest concentrations) affected the PAO (inhibition <20%) after long-term incubation.
Microbial community, fungal and bacterial, were shifted in the doped and undoped treatments. However, the strongest dissimilarities (PCoA analysis) were found in the Ag-PS-P treatments at the highest concentrations.

Conclusions: (heading must be in bold)
Microbial communities are affected by doped and undoped treatments, and the Ag-PS-P showed a toxic effect probably due to released Ag ions, producing PAO inhibition.

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Grassland afforestation: is it a threat to soil biodiversity?

Ms. Bruna Jorge[1], Bruna Winck[1], Luciana Menezes[2], Bruno Bellini[3], Valério Pillar[1], Luciana Podgaiski[1]

[1]Quantitative Ecology Lab, Department of Ecology, Universidade Federal do Rio Grande do Sul,, Porto Alegre, Brazil, [2]Grassland Vegetation Lab, Department of Botany, Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil, [3]Department of Botany and Zoology, Biosciences Center, Universidade Federal do Rio Grande do Norte, Natal, Brazil

Aim: Grassland afforestation with exotic fast-growing species has been increasing over the last ten years in south Brazil. Although the impacts of this conversion on aboveground biodiversity were already investigated, the responses of the soil biota and functions remains poorly known. Here, we compare soil Collembola communities and soil functions between areas of native grassland and grassland afforested by *Eucalyptus* trees in southern Brazil. Our results will further support the development of conservation strategies for sustainable land-use of subtropical grasslands, and promote a step ahead in the knowledge of its poor-know soil biodiversity.

Method: By using 10 paired transects (native grassland vs. *Eucalyptus* plantation), we assessed Collembola taxonomic and functional diversity and composition and their relationships with plant richness, soil microbial and soil physical–chemical parameters.

Results: Grassland afforestation decreased plant richness, soil pH and soil temperatures. These alterations were related to reduction of microbial biomass, soil basal respiration and soil enzyme activities (FDA and urease). Also, we detected distinct taxonomic and functional compositions of Collembola communities between native grassland and plantation areas, which indicate that environmental filtering triggered traits turnover from open to closed-canopy habitat. Collembola richness decreased, but Simpson index was not affected. Nevertheless, functional diversity increased with afforestation, probably due to the maintenance of some grassland-adapted species along with the forest-adapted species at the converted sites.

Conclusions: Although grassland afforestation is globally pointed out as a strategy favoring carbon sequestration, our results indicate a trade-off through reduction of soil's capacity to promote and regulate nutrient cycling.

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Impact of Non-Native Amynthas spp. on Soil Structure and Fungal Diversity in Deciduous Forest Soils

Dana Johnson[1], Bradley Herrick[2,3], Thea Whitman[1]

[1]Department of Soil Science, University of Wisconsin-Madison, Madison, United States, [2]University of Wisconsin-Madison Arboretum, Madison, United States, [3]Department of Forest and Wildlife Ecology, University of Wisconsin-Madison, Madison, United States

Aim: *Amynthas* spp. are epi-endogeic earthworms native to southeast Asia that have spread in the United States since the mid-1900s. In forest ecosystems, the introduction of *Amynthas* spp. has been shown to cause a decrease in surface litter, an increase in total carbon and nitrogen, and an increase in A horizon soil aggregation. There is also evidence that invasion of deciduous forests by other non-native earthworms has led to lower rates of mycorrhizal colonization. In this study, we test how *A. agrestis* and *A. tokioensis* in a U.S. deciduous forest impact soil fungal community composition via direct interactions and/or via changes in soil structure.

Method: We used *in situ* soil mesocosms to determine if the introduction of *Amynthas* spp. to soil: (1) impacts soil structure via changes in aggregation and (2) affects soil fungal communities by decreasing fungal diversity.

Results: We observed small increases in soil pH, decreases in bulk density, and no significant change in fungal community composition in soil amended with *Amynthas* spp. compared to control soil after a four-month incubation. One year later, we analysed the same mesocosms and found no significant relationship between the number of *Amynthas* spp. present and soil moisture, pH, or aggregation.

Conclusions: Despite temporary impacts of *Amynthas* spp. on soil properties, we found no effect on fungal community composition. This may be due to the presence of other long-established non-native earthworms in this forest or limitations in the spatial or temporal scale of this work.

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Farm level diversification and landscape variation influence soil microbiome and ecosystem functions

Khondoker Dastogeer[1], Hannah Waterhouse[1], Kenzo Esquivel[1], Timothy Bowles[1]

[1]UC Berkeley, Berkeley, United States

Aim:
Increasingly, the evidence suggests that farming diversification strongly influences soil organic matter and microbiome, which comprise the heart of soil health and functions. We aimed to know the influence of farm level diversification and landscape variation on soil microbial community assembly and diversity and ecosystem functions.

Method:
We collected soils from 28 organic lettuce farms on California's Central Coast, a highly productive agricultural region. Soil microbial communities, physicochemical properties, and selected ecosystem functions were analysed. The proportion of various landscape types within the 500m buffer of each farm was estimated by image analyses. Both local and landscape diversification scores were used as predictor variables in linear mixed models to know their effects on microbial diversity and abundance, their predicted functions, enzymatic activities, and various soil functions.

Results:
Our results revealed that increasing crop diversity increased bacterial but not fungal diversity. Also, farms that were surrounded by higher proportion of unvegetated had lower fungal diversity. Both local level and landscape level predictors had profound effect in bacterial and fungal community structure. We are testing the causal paths among landscape and local factors, microbiome communities, and soil functions to know the extent to which landscape and local effects on ecosystem functions are mediated through microbiome modulations.

Conclusions:
In addition to soil and climatic variables, farming management and landscape type define microbial diversity and community which in turn influence soil-based ecosystem services. The present study deepens our understanding of the relationship between farm diversification, the soil microbiome, and agroecosystem functioning.

Effect of Compost Added with Compostable Plastic Packaging on Wheat Health and its Rhizosphere Microbiome

Martina Coletta[1], Aldo D'Alessandro[1], Gianni Sagratini[2], Antonietta La Terza[1]

[1]School Of Biosciences And Veterinary Medicine, University Of Camerino, Camerino, Italy,
[2]School Of Pharmacy, University Of Camerino, Camerino, Italy

Aim:
Packaging waste is steadily increasing in Europe. Thus, compostable plastics (CPs) may represent an environmentally friendly alternative to petroleum-based plastics for the development of innovative packaging solutions. However, the potential impact of CPs presence in compost on soil ecosystems and crop health, still needs to be assessed. The present investigation aims to evaluate and compare the effects produced by "standard" compost (C) obtained from urban organic waste (UOW) and UOW added with 3% compostable bioplastics (CV), on wheat health and its rhizosphere microbiome.

Method:
Field experiments were conducted at Agricultural Research Station, CERMIS, Italy. During 2021-2022, three treatments (C, CV, and B -no compost) with five replicates each, were tested. Soil chemical-physical properties were measured before and after composts distribution to evaluate changes in nutrient concentrations and presence of possible pollutants. At the flowering stage, ten plants and associated rhizospheric soils were collected in each plot. Morphological and productive wheat traits were measured. Rhizosphere bacterial communities were analysed by 16S rRNA metabarcoding.

Results:
No significant differences between treatments were detected by means of wheat traits. C and CV compost fertilization significantly changed the bacterial communities with respect to the untreated control. But no significant differences were found between the C and CV communities, which also showed similar composition. This demonstrates the equivalence of the two composts.

Conclusions:
Results showed that CPs addition do not negatively affect compost quality neither wheat nor microbiome health. Thus, CPs represent a sustainable alternative to conventional plastic that will be crucial in the green European transition.

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Understanding hidden microbiodiversity in urban and natural environments using metabarcoding

Sjoerd Gremmen[1,2], Nafiesa Ibrahim[1], Kevin Beentjes[1], Jorinde Nuytinck[1], Vincent Merckx[1,2], Michael Stech[1]

[1]Netherlands Centre for Biodiversity Naturalis, Leiden, Netherlands, [2]IBED; University of Amsterdam, Amsterdam, Netherlands

Aim:

Microbial biodiversity in urban soils is understudied. Within current projects we aim to optimize molecular protocols and study the diversity and ecological functions of bacteria and fungi in Dutch cities. We aim to compare natural and urban soils and analyze biodiversity associated with common city trees and different urban topologies (e.g. pavement types).

Method:

In a pilot study, a nested sampling experiment was executed in a city park and a dune area close to Leiden. In addition, samples were taken in different streets (tree pits and pavings) in Leiden en Dordrecht. Soil was sampled to 15 cm deep using PVC tubes. Abiotic factors (pH/soil moisture) were determined and DNA was isolated and amplified using fungal ITS2 primers. OTUs/ASVs were determined from Illumina MiSeq data using the Dada2 pipeline.

Results:

Metabarcoding revealed a large fungal diversity (>5000 fungal ASVs) of mainly ascomycetes and basidiomycetes in city park and dune soils. Diversity differed more between than within locations and species accumulation curves indicate a dense sampling is required. Soil underneath pavings proved extremely alkaline (pH_{H2O} 8−10) and dry (H_2O content <10%). Very low DNA concentration (<1 ng/μl) were obtained; protocol optimization to sequence these samples are in progress.

Conclusions:

First results indicate that more natural urban soils (city park) are straightforward to analyze and harbor a large biodiversity. Soils underneath pavements seem to be extreme living environments, which either need to be analyzed by adapted lab protocols or may indeed accommodate significantly less biodiversity.

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Development of a Mesocosm Research Facility for Applied Research to Soil Ecology and Biology

Emiel Elferink[1], Martina Sura[1]

[1]*Van Hall Larenstein, Leeuwarden, Netherlands*

Helping to realize ecologically and economically healthy soils is the main goal of the Learning and Knowledge Center for Soil located in Oosterwolde the Netherlands. The LKC, founded in 2016, is acollaboration between 14 organizations and companies. Together we work on applied research and education on healthy soils. In 2022 we have realized a research garden with 100 so-called mesocosms. The mesocosms contain undisturbed soil cores of 1 meter deep and 1 meter wide. The mesocosms are equipped with an array of sensors that monitor soil conditions continuously. Per farm field 10 cores are collected. Fields differ in soil type and farming systems. Meso research is an addition to (macro) field research and highly controlled laboratory experiments (micro). By placing the mesocosms together, we investigate the interdependence of treatments and measures under the same natural conditions and monitor how soil ecology and biology changes. We will present the development of the research garden as well as the applied research projects we started to get better insight in soil ecology and biology development and how different treatments affects these.

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Tackling the diversity of urban green spaces for ground beetle communities

Alan VERGNES[1], Jérôme Cortet[1], Benoit Pongérard[1]

[1]*Univ Paul Valéry Montpellier 3 / CEFE, Montpellier, France*

Aim:
urbanization is a major land use change that leads to the alteration or destruction of natural or agricultural terrestrial habitats, and sometimes to the creation of new patches of habitats referred to as “green spaces”. The types of green spaces are highly diverse, reflecting the multiplicity of human uses of those vegetated patches: recreational, functional, aesthetic… The influence of urbanization features on soil epigeal biodiversity has now long been studied but mainly on urban-rural gradients. Studies that try to compare the response of communities between many types of green spaces are still rare.

Method:
we sampled ground beetles (*Coleoptera, Carabidae*), which are bioindicator insects, on 71 sites belonging to 10 types of green spaces (park, garden, roadside, etc.) in the area of Dijon metropolis (France). The effects of local environmental variables (type of site and vegetation cover) on abundance, diversity indices and the structure of communities were tested.

Results:
This study shows that the type of site effect on abundance and species richness of ground beetles, contrary to the vegetation cover.

Conclusions:
The results of this study clarify the existence of a strong local filter in urban environment and the importance of vegetation patches with low disturbance levels for insects. They also suggest that other factors may affect ground beetle communities.

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Diversity of Microorganisms in the Rhizosphere of the Only Two Higher Plants in Antarctica

Lenka Fisarova[1], Beata Soperova[1], Miroslav Kolarik[2], Jitka Viktorova[3], Miroslav Vosatka[1]

[1]*Institute of Botany of the Czech Academy of Sciences, Pruhonice, Czech Republic,*
[2]*Institute of Microbiology of the Czech Academy of Sciences, Prague, Czech Republic,*
[3]*University of Chemistry and Technology Prague, Prague, Czech Republic*

Aim:
Antarctica has a large number of unexplored species of microorganisms with potentially unique features and specific biological activities due to extreme climatic conditions. Aside from lichens, mosses and liverworts, plant life in Antarctica consists of coastal tussock grass and the only two flowering plants inhabiting continental Antarctica are Antarctic hair grass (*Deschampsia antarctica*) and Antarctic pearlwort (*Colobanthus quitensis*).

Method:
In this study, samples were taken from the roots and rhizosphere of these two species from Ross Island and Deception Island. Microorganisms were cultivated on potato dextrose agar, and their morphology was determined. Samples with different morphology were selected and their DNA was isolated. ITS sequences (fungal and yeast) and 16S rRNA sequences (bacterial) were amplified, sequenced and compared with database. Biological activities were tested *in vitro* in selected species, as well as the influence of bacteria on plant growth.

Results:
High diversity was found in detected samples. Most species were isolated from Antarctic pearlwort, including 107 isolates, where 22 different isolates of bacteria, fungi and yeasts were identified. Isolates included several taxonomical novelties. Biological activities tested were antioxidant, anticancer, antibacterial (e.g. against *Escherichia coli*, *Pseudomonas aeruginosa*, *Enterococcus faecalis*), antifungal (*Botrytis cinerea*, *Aspergillus fumigatus*, *Candida albicans*) and antiviral. When bacterial species were applied to plant roots, its synergy with arbuscular mycorrhizal fungi on the growth of plants was observed. Arbuscular mycorrhizal colonization was also found to be present in the roots of *D. antarctica*.

Conclusions:
Our findings demonstrate the diversity and specific bioactivities and thus potential use of microorganisms isolated from plants in Antarctica.

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Installing flower strips to promote soil biodiversity

Sara Acconcia[1], Andrés Valdezate[2], Oscar Aguado Martín[2], Luis Miranda[3], Javier Peris[3], Maria J I Briones[1]

[1]University Of Vigo, Vigo, Spain, [2]Andrena iniciativas y estudios medioambientales SL , Valladolid, Sapin, [3]Syngenta Crop Protection, Basel, Switzerland

Aim: The LivinGro® project focuses on using cover crops to create optimal conditions for enhancing above- and below-ground biodiversity. This study aimed at investigating the potential positive effects of installing flower strips to promote the diversity of macrofauna (earthworms) and mesofauna (microarthropods) communities.

Method: This preliminary study was carried out in two commercial olive groves located in RioSeco and Pozaldez (Valladolid, Spain) where the soil in between tree rows was either planted with a mixture of flowers or left uncovered. Earthworms were hand-sorted in the field from three soil quadrats (50 x 50 x 20 cm) and identified to species level. Microarthropods (mites and collembolans) were extracted from three intact soil cores (10 cm diameter x 20 cm deep) and identified to family level.

Results: Earthworm communities at both sites were low and dominated by two species *Aporrectodea trapezoides* and *Aporrectodea rosea.* In contrast, microarthropod communities were much more diverse, in particular at the bare soils where up to 20 microarthropod families were identified, compared with 18 being recorded in the vegetated plots. Diptera larvae and adults (Chironomidae), Prostigmata (Eupodidae) and Endeostigmata (Nanorchestidae) mites were particularly abundant at the vegetated plots, whereas a more diverse mite community, including Mesostigmata (Rhodacaridae and Macrochelidae), Prostigmata (Eupodidae, Rhagidiidae), Endeostigmata (Alicorhagiidae) and Oribatida (Oribatulidae) mites dominated the mesofauna communities at the bare plots.

Conclusions: These preliminary findings indicate that intensive practices have negative effects on macrofauna and that cover crops offer protection to the more drought-sensitive mesofauna.

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Relation of Soil Microbiome to Crop Nutritional Value – Dutch Farms Case Study

Martina Sura-de Jong**,** Emiel Elferink[1], Kika Lewak[1,2], Zhilei Gao[2], Luka Dorresteijn[1], Wouter Suring[1], Toke Heerkens[3], Pier Oosterkamp[2], Wynand Alkema[3], Petra Boorsma[4]

[1]Van Hall Larenstein University Of Applied Sciences, Leeuwarden, Netherlands, [2]ECOstyle BV, Oosterwolde, Netherlands, [3]Hanze University of Applied Sciences, Groningen, Netherlands, [4]Biosintrum, Oosterwolde, Netherlands

Aim:
The dynamics of the soil microbiota and their influence on crop nutritional value is still not fully understood. To unravel this correlation, a study is performed in close collaboration with farmers of the North of the Netherlands.

Method:
The agricultural soils and crops were collected on parcels of various farms (n=16 in 2020, n=50 in 2021). At each farm samples were taken from both soil that farmers indicated as ‘best’ and ‘worst’. ‘Best’ soil were those soils that delivered crops with a good yield, while ‘worst’ soil was indicated as a soil delivering poor yield. Soil was analysed for its physical-chemical properties. Soil microbiome (bacterial, protist and fungal community) was analysed using next generation sequencing. Crop material was investigated for its fatty acid, amino acid and carbohydrates (starch and sugar) content.

Results:
Although soil type shaped the richness and diversity of soil microbial community, analysis of beta diversity of individual microbial domains showed that ‘best’ and ‘worst’ soils harbour significantly different protist community. Furthermore, fungal diversity was correlated to soil organic matter, while fungal richness to fatty acids in crops. Bacteria and protists diversity and richness were correlated to crops nutritional components, such as multiple saturated and unsaturated fatty acids, amino acids and sugars; both in ‘best’ and ‘worst’ soil. Interestingly, protists diversity exhibited opposite correlations to specific crop fatty acids and amino acids in ‘best’ and ‘worst’ soils.

Conclusions:
In conclusion, this study shows there is a correlation between various soil microbial community measures and crops nutritional values.

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Understanding community assembly in arbuscular mycorrhizal fungi: from structural traits to fundamental and realized niches

Zuzana Kolaříková[1], Jana Rydlová[1], Martina Janoušková[1], Radka Sudová[1], Jakub Skřivánek[1], Renata Fričová[1], Petr Kohout[2]

[1]Institute of Botany, Czech Academy of Sciences, Průhonice, Czech Republic, [2]Institute of Microbiology, Czech Academy of Sciences, Prague, Czech Republic

Aim:

Arbuscular mycorrhizal fungi (AMF), almost ubiquitous plant symbionts, display interspecific variation in a range of traits, which may determine their distribution and symbiotic potential. We are interested in whether/and how AMF structural traits relate to the ability of these fungal species to proliferate in specific abiotic conditions, i.e. the species' fundamental niches.

Method:

We have started a series of greenhouse and growth chamber experiments with four plant species and a multitude of AMF isolates in order to assess the development of their intraradical and extraradical phase. Specifically, we focus on root colonization, activity and viability of intraradical fungal structures, spore production, extraradical mycelium length, morphology and metabolome.

Results:

Preliminary results show differences among AMF species- as well as among host plant-specific expressed over cultivation time. E.g., intraradical colonization and spore production were generally lower in Bromus erectus as compared to the other host plants. Claroideoglomus claroideum displayed higher activity of intraradical mycelium after 4 weeks, while Rhizophagus intraradices, AMF species with comparable root colonization levels, maintained high activity even after 18 weeks.

Conclusions:

Selected traits will be measured in future experiments focused on AMF development along gradients of environmental conditions and the intra- as well as interspecific variability of these AMF traits will be evaluated. We aim to link the realized-niche data derived from databases with information on fundamental niches and structural traits of AMF species in order to enable predictions of the species responses to environmental change.

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Effects of Livestock Grazing-Intensity and Soil Compaction on Soil-Mesofauna Depend on Land use History

Dennis Baulechner[1], Volkmar Wolters[1], Andrey Zaitsev[2,3], Katharina John[1]

[1]Institute Of Animal Ecology, Justus Liebig University, Heinrich-buff-ring 26, Giessen, Germany, [2]Senckenberg Museum of Natural History Görlitz, Görlitz, Germany, [3]Laboratory of soil ecosystem functions, A.N.Severtsov Institute of Ecology and Evolution, Russian Academy of Sciences, Moscow, Russia

Aim: Increasing demand in sustainably raised livestock favours the expansion of grazing systems on open land. However, the effects of these systems on the functional composition of soil fauna under conditions of intensive vs. extensive grazing are largely unexplored. Even less is known about the resilience of soil fauna after intensive grazing. The aim of our DFG Project ReSoilience is to contribute to close these knowledge gaps.

Methods: Mesofauna sampling was conducted on agricultural grasslands in the three model regions of the DFG Biodiversity Exploratories in Germany. We analysed functional community composition and assembly processes of Acari and Collembola (1) at the project's 150 grasslands which represent a gradient of land use intensity. (2) At 16 intensely used sites we analysed resilience of communities after one year of extensification, and (3) additionally in a subset of 27 sites we checked community assembly before and after experimental soil compaction.

Result: With increasing intensity, grazing reduced microarthropod functional diversity. At high intensity sites, it acted as an environmental filter that excluded functionally similar species. Resilience was low and regionally specific after extensification of grazing. Although the reduction in functional diversity after experimental compaction was comparable to that under intensive grazing, both the effect size and community resilience depended on the grazing intensity in the previous three years.

Conclusion: Our results show that the negative effects of long-term intensive grazing on soil-fauna cannot be reversed rapidly. Nevertheless, low grazing intensity can maintain soil-fauna diversity if livestock is moved regularly to ensure regeneration periods and avoid persistent stress.

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Modelling and mapping soil biodiversity patterns and functions across Europe: the EJP Soil- MINOTAUR project

Stefano MOCALI[1]

[1]*CREA, FIRENZE, Italy*

Aim:
The current status and trends in soil biodiversity across Europe are poorly known, and adequate taxonomical and functional indicators are needed to evaluate the vulnerability of soils to climate change. MINOTAUR aims to provide models, maps and policy-relevant indicators with validated reference values for monitoring soil biodiversity and associated functions. Moreover, it will aim to understand how agricultural practices can contribute to climate change mitigation and adaptation at regional and national levels across the EU.

Method:
The project collaborates with relevant EU research projects, international networks and programs to harmonize and integrate soil biodiversity data. Based on the collected data, specific policy-relevant indicators describing soil biodiversity taxonomical and functional status will be selected and validated under field conditions in 12 LTEs, where their sensitivity and ranges will be addressed in relation to soil type, climate and management practice. Finally, depending on the available datasets, we will model the spatial distribution patterns of soil fauna assemblages from the local to the wide scales in response to climate and habitat conditions.

Results:
The overall project strategy and the results of the first years will be presented. Collection and harmonization of the existing data and metadata on soil biodiversity available from previous EU and national projects available through the consortium, as well as external sources was carried out. Collaborations were established with existing databases (es. EUdaphobase) to identify knowledge gaps in existing databases.

Conclusions:
This project represents an ambitious attempt to provide reliable recommendations on soil management options for policy to address and enhance soil quality.

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ErIK2 - Machine Learning-Based Earthworm Identification Key and GIS Platform (Web and Mobile Application)

Davorka Hackenberger[1], Branimir Hackenberger[1,2], Domagoj Hackenberger[1,2], Tamara Đerđ[1,2]

[1]Department Of Biology, University Of Osijek, Osijek, Croatia, [2]SCIOM Ltd, Osijek, Croatia

Aim:

Taxonomic species identification is an essential part of biodiversity research. Despite advances in computer technology, there is still a lack of user-friendly software tools for earthworm species identification and simultaneous storage of data on the location of findings. This research focused on developing a machine learning-based earthworm identification key and GIS platform (ErIK2), an upgraded derivative of the software-based identification key (ErIK) previously developed by our team.

Method:

The ErIK2 platform comprises earthworm species identification keys (tabular and dichotomous key) and a GIS component. The machine learning-driven tabular key allows species determination based on morphological and anatomical features of the individual, while the dichotomous key considers user choices from a series of couplets. The GIS component allows input and display of data stored in a dedicated geospatial database. Sampling time and location of various earthworm species can be entered following species identification within the ErIK2 platform or independently from the species identification process.

Results:

The ErIK2 platform allows identification of 58 earthworm species distributed throughout Europe and ten endemic species being present exclusively in Croatia. The functionalities of the platform have been tested and confirmed on different operating systems, web browsers and smartphones. The ErIK2 web application is hosted on http://earthworms.eu/erik2, while the ErIK2 Application can be downloaded from Google Play.

Conclusions:

ErIK2 is an easy-to-use software platform that has the potential to become a central tool in mapping earthworm fauna distribution across Europe both in scientific research and citizen science projects.

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Temperature dependence of earthworm life history traits : a global synthesis

Jerome Mathieu[1], Pierre Ganault

[1]*Sorbonne University, Paris, France*

Aim: Temperature dependence of earthworm life history traits : a global synthesis

In the context of climate change, understanding the impact of temperature on reproductive traits is critical to anticipate population dynamics. However, our knowledge on soil organisms remains very limited by the little availability of life history trait databases at both intra and interspecific levels. Here we synthesize current knowledge of the temperature dependence of earthworm reproductive traits through a comparative analysis.

Method: Data synthesis

We compiled literature data from over 200 sources to build the EwLHT database of life history traits related to reproduction in earthworms.

Results: Strong temperature dependance

There is a strong temperature dependence of most life history traits - e.g. a strong decrease of cocoon hatching time with temperature - which suggests that climate change will have a deep impact on earthworm species population dynamics. However all species don’t respond in the same way, and life history traits can show opposite responses to temperature. Critically, data are lacking for the vast majority of earthworm species. Results also suggest a potential strong interaction with soil humidity, but data are too limited to confirm this trend.

Conclusions: The need for standardized data and other species

Temperature has a major impact on earthworm life history traits. but responses differ among species and life history traits. Critically, only a limited number of species were studied. This highlights the urgent need to better document life history traits in earthworms, with standardized experiments. This effort will be stimulated through the sWorm2 project.

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Building a verified image collection for computer vision identification of worldwide earthworm species in iNaturalist

Jerome Mathieu[1], Pierre Ganault, Erin Cameron, Thibaud Decaens, Lise Dupont, Carlos Fragoso, Anna Geraskina, Elena Golovanova, Mickael Hedde, Aiden Keith, John Reynolds

[1]*Sorbonne University, Paris, France*

Aim: Building a verified image collection for computer vision identification of worldwide earthworm species

Identifying species is a critical step in all ecological studies and a key way to engage citizens in science and conservation. However, soil organisms are noticeably difficult to identify in part because of the lack of identification tools. This is a clear bottleneck for monitoring programs and conservation efforts. Here we make a collaboration call to build a reference collection of pictures of earthworm specimens that were rigorously identified, in order to train both future earthworm taxonomists and the iNaturalist's computer vision identification engine.

Method: An iNaturalist Project

We will use the iNaturalist platform to store observations of earthworms that were identified by earthworm taxonomists. Pictures are uploaded to the project "Curated collection of Earthworms ID": https://www.inaturalist.org/projects/curated-collection-of-earthworms-id.

Results: iNaturalist is a suitable platform

The first tests show that iNaturalist is a suitable platform to develop this project. At the moment, there is a strong bias in favor of *Lumbricus terrestris*. Besides, many earthworm species are not included in the iNaturalist taxonomy database, but researchers have numerous pictures not uploaded to iNaturalist. We also need to develop interoperability with other platforms and initiatives such as BOLD, GloWorm and sWORM.2.

Conclusions: Earthworm taxonomists are invited to the project

All earthworm specialists are welcome to contribute with observations rigorously identified. Computer vision won't replace classic taxonomic work but can improve citizen awareness and involvement in soil biodiversity monitoring or invasive species tracking.

The amendments of small signalling molecules and soil-extracts influence the culturability of common sunflower microbiota

Eliška Suchopárová[1], Jakub Papík[1], Jáchym Šuman[1], Michal Strejček[1], Ondřej Uhlík[1]

[1]*UCT Prague, Praha 6, Czech Republic*

Aim: Plant-associated bacteria have been shown to have a high potential for various biotechnological purposes, including their application to increase the sustainability of agricultural practices. However, more than 90% of microorganisms have not yet been cultured as current cultivation approaches do not sufficiently reflect their natural living conditions. To address this, we aimed to investigate the effect of various growth media modifications on the diversity and structure of culturable rhizospheric and foliar endophytic bacterial populations of common sunflower (*Helianthus annus* L.).
Method: We (i) prepared leaf and soil extract-based solid media, which we believed would better simulate natural environment for endophytic and rhizospheric bacteria, respectively, and we (ii) tested how the addition of small signalling molecules (cAMP, cGMP, or acyl homoserine lactons) to microbial inocula prior to plating influenced their culturability. Obtained cocultures were subjected to total genomic DNA extraction and 16S rRNA gene amplicon sequencing using Illumina MiSeq.
Results: Our results show that, in the case of rhizospheric populations, our modifications had a significant effect on both the diversity and composition of culturable bacterial populations and led to the enrichment of specific bacterial genera, while the culturability of foliar endophytes was not influenced by media modifications nor the incubation with signalling molecules.
Conclusions: We show that different cultivation approaches resulted in yielding distinct rhizospheric populations, and, thus; only by combining multiple approaches to isolate potentially beneficial plant-associated microorganisms will we be able to seize their biotechnological potential most efficiently. This research was funded by Czech Science Foundation project 20-00291S.

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The impact of agricultural practices on the diversity and composition of soil biodiversity

Felipe Cozim Melges[1,2,3], Philipp Oggiano[1,4], Raimon Ripoll Bosch[3], Wim van der Putten[2], Ciska Veen[2]

[1]Farming Systems Ecology - Wageningen University and Research, Wageningen, Netherlands, [2]Netherlands Institute of Ecology (NIOO-KNAW), Wageningen, Netherlands, [3]Animal Production Systems - Wageningen University and Research, Wageningen, Netherlands, [4]Research Institute of Organic Agriculture - FiBL, Frick, Switzerland

Aim:

Agriculture has become a main driver of biodiversity loss, with intensive agricultural practices adversely impacting the biodiversity and composition of soil communities in agroecosystems. This led to the search for alternative practices (e.g. intensive to minimum tillage). Here, we present a global literature review to analyse how the diversity and abundance of functional groups of four important soil taxa, namely nematodes, earthworms, bacteria and fungi, were impacted by alternative practices.

Method:

A literature review was conducted in SCOPUS and WEB OF SCIENCE for cropland and grassland agro-ecosytems. We retrieved data from that literature review for the four soil taxonomic groups and further divided the data records by trophic groups, based on common and relevant classifications used in the current soil ecological literature.

Results:

We found that alternative agricultural practices in general increased the overall abundance of all taxonomic groups, however practices affected the diversity of taxa and abundance of functional groups differently. Furthermore, we found that all taxa had contrasting impacts among their functional groups for at least one of the reviewed practices, such as bulky organic fertilizers adversely affecting epigeic earthworms while enhancing endogeic and anecic groups. There was only one alternative practice, i.e., the use of cover crops, that was neutral to positive for the abundance of all functional groups across all taxa.

Conclusions:

Enhancing the abundance of different functional groups may require applying a combination of multiple alternative agricultural practices and understanding of potential contrasting effects between diversity and abundance of relevant functional groups.

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The Soil Invertebrate Genome Initiative (SIGI)

Miklos Balint[1,3,10], Jens Bast[2], Gemma Collins[3], Cyrille D'Haese[4], Miklós Dombos[5], Peter Decker, Carola Greve[3], Karin Hohberg[6], Kamil S. Jaron[7], Ricarda Lehmitz[6], Karen Meusemann[8], Leonie Schardt[3], Clément Schneider[6], Philipp Schiffer[2], Nikolaus Szucsich[9]

[1]Senckenberg Biodiversity And Climate Research Centre, Frankfurt Am Main, Germany, [2]University of Cologne, Cologne, Germany, [3]LOEWE Centre for Translational Biodiversity Genomics, Frankfurt Am Main, Germany, [4]Muséum National d'Histoire Naturelle, Paris, France, [5]Institute for Soil Sciences and Agricultural Chemistry, Budapest, Hungary, [6]Senckenberg Museum für Naturkunde Görlitz, , Germany, [7]Wellcome Sanger Institute, , UK, [8]LIB - Museum Koenig (ZFMK), Bonn, Germany, [9]Naturhistorisches Museum Wien, , Austria, [10]Justus-Liebig University, Gießen, Germany

Aim:

We launched the Soil Invertebrate Genome Initiative to co-ordinate genome sequencing of soil invertebrates.

Method:

The initiative was sparked by collaborations among researchers from several institutions, providing a platform to combine taxonomic and genomic expertise. Our whole-genome sequencing efforts are initially focused on representatives of a broad taxonomic range of soil invertebrates The involvement of many different taxon experts is an important characteristic of the initiative, ensuring accurate collection and identification of specimens which are then individually sequenced. Whenever possible, we employ non-destructive DNA extraction methods and deposit the specimen vouchers into museum collections to allow for later morphological verification. We are continuously adapting and developing new approaches to improve sequencing results, the amount of required DNA and the condition of the voucher after DNA extraction.

Results:

So far we generated short read genomes of over 200 species of mites, springtails, nematodes, myriapods, enchytraeids etc., and long read genomes for several species of springtails and mites. Analyses aim to link functional traits to genomic features, improve phylogenies, and support species identification from mixed/environmental nucleotide samples.

Conclusions:

As most soil metazoa are challenging to study, method developments are necessary to obtain genomes of reasonable quality. However, once these genomic resources are available, they enhance our ability to use environmental DNA and RNA for the identification of soil community structure and function, and support the development of efficient, large-scale monitoring procedures. These genomes also provide insights into the evolution and ecology of soil invertebrates and their roles in soil functioning.

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Mucoromycotina ‘fine root endophyte’ fungi – exploration of their endosymbiotic and rhizospheric bacteria

Grace Hoysted[1], Katie Field[2], Silvia Pressel[3], Martin Bidartondo[4,5]

[1]University College Dublin, Dublin, Ireland, [2]University of Sheffield , Sheffield , United Kingdom , [3]Natural History Museum , London, United Kingdom , [4]Imperial College London, London, United Kingdom , [5]Royal Botanic Gardens Kew, London, United Kingdom

Fungi have engaged in intimate symbioses with plants for >500 million years and bacterial associations are being increasingly appreciated for shaping phenotypes, function and ecology of plant-fungal interactions in diverse settings. Recently, we demonstrated that fungal partners of plant roots, known as mycorrhizal fungi, are more diverse than previously thought and include ‘fine root endophytes’ of the Mucoromycotina (MFRE). MFRE usually occur in plants co-colonised by Glomeromycota arbuscular mycorrhizal fungi (AMF). Like AMF, MFRE host endosymbiotic bacteria and our latest research, using novel monoxenic cultures and wild-collected plants and fungi, has shown MFRE associations also confer nutritional benefits on host plants. However, the role of the soil bacterial community in MFRE colonisation and function remains unexplored. Using novel techniques developed for MFRE fungal isolation and culture, we plan to manipulate MFRE singly and in combination with AMF and their associated bacterial communities to provide evidence of how different fungi communicate and interact in diverse ecosystems. Our research will have implications for microbial soil ecology, from controlled to field conditions, especially if diverse bacteria allow fungi to engage in unexpected partnerships and unlock their potential as bioenhancers of globally important crops.

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Cleaning Soil Invertebrate Samples using Computer Vision

Branimir Hackenberger[1,2], Tamara Djerdj[1,2], Domagoj Hackenberger[1,2], Davorka Hackenberger[1]

[1]Department Of Biology, University Of Osijek, Osijek, Croatia, [2]SCIOM Ltd, Osijek, Croatia

Aim:

The process of quantifying and monitoring soil invertebrate biodiversity is intensive and laborious. The application of modern computer vision and deep learning techniques can accelerate the sample processing and identification processes. However, the results of computer vision-based algorithms are highly dependent on the quality of the input data. As part of this research, an algorithm was developed for the recognition and removal of soil particles from photographs of soil invertebrate samples.

Method:

The computer vision and deep learning-based algorithm was trained on labeled photographs of invertebrate samples containing soil particles. The convolutional neural network for soil particle segmentation was trained on a total of 100 photographs of invertebrate samples collected at different locations, with various soil types. The software was written in Python and the artificial neural network was constructed and trained using Keras.

Results:

Performance of the developed algorithm was evaluated using a validation dataset which consisted of input-label pairs of invertebrate samples obtained from locations with different soil types. Photographs contained in the validation dataset have not been included in the training process. The developed algorithm achieved a precision of over 85% in recognition and removal of soil particles from photographs contained in the validation dataset. The mean Intersection-over-Union of the trained algorithm was over 60% for all soil types tested.

Conclusions:

The developed algorithm can be used for preprocessing photographs of soil invertebrate samples, and thus improve the results of previously developed computer vision-based algorithms for automatic determination of soil invertebrate biodiversity.

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Engage, Learn, Inspire: Building Leaders by Empowering Voices From the Ground

Victoria Valenzi[1], Miranda WadhamSmith[1], Lucia Gerbaldo[1]

[1]*FAO, Rome, Italy*

Aim:

The “Making every voice count for adaptive management” (MEV-CAM) initiative challenges traditional South-South knowledge management approaches by collecting and amplifying local and indigenous expertise. The unique knowledge these communities hold includes sustainable practices that encourage biodiversity to flourish, making it a vital global driver of drylands restoration.

Method:

MEV-CAM empowers communities and stakeholders to demonstrate their skills and share challenges and successes, visualizing the process of change itself through participatory tools. MEV-CAM digs deeper to extract best practices for scaling up, down, and deep to give communities ownership over the process of defining change by focusing on the impact at scale. MEV-CAM’s unique and innovative tools, such as participatory video (PV), are used to monitor change enhancing biodiversity by measuring the impact directly from the community level.

Results:

MEV-CAM has enabled communities from Malawi, Tanzania, Uganda, and Burundi to make PVs that document and share the best practices to encourage biodiversity in their areas. This has included the growth of beekeeping as a livelihood and contour farming to foster biodiverse ecosystems and soil health.

Conclusions:

MEV-CAM collects best practices, enabling communities to document and share their knowledge to facilitate more sustainable livelihoods, landscape restoration and biodiversity in local environments. MEV-CAM will be working directly with WeCaN’s Community of Practice for Women in Dryland Regions and Agrosilvopastoral Systems, a knowledge sharing platform for Southern women leaders to amplify and disseminate their skills and knowledge, to share these best practices more widely and empower women leaders on the ground to drive positive changes in biodiversity.

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Functional Approach Using Soil Protists as a Taxon-free Tool for Environmental Quality Assessment

Elizaveta Ermolaeva[1], Edward AD Mitchell[1]

[1]*Laboratory of Soil Biodiversity, University Of Neuchâtel, Neuchâtel, Switzerland*

Aim: Soil organisms are useful as bioindicators to assess the impact of ongoing climate change on ecosystem functioning. Peatlands, which represent a major reservoir of soil organic carbon, are threatened by anthropogenic influence. Water table depth (WTD) is a key factor controlling the carbon balance in peatlands. Testate amoebae are routinely used as WTD indicators using predictive models. These transfer functions require taxonomic identification based on shell morphology, but some taxa are commonly misidentified. An alternative approach is to use functional traits. Our aim was to assess the extent of taxonomic bias and to compare the performances of species-based and traits-based models.

Method: A set of light microscopy images of testate amoeba was compiled using samples collected across European peatlands. Species identifications with degree of confidence for each picture were analysed by researchers with contrasted expertise. We compared diversity metrics derived by each observer. For our second aim, we developed a trait-based transfer function with a trait database for the most commonly identified species morphotypes.

Results: The degree of identification bias differed among taxa leading to strong variation in diversity metrics. The functional traits model performed equally well compared to the morpho-taxa-based one.

Conclusion: As ecological information is being routinely lost due to species misidentifications and taxonomic uncertainty, taxon-free approaches potentially offer safe and robust alternatives for rapid and accurate ecological assessments. We conclude that functional traits models overcome limitations of taxonomy-based ones for WTD inference, and may also prove to be better-adapted for inferences of ecosystem functioning.

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The role of soil biodiversity in temperate forest restoration

Sam Bielen[1], Jasper Wubs[1], Wim H. van der Putten[1,2]

[1]NIOO-KNAW, Wageningen, The Netherlands, [2]Wageningen University & Research, Wageningen, The Netherlands

Aim:
Soil improvement aimed at vital and diverse forest with rich-litter species adapted to climate change and nitrogen deposition. This way we want to initiate a development that can transform the current negative impacts of these environmental changes into a positive forest and biodiversity development by testing different soil managements.

Method:
To test our aims a large field experiment is set up at the National Park 'De Hoge Veluwe'. We will test the influence of soil inoculation, rockdust, soil type, main occurring tree species and the planting of eight different tree species with fast degrading litter. In total, 640 plots will be studied for three consecutive years. Physical-chemical analysis, soil biodiversity, litter degradation, mineralisation and tree growth will be measured.

Results:
Similar studies which focused on grassland and heathland restoration already showed promising results. We also expect that restoration of degraded forests is possible with soil improvement.

Conclusions:
We will demonstrate what the best soil life in future-proof forests is and how it depends on soil conditions. In addition, we will demonstrate how soil transplantation can be most effectively conducted. Furthermore, this data will help stakeholders to make the right decisions in management.

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Microbial communities of peat soils and mofettes and their potential to transform lignin

Jakub Papík[1], Tereza Šmrhová[1], Michal Strejček[1], Ondřej Uhlík[1]

[1]*University Of Chemistry And Technology, Prague, Czechia*

Aim: Wetlands are some of the largest natural carbon sinks on Earth, removing CO_2 from the atmosphere and storing it in the form of organic matter. Climate change threatens these ecosystems in terms of their ability to store carbon, since rising temperatures can lead to drainage and increased organic matter decomposition. Our aim was to (i) characterize microbial communities in peat soils and mofettes in SOOS National Nature Reserve, Czechia, and (ii) their ability to transform lignin; the second most abundant plant biopolymer in the biosphere and a significant component of peat.
Method: To investigate lignin-transforming populations, we are employing a combination of shotgun metagenomics and metataxonomics, stable isotope probing with 13C-labeled lignin, and enrichment culture experiments with lignin as the sole carbon source under either aerobic or anaerobic conditions.
Results: Our preliminary results show that peat soils and mofettes host distinct microbiota, and we obtained lignin-transforming consortia that differed mainly in terms of their oxygen demands during incubation. Anaerobic enrichment cultures yielded a total number of 39 unique bacterial isolates, while aerobic enrichment cultures yielded 69 unique bacterial isolates, including a hitherto undescribed species which was found to have 16S rRNA gene sequence of 98.25 % to its closest cultured relative, *Altererythrobacter fulvus*.
Conclusions: The results of this ongoing study are expected to broaden our current understanding of lignin-transforming microbial populations in wetlands and the molecular mechanisms that lie behind plant-derived organic matter decomposition in these ecosystems. This research was funded by Czech Science Foundation project 20-00291S.

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If you can measure it, you can manage it: soil biodiversity management in South Africa

Tersia Conradie[1], Karin Jacobs[1]

[1]*Stellenbosch University, Stellenbosch, South Africa*

Aim: Microorganisms play a crucial role in several nutrient cycles. Managing these cycles is key to ensuring healthy crop production. We provide a tool through which farmers can monitor and manage changes in soil microbial communities over time by assessing microbial diversity, as well as functionality.

Method: A molecular fingerprinting technique is used to determine the soil microbial diversity, together with the functional potential of soils determined through various soil enzymatic analyses. Microbial diversity provides information on how diverse and evenly distributed the microbial communities are. Enzymatic activity of microorganisms provides information of how robust and functional these communities are. Each sample is compared to a database of the same crop, allowing the farmer to examine a single time point and monitor for changes over time.

Results: Microbial alpha-diversity indices and soil enzymatic activity is provided on a scale from low to high, together with a beta-diversity plot to determine how similar the community composition is to previous samples. Recommendations are made based on these results.

Conclusions: A highly diverse and evenly distributed microbial community is desired for optimal soil functionality. A loss in diversity due to a stress such as drought, may not result in a loss in functionality, as many microorganisms may perform similar functions. Testing for these functions provides information if the desired tasks are performed by each community even at low diversity levels. This is the first attempt in Southern Africa to use soil microbial diversity indices to inform the agricultural industry on farm management practices.

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Leveraging local and women’s in-depth ecological knowledge, as environmental stewards and guardians of biodiversity.

Lucia Gerbaldo[1]

[1]FAO, Camerana, Italy

The ***”WeCaN Nurturing Community of Knowledge Practice for Women in Dryland Regions and Agrosilvopastoral Systems” (*****WeCaN)** is a knowledge-sharing platform for women leaders on the ground to share good practices and drive positive changes in dryland restoration and soil biodiversity conservation.

Method:

The WeCaN community of knowledge practice built an international network of women’s farmers, small-scale food producers and women leaders to amplify, maximize, and disseminate specific women and local knowledge concerning species diversity, soil biodiversity and land restoration. Using the knowledge-to-action approach, the WeCaN Community collects, valorize and disseminates a new narrative about the women's role in biodiversity conservation, as food providers, custodians of seeds, keepers of medicinal plants, and guardians of biodiversity.

Results:

WeCaN has enabled over 200 women leaders to raise awareness of women’s specific expertise in biodiversity conservation and land restoration and the need to include them in decision-making. It has promoted themes, dissemination materials and activities relating to biodiversity in the dryland regions through articles dissemination, learning opportunities and knowledge exchange, engaging 20 women leaders in advocacy actions for soil biodiversity.

Conclusions:

The experiences and the best practices collected in 26 countries involved in the WeCaN community of Knowledge practice have confirmed that gender inequalities must be addressed as part of biodiversity conservation and land restoration. Going forward, WeCaN will be working directly with “***Making every voice count for adaptive management”* (MEV-CAM)** innovative knowledge documentation process used to scale up, deep and out best practices focused on soil biodiversity in the indigenous and local communities.

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Uptake of Soils Awareness-Raising/Education Workshops Evidences Interdisciplinary Demand for Soil Biodiversity Knowledge at University

Cairo Robb[1]

[1]University of Edinburgh, United Kingdom, [2]Magdalene College, University of Cambridge, United Kingdom, [3]CISDL, Canada

Aim:
Awareness raising and education about the diversity of soils and soil organisms, their contributions to human well-being, and the threats posed by lack of such awareness on the part of decision-makers from the classroom to the boardroom.

Method:
Capitalised on World Soil Day 2022 to launch a series of ‘Introduction to Soils Workshops’ at Magdalene College, University of Cambridge. Following an introductory talk and discussion, the first workshops (morning and afternoon) involved participants choosing and adopting the name of a soil dwelling organism, and taking part in hands-on soil texturing activity. The next will focus on soil structure and soil biodiversity, and involve Visual Evaluation of Soil Structure and hand-sorting soil animals.

Results:
With minimal publicity and little advance notice, 22 undergraduate and postgraduate students, researchers and lecturers (plus others) expressed interest in attending, spanning History, Languages, Archaeology, Geography, Astrophysics, Engineering and Natural Sciences. All who were able to participate in the workshops reported to have learned a lot and expressed a desire to attend a future workshop focussed on soil biodiversity. Additional feedback included that the workshops “put the whole thing in context” and highlighted “the importance of interdisciplinarity and communication on soils”. Some participants requested that future workshops address the impact of climate change and other anthropogenic activity on soil organisms.

Conclusions:
There is a desire - and an unmet need - among University students, researchers and staff, across many disciplines, for opportunities to learn about soils, soil organisms and soil biodiversity, and their relevance in decision-making.

Urochloa hybrid can inherit P-cycling genes related to microbial communities and their P-cycling abilities

Gabriel Silvestre Rocha[1], Luis Fernando Merloti[1,2], Luís Felipe Guandalin Zagatto[1], Lenir de Fátima Gotz[2], Anderson Santos de Freitas[1], Luísa da Costa Desgranges[1], João William Bossolani[3], Paulo Sérgio Pavinato[2], Cacilda Pimenta Borges[4], Tsai Siu Mui[1]

[1]Center for Nuclear Energy in Agriculture - University of São Paulo, Piracicaba, Brazil, [2]Luiz de Queiroz College of Agriculture - University of São Paulo, Piracicaba, Brazil, [3]School of Agriculture - São Paulo State University, Botucatu, Brazil, [4]Brazilian Agricultural Research Corporation (EMBRAPA - Gado de Corte), Campo Grande, Brazil

AIM

This work aims to understand how the genetic breeding of *Urochloa* (through hybridization between *U. brizantha* and *U. ruzizienensis*) modifies the soil microbial groups in soil depths and their related P-cycling abilities.

METHOD

Four *Urochloa* varieties, *U. brizantha* cv. Marandu (UM), *U. brizantha* BRS Paiaguás (UP), *U. ruziziensis* (UR) and the hybrid Ipyporã (UI) were evaluated in a 3-year field experiment with soil samples collected at three soil depths. The *pqqC* and *phoD* genes were amplified by qPCR as well as the barcodes for Bacteria, Archaea and Fungi communities. The phosphorus fractionation was conducted; the enzymatic activity was measured for both, acid and alkaline phosphatases. Data were analyzed in R.

RESULTS

There are differences in the Archaea, Bacteria and Fungi abundances, but with different patterns depending on the depth. AMF colonization varied according to the varieties, being higher in UM (60%) and lower in UI (42.8%). The *pqqC* gene specific for gluconic acid production, a marker gene of P-solubilizing Bacteria, was positively correlated with Archaea abundance ($R= 0.49$, $p< 0.01$) but has no correlation with Bacteria, only indicated previously by *in silico* analysis. Based on a Principal Component Analysis, it was possible to observe that microbiological components are important when genetic components are used to distinguish *Urochloa* varieties.

CONCLUSIONS

We concluded that each variety can shape the abundance of certain microbial groups to fulfill their strategies on P absorption for *Urochloa* genetic breeding. Our results also indicated a possible contribution of Archaea for P mineralization based on the *pqqC* gene.

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Biochar: Black diamond to improve plant performance and bacterial composition in growing medium

Vicky Levesque[1], Thomas Jeanne[2], Martine Dorais[3], Noura Ziadi[4], Richard Hogue[2], Hani Antoun[3]

[1]Agriculture and Agri-Food Canada, Kentville, Canada, [2]Institut de Recherche et de Développement en Agroenvironnement, Québec, Canada, [3]Université Laval, Québec, Canada, [4]Agriculture and Agri-Food Canada, Québec, Canada

Aim:
Peat is the most common substrate used as a growing medium in horticulture. However, the physicochemical properties need to be improved by adding aggregates such as perlite for plant growth. These aggregates are, however, expensive and not sustainable. To produce cheaper peat-based growing medium (PBGM), alternative materials to substitute part of aggregates have been investigated and biochar, carbon-rich material obtained by thermal combustion of biomass could be an interesting sustainable component. The aim of our greenhouse trials was to evaluate the effect of substituting perlite in PBGM by three types of biochar on tomato and sweet pepper, growth and yield, on retention of water and fertilizer and on the bacterial diversity found in PBGM.

Method:
Biochars tested were derived from maple bark pyrolysed at 550 °C (M550) and 700 °C (M700) and from pine chips pyrolysed at 700 °C (P700). Tomato and sweet pepper plants were grown in a greenhouse and fertigated with mineral fertilizer at full or half of the recommended level for 63 days.

Results:
Results indicated that the addition biochar increased tomato and sweet pepper fruit yield. Biochar also increased nutrient retention, while reducing nutrient loss in leachates. In addition, the presence of M700 or P700 biochars significantly increased beneficial bacteria for plant growth due to the improvement of physical and chemical properties of PBGM.

Conclusions:
Therefore, substituting perlite in PBGM with biochar appears to be a beneficial practice towards sustainable greenhouse production, and this practice merit further investigation with other crops such as indeterminate cultivars.

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Integrated monitoring for soil threats, biodiversity and ecosystem services in Italy supporting sustainable soil management

Carlo Jacomini[1], Francesca Assennato[1]

[1]*ISPRA, Rome, Italy*

Aim:
Within the European Joint Programme on SOIL, two projects SERENA and MINOTAUR are researching how to identify and select policy-relevant indicators describing soil threats, ecosystem services and soil biodiversity at European and National level.

Method:
The two projects will focus on soil biodiversity monitoring, in particular for meso-invertebrates, and on a framework of indicators to analyse soil ecosystem services, threats and relevant drivers for Europe.

Results:
The synergy between the two projects will allow further development of functional indicators. Moreover, they will provide an agreed definition of the knowledge base supporting the assessment of soil health, as well as where possible the quantitative relationships of soil biodiversity with soil functions, soil threats and soil ecosystem services under different conditions in terms of climate change, soil type, land use and management and human population dynamics.

Conclusions:
The focus on Italian national context (a very diverse and rich in soil biodiversity and soil threats situation) and the relevance in the environmental monitoring provided by ISPRA are discussed as a part of the preparatory work to support the implementation of the European Soil Strategy and the foreseen European Soil Health Law under definition, with the aim to improve environmental monitoring at national level and to support a truly sustainable soil management and land use.

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Soil Biodiversity Data Warehouse Supporting Soil Health Assessment

Paul Henning Krogh[1], David Russell[2], Photini Mylona[3], Lourdes Morillas[4], Jiri Schlaghamersky[5], Maria Tsiafouli[6], Mickaël Hedde[7], Ismael Navas-Delgado[8], Marjetka Suhadolc[9], Marko Debeljak[10], Žaklina Marjanović[17], Davorka Hackenberger[11], Jérôme Cortet[12], Anton Potapov[13], Vesna Tunguz[14], Stephan Jänsch[15], Andrey Zaytsev[2], Achim Schmalenberger[16], Lourdes Morillas[4], Stephan Lesch[2]

[1]Department of Ecoscience, Aarhus University, Aarhus C, Denmark, [2]Senckenberg Museum of Natural History, Görlitz, Germany, [3]Institute of Plant Breeding & Genetic Resources, Thermi, Greece, [4]University of Seville, Seville, Spain, [5]Masaryk University, Brno, Czechia, [6]Aristotle University of Thessaloniki, Thessaloniki, Greece, [7]INRA, Montpellier, France, [8]Universidad de Málaga, Málaga, Spain, [9]University of Ljubljana, Ljubljana, Slovenia, [10]Jozef Stefan Institute, Ljubljana, Slovenia, [11]Department of Biology, Osijek, Croatia, [12]Université Paul-Valery, Montpellier, France, [13]University of Leipzig, Leipzig, Germany, [14]Faculty of Agriculture, Istocno Novo Sarajevo, Bosnia & Herzegovina, [15]ECT Oekotoxikologie, Flörsheim, Germany, [16]University of Limerick, Limerick, Ireland, [17]Belgrade University, Belgrade, Serbia

Aim:

Creating the structures and procedures necessary for developing an open European-wide soil biodiversity data infrastructure. Stakeholders urgently need reliable tools for monitoring and evaluating the health condition of soils. The European COST Action network, EUdaphobase, has established a pan-European soil-biological data and knowledge warehouse, which can be used for understanding, protecting and sustainably managing soils, their biodiversity and functions.

Method:

EUdaphobase, is collating and testing the use of soil invertebrate biodiversity data for assessment of soil health ensuring the sustainable use of soil and delivery of soil ecosystem services. It aims to address the need for development of data standardization, data quality assessment, storage, and data distribution and create tools to assess the condition of soils based on soil biodiversity. Network partners are organized according to a data model consisting of quality assurance, IPR, harmonization and standardization of soil biodiversity data and methodological and environmental data (metadata) leading to assessment of soil health by using species traits and population abundances to model ecosystem services.

Results:

More than 30 countries are engaged in the network representing a vast potential of soil biodiversity data in Europe and beyond. Guidelines for data preparation and upload to the data warehouse are available. A range of projects (STSMs) have been launched to address the challenges of collating data and making data useful for the domain of environmental soil protection through relevant meta data.

Conclusions:

The current HORIZON Europe focus on developing a soil health index and link soil biodiversity to ecosystem services. This will require quality soil biodiversity baseline data and interoperability.

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Anthropocene effects on soil arthropods assemblages in a tropical urban coastal wetland in Puerto Rico

Gloria Ortiz-Ramírez[1], Elvira Cuevas[2]

[1]Department of Environmental Sciences, Faculty of Natural Sciences, University of Puerto Rico, San Juan, Rio Piedras, Puerto Rico, [2]Department of Biology, Faculty of Natural Sciences, University of Puerto Rico, San Juan, Rio Piedras, Puerto Rico

Aim: To determine soil arthropods' assemblages under spatio-temporal dynamics in a tropical coastal urban wetland, in the northern metropolitan area of Puerto Rico.
Method: During 2020, one hundred forty-eight samples were collected in a dry period (June) and the end of the wet period (October); in four 10m2 plots: two with autochthonous organic substrate, another two with allochthonous mineral soil embedded in the organic matrix. At each plot one substrate sample, 7.62 cm diameter x 5 cm depth was collected under three stratified random plants representative of four plant types: trees, shrubs, grasses, and ferns. Each sample was separated into loose litter and old litter/humus and placed in lighted Tullgren-Berlese extractors for one week. Phreatic level, soil water content, pH, and salinity were also measured.
Results: Two hundred forty-four morphotypes (detritivores, herbivores, predators, microbivore, and omnivores) belonging to twenty-two taxa groups were identified. Significant differences in soil fauna assemblages and abundance among plots and sampling periods were detected, highlighting the distinctly inter- and intra-specific responses of soil arthropods communities to wetlands periodic bio-physicochemical factors fluctuations.
Conclusions: Given that soil arthropods play an essential role in wetland biological processes, studying how climate and coastal urban wetlands bio-physicochemical factors influence their composition, becomes an important tool in adaptive wetland management to global and regional climate change, sea level rise and increased anthropic use of the region.