



**Natural resources and bioeconomy studies 46/2025**

# **5<sup>th</sup> Conference on Ecology of Soil Microorganisms 2025**

**15–19 June 2025, Helsinki, Finland**

**Suvi Sutela and Eeva Terhonen (Eds.)**

Natural resources and bioeconomy studies 46/2025

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Natural Resources Institute Finland, Helsinki 2025

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## **Welcome to ESM2025!**

We are pleased to invite you to the fifth conference on the Ecology of Soil Microorganisms, held again in Helsinki. This scientific event addresses questions related to individual microbes, i.e., archaea, bacteria, fungi, oomycetes, protozoa, viruses as well as microbial communities and their ecological networks. The aim of the conference is to advance understanding of the complex interactions across scales-from soil microbes and their viruses to their relationships with plants and larger ecosystem processes.

The conference program shows that understanding of soil microbiology and processes is increasingly expanding from amplicon-based analysis to sequencing of metagenomics, metatranscriptomics and proteomics as well as different in-situ and single-cell measurements. The new era of improved molecular analytics allow simultaneous analysis of soil viruses and invertebrates in addition to bacteria. We look forward to this trend which will eventually provide us with a new understanding of the truly complex networks of soil microorganisms and their functioning.

The organizers, together with the Natural Resources Institute Finland, warmly welcome experts from all related disciplines to join this state-of-the-art research forum and enjoy the unique atmosphere of Helsinki's Northern midsummer.

Taina Pennanen and Jenni Hultman

Chairs of the Organizing Committee

## Organisers

### Scientific committee

**MBU**

Petr Baldrian (Czech Republic)

**UC DAVIS**

Joanne Emerson (USA)



Jenni Hultman (Finland)

UNIVERSITY OF HOHENHEIM



Ellen Kandeler (Germany)

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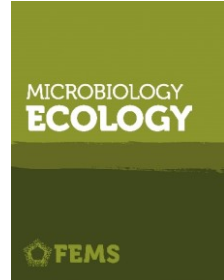
#### **Natural Resources Institute Finland**

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Kaisa Juupaluoma, Niina Romakkaniemi

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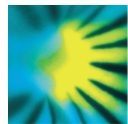


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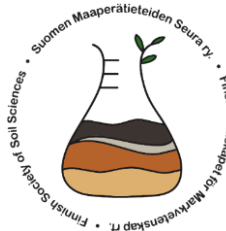
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## Single cell environmental microbiology with NanoSIMS

The NanoSIMS is a unique secondary ion mass spectrometer tool that combines exceptional spatial resolution with parallel acquisition of seven masses and the ability to complement other imaging techniques. These capabilities are key for studying complex microbial communities and soil-plant interactions.

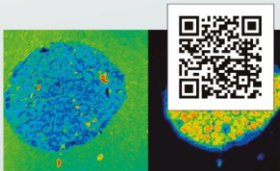
In **soil science**, NanoSIMS has been instrumental in visualizing nutrient cycling processes and understanding the spatial distribution of elements within soil aggregates. In **environmental microbiology**, it has enabled researchers to investigate microbial metabolism and interactions at the cellular level, providing insights into microbial ecology and function.

The newly released **NanoSIMS-HR** delivers breakthrough **innovations** that push the limit of environmental microbiology research:

- Lateral resolution  $\leq 30\text{nm}$
- x2.5 faster image acquisition
- Cryogenic compatibility

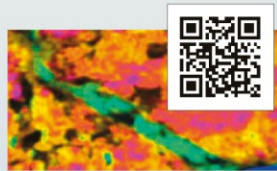
### Read some of our NanoSIMS users' success stories:

Caltech researchers used their NanoSIMS to analyze the anabolic activity in consortia of methane-oxidizing archaea and sulphate-reducing bacteria that help decrease methane release into the environment.



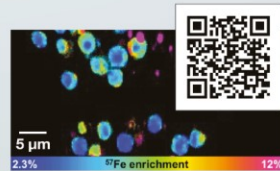
[cameca.com/go/caltech-geobiology](http://cameca.com/go/caltech-geobiology)  
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The University of Munich NanoSIMS was used to study the biogeochemical interactions among POM, microorganisms, and minerals at their interfaces, witnessing their interactions at the submicron scale.



[cameca.com/go/soil](http://cameca.com/go/soil)  
or scan the QR code

Scientists at University of Manchester investigated the temporal uptake and distribution of trace amounts of iron into wheat grain — and found something unexpected in their samples' bran layer cells...



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# Program

## Sunday 15.6.2025

14:00 REGISTRATION AND SPEAKERS SERVICE OPENS

### OPENING SESSION

- 15:30 Welcoming words, **Luke Vice President Sirpa Thessler**  
 15:40 Fungal community assembly processes from local to global scales, **Nerea Abrego**  
 16:25 How microbes find and adhere to roots? **Philip Poole**  
 17:10 Soil microhabitats - How do soil microorganisms benefit from their local environment? **Elen Kandeler**

17:40 GET TOGETHER

## Monday 16.6.2025

FOREST AND PEATLAND SOILS, chairs: Petr Baldrian, Taina Pennanen

- 9:00 Opening  
 9:05 Contrasting influence of ectomycorrhizal fungi on decomposition depending on forest fertility, **Björn Lindahl**  
 9:35 Fragile foundations of temperate forests: Microclimate effects on microbiome involved in fine woody debris decomposition and soil nutrient cycling, **Vendula Brabcová**  
 9:50 Meta-omics reveal microbial guild succession and functions during fungal necromass decomposition in forest soil, **Elsa Hilaire**  
 10:05 Microbial keystone taxa in stratified floors of beech forests, **Sebastian Blbinger**  
 10:10 Nitrogen addition increases soil carbon pool through increased microbial necromass formation but also modifies tree secondary metabolism in boreal forest, **Sylvia Adamczyk**  
 10:15 Ecological drift and host plant identity drive endophyte community structure in leaves along a gradient of soil primary succession, **Caio Cesar Pires de Paula**  
 10:20 Dispersal of soil bacteria in the context of human well-being, **Mira Grönroos**  
 10:25 COFFEE BREAK

FOREST AND PEATLAND SOILS, chairs: Håvard Kauseud, Nerea Abrego

- 11:00 Establishing genetic, phylogenetic and functional mechanisms that shape *Acidobacteriota* diversity of arctic tundra and boreal forest soils, **Max Häggblom**  
 11:15 The spatio-temporal distribution of soil fungi alters enzymatic activities along forest management gradients, **Kezia Goldmann**  
 11:30 Understanding local soil microbiomes in forest ecosystems: A perspective beyond broad-scale studies, **Nobuhiko Shigyo**  
 11:45 Short-term response of microbial communities in peatland forest soils to forest harvesting, **Alexandre Raimbault**  
 11:50 Do nitrogen-fixing Frankia nodules retain significant amounts of scarce micronutrients in a mixed-tree situation? **Tarja Lehto**  
 11:55 Reindeer grazing alters soil microbial activity in a northern peatland, **Tommi Välikangas**

12:00 LUNCH BREAK

13:00 POSTER SESSION

MICROBIAL NETWORKS AND HABITATS, chairs: Anne Winding, Bartosz Adamczyk

- 14:00 Dynamics of fungi and bacteria in soil and what they tell about the microbiome function, **Petr Baldrian**  
 14:30 How do microeukaryotes in boreal forest soil respond to forestry? **Ella Thoen**  
 14:45 Biogeography and diversity of soil microbial and mesofauna communities in different land uses with a gradient of soil disturbance in Eastern Canada, **Claudia Goyer**  
 15:00 Arbuscular mycorrhiza systematically suppresses ammonia oxidizing bacteria, but not archaea, across a range of soils, **Jan Jansa**  
 15:15 Do earthworms alter fungal community composition and activity in boreal forest soils? **Péter Garamszegi**  
 15:20 Adaptation of microbial communities' life strategies in urban areas along a management intensity gradient, **Fadwa Khalifallah**  
 15:25 Agricultural expansion in boreal regions: temporal responses of soil microbial functions after land clearing, **Lori Phillips**  
 15:30 Soil fungal communities in space and time, **Markus Gorfer**  
 15:45 COFFEE AND POSTERS

MICROBIAL NETWORKS AND HABITATS, chairs: Ely Morrién, Krista Peltoniemi

- 16:15 The co-occurrence of soil protists and prokaryotes is affected by rhizocompartment and wheat variety, **Anne Winding**

- 16:30 Delineating the co-existence strategy of different arbuscular mycorrhizal fungi for root colonization and foraging on root-free patches, **Anukool Vaishnav**  
 16:45 Mycellal exploration of arbuscular mycorrhizal fungi: intra- and interspecific variation among 29 isolates, **Rasmus Kjoller**  
 16:50 Soil and plant microbiome assemblages in pristine ecosystems of remote sub-Antarctic islands; responses to abiotic drivers of global changes, **Constance Bertrand**  
 16:55 Limited responses of ammonia oxidizers to simulated drought and heatwaves across arable soils in Europe, **Eduardo Pérez-Valera**  
 17:00 Gradients of C flux and microbial C use in the detritusphere, **Christian Poll**  
 17:15 How biochemistry may support microbiology? New tools and perspectives, **Bartosz Adamczyk**  
 17:30 Microbial necromass production and consumption define net necromass stocks, **Kate Buckeridge**  
 17:45 Deadwood as a key factor in soil carbon and energy flow through microbial communities, **Ewa Błońska**  
 17:50 Soil disturbances affect GHG emissions, organic carbon pool and microbial community in drained peatland forest, **Qian Li**  
 17:55 Forest management impacts on fine root input to peat carbon, **Tuula Larmola**

19:00 HELSINKI CITY RECEPTION (map)

## Tuesday 17.6.2025

VIRUSES IN SOIL, chairs: Eeva Vainio, Ville-Petri Friman

- 9:00 The magnificent, frustrating diversity of soil viruses, **Joanne Emerson**  
 9:30 Virus community dynamics and host defense evolution vary as a function of biogeochemical process rates in soil, **Christina Hazard**  
 9:45 Diversity of micropredators from Arctic and subarctic soils, **Tatiana-Demina**  
 10:00 Diversity of RNA virome in soil, **Rumakanta Sapkota**  
 10:10 Characterizing soil virus-nitrifier interactions and impact on nitrification, **Sungeun Lee**  
 10:15 Viral regulation of soil microbial communities and carbon cycling, **Ruiqi Wang**  
 10:20 Bacteria-phage coevolution drives patchy distribution of plant disease through resistance-virulence trade-offs, **Ville-Petri Friman**  
 10:35 Virus evolution and lifestyle in root-associated fungi, **Eeva Vainio**  
 10:50 Directional assembling of disease suppressive rhizobiome using probiotic-targeting phages, **Keming Yang**

11:00 COFFEE BREAK

SOIL CARBON AND NUTRIENT CYCLES, chairs: Petr Kohout, Kristiina Karhu

- 11:30 Using plant-soil interactions to increase stable carbon in soils, **Ely Morrién**  
 12:00 Disentangling the plant-microbial origins and stability of long-term soil carbon stores, **Rachel Yamamoto**  
 12:15 Plant diversity drives positive microbial associations in the rhizosphere enhancing carbon use efficiency in agricultural soils, **Luiz Domeignoz-Horta**  
 12:30 Development of biodiversity, nutrient cycling and soil organic stocks across a 150-year grassland chronosequence in a north European landscape, **Karina Clemmensen**

12:45 LUNCH BREAK

13:45 POSTER SESSION

SOIL CARBON AND NUTRIENT CYCLES, chairs: Karina Clemmensen, Jussi Heinonsalo

- 14:45 Exploring potential success factors for high soil multifunctionality: agricultural management, soil microbiome and soil carbon, **Gausje Koorneef**  
 15:00 Functional shifts in plant microbiomes along altitudinal gradients: Insights from DNA metabarcoding and metatranscriptomics, **Skylar Burg**  
 15:15 Presence of undersown cover crops but not their diversity, and especially soil depth affect microbial SOC stabilization and priming, **Jussi Heinonsalo**  
 15:30 Enhanced respiration rates from translocated tropical forest soils explained by lower 180 CUE, increased enzyme activities and substrate availability from decomposition of recalcitrant SOM, **Kristiina Karhu**

15:35	Phosphorus solubilization in <i>Bacillus</i> spp.: Advancing sustainable agriculture, <b>Stefanie Thaqi</b>
15:40	Regrowth alters rhizosphere nitrogen dynamics: Shifts in microbial community composition and functional profiles across different root parts, <b>Guoting Shen</b>
<b>15:45</b>	<b>COFFEE AND POSTERS</b>

**AGRICULTURAL SOIL MICROBIOMES, chairs: Maarja Õpik, Rasmus Kjoller**

16:15	Biodiversity and functioning of arbuscular mycorrhizal fungi in agricultural ecosystems at regional scale, <b>Maarja Õpik</b>
16:30	Organic phosphorus mineralization in soil: Microbial energetics and metabolic costs, <b>Nataliya Bilyera</b>
16:45	Global impacts of climate, management strategies and land degradation on biodiversity status of agricultural soils, <b>Pablo Sánchez Cueto</b>
17:00	Microbial functions induced by wood fibre amendments in agricultural fields, <b>Taina Pennanen</b>
17:20	Antimicrobial resistance dissemination potential of recycled fertilizers according to field trials, <b>Johanna Muurinen</b>
17:25	More generalistic AM fungal communities also produce less biomass in managed soils, <b>Tanel Vahter</b>
17:30	Copper and synthetic pesticides are major drivers of bacterial and fungal communities in vineyard soils, <b>Elias Barmettler</b>
17:35	Antibiotic resistance and microbial communities in the environment of an 18th-century slaughterhouse, <b>Minna Maunula</b>
<b>19:00</b>	<b>CONFERENCE DINNER (map)</b>

**Wednesday 18.6.2025**

**ECOLOGY OF SOIL MICROORGANISMS, chairs: Joanne Emerson, Max Häggblom**

9:00	Global distribution and biogeography of ericoid mycorrhizal fungi, <b>Petr Kohout</b>
9:30	Successive impoverishment of soil guilds alters grassland functioning: from universal to contextual effects, <b>Dajana Radujković</b>
9:45	The undescribed soil fungal lineages, <b>Leho Tedersoo</b>
10:00	Shrub expansion and associated microbial communities mediate shifts in organic matter characteristics and carbon stocks when colonizing subarctic grasslands, <b>Carles Castañó</b>
10:05	Does the interaction of fungi and plant roots drive soil carbon stabilization in boreal forests? <b>Anne Tyvjärvi</b>
10:10	The formation and breakup of the magic circle: 15 years of life of a fairy ring in Abisko, <b>Christoffer Bugge Harder</b>
<b>10:15</b>	<b>COFFEE BREAK</b>

**ECOLOGY OF SOIL MICROORGANISMS, chairs: Luiz Domeignoz-Horta, Katharina Kujala**

10:45	Microbial diversity-biomass relationships in soils across Europe, <b>José Siles</b>
11:00	Diverse and distinct soil archaeal communities in topsoil of arable, forest, and permanent grassland sites robustly detected by improved domain-specific metabarcoding, <b>Florian Gschwend</b>
11:05	Along the way from till to alpine meadow soils: diversification, specialization and microbial network decoupled, <b>Eva Kaštovská</b>
11:10	Identification of microbial keystones in complex soil ecosystems and determination of their activity, function and niche preferences, <b>Selma Vieira</b>
11:15	Labeling of active arsenate- and antimonate-reducing microbes in peat soil used for treatment of mining-affected waters, <b>Katharina Kujala</b>
11:30	Recycled nutrients, resilient microbes: unveiling soil microbial responses to alternative fertilization, <b>Rubén López-Mondéjar</b>
11:45	Deciphering the role of microbes and soil properties for natural disease suppressiveness, <b>Marie-Lara Bouffaud</b>
11:50	Enrichment and genomic analyses of methanogens from desert soil crust, <b>Weitao Tian</b>
<b>11:55</b>	<b>LUNCH BREAK</b>
<b>12:50</b>	<b>POSTER SESSION</b>

**MONITORING AGRICULTURAL SOIL MICROBIOMES, chairs: Christoph Tebbe, Sannakajsa Velmala**

13:50	Limitations and perspectives of monitoring the diversity of cropland microbiomes as soil health indicators, <b>Christoph Tebbe</b>
14:20	Shaping soil microbial communities and functionality by tillage intensity and crop diversification in Austrian agroecosystems, <b>Katharina Keiblinger</b>

14:35	Engineering the rhizosphere for mitigating biotic stress in arable land, <b>Shilpi Sharma</b>
14:50	Disentangling land-use effects on soil fungal communities across continents, <b>Felix Wesener</b>
14:55	Temporal developments of bacterial and fungal communities assessed over ten years of annual soil biomonitoring, <b>Janine Mall-Mielewczik</b>
<b>15:00</b>	<b>COFFEE AND POSTERS</b>

**EUROPEAN SOIL HEALTH, BIODIVERSITY, SUSTAINABLE MANAGEMENT, chair: Guusje Koorneef**

15:30	Microbial and biogeochemical responses to root exclusion across diverse European forests, <b>Tijana Martinović</b>
15:45	Legume-cereal intercropping for sustainable agriculture across Europe, <b>Shamina Imran Pathan</b>
16:00	Impact of agricultural microplastics on soil and microbial functions across Europe, <b>Sannakajsa Velmala</b>
16:15	Response of soil organisms to climate-smart sustainable soil management techniques - Highlights from EJP SOIL, <b>Sophie Zechmeister-Boltenstern</b>
16:30	SOILGUARD: Sustainable soil management to unleash soil biodiversity potential and increase environmental, economic and social wellbeing, <b>Tania Galindo-Castañeda</b>
16:45	Impacts of arable management practices on soil biological diversity - Outcomes from boreal case studies in SolidiverAgro, <b>Krista Peltola</b>
16:55	Soil health benefits from food industry side streams - the EU Mission Soil DelSoil project, <b>Ansa Palajärvi</b>
17:00	Introducing Precision: A Horizon project developing tailored solutions for agricultural practices in boreal regions, <b>Kaire Lait</b>
17:05	Project SOLO - developing a holistic and transdisciplinary soil research agenda for Europe, <b>Guusje Koorneef</b>
<b>17:10</b>	<b>PANEL DISCUSSION</b>
<b>17:45</b>	<b>SOIL MISSION MINGLE, REFRESHMENTS</b>

**Thursday 19.6.2025**

**MICROBIAL PROCESSES, chairs: Tim Ulrich, Tuula Larmola**

9:00	Soil microbial regulation of atmospheric trace gases: from enzymes to ecosystems, <b>Chris Greening</b>
9:35	Unravelling the role of hydrogen cycling microorganisms in agricultural soils, <b>Zahra Islam</b>
9:50	Wintertime microbial community activity in oroarctic tundra soils, <b>Sirja Viitamäki</b>
10:05	Like fish out of water? Cultivation and genomic characterisation of the first methanogens isolated from upland soils, <b>Roey Angel</b>
10:20	Legacy effects of fluctuating oxygen availability on the methane-driven interaction network, <b>Tanja Heffner</b>
10:25	Microbial adaptations in northern soils with naturally high baseline concentrations of arsenic and metals, <b>Lotta Purkamo</b>
<b>10:30</b>	<b>COFFEE BREAK</b>

**MICROBIAL PROCESSES, chairs: Ellen Kandeler, Jenni Hultman**

11:00	Pre-restoration baseline for microbial activity from two forestry drained fens in Northern Finland, <b>Jenni Hultman</b>
11:30	Cascading effects of Arctic tundra herbivory on above- and below ground biomass, soil biogeochemistry, and soil (microbial) food webs, <b>Andrea Söllinger</b>
11:45	Effect of warming on microbial decomposition of plant biomass in Arctic tundra soils using a stable isotope probing approach, <b>Gabriele Tosadori</b>
11:50	Composition of artificial root exudate treatment impacts soil functional outcome and plant productivity in metal-contaminated brown field soils, <b>Nina Goodey</b>
11:55	Mapping microbial genomic potential: Predicting plant litter decomposition from soil metagenomes across ecosystems, <b>Bala Singavarapu</b>
12:00	Unlocking novel microbial biosynthetic potential in a peatland microbiome, <b>Zander Human</b>
12:15	Into the heights and toward the poles: elevational and latitudinal trends in AM fungal community niche structure, <b>Inga Hilesalu</b>

**12.30 -12:45 AWARDING AND CLOSING CEREMONY**

# Posters program

## Posters Monday 13.00–13.55

Mugadza, Alois	MON P1	Promotion of sustainable and healthy soil: an overview of Zimbabwe's soil protection laws and policies.
Chen, Meirong	MON P2	The crucial role of sampling design in soil biodiversity assessment
Pandit, Aditi	MON P3	Unveiling the diversity and specificity of orchid mycorrhizal fungi associations: insights from geographic regions and methodological comparisons
Laine, Miikka B.	MON P4	Comparison of technologies for assessing fungi-to-bacteria-ratio of soil
Chandel, Neha	MON P5	Mechanistic understanding of metabolic cross-talk between <i>Aloe vera</i> and native soil bacteria for growth promotion and secondary metabolites accumulation
Singh	MON P6	Fostering equity in microbial ecology through data reuse: lessons from data collection and synthesis
Jurburg, Stephanie	MON P7	Fungal-bacterial interactions- a gateway to discover novel bioactive metabolites
Qurashi, Maryam	MON P8	Genome-assisted risk assessment of biocontrols
Saraiva, Joao Pedro	MON P9	Microbial ecology in mountain soils along elevation gradient: from forest to alpine meadow
Mahjoory, Yalda	MON P10	Tillandsia dunes as a habitat for microorganisms in the hyperarid Atacama Desert
Velte, Stefanie	MON P11	Reciprocal transport of carbon and nitrogen between plants and microbes in the grassland hyphosphere
Brandt, Luise	MON P12	Assessing the effects of environmental drivers on soil fungal diversity in desert ecosystems
Mani, Israel	MON P13	Disentangling the interplay between among earthworms, plants, and soil microbes in Amazonian dark earth
Leitão, Ricardo	MON P14	Presence and diversity of phosphorus solubilizing bacteria in alpine meadow and scree soils of Tatra Mountains
Choma, Michal	MON P15	Induced shifts in the maize rhizosphere microbiome under drought stress
Molefe, Rebaona	MON P16	Impact of regenerative management in hyper-arid ecosystem - microbial communities
Steinberger, Yosef	MON P17	Getting back to their roots: deadwood as a niche for ectomycorrhizal fungi
Ronold, Eivind Kverme	MON P18	Bacterial populations active during lignin depolymerization
Lara, Ana Catalina	MON P19	Ectomycorrhizal mycelial communities in a fragmented sub-Mediterranean Karst forest
Mrak, Tanja	MON P20	Global patterns of nutrient limitation in soil microorganisms
Cui, Yongxing	MON P21	A carbon utilization and nitrogen acquisition trait spectrum for ectomycorrhizal fungi
Jørgensen, Karolina	MON P22	Metabarcoding of arbuscular mycorrhizal fungi (AMF) communities endemic to the rhizosphere of the argan tree ( <i>Argania spinosa</i> (L.) Skeels): focus on southwest Moroccan forest ecosystems
Gachara, Grace	MON P23	Isolation and characterization of novel methanotrophs from peatland soil
Nweze, Justus Amuche	MON P24	Influence of canopy cover and soil moisture on mycobiome of protected forest in Mediterranean Croatia with insights on potential fungal ecosystem services
Mešić, Armin	MON P25	Long-term effects of ash-fertilization on the composition and functional gene pool of soil microbiome in drained peatland forests
Kattilakoski, Matilda	MON P26	Decadal adaptation of methanotroph affinity to peatland water table manipulations
Kohl, Lukas	MON P27	Peat methane-cycling microbial communities and biogeochemistry in the UNESCO Biosphere Entlebuch
Barney, Madison	MON P28	The microbial and viral communities in deep peat soils and their linkages
Pettersson, Kalle	MON P29	Intensive forest management of drained peatland: Effects on methane dynamics in anoxic conditions
Tláškal, Vojtěch	MON P30	Ammonia oxidizing archaea and bacteria respond dynamically to drought in rewetted fen peatlands
Burns, Anna	MON P31	Low-abundance soilborne pathogens inhibit the germination of <i>Picea jezoensis</i>
Iwakiri, Ayuka	MON P32	Soil food web interactions alter microbial community structure and function in temperate deciduous forest
Patmanova, Tereza	MON P33	Impact of shrub admixture in pine forest stands on soil bacterial and fungal communities and accumulation of polycyclic aromatic hydrocarbons
Lasota, Jarosław		

## Natural resources and bioeconomy studies 46/2025

Chmolewska, Dominika	MON P34	Translocated wet meadows: altered soil structure, moisture, N transformations, and microbial communities with saprophytic fungi increment
Řezáčová, Veronika	MON P35	Nutrient exchange within common mycorrhizal networks is altered in a multi-species environment
Ahlers, Laureen	MON P36	Warming in the Alps: Impacts on greenhouse gas fluxes and soil microbiomes
Stursova, Martina	MON P37	Diversity and functioning of the soil microbiome in naturally regenerating temperate beech forest in Slovenia
Moravcová, Andrea	MON P38	Direct vs. indirect climate effects on fungal communities and species responses: The role of vegetation-mediated pathways
Pathan, Shamina Imran	MON P39	Cultivar-dependent AMF colonization modulates metabolic pathways and bacterial communities in water-stressed wheat
Skrivanek, Jakub	MON P40	A comparison of the realized and fundamental niches of selected AM fungal species along a nitrogen gradient
Kaiserová, Johana	MON P41	Rapid soil changes following the expansion of heathland shrubs into grasslands: Implications for predictive models
Mészárosová, Lenka	MON P42	Post-fire dynamics of soil fungal communities: fungal community recovery and functional shifts across a burn severity gradient
Barbi, Florian	MON P43	Recovery of forest fungal communities across a gradient of burn severity
Bjørndal, Yngvild	MON P44	Microbial mechanisms controlling methane-temperature hysteresis in wetlands.
Sikorski, Johannes	MON P45	The temporal stability of active bacteria in grassland and forest soils across a time series spanning 12 years
Kostakou, Maria	MON P46	Spatial sampling strategies for soil biodiversity: insights from the SpaceMic project
Kastenholz, Lisa	MON P47	The mineral-organic horizon interface as an activity hotspot for methane-cycling microorganisms in kettle holes
Volles, Nils	MON P48	No recovery – three years of land-use reduction showed no effect on the methane sink function of grassland microbiomes
Soonvald, Liina	MON P49	The effects of vegetation shifts on soil microbial communities and carbon storage in subarctic soils
Zhelezova, Alena	MON P50	Microbial succession and aggregate formation in an indoor pot experiment with clean sand and willows
Itonen, Mats	MON P51	Global colonization success of soil fungi: do plant pathogens and mutualists track warming at different rates?
Terhonen, Eeva	MON P52	Fungal community shifts across Scots pine stand development: from early succession to maturity
Branysova, Tereza	MON P53	Climate effects on microbial communities across mountain forest ecosystems
Schmidt, Frida	MON P54	Forest management effects on the ericoid mycorrhizal fungal community in bilberry ( <i>Vaccinium myrtillus</i> ) roots

### Posters Tuesday 13:45–14:40

Karkman, Antti	TUE P1	The impacts of sewage sludge fertilization on soil resistome
Némethová, Ema	TUE P2	Impact of herbicides and fungicides on soil bacteria: unveiling neutral to positive dynamics based on the soil and active substance
Abeyawardana, Oushadee AJ	TUE P3	The effect of pesticides on fungal diversity and abundance varies across soils
Stoltenburg, Regina	TUE P4	Diversity and seasonal variation of soil microbial communities in response to different agricultural practices
Thioye, Babacar	TUE P5	Linking agricultural management to soil microbial dynamics: How organic matter, biocontrol, and crop management shape soil ecology
Lori, Martina	TUE P6	Microbial response to fertilization intensity and cropping systems: Insights from a 42-year-old long-term experiment
Mäkinen, Taru-Marja	TUE P7	Bio-based fertilizers and antibiotic-producing bacteria in the ecology of antibiotic resistance in Finnish agricultural soils
Pathan, Shamina Imran	TUE P8	Is a dual-plant system more efficient in nitrogen cycle closure? An Italian study on clover-wheat intercropping
Frąc, Magdalena	TUE P9	Preliminary results on bacterial and fungal microbiome transfer to wheat roots and rhizosphere in legume-cereal intercropping
Weinand, Tanja	TUE P10	Effects of different agroforestry systems on soil microbial communities

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Häkkinen, Laura	TUE P11	Microbial metagenomic study of the soil vertical profile under different land use and agricultural soil management
Tadrosová, Ma-nuela	TUE P12	Rhizodeposition-driven assembly of PGP taxa in the rhizosphere and plant endosphere
Sohlberg, Elina	TUE P13	Nature-based solutions for plant health management – the NaBaSolu project
Shrestha, Rashmi; Sietiö, Outi-Maaria	TUE P14	Undersown cover crop diversity impact on microbial carbon use efficiency in bulk soil
Teikari, Jonna	TUE P15	Metagenomic insight into the nitrogen cycle of northern agricultural soil
Thioye, Babacar	TUE P16	Understanding mycorrhizal dynamics in alfalfa cultivation: influence of plant age and soil tillage
Rüger, Lioba	TUE P17	The role of different soil microbiota fractions in plant nitrogen uptake
Jansriphibul, Kraiwut	TUE P18	Potential risk of spreading antibiotic-resistant genes from bio-solids
Patiño-García, María	TUE P19	Land use has a greater impact than seasonality on soil bacterial and <i>phoD</i> -harboring communities in a Mediterranean ecosystem.
Buckeridge, Kate; Pallez-Barthel, Marine	TUE P20	Does annual legume planting benefit soil microbial diversity and activity across Europe?
Hayden, Helen	TUE P21	Strategic tillage methods and crop type impact the soil food web in a Chromosol soil
Menichetti, Lorenzo	TUE P22	The ecological drivers of organic matter temperature sensitivity in forest soils across Europe
Picone, Riccardo	TUE P23	Wheat-faba bean intercropping can sustain soil nutrients and C cycles under different N fertilization levels
Vultaggio, Giulia	TUE P24	Organic and inorganic carbon storage in Dutch agricultural systems
Ruggaber, Julian	TUE P25	Rhizosphere metatranscriptomics of microbiome functions in carbon turnover assessed by a novel approach
Richy, Etienne	TUE P26	Soil carbon accumulation is enhanced by phosphorus limitation under long-term nitrogen fertilisation in a boreal forest
Bosch, Jason	TUE P27	Using SIP-metagenomics to characterise the microbial taxa responsible for transforming carbon compounds in arctic soil
Bukovská, Petra	TUE P28	Stable isotope probing to disentangle carbon for nitrogen trading in mycorrhizal hyphosphere
Soronen, Päivi	TUE P29	Spatial variation of soil nitrogen and carbon in Norway spruce-dominated stands with grey alder or birch admixture
Peng, Cheng	TUE P30	Long-term fertilization drives distinct nutrient dynamics and microbial activities in wheat rhizosphere and hyphosphere
Xu, Jie	TUE P31	Belowground nutrient transfer between Scots pine and bilberry mediated by ectomycorrhizas
Guasconi, Daniela	TUE P32	Effects of forest management and microbial diversity and community composition on soil respiration
Iturbe-Espinoza, Paul	TUE P33	Biochar affects extracellular enzyme activity and soil microbiome after 8 years
Karhu, Kristiina	TUE P34	Soil amino sugar measurement by high performance liquid chromatography – faster measurements and higher sensitivity compared to the gas chromatography method
Tuomela, Nea	TUE P35	Carbon released from thawing palsas and peatland is processed within site in a small Arctic catchment
Rzeczynska, Agnieszka	TUE P36	Linking microbial demand for limiting resources with microbial use of soil organic matter: insights from a 67-year field experiment
Kubove, Eva	TUE P37	Long-term potential for saprotrophic decomposition of humus following mycorrhizal removal in boreal forest
Packard, Erica	TUE P38	Heterologous manganese-peroxidase from ectomycorrhizal fungus <i>Cortinarius aurae</i> and its role in nitrogen mobilisation
Garcia-Pausas, Jordi	TUE P40	Impact of shrub clearing or burning as restoration strategies of encroached mountain grasslands on soil C and microbial functions
Yu, Wen-Fei	TUE P41	Plant diversity drives carbon retention in soils through root-driven microbial carbon processes
Marhan, Sven	TUE P42	Grassland management intensity affects nutrient limitation of soil microorganisms – two different analytical approaches reveal similar results
Pánek, Matěj	TUE P43	Interplay of taxonomy, ecological guilds, and nitrogen availability in shaping fungal biomass composition
Sietiö, Outi-Maaria	TUE P44	Effect of fungal necromass chemical quality and mean annual temperatures on its degradation rate

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Kohl, Lukas; Putkinen, Anuliina Rømcke, Åshild	TUE P45 TUE P46	Methane cycling in boreal upland and peat soils – links between functional gene composition, potential CH <sub>4</sub> production/oxidation and CH <sub>4</sub> fluxes Long-term effects of clear-cut forestry on fungal litter decomposer communities in boreal forests
Espinosa, María José Carpio	TUE P47	Microbial responses in bulk soil and rhizosphere to cereal-legume intercropping: implications for soil health and carbon dynamics
Sutela, Suvi	TUE P48	Molecular characterization and infection stability of a novel ormycovirus infecting mycorrhizal fungi <i>Lactarius tabidus</i>

### Posters Wednesday 12:50–13:45

Rohrbach, Stephan	WED P1	A world beyond peat: how microbial and ecological engineering can reduce agricultural peat consumption
Chawla, Kanika	WED P2	Exploiting the potential of soil microbiomes to control <i>Klebsiella pneumoniae</i> in arable ecosystems
Azziz, Gastón	WED P3	Soil microbial populations under different land uses at the Eastern Plains of Uruguay, from natural grasslands to rice fields
Alsina, Ina	WED P4	Evaluation of an innovative microorganism-enriched organic fertilizer on crop yield and microbiological activity of substrate
Drijvers, Fien	WED P5	Harnessing rhizosphere microbes for the optimization of Zn remediation by hemp
Lipsch, Lieke	WED P6	Can cover crops limit the spread of antibiotic resistance in agricultural soil microbiomes?
Spit, Jornt	WED P7	Granular organic fertilizers composed from multiple agri-food side flows impact soil microbial communities
Nosalj, Sanja	WED P8	Quantitative insights into soil bacterial and fungal populations under conventional farming practices
Li, Qian	WED P9	Protist-mediated control of enteric bacteria in agricultural soils irrigated with treated wastewater
Sinha, Argha	WED P10	Harnessing adaptive soil microbiomes for dryland cultivation of tomato
Edelman, Lucas	WED P11	Effects of prebiotics on <i>Zea mays</i> l. growth and rhizosphere microbial communities in drought stress: to understanding and beyond
Cajas, David Rodrigo	WED P12	Searching for target soil microbial communities to steer towards specific soil functions
Masse, Jacynthe	WED P13	Soil microbial diversity, structure and interactions under conventional and conversion-to-organic agricultural systems in Québec
Maffia, Angela Muscolo Adele	WED P14	Transforming agro-industrial waste into fertilizer: assessing the short-term effects on the rhizosphere microbial biodiversity of hazelnut saplings via a metagenomic approach
Mundra, Sunil	WED P15	Distinct functional responses of root and rhizosphere microbial communities in intercropping systems under arid conditions
Torppa, Kaisa	WED P16	Arbuscular mycorrhizal dependency in barley: the roles of variety age, agricultural management and fungal community composition
Vargas, Pablo	WED P17	Rootstock genetic background influences microbial community composition and enrichment of taxa associated with plant defense and nutrient availability
Moreno-Druet, Maria	WED P18	Limited and idiosyncratic thermal acclimation in soil saprotrophic fungi.
Marascalchi, Matheus	WED P19	Life cycle dynamics as a trait of arbuscular mycorrhizal fungi species
Fernández, Francisca Prieto	WED P20	<i>Pseudomonas veronii</i> and a bacterial consortium as Sb(V)-reducing bacteria: Unlocking Bioremediation Potential
Brzykcy, Julia	WED P21	Arctic seabird-affected soils as a source of microbial N <sub>2</sub> O emissions
Rijkers, Ruud	WED P22	Microbial community dynamics and functioning under three common plants encroaching the Canadian tundra
Schmoll, Monika	WED P23	An endohyphal bacterium contributes to light dependent metabolism and growth in the ubiquitous soil fungus <i>Trichoderma reesei</i>
Zambon, Sara	WED P24	Soil microbial diversity in Mediterranean oak forest ecosystems subjected to ungulate grazing and forest management
Roy, Friederike	WED P25	Linking CO <sub>2</sub> and CH <sub>4</sub> emission rates to microbial diversity in semi-natural and agricultural grasslands in Eastern Germany
Kynast, Danica	WED P26	Impact of small-scale spatial heterogeneities on methane-cycling microorganisms in semi-permanently flooded kettle holes

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Kolarikova, Zuzana	WED P27	Relating fundamental to realized niches of arbuscular fungi along a temperature gradient
Boeraeve, Margaux	WED P28	Recovery of soil fungal communities after clearcutting in previously fertilized and unfertilized forests
Janowski, Daniel	WED P29	Exploring climate-independent factors driving <i>Pinus sylvestris</i> root traits and bacterial endophyte communities in a common garden experiment.
Campeggi, Stephanie	WED P30	Conjugative gene transfer: advancing bioremediation of polyaromatic hydrocarbons in soils
Jeanne, Bongoua Affi	WED P31	Influence of rock phosphate application rates on soil bacterial density and community composition
Dubova, Laila	WED P32	Soil microbiological activity in differently managed urban meadows
Maček, Irena	WED P33	Successional dynamics of arbuscular mycorrhizal fungal communities in remediated soils after the removal of metal contaminants
Vieira, Caroline	WED P34	Opposite effects on plants of mycorrhiza establishment and soil microbial community manipulation with biocides
Hollá, Sandra Awokunle	WED P35	Mitigating short-term response of fungal communities in temperate forest soils to tree harvesting
Gelfand, Ilya	WED P36	Abiotic reactions drive post-wetting soil emissions of N <sub>2</sub> O and NO, but partially contribute to CO <sub>2</sub> emissions.
Reiser, Madlene	WED P37	Active and total prokaryotic communities in arctic-alpine soils are shaped by temperature and soil moisture along elevational and microtopographical gradients
Yakkou, Lamia	WED P38	Assessing heavy metal resistance and plant growth-promoting capabilities of earthworm's associated bacteria
Di Biase, Berenice, Steinkraus, Bruno	WED P39	Local microbial yield-associating signatures largely extend to global differences in plant growth
Kauserud, Håvard	WED P40	Long-term effects of clear-cut forestry on soil fungi and soil properties
Rissanen, Antti J.	WED P41	Conversion of methane to organic acids by aerobic methanotrophic bacteria
Anuforo, Philemon Chinemezu	WED P42	Effects of bacterial nitrogen transfer on fungal growth in nitrogen-deficient environments
Schoorens, Chloë	WED P43	Clearing the air: harnessing plant microbiomes for better malodor elimination
Belova, Valeriia	WED P44	Cross-kingdom interactions within arbuscular mycorrhizal fungi (AMF) hyphosphere
Burini, Giulia	WED P45	Response of soil microbial enzymatic activities to climate change and different tree species
Sarkar, Jagannath	WED P46	Aerobic bacteria in the sulfidic sediments of a marine hypoxic zone: sustenance and biogeochemical potentials
Kumar, Anil	WED P47	Diversity and function of novel members of the genera <i>Mucilaginibacter</i> and <i>Janthinobacterium</i> in Arctic tundra soils
Rocha, Alberto Vinicius S.	WED P48	Linking genomic traits to carbon necromass prediction in soil: a step-by-step guide for the soil ecology community
Medina, Rosa Paulina Calvillo	WED P49	SoWaFUN - Assessing fungal richness at the soil-water interface
Dammie, Nompumelelo	WED P50	The contribution of rare fungi to soil functioning
Abed, Raeid	WED P51	Salinity limits of photosynthesis, respiration, sulfate reduction and methanogenesis in microbial mats thriving at salt saturation in a salt flat from Oman
Ma, Bin	WED P52	Dynamic in situ detection in iRhizo-Chip reveals diurnal fluctuations of <i>Bacillus subtilis</i> in the rhizosphere

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## ORAL ABSTRACTS

### O1 Fungal community assembly processes from local to global scales

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Fungi represent one of the most diverse and ecologically important kingdoms of life. Despite their importance, the ecological processes that govern their distributions remain largely unexplored. A central debate in fungal ecology revolves around the roles of deterministic versus stochastic processes in shaping fungal community assembly. Drawing on studies conducted within my research group, I demonstrate how various ecological processes influence fungal communities at different scales. At local scales, experimental work provides quantitative evidence of how the interplay between biotic and abiotic filtering affects the colonization success and community dynamics of fungi. The relative influence of biotic and abiotic filtering on fungal colonization and succession is largely dependent on species-specific and phylogenetic constraints. By comparing experimental and observational data, I reveal that the role of stochasticity in shaping fungal communities is smaller than previously suggested. However, its significance varies with the successional stage of the communities, being more pronounced during the initial phase. Through sampling fungi directly from the air in a mainland-island study system, I show that fungi are generally dispersal-limited at regional scales, with wind speed being a primary environmental driver of dispersal distances. Results from a global study on airborne fungi indicate that fungi follow predictable latitudinal diversity gradients, similar to those observed in other major groups of organisms. The principal factor explaining the global spatial distributions of fungi is mean annual temperature. The moderate conservatism for sensitivity to climatic conditions found in our study suggests that fungi have continuously adapted to climatic conditions rather than being confined to their ancestral climatic niches. In fact, most species exhibited climatically restricted distributions, with the majority of genera and the vast majority of orders being detected across all climatic zones. Overall, I demonstrate how fungal community assembly can be understood within a predictable, scale-dependent conceptual framework.

## O2 How microbes find and adhere to roots

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Colonisation by bacteria of the zone surrounding plant roots (rhizosphere) is crucial to plant productivity, with plants secreting 10-30% of total photosynthate to the rhizosphere. Microarray, RNAseq and metabolic analysis combined with InSeq analysis of growth in the rhizosphere, colonisation of roots, bacteroid formation and regrowth from nodules has been used to dissect the stages in root colonisation and N<sub>2</sub>-fixation by *Rhizobium leguminosarum* in its interaction with pea. Ultimately successful root colonisation is driven by root attachment and biofilm formation and in recent work we have established that rhizobia have an exquisitely tuned system for identifying and attaching to the newly emerging root elongation zone of roots. We suggest this is a key step for any plant microbe as the newly emerging elongation zone is probably the only part of the root not already colonised by competitors(1-3).

1. T.L. Haskett *et al.*, Rhizopine biosensors for plant-dependent control of bacterial gene expression. *Environmental Microbiology* 25, 383–396 (2023).
2. T.L. Haskett *et al.*, Engineered plant control of associative nitrogen fixation. *Proc Natl Acad Sci U S A* 119, e2117465119 (2022).
3. B.A. Geddes *et al.*, Engineering transkingdom signalling in plants to control gene expression in rhizosphere bacteria. *Nat Commun* 10, 3430 (2019).

## O3 Soil microhabitats – how do soil microorganisms benefit from their local environment?

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The understanding of the interaction between soil microorganisms and their local environment has been improved in recent years through complex experiments under near-natural conditions. While the rhizosphere and the detritosphere are already very well studied, much less is known about the mineralosphere and hyphosphere. In this talk, different experiments on the colonisation and function of soil microorganisms in these two microhabitats will be presented. As part of the Biodiversity Exploratories project (<https://www.biodiversity-exploratories.de/en/>), we exposed goethite and illite to soils in grassland and forest ecosystems to study the microbial colonisation of these minerals under different land use intensities. In grasslands, fungi colonised the minerals faster and incorporated more  $^{13}\text{C}$  from amended labelled substrates into their biomass than bacteria. In forest soils, fungal colonisation of the minerals was driven by taxa-specific preferences for the C- and nutrient-poor microhabitat. By exposing so-called 'hyphoboxes' in a grassland soil, we wanted to test whether fungal hyphae connect different microhabitats and whether the interaction of fungi with bacteria stimulates the nutrient uptake by plants. Within these hyphoboxes, we separated a  $^{13}\text{C}$ - $^{15}\text{N}$ -labeled substrate, a hyphosphere, and a rhizosphere compartment by using different mesh sizes. The quality of the added substrate (recalcitrant root litter or labile arginine) affected not only the assembly of the hyphosphere microbial community but also N transport to plant roots. In conclusion, these experiments demonstrated how the local environment as well as microbial interactions determine the role of soil microorganisms in C and N cycling.

## O4 Contrasting influence of ectomycorrhizal fungi on decomposition depending on forest fertility

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Links between dominant mycorrhizal types, soil carbon storage and nutrient cycling are striking, but mechanisms are context dependent and evidence often contradictory. We propose that the influence of ectomycorrhizal fungi on decomposition depends, not only on traits of the mycorrhizal fungi, but also on traits of other interacting fungal guilds. In the least productive arctic and alpine forest ecosystems, saprotrophic and ectomycorrhizal decomposers are constrained by harsh conditions. Ericoid mycorrhizal fungi are versatile scavengers of organic resources but lack the potent oxidative enzymes required for efficient decomposition, leading to accumulation of large organic stocks. In the boreal forest, certain groups of ectomycorrhizal fungi – ectomycorrhizal decomposers – are efficient oxidizers of organic matter and take on the role as principal decomposers, facilitating cycling of organic N while reducing belowground carbon accumulation. With increasing soil fertility, efficient saprotrophic decomposers proliferate, N mineralization increases, and mycorrhizal decomposers become less prominent. In these ecosystems, ectomycorrhizal fungi may compete with saprotrophs for nitrogen, suppressing decomposition and promoting accumulation of organic matter – the ‘Gadgil hypothesis’. As forest fertility and productivity increase even further, litter quality changes, and fungal communities become increasingly dominated by opportunistic, C-limited saprotrophic ascomycetes. Here, ectomycorrhizal fungi may serve as a conduit of current assimilates into the soil and prime turnover of soil organic matter by saprotrophic microorganisms in the mycorrhizosphere. This context dependency may help to explain why ectomycorrhizal fungi correlate positively with belowground carbon pools on the largest scales, yet often seem to stimulate organic matter turnover in local studies.

## O5 Fragile foundations of temperate forests: Microclimate effects on microbiome involved in fine woody debris decomposition and soil nutrient cycling

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Fine woody debris (FWD) is a vital yet overlooked component of forest ecosystems, providing important microbial habitat and playing a key role in nutrient cycling. In managed forests with low deadwood stocks, FWD decomposition may enhance soil fertility by facilitating microbial nutrient turnover. However, effects of canopy cover—through its influence on microclimatic conditions—on microbial communities in decomposing FWD and surrounding soil remain poorly understood. In decade-long experiment, we followed FWD decomposition under closed/open canopy and assessed microbiome of surrounding soil. We characterized fungal and bacterial community composition, diversity, and key drivers of community assembly. Both fungal and bacterial communities were strongly influenced by microclimatic changes and deadwood origin. Fungal communities in FWD developed into structurally and functionally distinct pattern with limited convergence over time. Tree species-specific fungi dominated in early decomposition, whereas canopy-specific fungi persisted throughout. Bacterial communities in FWD and soil responded to canopy manipulation, with decomposition time being the primary driver of community structure. However, tree species and canopy conditions also played its role. We identified bacterial taxa involved in carbohydrate metabolism, fungal biomass degradation, and nitrogen fixation, underscoring their diverse functional contributions to FWD decomposition. These findings highlight the complex ecological interactions governing deadwood decomposition and nutrient cycling. While fungal communities exhibit strong dynamic shifts, bacteria appear to provide greater stability within the decomposer community, potentially sustaining decomposition and nutrient turnover despite environmental fluctuations. Future research should further explore microbial functional traits to better understand their roles in nutrient cycling under changing environmental conditions.

## O6 Meta-omics reveal microbial guild succession and functions during fungal necromass decomposition in forest soil

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In temperate and boreal European forests, soil fungal biomass is dominated by saprotrophic and ectomycorrhizal fungi, whose necromass constitutes a major reservoir of carbon (C) in soils. The decomposition dynamics of this organic matter, the relative stability of C necromass and the bioavailability of associated nitrogen (N) and phosphorus (P) are still poorly understood. We studied the decomposition dynamic of fungal necromass buried in temperate forest soil over six months. Several parameters were followed, such as mass loss, stoichiometric ratios and microbial enzymatic activities. The taxonomic composition of microbial communities associated with fungal necromass (necrobiome) was evaluated by metabarcoding, and microbial biomass of bacteria and fungi were estimated using qPCR. Finally, meta-transcriptomic was used to reveal the fungal functions involved in necromass decomposition processes. Unexpectedly, our results revealed that fungal biomass was more abundant than bacterial biomass within the necrobiome, and this proportion increased significantly during decomposition. Among bacteria, the proportion of copiotrophic species decreased by up to 50% during decomposition. Among fungi, while the Mortierellaceae family (saprotrophic fungi) dominated the early stages of decomposition, the proportion of ectomycorrhizal fungi increased in the later stages, particularly in recalcitrant necromass residues, i.e. relatively rich in melanin. Fungal necromass appears as a unique ecological niche, where a succession of microbial species and functions specific to its decomposition occurs. Combining knowledge from previous studies with our preliminary meta-transcriptomic results, sheds new light on the role of fungi in this specific soil microhabitat.

## O7 Microbial keystone taxa in stratified floors of beech forests

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The forest floor (FF) acts as boundary between mineral soil and atmosphere, serving as important hub for microbial nutrient turnover and transport in forest ecosystems. The FF is stratified into several layers differing in chemical, biological and physical properties. This study aimed to characterize the FF microbiome at fine vertical resolution, identify microbial key-stone taxa, and profile their capacities for catalyzing mineralization processes across temperate, beech-dominated forests. Samples were collected after litterfall from three beech-dominated forests differing in climate, spanning eight distinct layers of the FF and topsoil profile (OL0, OL1, OLF, OHF, OH, A5, A10, A20). Prokaryotic community composition was analyzed using 16S rRNA gene amplicon sequencing. Keystone taxa were identified through core microbiome and cooccurrence network analysis and their functional potential was assessed using complementary nanopore metagenomic sequencing. Amplicon data revealed strong stratification of the FF microbiome. We found larger compositional differences between the layers than between the different forest sites. Redundancy analysis showed that layer-specific physicochemical parameters had a strong influence on microbiome composition and functional capacity and this effect increased with depth. We could identify a set of shared species present at every site for the respective FF layer, which also acted as hub-species in cooccurrence networks. Functional profiling of these key-stone taxa regarding their potential to catalyze nutrient mineralization is currently ongoing. Our findings highlight that each layer represents a distinct ecological niche shaped by substrate quality, supporting a unique microbiome. FF sampling should therefore be carried out with caution regarding exact sampling depth.

## O8 Nitrogen addition increases soil carbon pool through increased microbial necromass formation but also modifies tree secondary metabolism in boreal forest

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Boreal forest soils contain a significant amount of global terrestrial C pool. Nitrogen (N) addition to these soils may even increase C pool providing a potential strategy for climate change mitigation. However, the main mechanism involved in the soil C accrual due to N addition and consequences for forest ecosystem functioning are not well-known. Here we used long-term N addition experiment on a N-poor Scots pine stand in Finland. Our results showed that N addition elevated C stocks, microbial biomass, necromass and the activity of extracellular enzymes, with no significant increase in greenhouse gas emissions. However, N addition decreased the production of plant secondary metabolites, tannins. Thus, N addition increased C stocks through elevated litter input feeding fungal biomass providing increased fungal necromass which was stabilised in the soil. Our study suggests that low N addition may increase C stocks though caution should be taken regarding potential changes in tree secondary metabolism.

## O9 Ecological drift and host plant identity drive endophyte community structure in leaves along a gradient of soil primary succession

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Endophytes play key roles in enhancing plant traits such as nutrient use efficiency, stress tolerance, and pathogen resistance. However, most research is conducted outside the context of natural ecosystems, and our understanding remains limited regarding how ecosystem changes across spatial and temporal scales influence endophytes and their ecological functions. Here, based on sequencing data, we present a field-study describing patterns of bacterial and fungal community dynamics in the foliar endosphere of four phylogenetically distinct plant hosts within the context of soil primary succession. Although successional stage influenced the structure of endophytic communities, particularly in fungi, it accounted for only a small percentage of the overall variability. Host plant identity and associated leaf tissue stoichiometry were stronger selective factors, while sampling time within a growing season also significantly influenced endophytic microbiome structuring. Together, these factors explained 10.1% and 11.8% of the variability in bacterial and fungal composition, respectively, and 27.4% of the variability in potential bacterial function. Null model results suggest that the remaining variability in community composition is primarily driven by stochastic assembly processes, particularly ecological drift. Our results indicate that foliar endophytic communities consist of a few dominant taxa with stable presence and many rare transients exhibiting high functional redundancy. Thus, endosphere colonization may enhance a plant's ability to adapt to environmental changes by dynamically restructuring endophytic assemblages throughout a single growing season and over the individual's lifetime.

## O10 Dispersal of soil bacteria in the context of human well-being

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Evidence is accumulating that contacts with soil microbes are beneficial for human health and immune system development. Thus, it is important to elucidate how soil microbes are transferred to humans. However, studies on microbial dispersal in this context are rare. In a recent correlative study, we used the relative numbers of bacteria shared between environmental and human samples as a measure of dispersal and studied how this measure was associated with living environment and study subject lifestyles. In an ongoing study, we use intervention to explore how outdoor activities change human microbiota and if bacteria in different green areas are transferred onto human skin and in saliva. Four ninth grade classes from southern Finland participated in either hiking, geocaching, playing location-based mobile games outdoors, or attended a drama camp indoors. The drama camp served as control for outdoor activities. Skin swab and saliva were sampled before and after the activities. Swab samples of adhesive tapes attached to participants' shoes were collected once during each activity and surface soils sampled to validate tape swab samples. Quantitative PCR was used to estimate bacterial abundance and 16S rRNA gene sequencing to estimate bacterial diversity and to dissect community composition. Bacterial abundance in the adhesive tapes was highest with the hikers, followed by study subjects participating in geocaching and mobile games, and lowest with the indoor drama campers. The bacterial abundance, however, in skin and saliva samples did not change with different intervention activities. Results of bacterial diversity and community composition were more variable.

## O11 Establishing genetic, phylogenetic and functional mechanisms that shape *Acidobacteriota* diversity of arctic tundra and boreal forest soils

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Members of the *Acidobacteriota* are ubiquitous and abundant in soils throughout the world, however the genetic taxonomic and functional diversity within this phylum remain poorly known. Our aim is to refine the phylogenetic and functional diversity of the ubiquitous, but elusive, members of the *Acidobacteriota* phylum so we can begin to link their diversity to different soil habitats and elucidate the mechanisms which shape these communities in soils. Bacteria excel at adapting to different environments, but the functional implications of community transitions need to be characterized. The overarching hypothesis is that resource partitioning, selective predation, and temporal separation of activity each contribute to the success of particular bacterial strains/species. With a focus on sub-Arctic tundra and boreal forest soil habitats laboratory- and field-based approaches are used to discern which species/strains are successful and explain why. From a set of long-term tundra and forest field sites we are collecting data on how the soil *Acidobacteriota* communities are selected across environmental gradients. The long-read capability of the Oxford Nanopore MinION is used to profile bacterial ribosomal RNA operons of soil communities and isolates to build a comprehensive rRNA operon sequence database of the *Acidobacteriota* with strain-level resolution. Assembled full *Acidobacteriota* genomes, multi-locus phylogenies, and annotated pangenome markers are utilized to differentiate *Acidobacteriota* species. By uncovering novel species and strains within the *Acidobacteriota* and improving the accuracy of their phylogenetic placements, we aim to enhance our understanding of this complex phylum and elucidate the mechanisms which shape microbial communities in soils.

## O12 The spatio-temporal distribution of soil fungi alters enzymatic activities along forest management gradients

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Forest management affects biodiversity and ecosystem functioning. However, currently little is known about how management intensifications impact the highly diverse group of soil fungi. In forests, fungi serve as symbionts, saprobes or pathogens, and also play a significant role in ecosystem functioning. Likewise, soil enzymes, partly fungal-borne, are crucial for decomposition and nutrient cycling in these ecosystems. Yet, functional shifts of fungal community and enzyme activities in spatial and temporal context along forest management gradients are scarcely studied. Our study covers 150 experimental forest plots in three study sites sampled at five time points to understand large- and small-scale as well as temporal distributions of fungi and enzymes in soils. The plots were established as part of a large interdisciplinary consortium funded by the German Science Foundation called "German Biodiversity Exploratories" with a design including a range of management regimes varying from almost natural to highly managed forests. By combining ITS2 amplicon sequencing data with the activities of three enzymes, indicative of different nutrient cycles, we aim to unravel spatio-temporal relationships under varying management intensities. We show that fungal communities and enzyme activity have a differential response to changes in anthropogenic factors. Plant-dependent groups, such as mycorrhizal or pathogenic fungi, respond stronger towards changes in management intensification than saprotrophic fungi. Furthermore, fungi showed not only host tree preferences but also various temporal appearance patterns at plot, local and regional scales. Enzyme activities increased over time, independent of study site and are strongly coupled with temporal shifts in soil fungal communities.

## O13 Understanding local soil microbiomes in forest ecosystems: a perspective beyond broad-scale studies

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A substantial body of research has focused on global gradients and broad-scale patterns of soil microbial communities, providing key insights into their environmental relationships. Recent studies, however, highlight the importance of local microbial dynamics in regulating the functions of forest ecosystems, which are required for ensuring productivity and biodiversity. Factors such as slope position, microtopography, and local soil conditions are crucial in shaping the composition and functional specialization of microbial communities. At small spatial scales (ranging from tens to hundreds of meters), soil microbial communities show remarkable variability driven by subtle yet significant changes in soil properties, including pH and moisture, which govern nutrient cycling and other biogeochemical processes (Shigyo et al. 2022 *CATENA*). Furthermore, locally adapted microbial communities are central to plant-soil interactions, affecting litter decomposition processes through site-specific linkages (Shigyo et al. 2024 *New Phytologist*). These findings indicate that fine-scale spatial variation, often overlooked in broad-scale research, is intricately associated with ecosystem processes. Such localized variability demands closer attention to the complex interactions among microbes, plants, and abiotic factors, thereby emphasizing the importance of context-dependent strategies. A renewed focus on local scales in soil microbial research can enhance our understanding of nutrient dynamics, carbon storage, and ecosystem resilience at finer resolutions. This increased attention to small-scale processes is necessary for improving predictive models, accurately capturing the complexity of forest soils, and guiding sustainable forest management strategies, particularly in the context of environmental changes such as climate variability and land-use shifts.

## O14 Short-term response of microbial communities in peat-land forest soils to forest harvesting

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Forest ecosystems cover around 4.6 billion hectares of the Earth's surface and are home to around two-thirds of the world's terrestrial biodiversity. However, over 30% of this area is exploited primarily for the production of timber and non-timber forest products, leading to a significant reduction in biodiversity and profound changes in ecosystem functioning. The effects of forest management have mainly been studied on fauna and flora, while soil micro-organisms and the ecosystem services they provide have been the subject of much less investigation. The role of soil micro-organisms in the carbon and nutrient cycles is increasingly recognised, not least because of their complex interactions with plant roots. The main aim of this study is to analyse the short-term responses of soil microbial community composition to different forestry practices, in particular thinning and clear-cutting, and to determine whether these practices have a significant impact on these communities. Using eDNA metabarcoding to analyse the various soil microbial communities, we found differentiated responses between trophic guilds as a function of forest management methods and inter-annual variations. The next objective is to examine whether these changes in the composition of soil microbial communities have led to alterations in the properties and functioning of forest ecosystems, particularly with regard to the decomposition of organic matter and the nitrogen cycle.

## O16 Reindeer grazing alters soil microbial activity in a northern peatland

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The rate of global warming is more rapid in the northern hemisphere compared to other regions of the world. Northern peatlands have a critical role in global carbon cycling but are also essential with regards to other greenhouse gases. Moreover, methane, carbon dioxide and nitrous oxide emissions from these soils are predicted to further increase in the future. While soil microbial activity is highly associated with greenhouse gas cycling, many of these processes are not yet well understood. In prior studies reindeer grazing in northern boreal forests, has been observed to affect the soil microbiome and the associated nutrient cycling. To shed light into the microbiome effects of grazing in northern peatlands, we performed deep metagenomic and metatranscriptomic analyses of plots exposed and unexposed to grazing by reindeers in the rich fen Puukkosuo in northeastern Finland. Our data show a distinct effect associated with reindeer grazing in the soil microbiome. Decreased microbial functional activity associated with nitrous oxide reduction to nitrogen was observed in areas exposed to grazing. However, the nitrite / nitrous oxide reductase ratio was significantly higher in metatranscriptomics data associated with the grazed areas, potentially suggesting altered microbial nitrogen cycling consequently to reindeer grazing. Furthermore, to better utilize the complementary nature of the omics datasets, an integrated multiomics approach was applied, with the power to classify samples with good accuracy into those from grazed or ungrazed areas by using only the measured soil microbial data.

## O17 Dynamics of fungi and bacteria in soil and what they tell about the microbiome function

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Dynamics of microbial communities is an important process that adjusts the microbiome composition to external conditions, e.g., seasonally, during ecosystem development or habitat succession after disturbance and in other instances. Microbial communities are also subject to changes that may appear random but still result in differences in microbiome composition in time. Repeated resampling of bacterial and fungal communities at specific locations in a forested area of Central Europe across multiple years demonstrated that microbial communities in forest litter and in soil undergo temporal change at a rate of 0.010–0.025 per year in units of Sorensen similarity, and the change in soil is slightly faster in fungi than in bacteria, with bacterial communities changing more rapidly in litter than in soil. Importantly, temporal development differs across fungal guilds (ectomycorrhizal fungi, saprotrophic fungi, unicellular yeasts) and bacterial phyla with different ecologies. While some microbial guilds show consistent responses across regional locations, others show site-specific development with weak general patterns. The factors that increase or decrease the rate of temporal turnover are so far rather guessed than confirmed. The temporal dynamics of fungal and bacterial communities in forest topsoils is largely independent, indicating that interaction between these two components of the forest microbiome are rather minor. The variety of paths that individual guilds of microorganisms follow in time along with the information on their climatic drivers allows us to hypothesize about the changes that the microbiome will undergo in the future.

## 018 How do microeukaryotes in boreal forest soil respond to forestry?

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Soil microeukaryotes are important components of the forest soil biome, yet are often overlooked in studies of microbial diversity. There is limited knowledge about their diversity and distribution patterns in forest soils, and even less about how they respond to anthropogenic influences such as forestry. To understand long-term responses to clear-cut forestry, we compare the diversity of soil microeukaryotes in mature, but previously clear-cut (CC) stands, with near-natural (NN) forests that have never been clear-cut. Soil samples were collected in twelve pairs of CC and NN forest stands in South-eastern Norway, and divided into seven soil horizons spanning two organic and five mineral soil horizons. Thickness and soil chemistry have been recorded and analyzed for each layer, allowing us to correlate these to the microeukaryotic community. To be able to phylogenetically resolve the largely unknown diversity of soil microeukaryotes, we are utilizing long-read metabarcoding with general eukaryotic primers targeting most of the ribosomal operon (*ca.* 4500 bp). We will present preliminary results on the phylogenetic diversity of microeukaryotes in boreal forest across different soil depths and assess how they respond to forestry and other environmental and edaphic factors in terms of community composition, diversity and richness.

## O19 Biogeography and diversity of soil microbial and mesofauna communities in different land uses with a gradient of soil disturbance in Eastern Canada

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Soil microbial and mesofauna communities play a crucial role in ecosystem functioning, supporting essential goods and services such as crop productivity, soil quality, and overall soil health. In Eastern Canada, deforestation and intensive agricultural practices altered soil health and organic matter, negatively impacting both natural ecosystems and agroecosystems. Despite their importance, the relationship between pedo-climatic and topographic factors and soil biodiversity across large spatial scales remains poorly understood. This study's objective was to assess the diversity of bacterial, fungal, nematode, and micro-arthropod communities across different land uses and a gradient of soil disturbance in Eastern Canada (<https://sis.agr.gc.ca/cansis/biome/index.html>). A comprehensive soil sampling strategy was employed across five provinces - Québec, New Brunswick, Nova Scotia, Prince Edward Island, and - Newfoundland and data on soil biodiversity, climate, and geomorphology were collected to create a robust dataset. This research represents the first phase of a long-term initiative to document Canadian soil biodiversity and aligns with the objectives of the International Initiative for the Conservation and Sustainable Use of Soil Biodiversity.

## O20 Arbuscular mycorrhiza systematically suppresses ammonia oxidizing bacteria, but not archaea, across a range of soils

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The role of arbuscular mycorrhizal (AM) symbiosis in plant phosphorus and micronutrient uptakes is well established, yet its role in plant nitrogen (N) acquisition and soil N cycling is less well understood. Here we focused on the interactions between AM fungi and ammonia oxidizing (AO) bacteria and archaea in a range of agricultural soils collected along a 200 km transect in the Czech Republic. The soils containing their indigenous microbiomes were incubated in root-free patches subjected or not to colonization by AM hyphal networks extending from mycorrhizal or nonmycorrhizal plants growing outside of the patches, respectively. The presence of AM fungal hyphae suppressed abundance of various microbial guilds such as bacteria, protists, and fungi. The strongest suppression was recorded for AO bacteria and no suppression whatsoever for AO archaea. Besides the effects assignable to AM fungal presence, significant parts of the dataset variability were also explained by soil pH (for AO bacteria) and soil organic carbon content (for AO archaea). Although we initially assumed that the observed effects could be explained by direct competition for free ammonium ions between AM fungi and AO microorganisms, the concentration of ammonium ions in the soils measured at the end of the incubation was slightly (but significantly) higher in the mycorrhizal as compared to the nonmycorrhizal pots, indicating more intricate network of interaction between AM fungi and other soil microorganisms in the soil, not completely unexpected given the complexity of soil N cycle.

## O21 Do earthworms alter fungal community composition and activity in boreal forest soils?

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While creating the drilosphere, earthworms interact with microorganisms and thereby can affect soil carbon and nutrient cycling. However, it is challenging to study interactions between earthworms and forest fungi *in situ*, which remain poorly understood. Particularly, controlled incubation experiments often exclude plant-associated ectomycorrhizal (EcM) fungi known to regulate carbon and nitrogen cycling in boreal forests. We sampled intact soil turfs including tree saplings from 12 northern boreal forests and placed them in an experimental forest in southern Sweden. The 12 forests represented a fertility gradient outside the current distribution range of burrowing earthworms. During spring, 2024, we introduced soil-dwelling earthworms (*Aporrectodea* and *Lumbricus spp*) into the mesocosms. We expect that in nutrient poor ecosystems, minimal earthworm activity will have limited effect on the EcM fungal community composition. However, in less acidic, more fertile soils, high earthworm activity will hamper fungi with extensive mycelia and lead to proliferation of opportunistic moulds. After the first growing season, earthworms could survive and reproduce in our experimental soils, and plant communities and soil properties started to respond to earthworm activity. These changes suggest shifts in fungal communities too, which we are studying with RNA and DNA sequencing.

## O22 Adaptation of microbial communities' life strategies in urban areas along a management intensity gradient

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Urbanization is a major 21st-century challenge. From 2000 to 2018, over one million hectares in Europe became urbanized, which is more than eight times the surface that reverted to agriculture. Characterizing urban soil microbial communities is a key priority for future research. This understanding is crucial for sustainable urban design, as it reveals the drivers of microbial community assembly and ecosystem functions. To this end, we investigated urban soil microbial communities in Blois, France, sampling 135 soils from eight land-use type: showcase-gardens, city parks, parklands, areas under trees, residential areas, roadsides, unused areas, and sports fields. Each type was assigned a management intensity score from 1 (least managed) to 4 (highly managed). Microbial communities were analyzed using Illumina sequencing, with fungal guilds identified via the FUNGUILD database, and proportions of oligotrophic and copiotrophic bacteria assigned. Our findings reveal that both management intensity and land use lead to adaptations in microbial functional groups. Highly managed areas, like showcase-gardens and sports fields, had significant differences in microbial community composition compared to less managed areas, like unused areas. Microbial network analyses showed that urban soil microbial communities exhibit less than half the connectivity observed in semi-natural ecosystems. Additionally, managed areas exhibit less connectivity compared to those in less managed areas. This suggests that urban soils, especially managed urban soils, support microbial communities that are less resilient and more fragmented. Urbanization leads to significant adaptations in microbial communities. Urban soil management strategies should prioritize reducing management intensity to maintain microbial resilience and ecosystem functions.

## O23 Agricultural expansion in boreal regions: temporal responses of soil microbial functions after land clearing

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Northern Canada is warming at more than double the global average. Increased growing days combined with northern food security concerns have prompted local governments to encourage agriculture expansion in boreal regions. Land conversion (LC) from forests to agricultural fields in these regions can lead to the loss of up to 76% of soil carbon and significant greenhouse gas emissions. There is a time-critical need to develop LC strategies that promote productive and functional cropping systems while reducing adverse environmental impacts, which will also reduce unnecessary deforestation. Different LC approaches, including conventional clearing and different mulch management strategies, were evaluated in the Ibex Valley, in south-west Yukon Territory. Starting from the first year of conversion, we used metabarcoding and quantitative PCR to assess how soil microbial communities responded to LC, with a specific focus on communities that underpin carbon and nitrogen cycling. The different LC approaches altered both the timeframe and the magnitude of microbial responses. Fundamental shifts in some bacterial and fungal communities occurred within months, while others remained relatively stable several years after LC. The presented research will discuss the rate at which different structural and functional communities responded to LC, and the implications of those responses for system sustainability and productivity.

## O24 Soil fungal communities in space and time

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Austria – albeit a small country – is especially rich in ecosystem and habitat types with influences from Atlantic, alpine, submediterranean and continental climates. Elevation ranges from ca. 120 m to nearly 3800 m. Many habitat types are, however, threatened due to climate change and human activities like agriculture, forestry, infrastructure work or tourism. Decline and loss of plant and animal species due to these changes is well documented, whereas less is known from fungal species. A comprehensive survey of soil fungal communities was carried out in semi-natural and near-natural ecosystems throughout Austria, from riparian forests in the Pannonian lowlands to alpine scrub and pastures. Samples were collected in ICP forest sites, LTER sites, national parks and natural forest reserves with well documented data on site characteristics, vegetation, soil properties, climate, disturbance history etc. From many sites, archived samples in soil libraries are available. Although archives were established for physicochemical analyses, initial experiments indicated that long-term stored soil samples are as well suited for DNA-based fungal community analyses. It is thus possible to compare soil fungal communities from the early 1990ies until the present for improved prediction of future developments. Dynamics in fungal community composition across space and time and data on major drivers of changes will be presented. Currently available data highlight the importance of habitat conservation for protection of a high fungal biodiversity across different ecosystems.

## O25 The co-occurrence of soil protists and prokaryotes is affected by rhizocompartment and wheat variety

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Soil protist communities and their interaction with prokaryotes in the rhizocompartment are known to influence plant growth while less is known of the drivers of protist communities and co-occurrence with prokaryotes within the rhizosphere compartments and between wheat varieties. We tested the hypotheses that rhizocompartment and wheat varieties varying in root structures and pathogen resistance impact the protist community structure and diversity, and that the co-occurrence of prokaryotes and protists depends on the wheat varieties selecting for different key protist-prokaryote interactions. The protist communities of four different wheat varieties in three rhizocompartments: rhizoplane, rhizosphere, and bulk soil, as well as their co-occurrence with prokaryote communities, were studied. In soil DNA protist abundance was determined using qPCR while protist and prokaryotic community composition were described by metabarcoding of 18S rRNA gene and 16S rRNA gene, respectively. Protist community diversity, structure, and abundance were significantly affected by the rhizocompartment and the wheat varieties. Specifically, protist richness increased with distance to the root surface. Differential abundance and Random Forest modeling revealed that Colpodea was relatively more abundant in the rhizosphere and Filosa-Sarcomonadea were relatively more abundant in the rhizoplane, compared to bulk soil. A co-occurrence network analysis of prokaryotes and protists showed a more intricate network with a higher number of nodes in the bulk soil. In conclusion, the rhizocompartment and the wheat variety drive the protist communities, which is consistent with the drivers of prokaryotic communities and demonstrates the interconnectivity of protist-prokaryotic interactions in soil rhizosphere.

## O26 Delineating the co-existence strategy of different arbuscular mycorrhizal fungi for root colonization and foraging on root-free patches

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Arbuscular mycorrhizal fungi (AMF) are crucial components of terrestrial ecosystems, yet their basic ecology of co-existence within the plant environment remains poorly understood. This study compared the root colonization and foraging behaviors of five AMF isolates from four families: Acaulosporaceae, Gigasporaceae, Claroideoglomeraceae, and Glomeraceae. Additionally, we examined their impact on plant growth and nutrient uptake. The rate of root colonization and foraging on root-free patches was assessed by measuring biomass abundance using taxon-specific genes through qPCR and amplicon sequencing (WANDA-AML2). A microbiome analysis was conducted to identify the core microbiome of extraradical AMF hyphae. Notable taxonomic differences were observed in fungal biomass across roots and root-free patches. Most isolates from the Glomeraceae family, specifically *Rhizophagus irregularis* and *Funneliformis mosseae*, exhibited the highest root colonization rates and actively foraged for root-free patches. In contrast, isolates from other families showed limited colonization, primarily restricted to the rhizosphere. Inoculating *Andropogon gerardii* with AMF isolates significantly increased the uptake of <sup>15</sup>N-labeled nitrogen from chitin and clover patches and reduced overall N losses from soil. Furthermore, the microbiome analysis revealed that extraradical hyphae carry their core microbial members during foraging in root-free patches. The findings suggest that the colonization strategies of AMF species vary significantly at the family level and are influenced by labor partitioning for foraging on different nutrient resources.

## O27 Mycelial exploration of arbuscular mycorrhizal fungi: intra- and interspecific variation among 29 isolates

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How changes in biological communities scales up to the ecosystem functioning are usually studied by averaging across individual species traits. For microbial communities, this is a challenge due to difficulties inherent to their cultivation. In the particular case of arbuscular mycorrhizal fungi (AMF), their colonization pattern is an important trait related to their functioning at both individual, plant host level, but also at ecosystem level. It has been proposed that there is a trade-off between internal root colonization and external soil proliferation which may be reduced to three overall functional life-history strategies: *rhizophilic*, *edaphophilic* and *ancestral*. Owing to the complexity of maintaining and experimenting with these obligate biotrophic symbionts only less than 5% of the described species have actually been mapped for these functional traits. In addition, any intra-specific variation among strains of the same species has mostly been ignored. In this study, we therefore set out to map soil *versus* root mycelial extension and colonization of a range of AMF isolates. From the AMF culture collection maintained at Estación Experimental del Zaidín, Granada, Spain, we selected 29 isolates from eight species, which thus included both intra as inter specific comparisons. Mycelial proliferation was measured at different distances (1, 3, 6, 12 cm from an enmeshed root system) after 70 days of plant growth. The AMF effect on overall root colonization and phosphorus uptake was conserved among AMF species while plant biomass was equally affected by species and strains. For root development, the intraspecific variation doubled variation of the species.

## O28 Soil and plant microbiome assemblages in pristine ecosystems of remote sub-Antarctic islands; responses to abiotic drivers of global changes.

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Plants interact with numerous microorganisms recruited in their environment and that colonize all of their organs, both below and aboveground. This biotic assemblage is referred to as a 'holobiont'. The associated microbiome, either transmitted vertically or recruited horizontally, plays crucial roles in the plant performance, by contributing to its nutrition, pathogen resistance, and stress tolerance. The uninhabited (to the exception of a scientific base) sub-Antarctic Kerguelen Islands are an ideal open-air laboratory to study plant-microbiome recruitment, diversity and evolution due to their geographic isolation, being thousands of kilometers away from the nearest continent. Fellfield ecosystems are inland pristine elevated bare areas subject to frost and wind exposure, and are home to most of the archipelago's endemic plant species. They represent key sentinel biological heritage sites that have evolved under low anthropic pressure and buffered climate. However, confronted to rapid rising temperatures and decreasing rainfall in the South Indian Ocean, these ecosystems and their holobionts may be at risk. We hypothesize that Kerguelen's isolation led to low  $\alpha$ -diversity in soil and plant-associated microbiomes, with limited microbial interactions for both endemic and introduced plant species. Additionally, we expect climatic variability along altitudinal gradients to affect microbial  $\beta$ -diversity, reducing diversity in high elevation fellfields. Using 16S and ITS DNA metabarcoding, we investigated soil and plant-associated microbial communities of the natives *Poa kerguelensis* (Poaceae) and *Pringlea antiscorbutica* (Brassicaceae), alongside the invasive *Poa annua* (Poaceae), across altitudinal transects.

## O29 Limited responses of ammonia oxidizers to simulated drought and heatwaves across arable soils in Europe

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With increasing droughts and heatwaves, understanding how nitrogen cycling and its associated microbial communities are affected is crucial to better predict the consequences for soil functions and ecosystem services. As part of the SOILGUARD EU project, we examined how soil ammonia-oxidizing bacteria (AOB), archaea (AOA), and comammox (complete ammonia oxidizers) responded to simulated drought- alone or in combination with heatwave- under both conventional and organic management practices. Field experiments were conducted in arable fields in Belgium, Denmark and Latvia, where drought was simulated for three months using rainout shelters, followed by a heatwave simulated using infrared heaters. Soil samples were collected before the climate change treatments, immediately afterward, and two months later. We characterized the abundance, diversity, and community composition of ammonia oxidizers using qPCR and Illumina-based amplicon sequencing of the *amoA* gene along with N-pools and nitrification activity. We found that simulated drought and heatwave had a small effect on the abundance and diversity of ammonia oxidizers. Community compositions were resistant to the climate change treatments, whereas the effects on the abundance and diversity were site-, management- and time-dependent. Comammox clade B abundance was the most sensitive to drought, whether alone or combined with a heatwave, whereas alpha-diversities responded only for AOA and AOB. Management practices strongly influenced ammonia oxidizers abundance and alpha-diversity, especially for AOA and AOB. Overall, these findings underscore that while the impacts of drought and heatwaves on ammonia-oxidizing communities are limited, they are both group- and site-specific and are further modulated by management practices.

## O30 Gradients of C flux and microbial C use in the detritusphere

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Plant litter entering the soil is a major pathway by which C enters the soil. We aimed to link the microbial filter function to changes in DOC quality within the detritusphere and with time. To address this research aim, we performed a 42 days microcosm experiment simulating the detritusphere in soil cores of increasing thickness (2, 4, and 8 mm). We studied the microbial filter function along the developing gradient of microbial activity by using differences in the natural <sup>13</sup>C abundance between maize litter and SOC, calorimetry, ultra-high-resolution FT-ICR mass spectrometry of leachates and analysis of microbial communities. The results show a fast development of gradients of substrate availability and microbial activity with pronounced activity in the 0–2 mm layer. Heat production peaked during the initial phase of the experiment much more pronounced and declined much faster than substrate availability. In comparison, microbial biomass increased immediately after litter addition but peaked towards the end of the experiment. Both were linked to an initial increase in bacterial abundance and fungal growth 14 days after litter addition, which may be related to shifts in substrate quality. DOC concentrations in leachates indicated an increasing microbial filter function with increasing thickness of the soil layer. Nitrogen leaching from soil cores strongly increased during the experiment, again pointing to a shift in quality of the leachates. Overall, the results indicate a temporal decoupling of substrate availability and use from microbial abundance in the detritusphere.

## O31 How biochemistry may support microbiology? New tools and perspectives.

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Although microbial living biomass carbon accounts for only 2% of the total soil organic carbon (SOC), microorganisms play a crucial role in the decomposition and accumulation of SOC. In boreal forests, especially ectomycorrhizal, ericoid mycorrhizal, and saprotrophic fungi drive SOC decomposition and even accumulation, as these fungi provide a large part of SOC (50–80%) in the form of microbial necromass. Thus, the role of microorganisms in SOC processes is unquestionable. With novel metagenomic and metatranscriptomic tools, we can study changes in microbial community structure, and estimate fungal guilds and microbial processes, however, these tools provide relative abundance data, not biomass of separate guilds and their activities. Recently, we developed methods to precisely estimate fungal biomass and necromass using liquid chromatography-mass spectrometry. Moreover, we are working on the development of other molecular markers of microorganisms to help to disentangle processes behind SOC stabilization in the soil. My talk will provide insights into these new biochemical methods, I will also provide my view on future directions in soil biochemistry and biochemistry behind plant-soil-microbial interactions. Only by a combination of microbiological, gas fluxes, and biochemical tools, we can understand the mechanisms behind soil processes to improve forest management and thus mitigate climate change with no harm to plant biomass production.

## O32 Microbial necromass production and consumption define net necromass stocks

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Microbial necromass carbon (C) is a conceptual and quantifiable link between microbial physiology and persistent soil organic C. Microbial biomass growth and death (necromass production) and microbial recycling of sorbed dead microbes for substrate (necromass consumption) create a production-consumption dynamic, that if quantified, should predict net necromass stocks as determined with amino sugars. We set out to test this framework in soils from three land uses (grassland, forest, arable) and two locations (Luxembourg, Sweden). To do so we quantified production as growth rate (calculated from CUE) and consumption as mining rate (necromass sorption and decay from particulate organic matter (POM) and mineral-associated organic matter (MAOM)), using <sup>13</sup>C-necromass generated from *Bacillus licheniformis* and *Trichoderma harzianum*. Preliminary results from grasslands indicate that necromass production, POM sorption and decay are larger with fungal necromass, with no site differences. MAOM sorption and decay were similar between necromass types, with small site differences for fungal necromass. Total sorption ranged from 40–65%, with decay rates ( $\sim 0.15\text{--}0.25 \text{ ng C g}^{-1} \text{ h}^{-1}$ ) slower than production rates ( $3\text{--}75 \text{ ng C g}^{-1} \text{ h}^{-1}$ ). The relationship between net necromass (production - decay) on fungal versus bacterial necromass in Sweden and Luxembourg grassland soils correlates positively ( $R^2=0.99$ ) with fungal and bacterial necromass stocks for the two sites as calculated from amino sugars ( $0.2\text{--}3 \text{ mg C g}^{-1}$ ), supporting our conceptual framework around net necromass. Critically, this also supports the concept that microbial necromass stocks are persistent (decay slower than production) but not stable, as both bacterial and fungal necromass are subject to microbial recycling.

## O33 Deadwood as a key factor in soil carbon and energy flow through microbial communities

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Climate change poses significant challenges to forest ecosystems, particularly influencing processes such as deadwood decomposition and carbon sequestration. This study explores the impact of decaying spruce wood on soil properties, enzymatic activity, and microbial structure across an altitudinal gradient in mountain ecosystems dominated by spruce monocultures. The research, conducted in the Babia Góra Massif, Poland, examined soils beneath highly decomposed spruce logs at various elevations (600–1200 m a.s.l.), focusing on physicochemical soil properties, enzyme activity, and microbial community composition. Our findings reveal that decaying wood significantly enriches soil with carbon and nitrogen, enhancing enzymatic activities such as  $\beta$ -glucosidase and phosphatase. These effects were consistent across altitudes, indicating that decaying wood universally acts as a substrate for microbial processes. Increased soil moisture content under decaying wood promotes decomposition and microbial activity. Interestingly, microbial community composition under deadwood exhibited minimal biodiversity changes compared to control soils, but metabolic activity was notably higher, suggesting shifts in microbial function rather than community diversity. The study highlights the significant role of decaying spruce wood in shaping soil properties and microbial processes in mountain ecosystems, emphasizing its contribution to carbon and nitrogen enrichment and enhanced enzymatic activities. These findings underscore the ecological importance of deadwood in forest ecosystems, particularly in the context of carbon cycling and climate change adaptation.

## O34 Soil disturbances affect GHG emissions, organic carbon pool and microbial community in drained peatland forest

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Soils in drained peatland forests are losing carbon stocks and increasing GHG emissions under warming climate. Natural disturbances like storms can exacerbate these changes by altering soil structure and nutrient inputs. Uprooted trees create pits, whereas fallen canopy cause excess litters to soil. Thus, disturbances increase the spatial heterogeneity of soil properties and microclimate, break root-fungal network, modify soil processes and carbon balance. To study the impacts of soil disturbances – topsoil removal and residues cover – on the GHG emissions, soil organic carbon (SOC) pool and microbial community, disturbance treatments were established in clearcut and canopy-covered peatland forest sites in southern Finland. Topsoil removal caused reduced CO<sub>2</sub> emissions but increased N<sub>2</sub>O emissions in both clearcut and canopy-covered forest during two-years treatment period. It also decreased the soil CH<sub>4</sub> sink, even switched clearcut to CH<sub>4</sub> source. Residue-covered treatment showed higher CO<sub>2</sub> and N<sub>2</sub>O emissions than control in canopy-covered forest. Both treatments increased the global warming potential in canopy-covered forest. The stable SOC fraction decreased after topsoil removal, while residues cover enhanced soil C stabilization by increasing the proportion of stable SOC. Topsoil removal altered fungal community composition and reduced fungal and bacterial biomass. Although bacterial communities showed stable in most treatments, clearcutting combined with topsoil removal led to a distinct shift, decreasing the relative abundance of methane-oxidizing bacteria. Our results revealed that soil disturbances cause global warming effects in short term and high spatial variation of soil microbes and SOC pool. Longer term studies are needed to understand the recovery after disturbances.

## O35 Forest management impacts on fine root input to peat carbon

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In peatland forests, most soil carbon may derive from roots and root-associated microorganisms rather than from the aboveground plant litter. Large uncertainties prevail in the quantity and quality of plant fine roots because it is very laborious to sort them from peat. We used modified ingrowth method and Fourier transform infrared (FTIR) spectroscopy to examine how forest management impacts fine root growth, depth and species distribution in two peatland forests: Ränskälänkorpi, Southern Finland and Kivalo in Northern Finland. Management options included rotation forestry with clear cuts vs. continuous cover forestry, i.e., selective cuttings. Woody roots dominated both under selective cutting and control plots in the south, whereas graminoid and herbaceous roots were more common in all management options in the north and in southern clear cuts. Most, up to 80–95% of the fine roots grew in the top 20 cm of soil. The amount or depth distribution of fine roots did not differ among most management options. However, fine root biomass production tended to be smaller and more evenly distributed by depth at the clear-cut plots with soil preparation. Thus, continuous cover forestry did not compromise the soil carbon input as fine root quantity or quality in the first years after harvesting. The lower root litter inputs or shifts in decomposability from low in woody roots to higher in herbaceous roots may in part contribute to net carbon loss from clear cut soils. To further assess root biomass quality, we will compare FTIR based to DNA based root species identification.

## O36 The magnificent, frustrating diversity of soil viruses

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Viruses have been recognized as abundant but virtually unknown members of the soil microbiome. Early insights into soil viral diversity, biogeography, and potential impacts on microbial ecology and biogeochemical cycling will be presented. Using shotgun viral metagenomic (viromic) approaches to recover and sequence the viral size fraction, tens of thousands of viral 'species' have been recovered from a wide range of soils, consistently indicating high viral diversity across terrestrial ecosystems. Soil viral communities are often strongly spatially structured, even over short distances, and they exhibit reproducible temporal successional patterns following rewetting of dry soil. The emerging paradigm is of a highly active and dynamic soil virosphere with the potential for substantial contributions to bacterial mortality, biogeochemical cycling, and food web dynamics in terrestrial ecosystems.

## O37 Virus community dynamics and host defense evolution vary as a function of biogeochemical process rates in soil

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Soil virus communities are dynamic and respond rapidly to environmental perturbations. However, understanding interactions between individual host and virus populations in soil are constrained by physicochemical complexity and vast diversity. Recently we have developed an approach that characterizes active viruses associated with methylootrophs by following the transfer of methane-derived <sup>13</sup>C from host to virus *in situ*, enabling a focused analysis of virus populations infecting taxonomically restricted and functionally coherent bacteria. To test the hypothesis that virus-host interactions and evolution are proportional to activity rates, soil microcosms with methane additions were established at three temperatures to generate different methane oxidation rates and incubated for 12 weeks. Microcosms were destructively sampled at weekly intervals and analyzed using three approaches: virus-targeted metagenomes ('viromes') to examine virus communities, 16S rRNA gene amplicons to exam host communities, and <sup>13</sup>C-enriched DNA to recover genome fragments containing clustered regularly interspaced short palindromic repeats (CRISPR) arrays to exam host-virus interaction and adaptation. Rates of methane oxidation were concomitant with virus community succession dynamics. Analysis of methylootroph CRISPR arrays revealed that the richness of virus populations infecting individual strains increased with host activity, and host ranges for individual viruses were limited to the family or sub-genus level. Intriguingly, community level analyses of CRISPR arrays suggested host adaptation in response to virus interaction during the course of the incubation. This study demonstrates that the use of molecular analyses facilitating analysis of taxonomically and functionally restricted populations provides detailed insight into host-virus dynamics and evolution *in situ*.

## O38 Phosphate amendment drives bloom of RNA viruses after soil wet-up

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Soil rewetting after a dry period results in a surge of activity and succession in both microbial and DNA virus communities. Less is known about the response of RNA viruses to soil rewetting—while they are highly diverse and widely distributed in soil, they remain understudied. We hypothesized that RNA viruses would show temporal succession following rewetting and that phosphate amendment would influence their trajectory, as viral proliferation may cause phosphorus limitation. Using 39 time-resolved metatranscriptomes and amplicon data, 2,190 RNA viral populations were identified across five phyla, with 37% of these predicted to infect bacteria (26%) or fungi (11%). Only 1.2% of viral populations had annotated capsid genes, suggesting most persist via intracellular replication without a free virion phase. Phosphate amendment altered RNA viral community composition within the first week and amended vs. unamended communities remained distinguishable for up to three weeks. While the overall host community remained stable, certain bacterial populations showed reduced abundance in phosphate-amended soils, likely due to increased viral lysis, as RNA bacteriophages, particularly *Leviviricetes*, proliferated significantly. Notably, 60% of the viruses with increased abundance under phosphate amendment belonged to basal *Lenarviricota* clades rather than well-known groups like *Leviviricetes*. We estimate RNA bacteriophage infections may affect  $10^7$ – $10^9$  bacteria per gram of soil, aligning with the total bacterial population ( $10^7$ – $10^{10}$  g<sup>-1</sup> soil), suggesting that RNA phages significantly influence bacterial communities post-wet-up, with phosphorus availability modulating this effect.

## O39 Diversity of RNA virome in soil

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Viruses are the most abundant entities in the soil, however, their role within the soil food web is largely unknown. Soil viruses are suggested to impact the diversity and abundance of the soil microbial communities and play a vital role in soil nutrient cycling. This study investigates the diversity of the RNA viruses across four soil types: beech and pine forest, grassland, and agricultural. We observed the highest viral abundances in the beech forest soil ( $4.1 \pm 2.4 \times 10^8$  viruses  $g^{-1}$ ) and the lowest in the agricultural soil ( $1.8 \pm 0.4 \times 10^8$  viruses  $g^{-1}$ ). Analysis of RNA virome data identified more than 6000 contigs broadly classified under phyla Kitrinoviricota, Pusuviricota, Duplornaviricota, Negarnaviricota, and Lenarviricota. We found that the grassland soil exhibited the highest alpha diversity for RNA viruses compared to agriculture and forest soils. Interestingly, a large number of contigs were unique to specific soil types. The phylum Pisuviricota, which includes plant hosts, was found in higher proportion in the grassland soils whereas Lenarviricota, particularly the bacteriophage *Emesvirus*, dominated forest and grassland soils. Conversely, the phylum Kitrinoviricota which mostly infects plants, dominated in the agricultural soil. This study indicates that soil types shape RNA viral communities, but their impact on plant ecology still needs to be determined. Overall, our results captured diverse viruses that belong to eukaryotic hosts including fungi, invertebrates, and plants, as well as bacterial hosts, indicating the crucial role of RNA viruses in the soil microbiome.

## O40 Characterizing soil virus-nitrifier interactions and impact on nitrification

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Characterizing host and virus population dynamics in soil is challenging due to high structural complexity and vast diversity. Viruses of nitrifiers have not been extensively studied in soil or other ecosystems but may have considerable impact on nitrification through interactions with specialized groups of chemolithoautotrophic ammonia-oxidizing microorganisms and nitrite-oxidizing bacteria that derive energy from oxidizing inorganic nitrogen (N) to fix inorganic carbon. While microbially-mediated nitrification is central to N-cycling, it contributes to nitrous oxide emissions and nitrate leaching from the inefficient use of applied fertilizers in agroecosystems. One of the major challenges in virus ecology is linking specific host and virus populations. Using soil incubations with stimulated nitrification rates, combined with differential inhibition and virus-targeted metagenomes, we recovered high-quality and complete virus genomes that could be associated with specific nitrifier taxa. To specifically identify viruses of nitrifiers, we established a reference nitrifier virus database composed of proviruses derived from nitrifier host genomes and metagenome-derived predicted viruses. We discovered that nitrifier viruses are diverse and active during nitrification and possess a range of predicted auxiliary metabolic genes that encode proteins involved in host energy metabolism. While nitrifier viruses have been cultivated from other environments, using our nitrifier culture collection containing representatives of all major soil relevant lineages, we have isolated nitrifier-infecting viruses from soil for the first time, and characterized their morphology, genomes and host range. This provides a new avenue for assessing the impact of viruses on nitrification and the potential for augmenting a process with major environmental impacts.

## O41 Viral regulation of soil microbial communities and carbon cycling

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Viruses are highly diverse and play critical roles in regulating microbial communities and biogeochemical cycling. Soil viruses exist in highly heterogeneous environments with varying physicochemical properties and complex microbial interactions making their ecological impact context-dependent. To study the ecological consequences of soil viruses, we conducted a fully factorial microcosm experiment where we manipulated viral abundances and the presence and absence of fungi across 4 soils with contrasting organic matter contents. This allowed us to detect generalizable patterns of how soil viruses affect microbial abundance and community composition as well as carbon cycling - and how soil fungi modulate this. We further analyzed carbon use efficiency (CUE) following viral manipulation using <sup>13</sup>C-labeled cellobiose. Our results show that viral addition significantly altered bacterial community composition in the short term and that this effect was dependent on soil organic matter content. Additionally, interactions between fungi and bacteria influenced the magnitude of the viral effects on bacteria. Furthermore, viruses affected soil CUE, indicating that viruses and their interactions have potential consequences for the soil carbon balance. These findings expand our understanding of soil viruses across diverse soil conditions and highlight the need to consider them as key regulators of microbial ecology and carbon cycling.

## O42 Bacteria-phage coevolution drives patchy distribution of plant disease through resistance-virulence trade-offs

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Bacteria-phage coevolution is pervasive in nature, affecting the global nutrient cycling and the composition and functioning of microbial communities. While coevolutionary adaptations often have correlated fitness effects, it is unclear how these changes cascade in food webs, affecting the ecology of the surrounding communities. Here, we used a combination of field, greenhouse and lab experiments to link coevolutionary patterns between phytopathogenic *Ralstonia pseudosolanacearum* bacterium and its phage parasites to bacterial wilt plant disease occurrence in tomato fields. By sampling four geographically disconnected fields, we establish that bacteria and phages are locally adapted: phages were the most infective on sympatric bacteria from the same fields, while bacteria isolated from healthy plants were relatively more resistant. The modularity of phage-bacteria coevolution could be explained by field-specific anti-phage defense system patterns and direct experiments where phages selected for field-specific mutations in different phage receptor genes. Crucially, phage resistance was costly and reduced virulence *in planta*, explaining why phage-resistant pathogens were more commonly associated with healthy plants. Our findings demonstrate that bacteria-phage coevolution can cascade through trophic networks, resulting in a patchy distribution of plant disease in tomato fields due to resistance-virulence trade-offs.

## O43 Virus evolution and lifestyle in root-associated fungi

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Fungal viruses (mycoviruses) are found in all different ecological guilds and taxonomical groups of fungi. They infect soilborne and root pathogens as well as root endophytes, mutualists and saprotrophs. Our research has focused on viruses of root rot pathogens such as *Heterobasidion* spp. and *Armillaria* spp., aiming at finding viruses that could be used in biocontrol against their hosts, but also investigating virus diversity, evolution, dispersal routes, host ranges and virus-virus interaction. We have also addressed the diversity and ecological role of viruses in ectomycorrhizal fungi and saprotrophic wood decay fungi. These investigations have revealed a highly diverse community of fungal viruses in the forest ecosystem. New findings based on virus phylogenetics and genome organization suggests that many viral taxa, previously believed to be exclusive to plants or insects, have related viruses in fungi. Having been an understudied topic in virology, mycovirus research has recently revealed also entirely new evolutionary trajectories and genome structures, such as ambiviruses with circular ambisense RNA genomes, and splipalmiviruses that encode divided RNA-dependent RNA polymerases in two independent genomic segments.

## O44 Directional assembling of disease suppressive rhizobiome using probiotic-targeting phages

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Using pathogen-specific phages or pathogen-inhibitive probiotics have been widely studied to control pathogen infection as successions of antibiotic-based therapy. However, the eco-evolutionary role of phages targeting on probiotics in pathogen invasion is merely studied. By using tomato plant infected by soil-borne phytopathogenic *Ralstonia solanacearum* as a model, we found co-evolving with phage can lead to a trade-up consequence of phage resistance and antibiosis activity of an agricultural probiotic strain *Stenotrophomonas maltophilia* with a multi-omics-based combination of greenhouse and lab experiments. This could be explained by the genome variation in phage receptor gene, inducement of phage defence system, reprogramming of secondary-metabolite. Moreover, this probiotic-targeting phage also recovered microbiome diversity during pathogen invasion and improved the antagonism of resident bacterium against pathogen. Therefore, we suggest these direct and cascading effects of probiotic-phage evolution give it the potential to precisely strengthen microbiome-wide disease suppressiveness against pathogen infection.

## O45 Diversity of micropredators from Arctic and subarctic soils

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Arctic and subarctic soils are rich in diverse microorganisms, including microbial predators, which contribute to ecosystem-wide processes in these climate-critical areas. To understand the natural diversity and ecological roles of microbial predators residing in (sub)Arctic soils, more cultivable isolates are needed. Here, we present Tunturi viruses isolated on *Acidobacteriota* strains from Kilpisjärvi soils [1] and *Bdellovibrio* and like organisms (BALOs) isolated on *Janthinobacterium* sp. and *Mucilaginibacter lappiensis* from Pallas soils, Finland. Tunturi viruses are tailed phages with three types of tails, and their genomes encode various proteins involved in interactions with their hosts, including putative auxiliary metabolic genes. Tunturi 5 is a jumbo phage, whose genome includes 43 tRNA genes as well as genes for proteins involved in tRNA processing. BALO isolates display small rod-shaped free-swimming cells with a single polar flagellum and are able to invade host cell periplasmic space. These BALOs represent new species within the classes *Bdellovibrionia* and *Bacteriovoracia*. Gene functions in the BALO genomes are predicted to be linked to protein synthesis, energy metabolism, and cell cycle. Both groups of the isolated micropredators, i.e., viruses and BALOs, seem to have narrow host ranges and many unknown gene sequences. New isolates can be used as laboratory model systems for future studies, revealing molecular details of predator-prey interactions in soil.

1. Demina T., Marttila H., Pessi I.S., Männistö M.K., Dutilh B.E., Roux S., Hultman J. 2025. Tunturi virus isolates and metagenome-assembled viral genomes provide insights into the virome of Acidobacteriota in Arctic tundra soils. *Microbiome*, in press.

## O46 Using plant-soil interactions to increase stable carbon in soils

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Plants and their soil microbial communities are connected by plant-root exudates that shape the soil microbiome. Monocultures of plants give a clearer plant-soil signal than mixtures of plant species, but the latter is what we deal with in natural systems. Grasses, herbs and legumes and their plant-root traits all have their own exudate types that alter plants and soil communities to cope with prolonged periods of drought and with repelling or attracting plant pathogens or symbionts. Having an insight in how plants shape soil microbiomes and how soil microbiomes shape plant communities are therefore crucial to sustain soil health and food security for the future but also important in the restoration of degraded soils. This talk will cover some possibilities to influence soil quality with plants steering the microbiome and how the microbiome steers the plant community in return. For the future of our planet, it will be important to use plant-soil interactions to keep our soils healthy and resilient to ensure food security for the generations ahead. My current and past work focusses on plant-soil interactions and microbiome steering via plants to increase soil carbon stabilization. I pledge that fungi are superheroes in this respect because they are very active in most soils even when low in biomass. Moreover, fungi have a high carbon use efficiency and if they are hyphal, their necromass tissue can be resilient against quick decomposition, and therefore can potentially contribute to stable carbon inputs.

## O47 Disentangling the plant-microbial origins and stability of long-term soil carbon stores

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Mineral Associated Organic Matter (MAOM) is the key element for the long-term preservation of soil organic matter (SOM) and the stabilisation of soil carbon (C) stocks. MAOM formation is attributed to two soil processes; firstly, the mineral adsorption of organic compounds directly derived from plants, such as organic residues and root exudates, and secondly, the mineral adsorption of microbial products formed after microbial decomposition. Disentangling the plant-microbial-soil interactions contributing to the stability of soil C is important, as uncertainty remains regarding the origins of long-term C stores. We examine the contributions of organic compounds of plant and microbial origin to MAOM formation in different soils, and the stability of MAOM formed with crop and pasture plants by tracking new MAOM-C using <sup>13</sup>C isotopic labelling. To identify contributions of plant-derived and microbe-derived C, five contrasting soils were collected from NSW. Ryegrass (*Lolium perenne* L.) and white clover (*Trifolium repens* L.) were sown, and a third treatment left unplanted. Plants were labelled continuously with <sup>13</sup>C depleted CO<sub>2</sub> in a growth chamber to determine photosynthetically-fixed C. Water-soluble metabolites, as the primary microbial path through which C passes, were also measured, as well as C-flux into necromass, and biomarkers identified to partition the C contributions of each microbial pool. Current results indicate broad trends in  $\delta^{13}\text{C}$  enrichment across soils, and clear differences in water-soluble metabolites and their load across plant types. Results will contribute to our understanding of long-term soil C formation and the improvement of soil C-sequestration programs.

## O48 Plant diversity drives positive microbial associations in the rhizosphere enhancing carbon use efficiency in agricultural soils

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Expanding and intensifying agriculture has led to a loss of soil carbon. As agroecosystems cover over 40% of Earth's land surface, they must be part of the solution put in action to mitigate climate change. Development of efficient management practices to maximize soil carbon retention is currently limited, in part, by a poor understanding of how plants, which input carbon to soil, and microbes, which determine its fate there, interact. Here we implement a diversity gradient by intercropping undersown species with barley in a large field trial, ranging from one to eight undersown species. We find that increasing plant diversity strengthens positive associations within the rhizosphere soil microbial community in relation to negative associations. These associations, in turn, enhance community carbon use efficiency. Jointly, our results highlight how increasing plant diversity in agriculture can be used as a management strategy to enhance carbon retention potential in agricultural soils.

## O49 Development of biodiversity, nutrient cycling and soil organic stocks across a 150-year grassland chronosequence in a north European landscape

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Many semi-natural grasslands traditionally used for grazing or hay production have been replaced by intensive arable land or forest due to afforestation or abandonment, which has led to a loss of biodiversity. Intensified agriculture has further decreased soil organic matter with consequences for multiple soil processes, and there is interest in increasing the proportion of perennial grasslands in the agricultural landscape. Here, we established a chronosequence consisting of 36 grasslands representing 6 age classes (2–150 years) since conversion from arable fields across three farms in a north European landscape. We investigated the time trajectories of development of plant, earthworm, fungal, arbuscular mycorrhizal and bacterial communities, as well as the inorganic nitrogen cycling potential of microbial communities, in relation to soil organic stocks. We found that increasing time since conversion to permanent grassland led to successions for all organism groups, but with different timelines. Soil carbon and nitrogen stocks increased by 50% in the upper 10 cm but were stable in the 10–20 cm layer, over the chronosequence. This corresponded to an average increase of 30 g carbon per square meter per year. The soil C/N ratio increased while the inorganic nitrogen cycling potential decreased with grassland age, suggesting a transition to an organic nutrient economy with less risk of nitrogen losses as grasslands aged. We also observed that bacterial, fungal and arbuscular mycorrhizal communities were more homogeneous across the youngest grasslands, while grasslands of over 50 years contained more divergent communities, of which some were of potential conservational concern.

## O50 Exploring potential success factors for high soil multifunctionality: agricultural management, soil microbiome and soil carbon

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Sustainable food production requires that soils produce sufficient yield with low environmental impact. Organic farming is often assumed to be more sustainable than conventional farming, but both farming systems comprise highly variable management practices. Here, we investigated how soil multifunctionality was related to management intensity in 57 Dutch conventional and organic arable fields. We furthermore explored whether relationships between management and soil functioning could be explained by characteristics of the soil microbiome and of soil carbon. We measured indicators for nutrient cycling, decomposition, soil structure provision, pathogen control and water regulation and integrated them into a single multifunctionality score. We similarly obtained a single management intensity score, using data from farm interviews about crop rotation, tillage, and organic matter inputs. We characterized the soil microbiome with 15 parameters, and soil carbon characteristics with 16 parameters. We show that increasing management intensity is associated with declining soil multifunctionality across all fields, whereas multifunctionality was not related with organic vs. conventional farming. Greater soil multifunctionality was also associated with less frequent tillage and more frequent grass-legume cover cropping. Bacterial biomass and soil organic carbon content, respectively, were the strongest biotic and abiotic predictors of soil multifunctionality. No other biotic parameters were related to soil multifunctionality, whereas the majority of soil carbon parameters was significantly related. Our results suggest that reducing management intensity will enhance soil multifunctionality in both conventional and organic farming, so that in highly intensive and productive agricultural systems, the paradigm of sustainable intensification should be replaced by “productive de-intensification.”

## O51 Functional shifts in plant microbiomes along altitudinal gradients: Insights from DNA metabarcoding and metatranscriptomics

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Soil microbial activity varies along altitudinal gradients, yet little is known about how altitude influences microbial activity within plant compartments. The plant microbiome – comprising microbial communities in the rhizosphere, phyllosphere, and endosphere – plays a crucial role in plant health, stress tolerance, and growth. As environmental stressors intensify, plant fitness will likely depend on co-evolutionary interactions with their microbiomes. Viewing the plant holobiont as an integrated system that provides additional genes and functions may better predict plant responses to climate change than considering plants and microbes separately. Here, we combined DNA metabarcoding and metatranscriptomics to examine bacterial and fungal communities in *Bistorta vivipara* roots and leaves across an altitudinal gradient. We identified both taxonomic composition and gene expression profiles to determine active microbial communities and their functional traits. We asked: (1) Do bacterial and fungal communities respond differently to altitude? (2) Does microbial activity vary more strongly between plant compartments than along altitude? (3) Which genes show differential expression across elevations? We hypothesized that (1) bacterial communities would be more stable than fungal communities due to greater functional redundancy among rare species, (2) microbial activity would be higher in roots than leaves, and (3) stress-related genes would be upregulated at high altitudes, while other functions would be downregulated to conserve energy. Our results will provide insights into how plant-microbiome interactions mediate responses to environmental change.

## O52 Presence of undersown cover crops but not their diversity, and especially soil depth affect microbial SOC stabilization and priming

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The use of diverse cover crops (CC) with deep-rooting traits have been proposed as a useful, agronomic tool to increase C sequestration in deeper soil layers. However, it is largely unknown how the counteracting processes, namely microbial carbon use efficiency (CUE) that stabilizes SOC and priming of old SOC that reduces SOC pools are affected by the use of diverse deep rooting plants. We investigated the effects of CC richness on microbial carbon use efficiency (CUE) and its link with priming effect (PE) at two soil depths (0–10 and 20–30 cm, topsoil/subsoil). We found that vegetation effects on CUE were depth dependent with lower CUE in topsoil compared to subsoil. Regarding CC diversity levels, we found no relation between CUE with increasing CC richness. Similar to CUE, vegetation effects on PEs were depth-dependent: in vegetated plots, priming was larger in subsoil. However, among different CC diversity levels, we found no relation between PEs with increasing CC richness. Our findings highlight strong depth-dependent interactions between CCs and microbial processes that may influence carbon cycling. Our results suggest that presence of CCs rather than optimizing their richness may be the main regulator of microbial processes determining the SOC processes. We observed that both CUE as well as priming are higher in subsoil. As both processes, the other stabilizing and the other reducing SOC pools, are activated in parallel, further studies are needed to determine the fate of SOC pools and the potential for C sequestration in subsoils using CCs.

## O53 Enhanced respiration rates from translocated tropical forest soils explained by lower $^{18}\text{O}$ CUE, increased enzyme activities and substrate availability from decomposition of recalcitrant SOM

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The magnitude of soil C losses due to warming is one of the biggest uncertainties in the global Earth system models. Previous studies have shown that soil C stocks in tropical highlands are highly vulnerable due to the microbial responses to warming often enhancing the C loss. We investigated how  $\text{CO}_2$  production and microbial  $^{18}\text{O}$  CUE changed in response to 3-years of passive warming of moist montane rain forest soils in Taita Hills, Kenya. In March 2020, replicated soil cores from 2200 m a.s.l. (Vuria) and from 1900 m (Ngangao) were translocated downwards to 1600 m (Macha) to simulate warming. Control soil cores were transplanted on site. In March 2023, 5 cores per plot (75 in total) were collected. Soil C contents, organic matter quality, and DNA-based microbial community composition were measured from all 75 samples, while enzyme activities,  $^{18}\text{O}$ -CUE and  $\text{CO}_2$  production during a 6 month's laboratory incubation at two different temperatures were measured from pooled samples ( $n=3$  plots per treatment and elevation). Microbial CUE decreased in the translocated soils at incubation temperature 25 °C, while the decrease was not statistically significant at 15 °C. Enhanced respiration rates (at the same incubation temperature) from the translocated soils could be explained by a combination of lower CUE, increased enzyme activities, and increased C availability from decomposition of recalcitrant substrates as supported by our organic matter fractionation (AWEN) results. We are currently investigating the role of microbial community in these changes in CUE and enhanced recalcitrant SOM decomposition in warmed soils.

## O54 Phosphorus solubilization in *Bacillus* spp.: advancing sustainable agriculture

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Phosphorus (P) solubilization is critical for sustainable fertilizers like sulfur-enriched bone char (BC<sup>plus</sup>), as its P content is not readily bioavailable. This process relies on diverse pathways and is essential for plant nutrition. We investigated the genomic potential, transcriptional responses, and metabolic adaptations to BC<sup>plus</sup> of two plant growth-promoting strains: *Bacillus licheniformis* DSM 13, from nutrient-rich compost soil, and the biofertilizer strain *Bacillus velezensis* DSM 23117. Genomic analysis revealed differences in P turnover genes, including the unique presence of *phoP* in *B. velezensis*. Phenotypic analyses in Belitsky Minimal Medium under three P conditions—full-P (1 mM KH<sub>2</sub>PO<sub>4</sub>), P-limitation (0.3 mM KH<sub>2</sub>PO<sub>4</sub>), and BC<sup>plus</sup>—showed efficient P solubilization by both strains, characterized by initial acidification followed by pH increases (24–48 h), likely due to OH<sup>-</sup> release during apatite dissolution. Transcriptomic analysis showed a rapid response of *B. velezensis* to BC<sup>plus</sup>, with upregulation of genes for organic acid production (*buk*, *pyc*) and P stress response (*phoH*) within 6 h. At 48 h, additional genes for succinic acid production (*gabD*), acid adaptation (*uvrA*, *ftsW*), and sulfur turnover (*sulP*, *yrkH*) were activated, underscoring its adaptability. In contrast, *B. licheniformis* showed limited adaptability, with upregulation of P-associated (*phnF*, *ugpBE*) and sulfur turnover genes (*sufS*, *cysI*) after 48 h, reflecting its nutrient-rich origin. Thiol export gene activation (*cydDC*) suggested proton release, while nitrate reduction genes (*narHJZ*, *nirBD*) indicated DNRA initiation, recently linked to P turnover. Ongoing metabolomics analyses complement these findings. These findings highlight *Bacillus* versatility in P solubilization, supporting tailored biofertilizer applications.

## O55 Regrowth alters rhizosphere nitrogen dynamics: shifts in microbial community composition and functional profiles across different root parts

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Plant shapes rhizosphere microbial communities and nutrient cycling during growth and regrowth after root residues decomposition, yet the spatial dynamics of these interactions in the rhizosphere of different root parts remain poorly understood. In this study, we combined visualization approaches with amplicon and metagenomic sequencing to investigate microbial activity and nitrogen metabolism at the *Zea mays* L. root-soil interface under growth and regrowth conditions. We found significant shifts in microbial community composition and functional profiles between growth and regrowth stages. Notably, amino-N availability declined in the regrowth, while leucine aminopeptidase activity exhibited divergent spatial patterns: decreasing in root tips but increasing in developed roots (seminal and lateral roots). Metagenomic data indicated that root tips had a lower relative abundance of genes related to nitrogen metabolism compared to developed roots, suggesting a gradient of microbial functional specialization across different root parts. Furthermore, regrowth selected for microbial taxa and pathway associated with fungal-derived biomass degradation (CAZymes), reflecting altered nutrient demands during secondary growth. These findings highlight the role of soil microbial community in seminal and lateral roots in the dynamic interplay between nutrient availability and microbial functional adaptation.

## O56 Biodiversity and functioning of arbuscular mycorrhizal fungi in agricultural ecosystems at regional scale

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Study of biodiversity patterns of arbuscular mycorrhizal (AM) fungi identified important driving factors, including edaphic and climatic parameters, host and fungal properties but also landscape properties, land management and disturbances. Here we asked how AM fungal diversity is structured in Estonian arable fields in relation to edaphic properties, land management and landscape structure. We conducted a country-level survey of agricultural land AM fungi. We found large differences in AM fungal richness among agricultural fields, relating to management type, pesticide application frequency, land use around the fields and to a lesser extent tillage. The latter compares to our collaborative, pan-European study that identified pronounced AM fungal richness and community composition differences among countries, but small overall differences related to tillage intensity. Smaller than expected positive effect of reduced tillage on AM fungal communities in the pan-European study made us speculate that availability of natural habitats around field could limit recovery of AM fungi. Estonian study indeed provided evidence of higher AM fungal diversity in fields that are surrounded by more natural land. Further investigation of historic land use around fields in Estonia detected a positive effect of 120-years ago natural habitats on the field soil AM fungi nowadays, demonstrating long-lasting legacy effect of landscape structure. Accumulating knowledge on AM fungal niche properties, developing computational approaches and improving high spatial density data are yielding new level of understanding on AM fungal distribution under changing environment and land management. This guides management of soil biota considerate for both agricultural productivity and ecosystem health.

## O57 Organic phosphorus mineralization in soil: microbial energetics and metabolic costs

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Microbially mediated processes increase phosphorus (P) availability to plants but are metabolically and energetically demanding. Microorganisms require energy to produce phosphatases to hydrolyze organic P into available phosphates. The processes of P acquisition and microbial activation also require cellular energy, which is transferred by P-containing substances like adenosine triphosphate (ATP). We hypothesized that energetic and metabolic costs for production of enzymes hydrolyzing P increase with complexity of organic P. We incubated soil and measured heat flux, enzyme activities, ATP and available P contents. The experiment included four treatments: 1) a control soil with added phosphate that requires no hydrolysis for microbial uptake; 2) sugar phosphate that requires hydrolysis by phosphomonoesterase; 3) DNA that requires hydrolysis by phosphodiesterase and phosphomonoesterase; 4) phytate that requires sequential hydrolysis by enzymes. Heat flux increased by 20% from phosphomonoester bonds in sugar phosphate to diester bonds in DNA but was 85–88% lower for six ester bonds in phytate ( $0.6 \mu\text{J g}^{-1}$  soil) (*i.e.*, exergonic reactions) as compared to the soil without organic P. Microbial uptake of phosphate required heat uptake of  $-1.1 \mu\text{J g}^{-1}$  soil (*i.e.*, endergonic reaction). Phosphomonoesterase activity increased with increasing substrate complexity, but enzymatic hydrolysis of phytate was limited by its low activity, demanding higher metabolic and energetic investments. These findings provide insights into the microbial energetics and metabolic costs of organic P mineralization in soil considering the energy balance of microbially-driven processes.

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## O58 Global impacts of climate, management strategies and land degradation on biodiversity status of agricultural soils

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Unsustainable soil management, climate change, and land degradation are threatening soil biodiversity and the ecosystem functions it supports. While the shift from conventional to organic agriculture is proposed to mitigate these pressures, evidence on its effectiveness across different regions, climates, and levels of land degradation remains limited. In this study, we used molecular methods to assess soil biodiversity in agroecosystems across four continents, examining environmental drivers of community composition and the impacts of transitioning from conventional to organic farming. Our results highlight temperature, precipitation, aridity, pH, and phosphate availability as key drivers of soil biodiversity, influencing the presence of oligotrophic, potential pathogen, and plant growth-promoting microbes in agricultural soils. Although the conversion to organic farming has a global impact on soil biodiversity, its effect is smaller compared to other environmental drivers. Notable interactions between management type and environmental factors, particularly climatic conditions, underscore the context-dependent nature of this transition. Regionally, soils in Belgium, Latvia, Denmark, and Spain were most sensitive to management practices. Organic soils in arid regions, such as Murcia (Spain), showed greater increases in biodiversity in degraded soils when compared to conventionally managed ones. Hence, our findings supports the hypothesis that a shift towards organic agriculture would maximize its beneficial impact for belowground diversity in soils that are highly degraded and exposed to arid conditions, such as the majority of our study areas in Spain, being a crucial tool to increase resilience and adaptation towards climate change and to achieve land degradation neutrality.

## O59 Microbial functions induced by wood fibre amendments in agricultural fields

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When forest soils are cleared for agricultural purposes, they frequently experience a reduction in essential fungal networks, resulting in a lower fungal presence compared to their natural counterparts. There are at least two reasons for this; removal of long-lived trees and other ground vegetation supporting symbiotic mycorrhizal fungal networks, and loss of woody biomass to feed and inhabit saprotrophic decomposer fungi. Boreal forest soils are naturally relatively acidic, which also favors soil fungi over bacteria and emphasize the role of fungi in the natural soils. Fungi are shown to be essential to soil health as presence of fungi and soil carbon turnover are interlinked leading also to soil carbon storage. We hypothesized that by adding forest-based substrates to agricultural soil we can increase particularly soil fungi, and thereby in a long run to promote soil health and even carbon sequestration. DNA-metabarcoding of microbial communities 3 yrs after the treatment in the field showed that when forestry-based side stream substrates were added to agricultural soils, fungal biomass increased and fungal community composition was diversified. An accumulation of mineral-associated carbon was also observed. However, soil DNA can be derived from dead organisms and therefore we performed metatranscriptome-based analyses to gain evidence of the true viability and functionality of the observed changes in microbial communities. After 5 yrs of the treatments, we still found upregulated fungal taxa and an increased levels of transcripts of numerous carbohydrate gene families indicating that there are active fungi in the soil and mobilizing of the carbon inputs.

## O60 Antimicrobial resistance dissemination potential of recycled fertilizers according to field trials

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Use of recycled fertilizers could offer solutions for reducing our dependence on fossil energy and for tightening the nutrient cycles. Recycled fertilizers include products manufactured from manures, wastes, composts, crop residues as well as mixtures of all these. As a part of a project aiming to produce a science-based toolkit for the use of recycled fertilizers in agriculture, we analyzed their antimicrobial resistance (AMR) potential using metagenomes from 528 soil samples. The samples were obtained from field trials in Finland, France and Spain conducted for analyzing agronomic efficiency and risks of recycled fertilizers. Samples were taken before, immediately after and six weeks after the application. The results show generally low AMR dissemination potential. Fertilizers containing poultry manure were an exception, possibly due to antibiotic use in production. Another group that seemed to facilitate more AMR were those whose manufacturing involved composting or fermentation. AMR genes were elevated in soils after application of fertilizers manufactured from manures, composts, or similar, but returned close to those of soil samples taken before the application within six weeks. However, in some cases the AMR genes that were present in the soil before application were enriched. This occurred mainly with those fertilizers that were manufactured from plant-based materials. These genes were not associated with mobile genetic elements. Given the large number of samples and carefully designed experiments, the results could give valuable understanding on the ecology of AMR. In our presentation, we will further elaborate and discuss the current and developing results.

## O61 More generalistic AM fungal communities also produce less biomass in managed soils

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Soils host about 60% of global biodiversity and support critical processes like food production and carbon sequestration. Arbuscular mycorrhizal (AM) fungi, forming symbioses with most terrestrial plants, are key for soil functions such as nutrient cycling and carbon sequestration. This study investigates the relationship between AM fungal diversity, biomass, and management intensity in agricultural soils. We found that intensive management leads to a decline in AM fungal species richness and biomass simultaneously. This decline is accompanied by a shift towards more generalist and ruderal Am fungal communities. Our results also show that AM fungal communities in intensively managed soils become more generalistic due to the decline in specialist taxa rather than an increase in the abundance of generalists. This means that habitat filtering, rather than competitive exclusion, is the main process structuring AM fungal communities in intensively managed soils. The study highlights the importance of preserving AM fungal diversity and biomass a precursor of niche occupancy, suggesting that intensive management practices negatively impact these crucial soil organisms.

## O62 Copper and synthetic pesticides are major drivers of bacterial and fungal communities in vineyard soils

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Soil microbial communities provide important ecological and agriculturally relevant functions that might be threatened by excessive use of pesticides. Vineyard soils are particularly exposed due to strong dependence on fungicides in viticulture. Therefore, we studied 61 conventional and organic vineyards across three regions with distinct climates and soil types. We assessed the long-term effects of copper and synthetic pesticide contamination on soil bacterial and fungal community composition. Microbial communities were characterized through metabarcoding (16S and ITS rRNA) and related to the concentrations of bioavailable copper and 146 synthetic pesticides. Copper caused a pronounced reduction in bacterial alpha diversity, whereas fungal alpha diversity was negatively related to synthetic pesticides, but not vice versa. Beta diversity of both bacteria and fungi was strongly affected by copper, exhibiting an effect size comparable to soil pH. Additionally, fungal beta diversity was associated with synthetic fungicides. A functional assessment based on the FAPROTAX and FungalTraits databases revealed that copper was negatively related to multiple nitrogen cycling and anaerobic respiration processes as well as the abundance of arbuscular mycorrhizal fungi. To our knowledge, this is the first large-scale field study documenting consistent negative effects of copper and synthetic pesticides on soil microbial diversity. The more pronounced impact of copper might be explained by its continuous accumulation over decades, while synthetic pesticide residues are more variable in concentration and composition. Both copper and synthetic pesticides may be detrimental for the functioning of the soil microbiome, which should be considered when trying to restore soil health in agriculture.

## O63 Antibiotic resistance and microbial communities in the environment of an 18th-century slaughterhouse

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Microbes, the first living organisms on Earth, have evolved to adapt to various environments. The microbial diversity in the human gut microbiome is crucial for health, and similarly, microbial diversity in agricultural environments is vital for soil health and interconnected health between humans, animals, and the environment (One Health). Although antibiotics were discovered in the early 1900s, microbes have produced antibiotics long before, and antibiotic resistance is ancient. However, the role of antibiotic-producing bacteria (APB) in resistance development is unclear. While the use of antibiotics causes a strong selective pressure for antibiotic resistance, other anthropogenic activities are also speeding up its spread. Manure and garbage piles in agricultural environments are habitats where both antibiotic producers and pathogens thrive, providing an opportunity to study the role of producers in the emergence of antibiotic resistance. This study explores the evolution of antibiotic resistance through agricultural history by investigating microbial communities, antibiotic resistance genes (ARGs), mobile genetic elements (MGEs), and potential APB from an 18th-century slaughterhouse in Turku, Finland. Twelve samples from archaeological excavations were analyzed using metagenomic sequencing. Additionally, dormant bacteria were cultivated, and their genomes were sequenced. From the metagenomes, 60 ARGs and 417 MGEs were detected. Nine gram-positive bacteria were isolated and identified: *Arthrobacter* sp., *Paeniglutamicibacter quisquiliarum*, *Paeniglutamicibacter sulfureus*, *Streptomyces* sp., *Microbacterium murale*, *Bacillus licheniformis*, *Peribacillus frigorigerans*, *Rhodococcus qingshengii*, and *Streptomyces clavifer*. Here, we present our current results, which will elaborate our understanding of the impact of agriculture on the emergence of antibiotic resistance.

## O64 Global distribution and biogeography of ericoid mycorrhizal fungi

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Ericoid mycorrhizal fungi play a crucial role in various ecosystems, contributing to processes such as soil carbon sequestration and forming mutualistic symbioses with Ericaceae. However, compared to other fungal groups, their biogeography remains largely enigmatic. Here, we integrate Bayesian regression models, hierarchical modeling, and geographic information systems to analyze a newly compiled, large-scale dataset with global coverage of ericoid mycorrhizal fungi. Our results reveal that ericoid mycorrhizal fungal diversity is predominantly concentrated at high latitudes, primarily driven by climate and soil chemistry. Surprisingly, their distribution appears to be more constrained by vegetation than their life history traits would suggest. Additionally, we provide strong evidence supporting a three-belt pattern of mycorrhizal fungal diversity: arbuscular mycorrhizal fungi reach their highest richness in the tropics, ectomycorrhizal fungi in temperate regions, and ericoid mycorrhizal fungi in the tundra. Furthermore, we demonstrate that the diversity and abundance of ericoid mycorrhizal fungi, are likely to decline due to climate change. Taken together, our findings reveal an exceptional biodiversity pattern, whereby most species are concentrated in the tundra regions, for an understudied but ecologically significant organismal group, ericoid mycorrhizal fungi.

## O65 Successive impoverishment of soil guilds alters grassland functioning: from universal to contextual effects

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Amid the biodiversity crisis, research on soil biodiversity and ecosystem functioning has expanded rapidly. Yet, the role of soil context in shaping this relationship remains underexplored. This study examined whether the link between the presence and richness of soil guilds and ecosystem functioning is consistent across grasslands with different soil types and identified functions most affected by biodiversity decline. We conducted a pot experiment simulating five grassland types, successively removing guilds by size to create four biodiversity levels – ranging from the most diverse (microorganisms, micro- and meso-fauna) to the least (impoverished microbial community). We then analyzed functions related to biomass production, nutrient cycling, and microbial interactions. Soil biodiversity did not affect plant aboveground biomass, microbial respiration, or nitrogen-fixing potential. However, nitrification potential and microbial nitrogen increased, while plant nitrogen, soil ureolysis potential, and bacterial parasites decreased with higher biodiversity. Moreover, the soil nutrient status influenced the response of certain functions: microbial carbon and bacterial chemoheterotrophs were promoted by biodiversity in nutrient-richer soils but suppressed in nutrient-poorer soils, along with root biomass. Collectively, the findings suggest that soil biodiversity can promote certain ecosystem functions while suppressing others; some effects are universal across grassland types while others depend on the soil context. We conclude that understanding the net effect of soil biodiversity on ecosystem health requires considering specific impacts on individual functions as well as soil nutrient status.

## O66 The undescribed soil fungal lineages

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Soil is the main habitat for fungi. While most fungi are known based on macro-morphological characters or cultures, a vast diversity of soil mycobiome remains unrecognized. By leveraging full-rRNA gene high-throughput sequencing of global soils, we show that phylogenetic diversity of soil fungi doubles the known diversity at the phylum and class levels. We argue that these lineages and their representative species warrant formal description following the DNA-based taxonomic principles.

## O67 Shrub expansion and associated microbial communities mediate shifts in organic matter characteristics and carbon stocks when colonizing subarctic grasslands

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Ongoing tree and shrub expansion in the Arctic can alter soil processes and organic matter characteristics. Particularly, soil nitrogen (N) and carbon (C) cycling may depend on which microorganisms that thrive under new vegetation types. We investigated grassland patches undergoing colonization by four tree/shrub species (*Betula pubescens*, *Betula nana*, *Salix glauca*, *Empetrum nigrum*) following a century of ceased reindeer grazing and milking activities. We quantified microbial communities involved in inorganic N transformations and profiled fungal communities in both stable grasslands and colonized areas to disentangle how microbial and plant characteristics relate to soil organic matter quality and carbon stocks. A decrease in archaeal ammonia oxidizers and a relative increase in root-associated fungi paralleling higher C:N ratios supported shifts towards organic N-cycling under all colonizing plants, except for *S. glauca*. The stable soil C fraction tended to increase under colonizing plants, except for *E. nigrum*. Root-associated fungi were linked to disparate trajectories of soil C, with root-associated ascomycetes linked to increasing, and root-associated basidiomycetes linked to decreasing C stocks. Decreased decomposition and accumulation of labile and stable C from plants and microbial necromass may drive heath vegetation to accumulate C, while organic matter decomposition by ectomycorrhizal fungi associated with trees and shrubs may lead to smaller soil C stocks. Our research emphasizes the need to predict which microbial communities will establish as vegetation changes in the Arctic to understand potential changes in soil processes and C stocks.

## O68 Does the interaction of fungi and plant roots drive soil carbon stabilization in boreal forests?

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Boreal forests are crucial carbon sinks storing approximately one-third of the world's soil carbon (C) stocks. However, climate change and global warming threaten to convert these soils into increasing sources of C emissions due to accelerated decomposition of soil organic matter. To mitigate these effects, understanding the mechanisms of soil C stabilization in the boreal ecosystems is crucial. Boreal forest vegetation, dominated by species like Scots pine and Norway spruce, hosts diverse fungal communities. These plants also produce secondary metabolites, notably condensed tannins, that can stabilize soil organic matter by forming complexes with fungal necromass. To investigate the impact of tannin-fungal necromass complexes on soil C stabilization, we conducted a field experiment in a Finnish pine forest. We used mesh bags filled with site-collected soil and added either fungal necromass alone, tannins alone, or both together. We used two mesh sizes: one allowing fungal in-growth but preventing plant root intrusion, and another permitting both plant roots and fungi. After burying the samples in the soil for one growing season, we measured concentrations of ergosterol, chitin, tannins, and soil stable C, and did metagenomic sequencing. Our preliminary results show that the presence of plant roots correlates with higher concentrations of fungal biomass, tannins, and stable C, highlighting the critical role of plant roots and tannin-fungal interactions in soil carbon stability. Ongoing analyses of fungal community composition and functional guilds aim to elucidate their role in soil carbon stabilization, providing insights into the complex interactions that maintain C sinks in boreal ecosystems.

## O69 Formation and breakup of the magic circle: 15 years of life of a fairy ring in Abisko

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The fairy ring, a fungal mycelium growing in gradually expanding ring-like structure, is a special fungal growth form appearing in several phylogenetically unrelated mushroom species. Its coherent mycelium enables several possible advantages, coordinated chemical warfare and subdivision of mycelium into generative and vegetative functions, and the impact on the surrounding vegetation is often visible from a long distance. After having followed a fairy ring of *Infundibulicybe gibba* in a subarctic tundra heath near Abisko for over 15 years, we show how it affects plants, soil microbial abundance and nutrient availability over time. A metabarcoding analysis of the fungal community shows *I. gibba* to competitively exclude other fungi in soil. By exuding cyanide and particularly chitinolytic enzymes, *I. gibba* appears to obtain nutrients particularly by killing and degrading other fungi on its path. Comparing this fairy ring with another longer (+40m) coherent fairy ring nearby also shows how these effects and competitive powers weaken over time, as the ring gradually breaks up into smaller fragments of 5–10 m. We discuss the possible advantages of the fairy ring growth form as an ecological strategy.

## O70 Microbial diversity–biomass relationships in soils across Europe

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Ecosystem functioning may rely on the relationships between soil microbial diversity and biomass. However, the impact of land use and climate on these relationships remains uncertain. Here, we (i) analyzed relationships and ratios between richness and biomass of bacteria and fungi in ~500 soils across Europe including three land-use types (woodlands, grasslands, and croplands) and climates (cold, temperate, and arid) and (ii) identified the driving factors of changes in richness:biomass (R:B) ratios. Richness and biomass of soil bacteria and fungi exhibited a unimodal pattern, peaking at intermediate biomass levels. This pattern was more evident in bacteria and clearer exerted by land use than by climate. Bacterial R:B ratios decreased with land use in the following order: croplands < woodlands < grasslands. Fungal R:B ratios decreased as follows: grasslands < croplands < woodlands. Climate was found to interact with the effect of land use. In this way, arid climate tended to increase bacterial R:B ratios in the different land uses; however, the agricultural practices associated to croplands seem to buffer this effect. In fungi, the interactive effect of land use and climate was less straightforward than for bacteria. According to random forests and structural equation modeling, soil organic carbon (SOC) and total nitrogen (N) in bacteria, as well as SOC in fungi, were identified as the primary predictors directly influencing R:B ratios. Therefore, factors related to land-use change and climate with impact on SOC and N contents are potential disruptors of soil microbial R:B ratios.

## O71 Diverse and distinct soil archaeal communities in topsoil of arable, forest, and permanent grassland sites robustly detected by improved domain-specific metabarcoding

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Diversity surveys of soil prokaryotes often rely on universal prokaryote PCR primers, which may underestimate archaea. To determine the capacity of different PCR primers to detect archaea, and to characterize their diversity in topsoil, we first compared metabarcoding results from 18 selected contrasting soils using four established PCR primer pairs including universal prokaryote and domain-specific PCR primers. Second, we applied the PCR primers yielding the most archaeal sequences to samples from 30 sites sampled annually over five years to characterize archaeal core communities. With 29 archaeal amplicon sequencing variants (ASVs), only few archaeal taxa were detected using the universal prokaryote PCR primers. This contrasted with the 801 archaeal ASVs obtained using domain-specific metabarcoding. Likely, this discrepancy is explained by the dominance of bacteria resulting in 0.5% archaeal reads detected using universal prokaryote PCR primers, while domain-specific metabarcoding yielded 99.7% archaeal reads. The five-year survey revealed site- and land-use-specific soil archaeal communities, which were composed of 2034 ASVs. Among these, we identified 957 core taxa, i.e., ASVs detected in at least 12 of the 15 samples from the same site, of which 54% were classified to known families, 41% to candidate families, and 5% remained unclassified. The percentage of unclassified core archaeal ASVs increased strongly at the genus level, reaching 48%. Our results allowed the definition of robustly detected soil archaeal core taxa and highlighted the need for domain-specific approaches to enhance the coverage of archaeal communities and to explore their vast, largely unexplored diversity, particularly at lower taxonomic levels.

## O72 Along the way from till to alpine meadow soils: diversification, specialization and microbial network decoupled

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High altitude alpine ecosystems with complex geomorphology (topography, exposure, slope) encompass microhabitats ranging from bare rock to vegetated soil surfaces in close proximity. These are inhabited by microbiomes of different sizes, diversity and ecological functions. We investigated the difference of microbiomes and their role in nutrient cycling and soil organic matter (OM) formation in till soils in freshly weathered scree areas and in closely adjacent short-stemmed meadow soils. The samples were taken at several sites in four mountain lake catchments (> 1850 m) in the central (granitic, acidic) part of the Tatra Mountains (Slovakia). We found that plant OM input with broader stoichiometric C/N/P ratios caused greater variability in the physico-chemical properties of meadow than till soils. Meadow soils showed a higher microbial, especially fungal abundance, a higher enzymatic activity directed especially towards C-mining and a high efficiency in the utilization of plant-derived metabolites (cellulose, xylose, phenols), as well as a lower species dependency within the microbiome (low network connectivity). The microbiomes of till soils, rich in ammonium-oxidizing archaea, experienced environment rich in mobile mineral nitrogen and phosphorus, and established tightly coupled community networks that ensured the formation of labile soil organic matter with rapid turnover but low nutrient storage capacity. The microbiomes of till soils from different valleys were more similar to each other than to the microbiomes of adjacent grasslands confirming the biogeographical theory of "everything is everywhere and the environment selects" and the key role of plants in formation of microbiomes during soil development.

## O73 Identification of microbial keystones in complex soil ecosystems and determination of their activity, function and niche preferences

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Determining the functional role of individual microorganisms and their relevance in the environment remains very challenging, especially in highly complex environments like soils. One approach is to detect and characterize keystone taxa, which are critical to the stability and functioning of the entire communities. We used co-occurrence networks from high-throughput sequencing data to elucidate significant associations and infer sequence types of particular importance to the overall microbial communities. This approach was applied to bacterial and fungal communities in 300 soils of the German Biodiversity Exploratories, which encompass grassland and forest ecosystems under different land use, sampled over a period of 11 years. 16S rRNA and the ITS2 were used as markers for bacteria and fungi, respectively. Keystones were identified by a ranking procedure based on the susceptible-infected-recovered model after perturbation of the original networks. Keystone taxa were specific to distinct soil environments and remained rather stable over time. We hypothesized that keystone taxa must be more active than co-occurring microorganisms as to exert their ecological influence. Accordingly, active bacterial taxa were identified using 16S rRNA/ 16S rDNA ratios and by determining bacterial growth rate from the peak-to-trough ratio of genomic sequence coverage. We found a significant overlap between keystone and active species, corroborating the network analysis approach. Niche preferences of keystone taxa were determined by modelling abundances against environmental parameters and metagenome assembled genomes (MAGs) representing bacterial keystones provided deeper insights into their functional potential. Our results help elucidate the ecological roles of individual microbial taxa in highly complex environments.

## O74 Labeling of active arsenate- and antimonate-reducing microbes in peat soil used for treatment of mining-affected waters

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Microbially catalyzed processes aid the removal of contaminants like arsenic or antimony in peatlands used to treat mining-affected waters in northern Finland. While arsenate and antimonate reduction have been identified as important processes in previous studies, the microbial players responsible for arsenate and antimonate reduction in these peatlands have yet to be identified. Bioorthogonal noncanonical amino-acid tagging (BONCAT) was used to label active arsenate- and antimonate-reducing microbes in flow-through pilot peatlands (50x15x15 cm) incubated under *in situ* relevant temperatures and water residence times. Pilot received inflow water with low concentrations of arsenate, antimonate, both or neither (as control) and were monitored for a total of three months. Arsenate and antimonate were efficiently removed in the pilots with most retention occurring close to the inflow. The methionine analogue homopropargylglycine (HPG) was added to the inflow water near the end of the experiment to label metabolically active cells, as these incorporate HPG into their proteins. At the same time, inflow water was also spiked with small concentrations of deuterium-labeled water as a tracer to follow the water flow through the pilots. After ensuring that HPG supplemented water had reached all parts, pilots were deconstructed, peat samples taken from different points and depths, and cells extracted for subsequent cell sorting. A fluorescent dye was attached to the incorporated HPG via azide-alkyne click chemistry, and labelled cells were separated from unlabeled cells using fluorescence-activated cell sorting (FACS). DNA was extracted from sorted and unsorted cells for amplicon-sequencing, the results of which are expected shortly.

## O75 Recycled nutrients, resilient microbes: unveiling soil microbial responses to alternative fertilization

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Nitrogen (N) is a fundamental macronutrient in terrestrial ecosystems, playing a crucial role in soil fertility and plant productivity. However, conventional mineral fertilizers can have detrimental environmental impacts, necessitating the exploration of sustainable alternatives. This study evaluates the ecological effects of substituting synthetic fertilizers with recycled byproducts – struvite, sludge, and their combination – on soil N cycling, microbial communities, and maize phenology in an agroecosystem context. Using a multi-omic approach integrating metagenomics, metaproteomics, and metagenome-assembled genomes (MAGs), we examined the taxonomic and functional composition of microbial communities involved in key N transformations, including nitrification, denitrification, dissimilatory and assimilatory nitrate reduction to ammonium (DNRA and ANRA), N<sub>2</sub> fixation, and N transport. Our results highlight that maize phenology exerts a dominant influence on the relative abundance of N-cycling genes, particularly those related to denitrification, nitrification, and N<sub>2</sub> fixation, surpassing the effects of fertilization treatments. Functional gene distribution was taxonomically structured, with *Nitrososphaeraceae* associated with nitrification and *Propionibacteriaceae* linked to denitrification. Fertilizer type significantly influenced microbial N-cycling processes, with struvite enhancing nitrification-related genes and sludge promoting denitrification pathways. Notably, metaproteomic analysis revealed increased glutamine synthetase abundance in the struvite+sludge treatment during germination, suggesting enhanced microbial N assimilation under these conditions. Our findings underscore the ecological significance of phenology-driven N cycling and demonstrate the potential of recycled fertilizers to modulate microbial communities in a way that supports sustainable nutrient management in agroecosystems.

## O76 Deciphering the role of microbes and soil properties for natural disease suppressiveness

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Crop plants are exposed to a wide range of soil-borne phytopathogens, particularly fungi, which are often difficult to control. However, in disease-suppressive soils, microbial interactions can significantly protect plants from specific soil-borne pathogens, thereby reducing disease incidence and plant damage. With natural disease suppressiveness, both disease suppressive and conducive soils typically coexist within the same landscape, resulting in marked differences in plant health between these soils despite similar climatic and agronomic conditions. These variations are primarily attributed to particularities of the soil microbiota, yet the underlying physicochemical soil properties that shape microbial communities remain poorly understood. As part of the BiodivERsA project SuppressSOIL, we aimed to develop an integrated understanding of the relationship between soil biodiversity and crop protection in disease-suppressive soils. By studying suppressive and conducive soils across several countries within the context of global change; marked by shifts in crops, cropping systems and climate; we conducted multi-omic analyses to investigate disease suppressiveness. Our findings revealed that suppressiveness (i) is strongly influenced by geography, involving distinct microbial communities, (ii) may confer protection against another pathogen infecting other crop, and (iii) has the potential to modify the plant physiology and metabolome. This project demonstrated that disease suppressiveness is linked to specific patterns of microbial biodiversity in the rhizosphere and plant metabolism. These insights will help define management strategies to improve crop health in the face of global change.

## O77 Enrichment and genomic analyses of methanogens from desert soil crusts

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Methanogens are the only organisms known to produce energy through methanogenesis, which occurs through one of three known pathways: hydrogenotrophic, acetoclastic, or methylotrophic. Nearly all our knowledge of methanogens is based on cultures isolated from anoxic systems or the study of anoxic environments. However, methanogens have been found to be present and active in desert soil crusts, an extreme and aerobic habitat. By which means they can survive and be metabolically active in these crusts remains unknown. We have enriched 6 new species in 7 strains of methanogens from a desert biological soil crust of the Negev Desert, Israel. The newly cultured organisms are affiliated with the *Methanobacterium*, *Methanosarcina*, and *Methanocella* genera. Species delineation was performed based on their genome sequences obtained using Illumina or PacBio. Phylogenetic analyses, conducted using GTDB-Tk, and insights from comparative genomics with close relatives from strictly anoxic habitats, will be shown. Special attention was given to the identification and characterization of genes involved in desiccation tolerance and oxidative stress response.

## O78 Limitations and perspectives of monitoring the diversity of cropland microbiomes as soil health indicators

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Cropland soil microbiomes maintain plant production by fueling biogeochemical transformations, supporting plant growth, and stabilizing soil structure. There is a general consensus that these beneficial activities should be preserved and utilized to improve soil health. In order to assess whether a specific management practice is good or bad for a soil microbiome and its particular activities, and making predictions for new technologies upfront, it is important to gain a more systematic understanding of how the different organisms constituting the soil microbiome depend on each other, are linked to soil functions, and, how they respond to management-induced environmental changes. Upscaling information from individual field studies is usually strongly limited due to uncertainty of temporal and spatial variation. Monitoring must be able to differentiate the impact of short-term individual events, i.e., precipitation or change of crops, from long-term effects, i.e., the accumulation of pollutants or climate change. With samples taken at 2-week intervals over a period of two years, on three neighboring fields that differed in terms of soil texture and tillage, we could demonstrate that bacteria, archaea, fungi and protists show distinct temporal dynamics and indicator potentials. Network analyses underlined the importance of fungi and protists for controlling the overall community composition. To monitor soil microbiomes at national scale we selected ca. 200 sampling points focusing to train datasets with microbiomes from assumingly “healthy” and “degraded” soils. Linking microbiome data to the physicochemical properties of the respective soils should show how useful soil microbiome analyses are for future soil monitoring.

## O79 Shaping soil microbial communities and functionality by tillage intensity and crop diversification in Austrian agroecosystems

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Effective agricultural management enhances soil microbial communities, driving sustainability and soil health. This study investigates the soil microbial abundance, diversity and functionality under diverse cropping systems and varying tillage intensities in two long-term field trials in Lower Austria. We hypothesize that decreased tillage intensity and increased crop diversification will foster more diverse and active soil microbial communities, with subsequent improvements in soil health. Our long-term monitoring sites were subjected to varying tillage practices (plough, cultivator, disc-harrow, direct-seeding) and different cover crop diversification schemes. Soil samples were collected at multiple intervals to assess key soil health indicators, including soil organic carbon (SOC), total nitrogen, dissolved organic carbon, total dissolved nitrogen, microbial biomass carbon, fungal biomass and potential enzyme activities (leucine aminopeptidase (LAP), N-acetyl- $\beta$ -glucosaminidase (NAG),  $\beta$ -glucosidase (GLU), phosphatase (PHO)). Bacterial and fungal community composition was analyzed using amplicon sequencing. Preliminary results indicate beneficial effects with decreasing tillage intensity, particularly crop diversification, on SOC, microbial biomass and enzyme activities (LAP, NAG, GLU). Improved aggregate stability in diversified plots, indicate more suitable soil structural conditions for microbial growth and functionality. While tillage intensities strongly influence the overall microbial community structure, the fungal community diversified in response to soil ecosystem disturbances. Further analyses will explore the link between microbial community composition, bacterial and fungal growth and carbon-use-efficiency across soil depths, and the long-term implications of these management practices for soil health and resilience. This research provides insights into possible agricultural production systems to promote the functionality shape soil microbial communities for sustainable and resilient agroecosystems.

## O80 Engineering the rhizosphere for mitigating biotic stress in arable land

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Organic farming involves application of bio-amendments for promoting plant growth and exerts positive impact on microbial diversity, thereby enhancing soil health. The soil from organic fields exhibits disease-suppressiveness, which is the ability of soil to minimize the negative impacts of soil-borne phytopathogens offered by key biocontrol microorganisms in rhizosphere soil. However, soil microbiome's mechanism in conferring disease suppressiveness to broad range of phytopathogens remains to be deciphered. This study compared the microbial diversity of organic and conventional field soils, maintained over 1.5 decades, and examined if the potential of disease-suppressiveness can be transferred to transform a conducive soil into suppressive soil. After validating the disease-suppressive potential, enumeration of bacterial biocontrol strains was performed to generate a culture bank. Active metabolites contributing to observed biocontrol activity were identified. Disease suppressiveness of both soil types was assessed by *in planta* assays. When wheat plants were exposed to *Rhizoctonia solani* and *Fusarium oxysporum* a higher disease-suppressive potential of rhizosphere microbiome from organic soil was observed against these phytopathogens. Further, soil transplantation experiments conducted in polyvinyl chloride pipes assessed the impact of mixing conducive and suppressive soil on the growth of wheat plants infested with these phytopathogens. Changes in the abundance of structural and functional microbial markers for disease suppressiveness were observed in the transformed soil during wheat growing season. The study highlights that soil microbiome application can be an environment-friendly approach for strategizing disease management in agroecosystems.

## O81 Disentangling land-use effects on soil fungal communities across continents

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Soil fungal communities have a significant effect on agroecosystem functioning and are themselves critically altered by land use. However, large-scale assessments of land-use impacts on their diversity remain limited. We use GlobalFungi, the most comprehensive dataset to date, to analyse fungal richness and community composition across European grasslands and croplands, disentangling land-use type and intensity from climatic and edaphic factors. We identified a hump-shaped relationship between land-use intensity and overall fungal richness, with higher diversity at intermediate management levels. Using hierarchical modeling of species communities (HMSC), we find significant effects of land use on fungal community composition. Fungal functional groups exhibited divergent responses: pathogen richness significantly increased in croplands, while mutualistic arbuscular mycorrhizal fungi declined with intensification. These trends were consistent across Europe's spatially balanced sampling network, which includes gradients of management practices. To assess global relevance, we compared European patterns with preliminary data from China and Australia, revealing similar effects of agricultural land use on fungal richness. Our findings highlight the vulnerability of key functional guilds to land-use changes and underscore the need for management strategies that balance productivity with soil biodiversity conservation.

## O82 Temporal developments of bacterial and fungal communities assessed over ten years of annual soil biomonitoring

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Due to their importance for soil quality, microorganisms are receiving increasing attention in soil monitoring programs, which may get further support by the proposed European Soil Monitoring Law. However, data on long-term spatio-temporal variability of soil microbial communities, which is needed to determine accurate sampling intervals, is still lacking. Since 2012, soil bacterial and fungal communities were assessed every spring using metabarcoding at 9 arable and 10 grassland sites of the Swiss Soil Monitoring Network. During this period, land-use changed from grassland to arable land at three sites providing the opportunity to investigate its long-term effects. The dataset allowed assessing long-term developments of soil bacterial and fungal communities and estimating environmental drivers of temporal and spatial community variability. Over ten years, differences between communities of different sites and land-use types remained stronger than temporal changes. While the temporal variability was significantly higher at arable sites for fungal but not for bacterial communities, temporal community shifts were detectable in both land-use types and for bacteria and fungi. Environmental factors correlating to these temporal community shifts included soil pH, organic carbon content for bacteria, and mean annual temperature for both bacteria and fungi indicating potential long-term effects of climate change on soil microbial communities. These results reveal slightly different long-term temporal developments of soil bacterial and fungal communities and provide valuable data for the design of new soil biomonitoring programs suggesting that sampling intervals may be enlarged from one to several years in favor of additional sampling sites covering more soil habitats.

## O83 Microbial and biogeochemical responses to root exclusion across diverse European forests

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Tree roots play a critical role in shaping soil microbial communities and biogeochemical processes through rhizodeposition, symbiotic associations, and nutrient cycling. However, how root exclusion (whether due to natural or management-induced disturbances) affects microbial communities and soil functioning across forests with different climate and management histories remains poorly understood. In this study, we examined the effects of root exclusion via trenching across 12 forests in Europe, representing diverse climatic regions and management intensities. We analyzed microbial community composition (fungi and bacteria), microbial biomass, enzyme activity, soil chemistry (C, N, P availability, pH), and CO<sub>2</sub> flux measurements to assess changes in microbial community composition and processes one year after root exclusion. Our results indicate a consistent decline in microbial biomass and enzymatic activity in trenched plots, suggesting reduced labile carbon inputs from roots. Bacterial communities exhibited shifts toward oligotrophic taxa, while ectomycorrhizal fungi declined in relative abundance, replaced by saprotrophic fungi that likely opportunistically utilized remaining organic substrates. CO<sub>2</sub> fluxes were significantly reduced in trenched plots. However, the magnitude of microbial and biogeochemical shifts varied across sites, likely influenced by forest type, soil properties, and management history. These findings highlight the critical role of root-associated microbiome in nutrient cycling in forest soils and provide insights into the potential consequences of altered root-soil interactions under changing environmental conditions.

## O84 Legume-cereal intercropping for sustainable agriculture across Europe

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The LEGUMINOSE project seeks to transform European farming by championing and implementing legume-cereal intercropping systems as a sustainable agricultural method. This initiative addresses various goals, from developing crop combinations to exploring economic prospects and tackling adoption challenges, with the aim of boosting ecosystem services, enhancing soil quality, and increasing crop durability. The project employs a collaborative approach, engaging stakeholders throughout the supply chain and fostering international partnerships to promote knowledge sharing and skill development. Through the use of on-farm living labs, cutting-edge technologies, and policy suggestions, the project has the potential to reshape farming practices, supporting the EU's sustainability objectives and promoting a more resilient and eco-friendly food production system. The project's success could lead to widespread adoption of intercropping, resulting in substantial environmental, economic, and social advantages across Europe and beyond. A key objective of the project is to evaluate the multifaceted benefits of intercropping in improving ecosystem services, showcasing its effects on soil organisms, particularly soil microorganisms and their functions. To accomplish this, 7 research field trials have been established across Europe. During the soil mingling session, some results and data on soil microbiome and their functions, collected in the first two years of the project from these research trials, will be presented. These preliminary findings will provide the groundwork for the ensuing discussion among participants during the session.

## O85 Impact of agricultural microplastics on soil and microbial functions across Europe

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Agricultural plastics (APs) such as mulching films aid in maintaining soil moisture and reducing pesticide use but may lead to microplastic (MP) soil contamination through degradation. This study examined the impact of conventional (PE) and biodegradable (PBAT-BD) agricultural MPs on soil properties, aggregation, microbial diversity and functions, litter decomposition, and greenhouse gas (GHG) emissions in three European countries with distinct pedoclimatic conditions (Finland, Germany, and Spain) over two growing seasons (2022 and 2023). MPs were introduced at concentrations of 0.005% and 0.05% (w/w dry soil). MP-contamination affected soil properties, aggregation, microbial diversity, and functions, and GHG emissions. However, the effects were inconsistent across different locations and treatments. Microbial activity was consistently reduced by both PE and PBAT-BD MPs, especially at higher concentrations and following the second harvest season. Notably, nitrogen cycling, and microbial functions were affected by MPs in Germany and Spain, particularly at higher MP concentrations (0.05% w/w). Despite natural soil variability, these findings highlight the potential ongoing effects of MPs on soil health, which were more pronounced in southern Europe due to varying pedoclimatic conditions. The study underscores the need for regionally tailored risk assessments to protect soil from plastic pollution. Our results emphasize that even low MP concentrations can affect soil nitrogen cycling and microbial functions, necessitating further investigation into the long-term implications of agricultural MP contamination under natural field conditions.

## O86 Response of soil organisms to climate-smart sustainable soil management techniques – highlights from EJP SOIL

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The EJP SOIL program, running over five years, has made substantial contributions to addressing the challenges of sustainable and climate-smart soil management across Europe. Through a combination of surveys, reviews, and experimental studies, the program provided critical insights into its six Expected Impacts (EIs), including fostering sustainable soil management, enhancing carbon sequestration, and supporting climate change adaptation and mitigation. Eight projects specifically investigated the role of soil organisms—EnergyLink, MaxRoot-C, MixRoot-C, AgroEcoSeqC, MINOTAUR, TRACE-Soils, SOMMIT, and INSURE—delivering new knowledge on how soil biota interact with climate-smart management practices. Key findings demonstrate (1) how microbial energy turnover influences carbon sequestration processes, (2) the contribution of roots to soil organic carbon inputs and their interactions with microbial communities, and (3) the potential of mixed plant species compositions to enhance microbial biodiversity and its role in stabilizing soil organic matter. Additionally, these projects examined whether carbon sequestration measures consistently improve the greenhouse gas (GHG) balance or whether trade-offs with non-CO<sub>2</sub> emissions, such as N<sub>2</sub>O, may occur. Critical questions also emerged regarding the need to improve models to incorporate microbial dynamics and identify reliable indicators for monitoring soil organisms. This presentation highlights key findings on how soil management affects soil biota. As EJP SOIL results continue to emerge, these insights will guide future research and support sustainable soil management to address climate change and food security. Knowledge on soil organisms will play a pivotal role in this effort.

## O87 SOILGUARD: Sustainable soil management to unleash soil biodiversity potential and increase environmental, economic and social wellbeing

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We studied the capacity of sustainable soil management to mitigate the impacts of climate change on soil biodiversity and functioning across six European sites (five arable lands, one grassland) during 2022 and 2023. To simulate drought and heatwaves realistically, climate projections were calculated using 11 EURO-CORDEX regional climate models. The resulting indexes were applied in field simulations using shelters, and infrared heaters. Two adjacent managed fields, one conventionally (high-input agriculture, monoculture grassland) and another alternatively (organic agriculture, mixed-species grassland), were used at each site. DNA-based measurements of soil biodiversity (prokaryotes, eukaryotes) and multifunctionality metrics (physical and biochemical properties) were determined, and their interactions analyzed. Each site harbored a unique soil biodiversity, with site explaining 11–79% of the variance in biodiversity, while management effects were site-dependent (~2% general, ~10% at each site). Simulated climate effects were masked by site and management but were consistently detectable, with stronger effects on eukaryotes than prokaryotes. Ongoing taxon-level analyses reveal management-specific genera across all sites. Region-specific responses of soil functions showed conventional management had lower resilience to climate change in Belgium, Denmark, and Ireland, while Spain showed the opposite pattern. No evidence was found that soil multidiversity enhances the resilience of multifunctionality to climatic simulations. Synergies were observed between nutrient cycling indicators, C stock, mycorrhizal abundance, and N transformation rates, with little evidence of functional trade-offs. Management or climatic treatments did not exacerbate these trade-offs. We provide a basis for recommendations on soil management regimes to buffer climate change effects on soil biodiversity and multifunctionality.

## O88 Impacts of arable management practices on soil biological diversity – Outcomes from boreal case studies of SoildiverAgro

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The SoildiverAgro project studied the impact of farming practices on soil biodiversity, yield, and profitability across six European regions through 17 field case studies. In Finland, four case studies were conducted and monitored for three years. Two experiments focused on the effects of ploughing in wheat fields under long-term organic farming and reduced tillage. Spring ploughing in spring wheat and autumn ploughing in winter wheat were examined. The other two experiments assessed organic soil amendments from forest industry side-streams and catch crops in early potato fields, which are prone to soil structure deterioration and erosion. Ploughing had minor effects on soil biodiversity, with autumn ploughing having slightly more impact than spring ploughing. Although ploughing did not change soil microbial or fungal communities, it reduced genes involved in carbon and nitrogen cycles and decreased nematode total abundance. Autumn ploughing led to a decline in earthworm biomass, indicating decline of large, deep burrowing earthworms. Thus, occasional ploughing, especially in spring, could be used for e.g. weed control or phosphorus management without causing harm to soil communities in well-functioning organically farmed field managed with reduced tillage. Organic soil amendments from forest industry side-streams had no effect on soil biodiversity in early potato fields. Catch crops did not influence soil microbes, fungi, or earthworms but reduced nematode abundance and increased their overall biodiversity, suggesting potential benefits for pest and disease management. Low earthworm abundance and richness in potato fields were likely due to coarse soil texture, annual ploughing, and pesticide use. Longer research periods may yield more reliable results.

## O89 Soil health benefits from food industry side streams – the EU Mission Soil DeliSoil project

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Scientific and political interest in the concept of the circular bioeconomy is attracting growing attention to biomass use as a basis for renewable resources. The EU Horizon-funded DeliSoil project is contributing to the EU's Mission "A Soil Deal for Europe" by delivering new technical solutions to produce fertiliser products from food industry side streams with reduced environmental risks. With the ultimate goal of enhancing soil health, project aims to improve the sustainability of food systems by producing soil improvers from circular food production processes. Organic matter and nutrients in food industry side streams can be reused but instead often are deposited into the nearby environment, landfills, or waterways where they can cause greenhouse gas emissions and eutrophication. Food processing and production residues have high valorisation potential, due to their large, concentrated, and homogeneous side streams. Soils are healthy when they are in good chemical, biological, and physical condition, and thus able to continuously provide their important ecosystem services. The effects of different innovative soil improvers on selected soil health and plant parameters were evaluated in pot and field experiments (some still ongoing). A selection of products was also tested in combination with microbial-based inoculants to explore ways of improving their performance. Preliminary yield analysis revealed that the different soil amendments tested had varied impacts on crop yield, providing a first comprehensive evaluation of how each soil amendment affected both soil health and plant growth indicators. A detailed soil microbiome analysis allows us to identify new biomarkers of soil health.

## O90 Introducing Precilience: a horizon project developing tailored solutions for agricultural practices in boreal regions

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Precilience ([www.precilience.eu](http://www.precilience.eu)) is a Horizon Europe project conducted in Finland, Sweden, Norway, Denmark, and Estonia to develop precision solutions in collaboration with farmers, foresters, landowners, and other stakeholders to enhance climate resilience. One of the project's work packages focuses on evaluating various soil management practices across different soil types to identify the most effective solutions for each region. As part of this effort, the project assesses the effects of different tillage treatments. In Estonia, three locations have been selected, while in Norway, two locations are included in the study. The experiment compares no tillage, minimal tillage, and intensive tillage as well as spring tillage over autumn tillage to evaluate their impact on soil health, pathogen communities, crop yield and water quality. While tillage can improve soil drainage and aeration, it can also contribute to soil erosion, nutrient loss, and reduced biodiversity. In terms of pathogen presence, no-tillage can increase pathogen survival, as crop stubble often leads to higher disease severity. However, these effects are highly dependent on soil conditions, demanding research tailored to different climatic and field conditions. The findings of this project will contribute to region-specific tillage recommendations, improving agricultural practices in a changing climate. Furthermore, by working closely with stakeholders, the project ensures active participation and knowledge exchange, helping agricultural communities prepare for future challenges.

## O91 Project SOLO – developing a holistic and transdisciplinary soil research agenda for Europe

Guusje Koorneef, Justine LeJoly, Wim van der Putten

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Healthy soils provide the basis for human life and the functioning of ecosystems. The aim of the EU's Soil Strategy is therefore to increase the status of healthy soils from 30 to 70% in Europe by 2050. To achieve this aim, it is essential that relevant knowledge and tools are in place at the right location, requiring the mutual exchange and creation of knowledge between science and society. The aim of research project SOLO, funded by the Soil Mission, is therefore to provide actionable roadmaps for future soil research and innovation in Europe. The transdisciplinary approach of SOLO ensures the involvement of a wide range of stakeholders via the establishment of think tanks, one for each Soil Mission objective and an additional one focusing on the conservation of soil biodiversity. These think tanks identify knowledge gaps, bottlenecks and other critical actions required for the success of the Soil Mission. Potential differences in the regional implementation of the Soil Mission are assessed by four co-creation Regional Nodes, generating their own roadmaps for their specific region and focus land use. An overarching transdisciplinary roadmap integrates the thematic and regional roadmaps and assesses potential synergies and trade-offs in increasing the sustainability of soil management. In this presentation, the unique methodology of SOLO will be demonstrated as well as the roadmaps that have been, or will be, in open review and accessible for all European Soil researchers, in 2025.

## O92 Terrestrial microbial oxidation of atmospheric trace gases

Chris Greening

Monash University, Melbourne, Australia

The atmosphere provides most of the oxygen, carbon, and nitrogen that we depend on, but until now has been thought to lack sufficient energy to sustain life. Here I will demonstrate that diverse terrestrial microbes live by harvesting the small amounts of hydrogen, carbon monoxide, and methane from air. Through research focused on the model soil bacterium *Mycobacterium smegmatis*, I will explain the physiological role, genetic regulation, and structural basis of this process. Culture-based and culture-independent evidence will be presented that microorganisms from multiple phyla and diverse environments also meet their energy needs through this process. Finally, I will reveal that certain oligotrophic soil ecosystems are primarily powered by atmospheric energy sources, including hyper-arid deserts and aerated caves. These findings redefine the minimal requirements for life and have broad climate, medical, and astrobiological implications.

## O93 Unravelling the role of hydrogen cycling microorganisms in agricultural soils

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Soil microorganisms have been recognised as key players in nutrient cycles, with recent studies highlighting their effects on the cycling of the atmospheric trace gas hydrogen (H<sub>2</sub>). Within agroecosystems, a primary source of H<sub>2</sub> is as a by-product of nitrogen fixation, with legumes often associated with a temporary supersaturation of H<sub>2</sub> around legume nodules. The temporary nature suggests that the H<sub>2</sub> produced is rapidly recycled by closely associated microorganisms or internally if they harbour high-affinity uptake hydrogenases. Using a multidisciplinary approach, we combined traditional gas chromatography, metagenomics and metatranscriptomics to characterise the effect of exogenous fertiliser addition on the resilience of agroecosystem H<sub>2</sub> cycling. Five agricultural soils with diverse physicochemical properties were assessed for their ability to oxidise two concentrations of H<sub>2</sub> within microcosms. All soils were able to rapidly oxidise the excess concentration of H<sub>2</sub> (10,000ppmv) to close to atmospheric levels, albeit at different rates, suggesting that soil physicochemical properties play a key role in H<sub>2</sub> uptake rate. In a soil microcosm amended with excess H<sub>2</sub>, fertiliser or a combination, the soil's uptake was robust, with only a slight increase in uptake lag time observed for the combined condition. Metagenomic and metatranscriptomic profiling highlighted that the predominant hydrogenase is the persistence-linked group 1h [NiFe] and that expression increased in the presence of both excess H<sub>2</sub> and the combined fertiliser+H<sub>2</sub> condition. Understanding the role H<sub>2</sub> cycling plays in agricultural soils and how they are affected is paramount for the future development of novel and sustainable practices to futureproof Australian agriculture.

## O94 Wintertime microbial community activity in oroarctic tundra soils

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Microbial communities play a central role in regulating greenhouse gas balance in soil ecosystems. In the Arctic tundra, where winter lasts up to ten months, microbial activity persists in cold, snow-covered soils. However, their wintertime functions remain poorly understood. Metatranscriptomic samples were collected with gas flux measurements to investigate the functional activity of bacterial and archaeal communities in oroarctic tundra soils in late winter across key vegetation types. Transcription of central carbohydrate metabolism and various stress-related genes, together with high CO<sub>2</sub> fluxes, indicated active microbial metabolism in winter. Vegetation and pH were strong drivers of the functional activity and microbial community composition during winter, similar to that in summer, indicating that vegetation type and pH determine the bacterial community composition in oroarctic tundra soils throughout the year. Furthermore, the results indicate that shrublands and meadows act as methane sinks during winter, while all vegetation types are small sources of N<sub>2</sub>O. This suggests that microbial communities are involved in the CH<sub>4</sub> and N<sub>2</sub>O cycles even in winter.

## O95 Like fish out of water? Cultivation and genomic characterisation of the first methanogens isolated from upland soils

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Methane is a potent greenhouse gas produced almost exclusively by anaerobic methanogenic archaea. Accordingly, methanogens were thought to occur only in anoxic environments such as water-logged soils, aquatic sediments, and animal guts. However, recent works challenged this notion by showing the presence and activity of certain methanogens in oxic environments. An extreme example is the detection of active methanogens in arid biological soil crusts (biocrusts), which are not only oxic but also experience prolonged desiccation periods. Methanogens are non-spore-forming, and their genetic and physiological mechanisms for dealing with oxygen and desiccation are mainly unknown. Here, we separately enriched methanogens belonging to the *Methanosarcina*, *Methanocella*, and *Methanobacterium* genera from biocrusts originating from desert soil in Israel, representing the first methanogen isolates from oxic soils. *Methanosarcina* and *Methanocella* belong to the so-called Class II methanogens that are genetically equipped to cope with oxidative stress. However, *Methanobacterium*, which was most abundant in these soils, is a Class I methanogen and is expected to be particularly sensitive to oxygen. Through controlled experiments coupled with comparative (meta)genomics, transcriptomics, microscopy, and physiological assays, we studied the effects of oxygen and desiccation stress on our isolates and compared them to their closest relatives from public culture collections. Our data provide first insights into their unique adaptation mechanisms and add previously unknown physiological breadth to the group of archaeal methanogens.

## O96 Legacy effects of fluctuating oxygen availability on the methane-driven interaction network

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Aerobic methanotrophs primarily thrive at oxic-anoxic interfaces where the availability of their main substrates, oxygen and methane overlaps. This ecological niche is exposed to regular oxygen fluctuations, affecting the methanotrophic community, as well as the associated methane-driven interaction network. Thus, stable isotope probing with <sup>13</sup>C-CH<sub>4</sub>, coupled to a co-occurrence network analysis, was performed with river sediment following preincubation under different oxygen conditions to determine their legacy on the methane-driven interaction network. The oxygen fluctuation differentially shaped the methane-driven bacterial communities. Low oxygen availability (continuous microoxic reference and low oxygen fluctuation) led to a more complex and connected interaction network, compared to high oxygen fluctuations or continuously high oxygen availability. This was particularly evident in the microoxic reference where higher methane uptake rates were detected in the short-term, demonstrating the ability of aerobic methanotrophs to respond quickly when conditions turned favourable, thereby promoting cross-feeding with non-methanotrophs. Overall, our findings highlight the resilience of aerobic methanotrophs to transient hypoxia and frequent oxygen fluctuation, and how their legacy shapes the associated methane-driven interaction network.

## O97 Microbial adaptations in northern soils with naturally high baseline concentrations of arsenic and metals

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Microbes have evolved to tolerate and even utilize harmful high concentrations of elements in their environment, and metabolic mechanisms related to the tolerance of high metal concentrations are known. Microbes play a vital role in plant survival under extreme conditions, where they can promote plant growth by mitigating metal-induced toxicity, provide essential nutrients, fix nitrogen, and produce growth-promoting substances. The aim of our study is to identify microbial groups adapted to high metal concentrations in northern environments, understand the factors influencing the development of microbial communities and assess the properties of microbes adapted to naturally high concentrations of harmful substances. A total of 91 soil samples were collected from 9 different sites in Finland. DNA was extracted using PowerSoilPro Kit (Qiagen), and bacterial (16S rRNA) and fungal (ITS1) amplicons were sequenced (EurofinsGenomics Inc.). Sequence data was analyzed using DADA2 approach and further ecological analyses and statistical tests were performed using e.g. phyloseq and vegan packages in R. Most abundant bacteria in the samples affiliated with proteobacterial Xanthobacteraceae, Oxalobacteraceae and Nitrosomonadaceae families. The highest diversity was detected in samples originating from Kuotko site (median Shannon H' 5,25). According to NMDS analysis, Cu concentrations were most the significant environmental factors affecting the community structure in Kuotko, while Cr and Ni had highest impact on Pahtavaara site. Microbial communities in Rämepuro were mostly affected by pH. Further analyses are currently underway. The results of this study can improve the understanding of vegetation development in cover solutions for mining waste areas in cold climate.

## O98 Pre-restoration baseline for microbial activity from two forestry drained fens in Northern Finland

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Rewetting of peatlands allows their development towards natural condition and functionality. Restoration of the C sink function can result as climate change mitigation in the long-term. However, there is a need for more studies on the C, greenhouse gas (GHG) balances and microbial community functions of both forestry drained and rewetted peatland sites. In 2024 two drained peatland forests were restored through rewetting. The sites are in Pallas in the zone of aapa mires, north-boreal Finland, which is close to the northern limit of historical forestry drainage actions. The fens were drained in the 1960–1970s, but the wet central parts of the peatlands are less affected by drainage and mainly treeless. We have measured CO<sub>2</sub>, CH<sub>4</sub>, and N<sub>2</sub>O fluxes using chamber and snow-gradient methods from fall 2022 onwards year-round. In summer 2023 we also monitored microbial communities and functions throughout the snow free season using metagenomic and metatranscriptomic approaches. Here I will present the pre-restoration baseline for microbial activities, i.e. representing forestry drained conditions with the current tree stand in both drained and more pristine areas. Genes involved in CH<sub>4</sub> cycling were present and active in all sites but methanogenesis was more pronounced in pristine areas. Similarly, denitrification genes were active in all sites but there were differences in NorB and NosZ gene expression and abundance, possibly leading to N<sub>2</sub>O emissions. Intriguingly, trace gas metabolism, for example CO oxidation and hydrogen metabolism were highly abundant in all samples.

## O99 Cascading effects of Arctic tundra herbivory on above- and belowground biomass, soil biogeochemistry, and soil (microbial) food webs

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Climate change affects Arctic herbivores and their grazing pressure. Here we investigated the effects of grazing geese and reindeer on High-Arctic tundra (Thiisbukta peatland, Svalbard), by studying the effects of short- and long-term exclusion of herbivores *in situ* at five replicated sampling sectors, each including 4- and 14-year exclosure plots (Ex-4, Ex-14) and herbivory control plots (Hr). Preventing herbivory altered a moss-dominated vegetation (Hr) to a mix of mosses and vascular plants (Ex-4) and a vascular-plant-dominated vegetation (Ex-14). Root biomass, lignin derivatives, inorganic phosphorus, glucose, and N-acetyl-glucosamine contents were significantly increased in Ex-14, while soil pH and moisture decreased. Metatranscriptomics revealed a substantial, often gradual, restructuring of the soil communities after the exclusion of herbivores on multiple trophic and functional levels. For example, eukaryotic micro-predators and bacterivorous bacteria decreased in relative abundances while prokaryotic viruses increased. Prominent changes in relative abundances of meso- and macrofauna included decreased abundances of *Platyhelminthes*, *Monogononta*, and *Maxillopoda* and increased abundance of *Insecta* and *Arachnida*. *Fungi*, especially mycorrhizal fungi and plant pathogens, showed the strongest positive response to the exclusion of herbivores, coinciding with increased relative abundances of viruses targeting *Fungi*. Furthermore, with increasing coverage of vascular plants, soil microbial respiration rates increased, while total microbial biomass did not differ significantly, but microbial turnover times shortened, suggesting a faster microbial loop and accelerated soil organic matter decomposition. Thus, our results demonstrate how aboveground changes can substantially alter belowground communities and the trophic interactions that control carbon cycling in High-Arctic tundra ecosystems.

## O100 Effect of warming on microbial decomposition of plant biomass in Arctic tundra soils using a stable isotope probing approach

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Climate models predict that the Arctic will be significantly affected by climate change resulting in warmer summers and thicker winter snowpacks, both leading to higher soil temperatures. A warmer soil may promote plant growth, i.e. a higher amount of plant biomass (either litter or root exudates), and higher activity of microbial communities that play key roles in organic matter decomposition. The main aim of our study was to investigate the response of bacterial and fungal communities in the decomposition of plant-derived substrates in tundra soils under a scenario of increased summer temperatures and snow cover, using a stable isotope probing approach. For our study, we used in situ climate manipulation experiments established in Western Greenland (Disko Island) where we collected soil samples after eight years of warming treatment. Collected soil samples were used for microcosm incubations with different <sup>13</sup>C-stable-isotopically labelled substrates (cellulose, glucose, acetate) to track the decomposition via respiration (analysis of <sup>13</sup>C-CO<sub>2</sub>) and incorporation into microbial biomass (analysis of <sup>13</sup>C-PLFAs and <sup>13</sup>C-fraction of DNA using 16S and ITS amplicon sequencing). Results revealed that warming induced higher respiration of plant-derived biomass for all substrates, and enhanced bacterial, but not fungal, biomass formation. In addition, to get a deeper understanding of the effect of warming on microbial communities, we will complement these results with DNA-SIP amplicon data. Altogether, this study contributes to the understanding of microbial decomposition of plant biomass stressing higher microbial respiration associated with warmed tundra soils of the Arctic.

## O101 Composition of artificial root exudate treatment impacts soil functional outcome and plant productivity in metal-contaminated brownfield soils

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Root exudates, composed of sugars, organic acids, and amino acids, facilitate symbiotic relationships between plant roots and microbes and are essential for vegetation. Anthropogenic heavy metal accumulation can disrupt these relationships and lower extracellular soil enzyme activities, leading to barren landscapes. We investigated the impact of artificial root exudate (ARE) composition on extracellular soil enzyme activities, soil respiration, and plant productivity in metal-contaminated, barren, post-industrial soils. Seven treatments were applied: sterile water (control), two sugars, two organic acids, two amino acids, two mixtures containing one sugar, one organic acid, and one amino acid (LDA and LDB), and a high-diversity mixture (HDM) with two of each compound type. Results showed that LDA and LDB treatments significantly increased soil respiration and sunflower germination rates. These two treatments also supported robust soil enzymatic function and plant productivity without plant deformation. These treatments also increased the abundance of the fungal class Eurotiomycetes. AREs provided nutrients, stimulating fungal growth and Eurotiomycetes may have had an advantage because they include species that are metal-tolerant through mechanisms like metal sequestration and oxidative stress resistance. The increased presence of Eurotiomycetes may have improved soil function by immobilizing heavy metals or transforming them into less bioavailable forms. Our findings indicate that a simple ARE solution containing one sugar, one organic acid, and one amino acid effectively transformed a barren, contaminated soil into a vegetated environment by enhancing microbial function and plant productivity. This research provides a foundation for using low-cost waste-derived ARE treatments to enable phytoremediation of barren brownfields.

## O102 Mapping microbial genomic potential: predicting plant litter decomposition from soil metagenomes across ecosystems

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Plant litter decomposition is critical for nutrient cycling in soils, particularly in grasslands and forests, which together cover about 70% of Earth's land surface. However, how microbial genomic potential for litter decomposition varies across these ecosystems remains poorly understood. The International Soil Biogeography Consortium (iSBio) integrates microbial genomic diversity with soil functional data across environmental gradients. Here, we utilized decomposition data from the TeaComposition initiative across 350+ sites, combined with soil metagenomics from 314 metagenome assemblies. Focusing on European grasslands and forests, we identified 96 CAZyme families and 2,628 subfamilies involved in lignin, pectin, cellulose, and hemicellulose decomposition pathways. Of these, 297 CAZyme subfamilies ( $p < 0.05$ ) from AA, GH, CE, and PL families showed differential abundance across grasslands, broadleaf forests, and coniferous forests. Gene relative abundances associated with decomposition pathways were highest in coniferous forests, followed by broadleaf forests, and lowest in grasslands. Similar patterns were observed for CAZyme family richness and evenness, mirroring litter mass loss rates. Acidobacteriota and Actinomycetota had a predominant contribution to the gene abundances involved in the early breakdown steps of lignocellulosic substrates, while Pseudomonadota contributed more to later stages. Basidiomycota played a greater role in forests, particularly during the initial stages of decomposition. Soil properties such as pH and C:N ratio, along with climatic factors (primarily temperature and precipitation), collectively explained 65% of the variation in microbial genomic potential for litter degradation. These findings underscore the importance of integrating microbial genomics with large-scale surveys to refine models of soil nutrient cycling across diverse ecosystems.

## O103 Unlocking novel microbial biosynthetic potential in a peatland microbiome

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Peatland microbiomes consist of many taxa from understudied branches of the bacterial tree of life which represent novel functions and biosynthetic capabilities beyond those found in easily cultivated groups. In this study, we used metagenomics combined with metatranscriptomics to identify novel biosynthetic gene clusters (BGCs) and assess their environmental relevance *in situ* within the Schlöppnerbrunnen fen, a slightly acidic, Fe-rich peatland. Our analysis showed that Acidobacteria dominated the community, comprising up to 45% of reads aligned to metagenome assembled genomes (MAGs), while Pseudomonadota, Actinomycetota, and Desulfobacterota were also abundant. We detected 10,354 BGCs, which were clustered into 8,724 non-redundant gene cluster families (GCFs). Ribosomally synthesized and post-translationally modified peptides (RiPPs) represented the largest fraction (2,633 GCFs), followed by non-ribosomal peptide synthases (NRPS, 1,944) and terpenes (1,420). Notably, the majority of RiPPs were unique lassopeptides, ranthipeptides, and lanthipeptides, compounds often associated with antimicrobial activities. Most BGCs appear to encode novel compounds, with many clusters showing high divergence from known BGCs. Several MAGs had exceptional biosynthetic potential, including 25 Pseudomonadota and 14 Acidobacteriota with more than 10 BGCs per genome. Furthermore, metatranscriptome data showed that BGCs from the Acidobacteria dominated the upper peatland depths compared to the Actinomycetota, Desulfobacterota, and Pseudomonadota in deeper layers. Terpenes were most highly expressed BGC class, while different classes of RiPPs were highly expressed in the upper peat layers. We suggest RiPPs in the upper layers play a key role in ecological interactions while terpenes, at lower depths, may be important in adaptation to environmental stress.

## O104 Into the heights and toward the poles: elevational and latitudinal trends in AM fungal community niche structure

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Earlier theory predicted that the volumes of ecological niches decrease with latitude, and that species distribution limits are primarily determined by abiotic factors at high latitudes and biotic factors at low latitudes. Additionally, it has been hypothesized that analogous trends in community structure emerge along latitudinal and elevational gradients. In this study, we tested these predictions using distribution and niche data for arbuscular mycorrhizal (AM) fungi. We found that temperature niche volumes increased with latitude, while precipitation niche volumes decreased. These trends coincide with increasing temperature variability and decreasing precipitation variability with latitude. Niche differentiation decreased with latitude, indicating a shift from habitat filtering at high latitudes towards more neutral coexistence of species within the regional species pool at low latitudes. Furthermore, latitudinal changes in community niche structure mirrored those observed along elevational gradients.

## POSTER ABSTRACTS

MON P1 Promotion of sustainable and healthy soil: an overview of Zimbabwe's soil protection laws and policies.

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The importance of soil protection in Zimbabwe is twofold: firstly, because the country's food security and biodiversity are contingent on this rich and stable resource; and secondly, because effective soil protection is essential to ensure sustainable development. In order to ensure the effective governance of soil protection, it is essential that legislation is in place, accompanied by robust enforcement mechanisms and a network of effective, independent, and efficient institutions. The present study undertakes a thorough analysis of Zimbabwe's current legislative framework pertaining to soil protection. The study further provides legal recommendations for the formulation of future legislation, with the objective of safeguarding Zimbabwean soil and ensuring its sustainable utilisation. The study is further strengthened by the consideration of the impacts of climate change on Southern Africa, emphasising the significance of healthy soil and land, the repercussions of soil degradation. The paper examines drivers of soil degradation and the causes of soil threats found in Zimbabwe. The paper will also encompass the examination of pertinent international legal instruments and the legislative framework governing soil protection in Zimbabwe.

## MON P2 The crucial role of sampling design in soil biodiversity assessment

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Unbiased biodiversity surveys start with an appropriate sampling design standardised for all sampling sites. In meta-analytical works, bias caused by differences in sampling design between source studies cannot be eliminated by statistical standardisation and hinders the understanding of the true patterns. Here, based on PACBIO and Illum sequencing of animal, bacteria and fungi, we compared soil sampling designs from widely known global metabarcoding-based biodiversity projects. The difference in diversity estimates revealed that different sampling designs applied in the same sampling sites reached 75, 6, and 16 times for animals, bacteria, and fungi, respectively. More importantly, different designs retrieved significantly different communities. We disentangled the effects of sampling area, size and depth on revealed diversity and composition. We also evaluated how different approaches to sample pooling (to save labour and resources) affected biodiversity estimates. Importantly, pooled sampling reduced the differences between sample designs, while could not overcome the effect of sampling factors. A large number of pooled subsamples were used in the diversity assessment, while with fewer subsamples, pooling had a positive effect. Based on the expenses at different stages of sample processing and sequencing, we calculated how many resources are saved by sample pooling relative to unpooled sampling and how they are connected to the effectiveness of species detection.

## MON P3 Unveiling the diversity and specificity of orchid mycorrhizal fungi associations: Insights from geographic regions and methodological comparisons

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Orchids are threatened due to their great ornamental and medicinal values, and their seed germination entirely dependent on compatible orchid mycorrhizal fungi (OMF). However, understanding the diversity and specificity of orchid-fungus associations is crucial for understanding ecology of these symbiotic relationships and for orchid conservation purposes. Here, we present results demonstrating the diversity of OMF isolates obtained from four orchid species, *Anacamptis morio*, *Dactylorhiza sambucina*, *Orchis mascula* and *Platanthera bifolia* growing in Czech Republic, Sweden and Italy. These orchids are known to associate with Ceratobasidiaceae and Tulasnellaceae fungi, showing variation in the specificity of orchid-fungus associations. The orchid roots were screened for OMF using culture-dependent (isolation from intracellular hyphae coils) and culture-independent (Next Generation Sequencing of root sections) techniques. The culture-independent method revealed a greater fungal diversity than the culture-dependent one, but despite the lower detection, the fungal strains isolated were in majority the abundant OMF in adult roots. The poster presents a comparison of the diversity and specificity of orchid-fungal associations across different geographic regions and orchid taxa obtained by these two methodologies and compares their efficiency for OMF detection. The scientific outcomes can provide deeper insights into the functional implications and evolutionary dynamics of these symbiotic relationships.

## MON P4 Comparison of technologies for assessing fungi-to-bacteria-ratio of soil

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Measuring bacterial and fungal biomass may offer insights into agroecosystem health. Nevertheless, few studies have directly compared the ability of different methods to assess the abundance of these two microbial groups and their ratio (F/B ratio). This study compared the ability, precision, and repeatability of three commonly used laboratory methods - phospholipid fatty acid (PLFA) analysis, quantitative PCR (qPCR), and droplet-digital PCR (ddPCR) - alongside a commercially available microbial carbon testing tool (microBIOMETER®), to assess the F/B ratio and microbial abundance in agroecosystem soils. We also reviewed recent literature on common measurement and reporting practices. PLFA and ddPCR provided the most reliable outcomes, with PLFA being the most precise, repeatable, and widely used (81 % of reviewed studies). However, significant variability in analytical procedures exists between laboratories, and key details, such as storage conditions, are often underreported. MicroBIOMETER® can offer a low-cost option for assessing total microbial biomass but did not match PLFA results in determining the F/B ratio. ddPCR offered better precision than qPCR but had a narrower dynamic range. Therefore, the optimal approach is to use the two methods in parallel. In conclusion, we recommend future studies adopt PLFA analysis as the primary method for assessing microbial abundance and F/B ratio of soils, as PCR-based measurements are influenced by several unavoidable biases. Furthermore, we suggest improvements to the PLFA method to ensure more reliable comparisons across laboratories. Altogether, our study gives guidelines for improving the monitoring of F/B ratio and microbial abundance in agroecosystems.

## MON P5 Mechanistic understanding of metabolic cross-talk between *Aloe vera* and native soil bacteria for growth promotion and secondary metabolites accumulation

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Plants release a wealth of metabolites into the rhizosphere that can influence the composition and activity of microbial communities. These communities, in turn, can affect the growth and metabolism of the host plant. The relationship between medicinal plants and their associated microbes has been suggested, yet the mechanisms of indigenous microbial selection and their significance in medicinal plants remain largely unknown. This study investigated how *Aloe vera* selects its rhizosphere bacteria and their functional roles in supporting the plant. We utilized two native plant growth promoting rhizobacterial (PGPR) strains of *Aloe vera*: *Paenibacillus* sp. GLAU-BT2 and *Arthrobacter* sp. GLAU-BT16, as either single or consortium inoculants for plant growth experiment. We analyzed non-targeted root metabolites while observing both single and consortium bacterial inoculants and confirmed their exudation in the rhizosphere metabolites. The GC-MS analysis of metabolites revealed that the bacterial inoculation amplified the abundance of flavonoids, terpenes and glucoside metabolites in the root, which exuded out in rhizosphere as well. Flavonoids were the most prevalent metabolite group in individual and consortium inoculants, highlighting their crucial role in interacting with rhizosphere microbes and shaping their community. Additionally, the bacterial inoculants significantly increased antioxidant activity, total phenolic and flavonoid contents in *Aloe vera*'s leaf. In conclusion, we propose a model of circular metabolic communication, where rhizosphere bacteria stimulate flavonoid content in the plant, and in turn, plant releases some of these flavonoids in the rhizosphere to maintain the indigenous microbial community for its own benefit.

## MON P6 Fostering equity in microbial ecology through data reuse: lessons from data collection and synthesis

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Data collection, management, and reuse are increasingly important in ecology and biodiversity research. In microbial ecology, sequencing has altered our relationship to the invisible microbial world and created massive amounts of reusable microbiome data. Data reuse in microbial ecology can integrate bacteria into macroecology and fill major gaps in the field, however, meta-analyses are currently overwhelmingly performed by researchers from the Global North. Fostering microbiome data reuse globally may not only advance science but may serve to invert knowledge flows in microbial ecology. I will present the Microbial Community Database (MiCoDa), an open database of 16S rRNA amplicon sequencing data. MiCoDa data was collected from sequence archives as well as through community-oriented data collection and reuse events, which have been organized in Latin America and Africa and soon, across Asia. MiCoDa was developed with equity and accessibility as central aims, and addresses many of the issues limiting data reuse in the Global South, including access to computational capacity and existing credit and acknowledgement systems for data creators and data reusers. Today, MiCoDa is one of the largest bacterial databases in the world, boasting over 35,000 curated microbiome samples. The database fosters interoperability between INSDC databases, publication DOIs, and the Global Biodiversity Information Facility (GBIF) to stimulate interoperability and proper citation practices. In addition to describing the MiCoDa model of data collection and its main motivations, this presentation will demonstrate the potential of MiCoDa for data reuse.

## MON P7 Fungal-bacterial interactions- a gateway to discover novel bioactive metabolites

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Forests store vast amounts of carbon in deadwood, which presents a physically and chemically challenging environment for microbes. Filamentous fungi, particularly in class *Agaricomycetes* of *Basidiomycota*, have been studied for their role in decomposing deadwood through white rot, brown rot, intermediate or soft rot decay. During this process, fungi interact with other fungi and microbes sharing the same habitat. Bacteria from the phyla *Acidobacteria*, *Pseudomonadota*, *Bacillota*, and *Actinobacteria* have been reported to co-exist with wood-decay fungi, though their interactions remain largely unknown. Our aim is to study metabolic pathways and changes in gene and enzyme expression incurred due to these interactions via omics approach, specifically meta-genomics and transcriptomics, together with analysis of the produced metabolites. We cultivated three species of wood decay fungi i.e. *Fomitopsis pinicola*, *Phlebia radiata* and *Schizophyllum commune* representing different decay types and substrate specificity, both individually and in combination with five bacterial species isolates of *Pseudomonadota* and *Actinobacteria* to analyze their growth, colonial interactions and secreted metabolites on various media. Interaction zones indicating antagonistic reactions between fungal hyphae and bacterial colonies were observed. Metabolic activities were analyzed by enzyme assays and UPLC chromatography - mass spectrometry. These simulations will offer insights into the biological processes occurring during wood degradation. Additionally, microbial co-cultures may produce novel natural compounds and bioactive secondary metabolites, which can be explored for potential applications.

## MON P8 Genome-assisted risk assessment of biocontrols

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Dependency on chemical pesticides in agriculture has raised significant concerns regarding environmental sustainability and human health. Biocontrols such as microbial pesticides, offer a promising alternative to conventional practices. These environmentally friendly solutions have the potential to reduce chemical residues in food, lower risks to pollinators and beneficial organisms, and mitigate the development of pesticide resistance. Despite their advantages, the widespread adoption of biocontrol agents requires rigorous risk assessment to ensure their safety and efficacy. Traditional assessment methods can be time-consuming and inconsistent, highlighting the need for streamlined bioinformatics tools to facilitate rapid and comprehensive risk analysis based on whole genome sequences. These approaches can facilitate the prediction of potential ecological impacts, assess potential transferability e.g. of antibiotic resistance, and improve regulatory decision-making. To improve, harmonize and streamline the assessment of biocontrol, an analysis of the genomes of 100 randomly selected approved biocontrol agents was conducted. Of the 98 unique species in the dataset, almost half belonged to *Corynebacterium*, *Streptomyces* and *Bacillus*. Genes were recovered that conferred, on average, resistance to nine antibiotics with vancomycin and tetracycline being the most frequent. Additionally, species of *Corynebacterium* had the highest number of resistances to antibiotics (12). *Corynebacterium* also showed the highest number of antimicrobial resistance genes located within mobile genetic elements (32) which should be further followed up with experimental assays. These findings, obtained in an automated and harmonized manner, underscore the importance of robust bioinformatics tools to support rapid, evidence-based risk assessment, ensuring that biocontrol solutions remain both effective and environmentally responsible.

## MON P9 Microbial ecology in mountain soils along elevation gradient: from forest to alpine meadow

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Mountain ecosystems provide wide gradients of environmental conditions at local scale. Ecosystems along these gradients differ in many aspects such as vegetation, soil properties and microclimate, and, accordingly, soil microbiome composition and its functioning. We studied an ecosystem gradient in Furkotská Valley, High Tatras (Slovakia), across three zones: forests (<1600 m), subalpine meadows and dwarf shrubs (1800–1900 m), and alpine meadows and scree (>1900 m). Soil samples were collected and analyzed for microbiome composition and functional potential. Microbial communities were assessed via soil DNA using qPCR for group-specific marker genes (e.g., 16S and 18S rRNA for bacteria and fungi, respectively, and ammonia-oxidizing (*amoA*) for archaeal and bacterial nitrifiers). 16S rRNA and ITS sequencing identified bacterial and fungal composition. qPCR results showed significant microbiome differences along the gradient. Bacterial abundance increased with vegetation complexity, peaking in forests and reaching its lowest in scree. Fungal abundance was higher in meadows and dwarf shrubs. The *amoA* gene for archaea was most abundant in scree and meadows, while forests had lower values. However, the *amoA* gene for bacteria varied, being lowest in scree, moderate in dwarf shrubs, higher in meadows, and highly variable in forests. Preliminary results indicate microbiome composition and function vary with elevation. Further analyses will integrate microbiome composition with soil chemistry and microbial activity to better understand these differences.

## MON P10 *Tillandsia* dunes as a habitat for microorganisms in the hyperarid Atacama Desert

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The Atacama Desert in northern Chile is characterized by hyperaridity, high UV-radiation, and low soil organic carbon levels, limiting microbial life to specific habitats that provide sufficient nutrients and water. *Tillandsia landbeckii*, a plant species highly adapted to hyperarid conditions, exists in dune systems as spatially isolated monocultures growing in banded patterns. Often, these dunes contain several layers of buried plant residues, which may serve as organic carbon resources for soil microorganisms. Aim of this work is to understand the role of *Tillandsia* dunes as habitats for microbial life. One-meter-long push cores were recovered from four *Tillandsia* dunes located in different regions of the Atacama Desert and dissected into 9 to 14 layers. Samples were used to assess microbial viability and community structure with increasing depth. Radiocarbon dating of plant residues revealed that initial plant colonization events occurred between 198 and 1712 cal yr BP. Like plant residues, dead microbial biomass may experience prolonged preservation in dunes. Thus, we extended classical microbiota profiling by distinguishing between intracellular versus extracellular DNA and by viable cell counts. Colony counts indicated a decline in viable cell numbers with increasing depth, which was roughly reflected by qPCR results targeting the bacterial 16S rRNA gene and fungal ITS1 region. 16S rRNA gene amplicon sequencing revealed sampling site specific microbiotas with distinct depth profiles. Within each core the microbiota of intracellular compared to extracellular DNA fractions was also distinct. The cell counts and specific iDNA profiles point to long-term preservation of microbial life in *Tillandsia* dunes.

## MON P11 Reciprocal transport of carbon and nitrogen between plants and microbes in the grassland hyphosphere

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In the plant-arbuscular mycorrhizal fungi (AMF) symbiosis, the plant exchanges photosynthetically fixed carbon (C) for nutrients (e.g., nitrogen, N) acquired by the fungus. This C may be transferred via fungal exudates to bacterial communities in the AMF hyphosphere, which assist the fungus in nutrient acquisition by decomposing organic substrates. In addition, saprotrophic fungi play a role in plant C uptake by rapidly processing rhizodeposits and channeling them into the hyphosphere. However, which microbes benefit from plant-fixed C in the hyphosphere and the temporal dynamics of this C allocation remain unclear. We developed 'hyphoboxes' separating the (mycor)rhizosphere from the hyphosphere with a 50 µm mesh. A substrate compartment containing root litter and <sup>15</sup>N-labeled urea was isolated within the hyphobox by an air gap to restrict colonization to fungi and their associated bacteria. Hyphoboxes were buried in soil (Leptosol) for three months at an experimental grassland plot of the Biodiversity Exploratories in south-west Germany to allow establishment of microbial communities. We then performed <sup>13</sup>CO<sub>2</sub> pulse labeling of the aboveground plant biomass and sampled hyphoboxes 1, 3, and 7 days after labeling to explore the temporal dynamics of C allocation to hyphosphere microbes. As expected, we observed a reciprocal transport of plant-derived <sup>13</sup>C into the hyphosphere and of urea-derived <sup>15</sup>N into plant roots. Moreover, we characterized hyphosphere microbial communities by amplicon sequencing and visualized the <sup>13</sup>C and <sup>15</sup>N distribution in the hyphosphere using NanoSIMS. Our findings provide new insights into the complex interactions between plants, fungi, and bacteria in belowground nutrient cycling.

## MON P12 Assessing the effects of environmental drivers on soil fungal diversity in desert ecosystems

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Climate change is significantly altering desert ecosystems by impacting soil fungal communities that are essential for nutrient cycling, organic matter decomposition, and plant symbiosis. Rising temperatures and reduced precipitation lead to drier soils through enhanced evaporation, favouring drought-tolerant species while reducing overall biodiversity. Shifting rainfall patterns disrupt fungal growth cycles and spore dispersal, unbalancing the ratio between saprotrophic fungi that decompose organic material and mycorrhizal fungi that form vital symbiotic relationships with plants, ultimately compromising plant nutrient uptake and water absorption. Increased temperatures also accelerate decomposition processes, which alter soil carbon dynamics, nutrient availability, and pH levels, further influencing fungal community structure. In our study, we analysed soil samples from desert regions to examine fungal species composition along with measurements of soil nutrient content, temperature, and vegetation, thereby providing precise observations of these climatic impacts. Notably, even small shifts in climate can lead to significant ecological changes that affect the entire desert ecosystem. We are currently working on understanding desert soil fungal organisms, focusing on their adaptive strategies in response to climatic stressors and investigating how other environmental factors, such as soil nutrient dynamics and microbial interactions, further influence these communities.

## MON P13 Disentangling the interplay between among earthworms, plants, and soil microbes in Amazonian dark earth

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This study aimed to elucidate the roles of earthworms, plants, and soil microbes in enhancing soil functionality through an experimental system mimicking key components of Amazonian Dark Earths (ADEs). ADEs are highly fertile, anthropogenic soils characterized by elevated organic carbon, enhanced nutrient availability, and an unusually diverse microbial community resulting from ancient human activities such as charcoal deposition and organic waste management. In this study, maize was cultivated in pots containing nutrient-poor soil, amended in a factorial design with earthworms, biochar, and manure as a source of organic matter. Both individual and combined amendments were evaluated, with the highest plant biomass observed in pots receiving all amendments simultaneously, indicating strong synergistic effects on plant growth. Bacterial community composition was concurrently assessed via 16S rRNA metabarcoding in three compartments: bulk soil, root tissues, and earthworm guts. Despite distinct community structures among compartments, a stable core microbiome was evident. Notably, *Bradyrhizobium* was the dominant genus in the core microbiome, being most abundant in the root compartment, where it is selectively recruited by the plant. Also, its relative abundance in the earthworm gut was lower in the absence of plants, suggesting that plant presence further enhances its occurrence. In bulk soil from the treatment combining all amendments, which also supported the highest plant biomass, *Bradyrhizobium* abundance was remarkably higher. These findings demonstrate that integrating the soil amendments characteristic of ADEs can substantially improve plant growth and modulate soil bacterial communities, emphasizing the critical role of synergistic biotic interactions in soil functionality

## MON P14 Presence and diversity of phosphorus solubilizing bacteria in alpine meadow and scree soils of Tatra Mountains

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Phosphorus solubilizing bacteria (PSB) release bioavailable phosphorus (P) from insoluble inorganic forms. PSB play a vital role in soils deficient in available P, e.g. young, undeveloped soils, where they facilitate P availability and mobility. Recently, high increase in leaching of P was observed from soils in alpine zone of Tatra Mts., Slovakia, particularly from the undeveloped, unvegetated soils in scree areas. Among the potential mechanisms that could explain this phenomenon is the increased activity of PSB induced by climate change. We aimed to compare presence and diversity of PSB in scree and adjacent alpine meadow soils. We isolated PSB from meadow and scree soils collected in four catchment-lake systems in Tatra Mts. and identified the isolates by 16S rRNA gene sequencing. To estimate the relative abundance of identified PSB in soil microbiomes, soil DNA amplicon sequencing (V4 region of 16S rRNA gene) was performed. We detected PSB from different lineages (e.g. *Burkholderia-Paraburkholderia-Caballeronia* sp., *Psudeomonas* sp., *Collimonas* sp.) in both meadow and scree soils. These PSB comprised rather minor part of the soil bacterial communities: ~0.4–0.7% and ~0.1–0.3% in meadow and scree soils, respectively, with majority of PSB taxa shared between the two soils. We haven't found any significant difference in PSB communities between scree and meadow soils, suggesting that other factors, such as varying rates of abiotic weathering and/or the plant- and microbiome-related P immobilization capacity, may explain the differences in P leaching rates between these two soil types.

## MON P15 Induced shifts in the maize rhizosphere microbiome under drought stress

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Drought stress has a significant impact on global maize production, but the effects on the maize rhizosphere microbiome are not well understood. This study explored how water stress influences microbial composition, diversity, and structure in the rhizosphere of drought-sensitive (CRN-3505) and drought-tolerant (Monsanto DKC 72-70) maize cultivars. We hypothesized that drought would induce shifts in microbial composition, favoring drought-resistant microbes, while favorable water conditions would enhance microbial diversity and abundance. Using shotgun metagenomic sequencing, we analyzed rhizosphere soil samples from both cultivars under three water treatments: 60% water holding capacity (WHC) (severe drought), 80% WHC (moderate drought), and 100% WHC (well-watered). Our results showed that bacteria dominated all groups, followed by fungi and archaea. Principal Component Analysis revealed distinct microbial signatures associated with each water level and cultivar. For example, Proteobacteria were prevalent in the W\_60R of Monsanto DKC 72-70, while Ascomycota was more abundant in the Y\_60R of CRN-3505. Alpha diversity indices indicated the highest evenness in W\_80R for Monsanto DKC 72-70 and Y\_100R for CRN-3505, with Shannon diversity values of 3.09 and 3.06, respectively. Beta diversity analysis (PCoA) showed significant differences across all groups (ANOSIM  $R = 0.51$ ;  $p < 0.01$ ). These results demonstrate that drought stress causes significant changes in the maize rhizosphere microbiome, with potential implications for plant growth, nutrient uptake, and pathogen resistance. This study offers critical insights for developing microbiome-based strategies to improve drought tolerance in maize, promoting the cultivation of climate-resilient crops.

## MON P16 Impact of regenerative management in hyper-arid ecosystem - microbial communities

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The utilization of cover crops is becoming a foundational practice in sustainable agriculture, owing to their significant advantages, such as enhanced nutrient availability and improved soil health. Soil bacteria are pivotal as primary decomposers of plant residues, playing crucial roles in nutrient cycling. This study confidently investigates the impact of regenerative management practices on soil microbial community composition in almond orchards located within a hyper-arid ecosystem. Utilizing high-throughput sequencing techniques, we compared microbial communities from two adjacent almond orchards managed under organic (ORG) and regenerative agriculture (RA) practices, in addition to an uncultivated (UC) site, where the responses of soil bacterial communities to intercrop mulch from cover crops have been largely underexplored. Our findings unequivocally demonstrate that RA management significantly enhances soil organic carbon levels and transforms microbial community structure in hyper-arid ecosystems. Specifically, RA practices lead to increased overall bacterial abundance and enrich key taxa within the microbial community. These modifications have profound implications for nutrient cycling processes in these ecosystems, indicating that the adoption of RA practices is critical for enhancing the functional capacity of soil microbial communities in hyper-arid environments.

## MON P17 Getting back to their roots: deadwood as a niche for ectomycorrhizal fungi

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Deadwood is an important component of forest ecosystems and an integrated part of the soil. Saprotrophic fungi are the main agents of wood decay, exhibiting strong successional patterns during the process of decomposition. However, some ectomycorrhizal (ECM) fungi occur in deadwood at advanced decay stages. The ECM lifestyle evolved multiple times from saprotrophic ancestors, leading to a significant loss of most in their decomposition capacity. During decay, deadwood is depleted in carbon, but accumulates nitrogen in recalcitrant organic forms. In nitrogen-limited forests, these patches of nutrients may be important sources for plant and microbial growth. Supplied with carbon from their hosts, certain ECM species that have retained some saprotrophic capacity may thus be uniquely suited for accessing these nutrients. Here, we investigate whether some ECM fungi are preferentially occurring in deadwood above soil, and further, which traits that characterize ECM fungi occurring in deadwood. To address this, we compare the distribution of ECM fungi in a ITS2 metabarcoding dataset drilled from 470 spruce logs across all decay stages, as well as 168 soil samples, all sampled from 24 spruce forests in southeastern Norway. We observed a specific set of ECM species associated with deadwood, and further, that agaricoid and corticioid ECM species exhibit different occurrence patterns. Notably, agaricoid ECM species showed a strong correlation with logs that have a high nitrogen content, a relationship more marked for species with longer-ranging exploration types.

## MON P18 Bacterial populations active during lignin depolymerization

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Lignin is the most abundant and chemically prolific resource in nature. The effective and comprehensive utilization of lignin has become an important topic with the advent of global politics and industrial practices into being more sustainable, and less oil-dependent. Understanding how microorganisms transform lignin into potentially interesting added-value products, and identifying key enzymes is not new, however, exploring the depolymerization potential of bacterial populations and shifting the focus in bacteria beyond the funneling pathways is a recent development. In this work, we identified active bacterial populations from lignin-degrading enriched garden soil using a combination of isotope probing with pure lignin and metagenomics. The results showed that a diversity of bacterial populations are active during the depolymerization of lignin, pointing to the participation of bacterial population in the active degradation of lignin in nature.

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## MON P19 Ectomycorrhizal mycelial communities in a fragmented sub-Mediterranean Karst forest

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The presence of common mycelium networks of ectomycorrhizal (EcM) fungi could play a crucial role in the survival of tree seedlings and adult trees in the harsh environment of the sub-Mediterranean Karst. The sharing of symbionts can be affected by the identity of tree species involved in the symbiosis, host specificity of EcM fungi, spatial distance, variability in soil parameters, and the ability of EcM fungi to form extensive mycelia. We investigated ectomycorrhizal mycelial communities in a fragmented secondary forest of sub-Mediterranean Karst region of Slovenia using in-growth mesh bags. The tree species *Quercus pubescens*, *Ostrya carpinifolia* and *Pinus nigra* were included in the study. Metabarcoding was used to identify the community composition of fungi developed in mesh bags. Although most ectomycorrhizal taxa were shared among the investigated tree species, tree species identity was a significant determinant of mycelial communities, with geographical distance and soil parameters as additional shaping parameters. The highest potential for spatial spread was identified for the mycelial communities of *Pinus nigra*, but its community members were predominantly EcM fungi with high host specificity.

## MON P20 Global patterns of nutrient limitation in soil microorganisms

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The nitrogen (N) and phosphorus (P) limitations in soil microorganisms have profound implications for key soil functions such as organic matter decomposition and soil carbon (C) sequestration. However, the extent and magnitude of microbial N and P limitation in soils worldwide remain largely unknown compared to N and P limitation in plants. Herein, we evaluated global patterns of microbial N and P limitation by combining profiles of extracellular enzymes (*i.e.* ecoenzymes; 5,259 observations) with multiple sets of observational and experimental data from natural (*i.e.* outside of agricultural and urban areas) terrestrial ecosystems. Our analyses reveal widespread indications of microbial P and N limitation (65 and 40% of observations, respectively) in soils worldwide, with unexpectedly frequent N and P co-limitation in the tropics. This co-limitation could be attributable to elevated microbial N demand for the synthesis of P-acquiring enzymes under P limitation, and thus likely as a secondary N limitation resulting from the inherent P deficiency in tropical soils. Upscaling prediction (0.1 × 0.1 spatial resolution) further indicated certain regions such as the Amazon Basin, Tibetan Plateau, and Siberian regions, which harbor substantial soil organic C, showed signs of strong N and P limitation in soil microorganisms, suggesting a high sensitivity of soil C cycling in these regions to nutrient perturbations. As the first global assessment of spatial variation in microbial N and P limitation, these findings provide clues to explain the long-standing “Tropical N Paradox” and could be useful for understanding and predicting soil biogeochemical cycles in a changing world.

## MON P21 A carbon utilization and nitrogen acquisition trait spectrum for ectomycorrhizal fungi

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Trait spectra have been used in various branches of ecology to explain and predict patterns of species distributions. Several categorical and continuous traits have been proposed as relevant for ectomycorrhizal fungi, but a spectrum that unifies co-varying traits remains to be established and tested. Ectomycorrhizal fungi are pivotal for nutrient cycling in the generally nitrogen limited boreal forest, and utilize carbon delivered from their hosts to mobilize nitrogen that they either retain in their own biomass or deliver to the host. We propose that the extent to, and the mode by which, the fungi use host carbon to explore the soil for nitrogen can be described by a carbon utilization and nitrogen acquisition spectrum, which encompasses several morphological, physiological and metabolic traits. The trait spectrum is linked to the concept of apparent carbon use efficiency and resolves the contradiction that species with high supply of host carbon can maintain nitrogen transfer despite building large mycelial biomass. We suggest that ectomycorrhizal fungal species are distributed along this spectrum, with lifestyles ranging from “absorbers” with a niche in high productive forests with high availability of soluble N to “miners”, focused on exploitation of organic matter in forests with low N availability.

## MON P22 Metabarcoding of arbuscular mycorrhizal fungi (AMF) communities endemic to the rhizosphere of the argan tree (*Argania spinosa* (L.) Skeels): focus on Southwest Moroccan forest ecosystems

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Mycorrhizal populations play pivotal roles in multiple ecosystem processes with recent research findings linking mycorrhiza strain types to specific functions such as biodiversity conservation, reinforcement of ecosystem sensitivity to carbon dioxide, increased soil fertility and deposition of essential macronutrients and carbon sequestration. Investigation into the AMF diversity in any ecosystem, but especially forestland areas, is an important biological parameter that can be used to conduct assessment of environmental disturbances and inevitable climate stressors. The investigation of indigenous soil mycorrhizae, such as those endemic to the Argan forestlands of Morocco stands to bring immense benefits to biodiversity conservation, including ecosystem restoration, improvement of environmental tolerance to local conditions, low ecological risk and quick acclimatization to the harsh effects of climate change. Metabarcoding will make it possible conduct the simultaneous identification of not only one, but multiple mycorrhiza species and taxa that will in turn make it easier to obtain a comprehensive overview in terms of diversity of these AMF consortia. In addition, it will be possible to analyze a larger number of samples at once, in comparison to other conventional methods of mycorrhiza morphological characterization. The choice of metabarcoding is also preferred because the project strives to achieve higher taxonomic output, which will be possible since metabarcoding targets the ITS region of mycorrhizal fungi that is known to contain variable sequences. Hence, it will be possible to detect or capture the unique or rare AMF strains that might be overlooked or skipped during analysis with other conventional molecular techniques.

## MON P23 Isolation and characterization of novel methanotrophs from peatland soil

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Peatlands store 30% of global soil organic carbon and are hotspots for methane cycling. Methanotrophic microorganisms in these ecosystems serve as a methane filter, significantly reducing emissions of this potent greenhouse gas. Yet, the identity, activity profiles, and metabolic capacities of peatland methanotrophs are not fully known. Using fluorescence-activated single-cell sorting (FACS), we isolated two new bacterial methanotrophs from Czech peatland soil, *Ca. Methylocystis sumavensis* JAN1 and *Ca. Methylosinus bohemicus* JAN2. While the new *Methylocystis* species is closely related to others isolated from peat, the new *Methylosinus* species falls within a cluster of hitherto uncultivated methanotrophs from this genus. Both isolates are acidotolerant but have their growth and activity optima at neutral pH, consuming  $0.52 \pm 0.01$  and  $0.14 \pm 0.01$   $\mu\text{mol}$  methane per  $\mu\text{g}$  protein per hour under optimal conditions, respectively. Although both isolates are genomically similar to previously described species, *Ca. Methylocystis sumavensis* JAN1 possesses a chromosome-encoded clade II nitrous oxide reductase (NOS). This operon was previously only found in few *Methylocystis* species from acidic environments, implying a role in denitrification coupled to anaerobic methane oxidation. *Ca. Methylosinus bohemicus* JAN2 carries two plasmids containing the same NOS operon, as well as genes for urea metabolism and transport, for [NiFe] hydrogenases, and nitrate transport. Our results reveal unique metabolic traits of new methanotroph species, highlighting their adaptation to peat ecosystems and broaden their roles beyond aerobic methane mitigation.

## MON P24 Influence of canopy cover and soil moisture on mycobiome of protected forest in Mediterranean Croatia with insights on potential fungal ecosystem services

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Fungi play an important role in soil processes, such as the decomposition of organic matter and biogeochemical cycling of essential elements. This study focused on the fungal communities in Soline Hill, a protected forest park in Mediterranean Croatia, known for its dense holm oak maquis and specific microclimate. This study aimed to explore the influence of canopy cover and soil humidity on forest mycobiome and analyze whether enzymatic activity indicates potential fungal ecosystem services. For this purpose, 40 soil samples were collected and ITS2 gene region was sequenced using Illumina MiSeq. For each sampling point, a detailed botanical survey was done, forest canopy cover was estimated, soil moisture content and enzymatic activity were measured. The results showed that saprotrophs dominated in all canopy cover categories, especially under closed canopy (70–80%), while the relative abundance of ectomycorrhizal fungi was the highest under fully closed canopy (90–100%). Moisture correlated negatively with ectomycorrhizal fungi ( $r = -0.53$ ,  $p = 0.0005$ ). Enzymatic activity varied, lipase showed the highest activity and  $\alpha$ -glucosidase the lowest. Ectomycorrhizal fungi were negatively correlated with cellobiohydrolase and chitinase activity, while saprotrophs were positively correlated with all measured enzymatic activities, particularly with the  $\beta$ -galactosidase. In conclusion, fungal communities are influenced by forest canopy cover and soil moisture. Saprotrophs thrive in humid conditions, and the association with  $\beta$ -galactosidase activity suggests their role in facilitating the decomposition of complex C sources, whereas ectomycorrhizal fungi are less affected by moisture. These findings are essential for understanding the biogeochemical and ecological functions of Mediterranean forests.

## MON P25 Long-term effects of ash-fertilization on the composition and functional gene pool of soil microbiome in drained peatland forests

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Finland aims to increase the use of wood ash in fertilizing drained peatland forests to improve annual carbon capture in the land use sector. While wood ash increases tree growth, its effects on the soil greenhouse gas (GHG) cycle and soil microbial communities are not fully understood. To gain a comprehensive understanding of the overall GHG balance of a forest, it is crucial to understand the role of the soil microbiome. We investigate the impact of ash-fertilization on soil microbial communities and their functional gene pool, as changes in these can impact GHG cycling, carbon storage, and overall biodiversity in drained peatland forests. The experiment consists of seven ash-fertilized peatland forest sites in Finland, representing three drained peatland forest site types with different nutrient levels. Each site has an ash-fertilized plot and an adjacent unfertilized control plot. The plots have been fertilized (5–10 tons of ash per hectare) at different times, the oldest in 1979 and the most recent in 2014. DNA was extracted from a total of 168 soil samples, followed by metagenomic sequencing and analysis. Our findings reveal that location and site type influence microbial community composition more than ash treatment. This indicates that microbial communities in drained peatland forest soils are diverse and vary between forests. To further understand impacts on the GHG cycle, we are analyzing genes related to GHG cycling. These analyses will show how ash-fertilization affects the functional potential of microbial communities in these soils.

## MON P26 Decadal adaptation of methanotroph affinity to peatland water table manipulations

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Peatland methanotrophs mitigate greenhouse gas emissions through oxidizing methane in shallow peat layers forming a filter that removes methane during diffusive transport towards the peat surface. Beside the abundance of methanotrophs the effectiveness of this filter also depends on their affinity towards methane and oxygen, which might be affected by land management practices like drainage and restoration. Here, we quantified the long-term effects of water-table depth (WTD) and WTD manipulation on the methanotroph affinity towards methane and oxygen. Samples were collected at the Lakkasuo peatland in central Finland. Within this site, we collected samples (10–20cm depth) from four sites along a drainage/WTD gradient (drained forest, drained open peatland, undrained control, high WTD location). Affinities ( $k_M$  values) towards methane and oxygen were determined in laboratory incubations with 50–50 000 ppm methane and 3–21% oxygen. At the same time, we surveyed the of the methanotroph communities at these sites through targeted metagenomics (results pending). Methane affinity decreased from dry to wet locations from 550 to 18 000 ppm, indicating the establishment of relatively high affinity methanotrophs in drained peat. Substrate saturation toward oxygen was evident over 5–10% oxygen, but the precision was insufficient to identify differences along the gradient. Our results demonstrate that significant changes in methanotroph kinetics occur in response to WTD depths manipulations which may need to be considered in peatland methane models. Parameters derived from pristine peatlands may not be accurate immediately after rewetting when methanotroph communities are still adapted to low methane and high oxygen concentrations.

## MON P27 Peat methane-cycling microbial communities and biogeochemistry in the UNESCO Biosphere Entlebuch

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Peatlands act as natural carbon sinks while also emitting methane. Native microbial communities, including methane-producing and methane-consuming bacteria and archaea, regulate carbon dynamics in peatlands. Yet the factors governing the balance between carbon storage and emission are not fully understood. In this work, we examine the biogeochemistry, microbial community composition via 16S amplicon sequencing, and land use of six peatlands across Switzerland. Keystone microbial species were observed across all sites, with some exclusive to the top (10 cm) or bottom (40 cm), and overall microbial composition seemed to be influenced specifically by pH, calcium, sodium, and manganese ( $P < 0.05$ ). 16S amplicon based functional predictions (PICRUSt2) revealed different abundances of key metabolic pathways for carbon and nitrogen cycling across sites, including a ~11-fold increase in acetoclastic methanogenesis between the lowest- and highest- ion sites. We detected a large diversity of methane-cycling microorganisms, including 9 genera of methanotrophic bacteria (MOB) and 8 of methanogenic archaea (methanogens). MOB generally dominated the top layer (10 cm), with *Methylocapsa* being the dominant MOB genus (0.02–2.7% of the community). Methanogens were more abundant in deep layers (25 and 40 cm), where Rice Cluster II, a putative hydrogenotrophic methanogen, was the dominant methanogen (0.003–13.9% of the community). Interestingly, “*Candidatus Methanoperedens*”, a methane-consuming anaerobic archaeon, was detected at 40 cm in a site that recently underwent rewetting. Overall, these findings highlight that biogeochemistry and historical land use influence microbial communities, including methane-cycling microorganisms, and thus the carbon balance of peatland ecosystems.

## MON P28 The microbial and viral communities in deep peat soils and their linkages

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Peatlands are carbon-rich ecosystems that are important to global carbon and other nutrient cycles. They act as crucial carbon sinks but are threatened by climate change and land-use changes, which could turn peatlands into sources of carbon to the atmosphere. The key component in these functions are the microbial communities. The balance between methanogens producing the greenhouse gas methane and methanotrophs oxidizing it, and whether peatlands act as carbon sinks or sources is determined by the environmental conditions limiting microbial degradation of organic carbon stored in peat. Both viruses, which can modulate and alter the functions of the host microbes, and deep peat are understudied. That is why metagenomic short- and long-read sequencing were used to study the bacterial, archaeal, and viral communities in peat from up to the depth of 350 cm. The taxonomic and metabolic composition of the microbial communities were characterized, and potential virus-host linkages were studied with computational host prediction and shared methylation patterns between hosts and viruses. Despite the expectations that microbial communities would differ based on peat depth, the changes in microbial communities seem to be connected to some other factor.

## MON P29 Intensive forest management of drained peatland: effects on methane dynamics in anoxic conditions

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Gas fluxes from boreal peatlands have the potential to influence the concentration of greenhouse gases in the atmosphere. In addition, some of the boreal peatlands are under intense human influence and are used for timber production. The most widespread timber harvesting practice, clear-cutting, has effects on soil and groundwater regimes and microbial functions that are not fully understood. We hypothesized that clear-cutting and subsequent water table elevation create a niche for anaerobic methanotrophic microbes that mitigate the effect of methane emissions from peatlands. Clear-cutting forest management, soil depth and pH were found to be drivers of microbial community composition. Based on amplicon community profiling, we detected the presence of the genus *Candidatus Methanoperedens* – a member of the anaerobic methanotrophic archaea, in submerged peat layers. The rate of methane production in the submerged peat layers was low two years after clear-cutting. Methane oxidation was detected in anoxic microcosms with an excess of added nitrate as an electron acceptor. However, metagenomic characterization of an active microcosm revealed the presence of aerobic proteobacterial methanotrophs and the absence of anaerobic methanotrophic archaea. This study demonstrates that methanogenesis is not extensive in newly submerged peat soil layers and suggests that aerobic methanotrophs may be capable of oxidizing methane under low-oxygen or anoxic conditions through an unidentified metabolic pathway. The activity of these methanotrophs potentially reduces the amount of methane produced in deeper soil layers.

## MON P30 Ammonia oxidizing archaea and bacteria respond dynamically to drought in rewetted fen peatlands

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Impacts of drought on ammonia oxidizing microbes in peatlands remain unclear, despite their role as a rate-limiting step in nitrification and increasing prevalence of drought. This study aims to identify trends in archaeal (AOA) and bacterial (AOB) ammonia oxidizer abundances and their feedbacks to summer drought in a percolation (PW) and coastal rewetted fen (CW) in northeastern Germany. AOA and AOB abundances were quantified via *amoA* gene copies with qPCR and transcript copies with RT-qPCR from *in situ* peat soil bi-monthly between April 2018 and February 2019, supported by 16S rRNA amplicon sequences and metatranscriptomes. The magnitude of the nitrifying microbiomes' drought response was unexpectedly more pronounced in PW than CW, despite PW exhibiting higher hydrological stability. RT-qPCR showed that PW had an increase in bacterial and archaeal *amoA* transcripts during drought. Additionally, there was evidence in the PW metatranscriptome for shifts in soil nitrogen cycling, first from a decrease in nitrogen fixation after drought onset, then due to a late-drought increase in assimilatory nitrate reduction to ammonium. In contrast, CW had no significant shifts in RT-qPCR *amoA* transcripts or nitrogen cycling mRNA transcript abundances during the drought. This suggests that ammonia oxidizers react significantly to drought, responding to changes in soil nitrogen sources and amplifying shifts in nitrogen cycling gene transcription. Frequent droughts would increase the role of ammonia oxidation in rewetted fens; however, this response may vary between peatland types based on whether the ecosystem is frequently exposed to hydrological changes or is accustomed to hydrological stability.

## MON P31 Low abundance soilborne pathogens inhibit the germination of *Picea jezoensis*

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Soilborne pathogens influence the natural regeneration in forest by inhibiting seed germination and seedling growth. The germination of *Picea jezoensis* is limited by soilborne pathogens under snow but the causal agents are unclear. To investigate the pathogen community, we conducted sowing experiment in 12 plots at 500 m and 700 m altitudes in Hokkaido, Japan. A total of 300 seed bags were put on the soil surface before snowfall, and the fungi infecting the seeds were isolated from ungerminated seeds after snowmelt. Additionally, metabarcoding analysis was performed to investigate the pathogen presence in litter and soil layers. A total of 26 fungal species were isolated from seeds, with *Herpotrichia juniperi* and *Neonectria candida* being dominant (63% of seeds). *H. juniperi* was found in all plots and was more frequent at higher altitude (36–80%), whereas *N. candida* was more common in lower altitudes (20–63%) but rare in higher altitudes (0–8%). Metabarcoding analysis revealed that the relative abundance of *H. juniperi* was 0.3–1.1% in litter and 0.03–0.2% in soil, while that of *N. candida* was 0.0–0.1% in litter and 0.0–0.08% in soil across the altitudes. The average of relative abundance of other species were 0.0–1.2% in litter and 0.0–0.1% in soil. Our results suggest that various fungal species contribute to germination inhibition of *P. jezoensis*. The low abundance of pathogens in litter and soil indicates that the entire fungal community may not fully explain their impact on germination and forest regeneration.

## MON P32 Soil food web interactions alter microbial community structure and function in temperate deciduous forest

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Decomposition of soil organic matter, driven by microbial decomposers, is vital for nutrient cycling in forest ecosystems. The process is influenced by substrate quality as well as complex interactions between organisms of the trophic cascade. The present work examined the combined effect of top-down (via predation by microbivore earthworms and predacious centipedes) and bottom-up (via inputs of cellulose, source of nitrogen and phosphorus) control on soil chemistry, structure of soil prokaryotic and eukaryotic communities, and decomposition activities. From *in situ* mesocosms in a deciduous forest, soil samples from two horizons (FH and A) were collected 10 days after the beginning of the experiment. Amplicon sequencing revealed that while soil communities did not differ between treatments within the soil layer, they were strongly shaped by the horizon, particularly in the case of eukaryotic organisms. Enzymatic activities, assessed via fluorogenic substrates, were generally higher in the FH horizon, likely due to its greater organic matter content. Acid phosphatase,  $\beta$ -glucosidase, cellobiohydrolase, and leucine aminopeptidase exhibited particularly high activity compared to the A horizon. Cellulose addition and centipede presence enhanced most enzymatic activities compared to nutrient inputs alone, though leucine aminopeptidase and chitinase were unaffected by treatments. Our findings highlight the influence of nutrient inputs and macrofaunal interactions on decomposition activity and thus, nutrient dynamics in the forest soil environment. However, the microbial community composition was more strongly influenced by soil horizons than by short-term experimental treatments. Future data from additional sampling times will provide further insights into these intricate ecosystem processes.

## MON P33 Impact of shrub admixture in pine forest stands on soil bacterial and fungal communities and accumulation of polycyclic aromatic hydrocarbons

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Polycyclic aromatic hydrocarbons (PAHs) are a group of persistent and toxic pollutants. The species composition of forest stands plays a significant role in determining the quality of soil organic matter, which in turn influences PAH content. This study aimed to assess the role of shrubs in modulating PAH accumulation in forest soils. The research focused on soils from pine stands in the Rybnik Forest District, an area experiencing some of the highest levels of industrial emission deposition in Europe. Pine stands with and without shrubs (alder buckthorn *Frangula alnus* and European hazelnut *Corylus avellana*) growing under identical soil conditions were selected for analysis. Soil samples were collected from the organic horizon (O) (0–7 cm depth) and the humus mineral horizon (A) (7–15 cm depth). Analyses included measurements of organic carbon (C) and total nitrogen (N) concentrations, pH, alkaline cation content, soil enzyme activity, and PAH levels. The taxonomic composition of soil bacterial and fungal communities was also examined. The results showed that soils influenced by shrubs exhibited the highest enzyme activity, which was positively correlated with total N, organic C, and pH (H<sub>2</sub>O and KCl) and negatively correlated with the C/N ratio. The highest PAH concentrations were observed in soils from pine stands without shrub admixture. The findings highlight the significant role of shrubs in influencing the properties of surface horizons in forest soils, particularly in reducing PAH accumulation. Shrubs enhance soil biochemical activity, resulting in lower PAH levels by contributing more readily decomposable organic matter.

## MON P34 Translocated wet meadows: altered soil structure, moisture, N transformations, and microbial communities with saprophytic fungi increment

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Turf translocation, an undertaking to prevent the destruction of valuable habitats, can challenge soil biota. We sampled translocated wet meadows (ca. 0.8 ha) before and after translocation to assess soil function and microbial communities' stability. Examining plots at the receptor area helped to compare the neighbourhood and possible interactions. Soil moisture, compaction, reactivity, and nutrient availability were investigated. The microbiological features evaluated included taxon-specific markers for quantitative PCR and Fatty Acid Analysis, N transformation (ammonia oxygenase gene quantification, nitrification potential), and the composition and diversity of bacteria, archaea, fungi, and protists, using soil DNA metabarcoding. Translocated soils were compacted, had lower water retention, and N-transformations were altered: N immobilisation prevailed over ammonification, nitrification increased, the ratio of ammonia oxidising archaea to bacteria dropped. A high diversity of fungi, especially saprotrophic, and changes in relative abundance of Ascomycota and Basidiomycota were observed. The root colonisation by mycorrhiza was stable, but their other indices in soil varied (morphospecies number, relative abundance of Glomeromycota). The community structure of Chlorophyta and Alveolata tended to be habitat-specific, with a trend of soil algae to increasing diversity. The observed changes in soil microbiome were mostly related to soil compaction and loss of moisture. In conclusion, translocated turf underwent a functional switch, which depended on the habitat changes following translocation and provided a suitable environment for copiotrophic species: AOB and saprotrophic fungi particularly. Excess of saprophytic fungi can be undesirable for plants, the main target of conservation, as they release less ammonia, and contribute to soil acidification.

## MON P35 Nutrient exchange within common mycorrhizal networks is altered in a multi-species environment

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Although it is known that arbuscular common mycorrhizal networks (CMNs) mediate belowground interactions between one or two species, little is understood about their role in mediating interactions among multiple, co-occurring plant species. We investigated the CMN-mediated interactions among two Central European species, *Inula conyzae* and *Crepis biennis* within pots and the impact of a third plant, an invasive *Echinops sphaerocephalus*, on these relationships. We examined changes in C-to-P exchange within a CMN formed by *Funneliformis mosseae* sourced from Central Europe by tracking plant C cost with  $^{13}\text{C}$  signatures of 16:1 $\omega$ 5 and P acquisition to hosts with  $^{33}\text{P}$  only accessible to CMNs. When only native plants were present, the C cost was consistent for both species, despite CMNs favoring *C. biennis* with P uptake. In the presence of *E. sphaerocephalus*, CMNs also favored *C. biennis* with P, but while *C. biennis* and *E. sphaerocephalus* provisioned similarly large portions of  $^{13}\text{C}$ , *I. conyzae* provided less. Mycorrhizal P acquisition, therefore, was the costliest for *E. sphaerocephalus*, which likely mitigated some *I. conyzae*'s C cost even though both received a low proportion of  $^{33}\text{P}$  from CMNs. *E. sphaerocephalus* altered mineral nutrient and C exchange proportions between native plants and their CMN, suggesting that this species alters belowground plant interactions and that not only specific characteristic of plant host and fungal partner, but also the wider plant community mediates resource exchanges between CMNs and individual plants.

## MON P36 Warming in the Alps: impacts on greenhouse gas fluxes and soil microbiomes

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Alpine ecosystems are highly vulnerable to climate change, yet the effects of warming on high-altitude soils remain largely unexplored. In particular, it is unclear how soil microbial communities will adapt to rising temperatures and how this will influence greenhouse gas (GHG) fluxes, including methane (CH<sub>4</sub>) and carbon dioxide (CO<sub>2</sub>). Understanding these microbial responses is crucial for predicting future carbon cycling in these fragile environments. To address this knowledge gap, we installed open-top warming chambers (OTCs) in permafrost-affected soils at ~3000 meters above sea level across a vegetation gradient. These OTCs passively increase soil temperatures, allowing us to study microbial adaptation to warming under realistic field conditions. Preliminary results show that GHG flux responses vary considerably between sites. Non-vegetated soils exhibit minimal biological activity, whereas vegetated soils release CO<sub>2</sub> and remove CH<sub>4</sub>, suggesting active microbial methane oxidation. Seasonal variations strongly influence gas fluxes, highlighting the importance of long-term monitoring. Microbial community analysis reveals significant differences in bacterial composition between sites and between natural and experimentally warmed soils. Warming effects on bacterial communities may further alter GHG fluxes, with potential consequences for alpine carbon cycling. Additionally, biogeochemical soil variables, including soil moisture, pH and C content, play key roles in shaping microbial community structure and function. This study provides new insights into how alpine permafrost-affected soils respond to warming, emphasizing the role of microbial communities in regulating GHG fluxes. Understanding these dynamics is crucial for predicting the future role of alpine ecosystems in the global carbon cycle under climate change.

## MON P37 Diversity and functioning of the soil microbiome in naturally regenerating temperate beech forest in Slovenia

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Forest harvesting and natural disturbances represent dramatic events in the development of an ecosystem that can turn forest soils into temporary C source rather than a C sink. Furthermore, forest management practices change soil microbial biodiversity and affect various groups of soil microbes and the processes that they mediate. The goals of this study are to compare the effects of forest stand manipulation on gross ecosystem properties and processes. Soils from two different forest management practices and from unmanaged forests were analyzed for microbial biomass (PLFA, NLFA), microbial (16S rRNA gene, ITS2, and arbuscular mycorrhiza fungi marker) and understory plant community (trnA) composition (Illumina Sequencing), decomposition potential of microbial community, extracellular enzyme activity and soil physicochemical parameters along with vegetation data to describe microbial community development and to identify how functional guilds of microbes and microbe-mediated ecosystem processes change in forest soils after a decade of natural regeneration. Development of microbial communities after logging is site specific and differences between management types do not show common pattern. Fungal community structure and function was affected by applied forest management and underwent serious changes affecting the decomposition potential of the soil and these changes were detectable after 10 years of natural regeneration, while bacteria and AM fungi communities were not affected. The soil nutrient content seems to be a main driver in soil processes. High content of N and P and higher pH resulted in different pattern of community development with higher bacterial and arbuscular mycorrhizal fungi biomass and higher decomposition potential.

## MON P38 Direct vs. indirect climate effects on fungal communities and species responses: the role of vegetation-mediated pathways

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Climate is a major driver of fungal community composition, but distinguishing its direct effects (e.g., temperature and precipitation changes) from indirect effects mediated by vegetation remains a key challenge. Many predictive models rely on correlations between climate and fungal distributions, making it difficult to determine whether observed shifts are driven by climate itself or by climate-induced vegetation changes. To address this, we analyzed fungal community composition and species-level responses along eight elevational gradients in Europe, leveraging sites with stable and varying vegetation to isolate direct climatic influences from vegetation-driven effects. Our results show that ectomycorrhizal fungi respond primarily to direct climate factors. In contrast, plant pathogens, root endophytes, and saprotrophs are influenced by both direct and indirect effects, with vegetation-mediated impacts even more striking. At the species level, these patterns were largely mirrored: ectomycorrhizal fungi were structured mainly by direct climate effects, while root endophytes and litter saprotrophs were influenced by both direct climate factors and, more strongly, by climate-driven vegetation shifts. Our findings challenge the conventional view that climate alone dictates fungal distributions. Instead, they underscore the need to integrate both direct and indirect pathways into predictive models. Without accounting for vegetation-mediated effects, we risk severely underestimating how fungal communities – and the critical ecosystem processes they regulate – will shift in a warming world.

## MON P39 Cultivar-dependent AMF colonization modulates metabolic pathways and bacterial communities in water-stressed wheat

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Arbuscular mycorrhizal fungi (AMF) play a crucial role in mitigating drought stress in durum wheat (*T. turgidum* subsp. *durum* (Desf.)), but the influence of cultivar-specific mycorrhizal affinity on metabolic and microbial responses remains largely unexplored. The present study explored the mycorrhizal relationships of two durum wheat varieties, Iride and Ramirez, and their effects on root metabolism and the bacterial communities in both roots and soil under optimal watering and drought conditions. Iride exhibited high AMF colonization affinity, while Ramirez showed low affinity. Untargeted metabolomics revealed more pronounced alterations in metabolic pathways in the highly colonized variety under water deficit conditions, with AMF contributing to the regulation of amino acids, alkaloids, phenylpropanoids, lipids, and hormones in both varieties. The 16S metagenomics approach revealed a suppression effect of drought on bacterial taxa, including drought-tolerant taxa, particularly in non-inoculated plants. However, AMF provided a protective effect, especially in the Iride variety, maintaining the abundance of drought-depleted taxa such as Planctomycetes, Bacteroidetes, and Verrucomicrobia. Drought also reduced the network complexity of root and soil bacteria, with a more pronounced effect in the Ramirez variety. These findings highlight the significance of considering cultivar-specific mycorrhizal affinity in understanding the complex interplay between plant genotype, AMF symbiosis, and microbial communities in drought stress tolerance, paving the way for the development of targeted strategies to improve crop resilience to water scarcity.

## MON P40 A comparison of the realized and fundamental niches of selected AM fungal species along a nitrogen gradient

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Despite the close association between arbuscular mycorrhizal fungi (AMF) and their host plants, both partners in this symbiosis can respond differently to environmental changes, such as nitrogen availability in the soil. Most predictions of AMF responses to global changes often only consider realized niches. Still, these do not capture the full "potential" of the species, as they are always derived from fundamental niches (full range of conditions where certain species can proliferate and grow) and are influenced by biotic interactions with other species. This study aims to compare the realized and fundamental niches of selected AMF species along previously mentioned nitrogen gradient which is highly prone to change due to anthropogenic activities. This research employs a combination of experimental and database approaches. The newly published GlobalAMFungi (Větrovský et al. 2023) database is utilized to estimate the realized niches of AMF species, while controlled experiments assess their fundamental niches along nitrogen gradient. Preliminary results from two greenhouse experiments suggest that AMF species exhibit distinct preferences along the nitrogen gradient. Notably, in one experiment, *Rhizophagus irregularis* achieved dense root colonization even at high nitrogen levels, which were detrimental to host plants and other AMF species. Knowledge of the fundamental niche in nitrogen axis of AM fungi and its comparison with the realized niche should help us to better predict the impacts of global changes due to nitrogen deposition on AM fungi.

## MON P41 Rapid soil changes following the expansion of heathland shrubs into grasslands: Implications for predictive models

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Climate change and decreased land management practices lead to shifts in vegetation range. One instance of this process is the encroachment of heathland shrubs into grasslands, which has been observed increasingly. Changes in soil microbial communities and chemistry accompany these vegetation shifts. However, the rates at which said transformations occur remain unclear, challenging the accuracy of predictive models under ongoing environmental change. In this study, we address this knowledge gap by using high-resolution spectral maps to visualize the change in vegetation cover over the course of ten years on Luční hora (Giant Mountains) in Czechia. There, *Nardus stricta* alpine grassland is being overgrown by shrubs of the *Ericaceae* family, namely *Vaccinium myrtillus*, and *Calluna vulgaris*. We analyzed soil samples from areas where vegetation cover has not changed and areas where shrubs encroached to assess changes in soil chemistry and microbial communities. Our findings show that soil abiotic and biotic changes can occur rapidly following vegetation shifts, but the rate and sequence of changes depend on the expanding species. In the case of *V. myrtillus*, all soil parameters – including chemistry, fungal, and bacterial communities – were fully adjusted within 10 years post-expansion. Contrastingly, for *C. vulgaris*, vegetation shift initially alters fungal community composition, leading to subsequent changes in soil chemistry, with bacterial communities responding only after these shifts. These findings highlight species-specific dynamics in soil transformation and contribute to improving predictive models of soil change in response to vegetation shifts driven by climate change and human activity.

## MON P42 Post-fire dynamics of soil fungal communities: fungal community recovery and functional shifts across a burn severity gradient

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Wildfires have become increasingly prevalent in forests worldwide, posing significant ecological and environmental challenges. Given the crucial role that soil fungi play in nutrient cycling and carbon sequestration, understanding how fungal communities respond to forest fires is pivotal for assessing ecosystem resilience and post-fire recovery. To examine post-fire fungal development, we established 24 long-term plots across a burn severity gradient in a mixed temperate forest, sampled biannually. Over 26 months, we tracked changes in soil fungal biomass, community composition, mycelial production, and functional potential. We observed a tenfold reduction in soil fungal biomass across burn severities, with no signs of recovery up to 21 months post-fire. Wildfire significantly reduced soil fungal richness regardless of burn severity, with ectomycorrhizal taxa being particularly affected. While fungal community composition was significantly altered by fire, there were no differences between burn severities. Mycelial production was virtually absent at severely burned sites 14 months post-fire but resumed between 21- and 26-months post-fire, reaching control levels. By the second year, the relative abundance of ectomycorrhizal fungi significantly increased at severely burned sites compared to the first year. Wildfire significantly reduced microbial activity – measured by enzymatic activity and soil respiration – for up to 14 months post-fire. Our findings reveal that while mycelial production resumes within two years, fire-induced disruption to microbial diversity persists beyond this period, underscoring the long-term ecological impact of wildfires.

## MON P43 Recovery of forest fungal communities across a gradient of burn severity

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Wildfires are becoming more frequent and intense due to ongoing climate change, impacting vegetation, soil structure and soil microbial community, such as fungi, which play key roles in carbon storage, soil fertility, and therefore ecosystem recovery. While mild wildfires mainly burn understory vegetation and tree surfaces, severe fires can kill trees and transform the organic horizon into highly aromatic pyrogenic compounds. Therefore, understanding how fire severity affects fungal communities is essential for better predicting and managing post-fire forest regeneration. In August 2022, a wildfire consumed over 1300 ha of forest in the Saxon-Bohemian Switzerland region (Czechia). Since the event, soil samples have been collected each May and October from sites affected by mild and severe fires, as well as from nearby unburned control sites. Total DNA has been extracted and sequenced to analyze fungal metagenomes. This study presents early post-fire results. Through two approaches- full metagenome assembly and targeted functional gene analysis - we aimed to characterize early post-fire fungal communities, identify their key functional traits, particularly their decomposition ability, and assess fire severity effects. Specifically, we tested two hypotheses:

- Ectomycorrhizal fungi would reestablish faster after mild fire, where tree survival was higher. Necromass decomposition could be a prevalent trait among fungi, supported by tree carbon allocation, as it constitutes an important source of nutrient.
- In contrast, saprotrophs would dominate after severe fire, characterized by rapid colonization or the ability to degrade pyrogenic aromatic compounds, reflected in higher share of peroxidase and laccases coding genes.

## MON P44 Microbial mechanisms controlling methane-temperature hysteresis in wetlands.

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Recently, high methane emissions in autumn relative to the same temperatures in spring was demonstrated in wetlands globally. However, the underlying mechanisms of this lagged response in methane emissions to summer warming, here called methane-temperature hysteresis, remain unclear. This limits our ability to predict future trajectories in methane emission patterns in response to global warming. To explore the mechanisms behind methane -temperature hysteresis in northern wetlands, we performed an anoxic laboratory temperature experiment using peat soil from four different sites, located in: Svalbard, Norway (mainland), Canada and Greenland. We exposed the soils to a 9-week temperature-ramp (2–10–2°C) changing two degrees per week, simulating a transition from spring to autumn. Methane accumulation rates, substrate availability, RNA and DNA content and community composition and size were monitored throughout the experiments. Three out of four sites expressed methane-temperature hysteresis (Svalbard, Norway and Greenland). In the soils from Svalbard and Greenland, a temperature threshold of 6 °C triggered overconsumption of methanogenic substrates that had accumulated at low temperatures fuelling an increase in the methanogenic community size, trends persisting after initiation of cooling. In soils from Svalbard and Norway, RNA/DNA ratios increased during cooling, indicating increased investment into protein biosynthesis. Svalbard was the only site expressing methanogenic community composition changes. Our study demonstrates that methane-temperature hysteresis arises from a combination of site-specific microbial temperature responses. Exploring these mechanisms in more detail will help us improve future predictions of methane emissions from warming wetlands.

## MON P45 The temporal stability of active bacteria in grassland and forest soils across a time series spanning 12 years

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The twin crises of climate change and biodiversity loss pose two of the greatest risks to humanity's ability to further thrive on Earth. While their detrimental effects on plants and animals are fairly well understood, the situation is less clear for bacteria, for example in soils. Here we use the fully factorial sampling design of the German Biodiversity Exploratories, covering a total of 150 grassland and 150 forest plots across three regions in Germany. The plots were sampled in May in 2011, 2014, 2017, 2021 and 2023, yielding a total of 1500 amplicon sequence data sets for 16S rRNA transcripts. We analysed the resulting several 100k amplicon sequence variants (ASVs) for their abundance variability in a scaled rank abundance distribution across all five time points per plot. Interestingly, a surprisingly high fraction of approximately 70 to 80% of all ASVs stably maintained their rank position, regardless of whether they were abundant or rare. In forests, the proportion was slightly lower, but still above 50%. While ASVs were stable over time, the specific rank position of ASVs could vary significantly between habitats and regions and also across different taxonomic or functional groups. Our approach allows to attribute both the level of abundance and the question of temporal stability or variability of abundance to habitats and to their temporal dynamics of specific environmental variables at the level of individual ASVs. This markedly improves understanding of soil ecology at ASV level.

## MON P46 Spatial sampling strategies for soil biodiversity: insights from the SpaceMic project

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Soil biodiversity is crucial for ecosystem function, but is spatially variable, making its characterization difficult. Monitoring soil biodiversity requires targeted sampling strategies that integrate ecological principles, such as distance decay relationships, into their design. We present key findings from the SpaceMic project, within the framework of the German Biodiversity Exploratories, investigating how spatial sampling designs influence metabarcoding-derived biodiversity estimates in grasslands and forests. Using 16S, 18S, and ITS marker genes, we examined the effects of sample extent and sample number on alpha, beta and gamma diversity across 54 plots. Our results reveal a critical trade-off: homogenizing multiple soil samples into a single composite increased observed plot diversity with sample number, but likely at the cost of capturing the full spectrum of diversity. Sample extent had minimal impact on plot-level diversity, suggesting flexibility in plot size for research studies, but highlighting the importance of consistent plot dimensions within a given study. We recommend a standardized, spatially explicit sampling design incorporating both single and composite samples per plot. This dual approach maximizes information capture while ensuring comparability, essential for robust biodiversity research. Our findings offer practical guidelines for optimizing soil sampling, improving reproducibility, and strengthening the ecological insights gained from biodiversity research.

## MON P47 The mineral-organic horizon interface as an activity hotspot for methane-cycling microorganisms in kettle holes

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Kettle holes are characterized by layers of peat and colluvial mineral soil, seasonal wet-dry cycles, and often significant nutrient input from surrounding agricultural land. They are at least temporarily sources for atmospheric methane. Different groups of methane-cycling microorganisms thrive under these conditions with unknown spatiotemporal distribution and activity patterns determining methane fluxes. We investigated whether soil horization along with changing water table and seasonal variations relate to changes in abundance and especially activity of these methane-cycling organisms in a model kettle hole near Christianenhof, Brandenburg, Germany. Soil cores were taken next to five permanently installed automatic GHG measuring chambers within the kettle hole over a full plant growth period and separated depending on soil horization. The abundance and gene expression of functional marker genes *pmoA* and *mcrA* was determined by quantitative PCR. Activity of methanogens and anaerobic methanotrophs peaked under water-saturated conditions in early spring, when overall abundance was lower and more even across soil horizons, than in summer when dry phases occurred irregularly. Aerobic methanotroph distribution remained rather stable between horizons throughout the plant growth period, though with lower overall abundance in winter and early spring. The highest copy numbers of methanotrophs and methanogens were detected near the mineral-peat transition zone, indicating that this is a hotspot for methane-cycling microbes. In the future, physicochemical properties of the soil and methane flux data will be correlated with our microbial data to develop a deeper understanding of the causes of the strongly fluctuating methane fluxes in kettle holes.

## MON P48 No recovery – three years of land-use reduction showed no effect on the methane sink function of grassland microbiomes

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Grassland soils are important methane (CH<sub>4</sub>) sinks through CH<sub>4</sub> oxidation by methanotrophs, but intensive management with high nitrogen inputs reduces this potential. While long-term recovery of the CH<sub>4</sub> sink is well established, little is known about the scope of short-term land-use intensity (LUI) reduction in grassland. We investigated the effects of an experimental three-year prolonged LUI reduction (no fertilization, no grazing, and only one mowing event per year) on 45 grassland sites across three pedoclimatic regions in Germany. As a baseline for the functional potential of LUI reduction, we also studied 15 sites with historically low LUI. We measured the potential CH<sub>4</sub> oxidation rate (PMOR), CH<sub>4</sub> production potential and the abundance of functional genes for CH<sub>4</sub> oxidation by methanotrophs (*pmoA*) and CH<sub>4</sub> production by methanogens (*mcrA*). After three years, LUI reduction had no significant effect on microbial activity or abundance in any region. However, historically low-LUI sites exhibited higher CH<sub>4</sub> oxidation potential and greater Upland Soil Cluster  $\gamma$  (USC $\gamma$ ) methanotroph abundance than sites with three years of LUI reduction. USC $\gamma$  and USC $\alpha$  abundance was correlated with PMOR while that of general *pmoA* functional genes was not. High correlation between general *pmoA* and *mcrA* highlight a methane filter function that is independent from reduction of LUI across regions. Our study consistently proved that three years of reduced LUI are not enough to recover the CH<sub>4</sub> sink function of grasslands and USC $\gamma$  methanotrophs may play a key role mediating recovery in the future.

## MON P49 The effects of vegetation shifts on soil microbial communities and carbon storage in subarctic soils

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In recent years, Arctic regions have experienced shifts in vegetation. Meadows and other highly productive vegetation types are transitioning to landscapes dominated by slower-growing, slower-decomposing shrubs, accompanied by treeline expansion. These changes in plant cover are closely linked to mycorrhizal associations. To study the impact of vegetation transitions on soil fungal communities, soils containing arbuscular mycorrhizal, ectomycorrhizal, and ericoid mycorrhizal fungi were collected from various sites in the Tromsø region in 2020. In an experimental setup, these soils were used as habitats for seedlings of plant species with either similar or contrasting mycorrhizal types, which were then grown for three years under typical Tromsø weather conditions. By the third year, measurements were taken on soil chemical composition, plant processes, and microbial community changes. Across all soils, ectomycorrhizal fungi dominated most treatments, while arbuscular mycorrhizal fungi exhibited low overall abundance. The results showed that total fungal richness, as well as ectomycorrhizal and ericoid fungal richness, varied depending on planting type, soil type, and sampling time. The lowest total fungal richness was observed in arbuscular and ectomycorrhizal woody plantings, whereas ectomycorrhizal and ericoid fungal richness were highest. PERMANOVA analysis indicated that fungal community composition differed between soil types. Furthermore, within each soil type, fungal community composition varied according to planting type. These findings suggest that shifts in vegetation significantly influence soil fungal communities, which, in turn, may have lasting effects on carbon storage in the subarctic tundra.

## MON P50 Microbial succession and aggregate formation in an indoor pot experiment with clean sand and willows

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Different species of willow (*Salix sp.*) were historically used for slope stability improvement and afforestation on sandy soils. Willows can be grown from cuttings harboring microbial symbionts that may help successful plant establishment. In an indoor pot experiment we estimated change of physical, chemical and microbiological parameters of clean sand during the growth of willows. Samples were taken from different pots that were disassembled on days 30, 60, 90, and 150. Sand aggregation around roots was observed in pots sampled at day 150 (aggregate diameter ranged from 0.66 to 4.5 mm, with average 1.64 mm). Sequencing of gene libraries (bacterial 16S rRNA, fungal ITS2) was performed for 64 samples of DNA extracted from bulk sand and aggregates. Bacterial community structure changed with time, and Shannon index significantly increased from day 30 to day 150. Alpha- and Gammaproteobacteria were dominant in all samples (up to 45 and 64%, respectively). Bacteroidota, Planctomycetota, Chloroflexota abundances increased along the succession. In aggregates, bacterial community was dominated by plant-associated bacteria like *Sphingobium sp.*, while Firmicutes were significantly reduced compared to sand samples. No clear trends could be observed for fungal communities, as distribution of fungal dominants in sand samples was more scattered. In aggregates, *Plectosphaerella*, *Neopyrenochaeta*, *Chaetomium*, *Clonostachys* and some other endophytic and plant-pathogenic genera were found. Our findings show that the growth of willow cuttings leads to sand fixation by root reinforcement, and plant-induced sand aggregation happened after 5 months.

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## MON P51 Global colonization success of soil fungi: do plant pathogens and mutualists track warming at different rates?

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Climate change rapidly redistributes species, but their ability to track suitable environments can be influenced by mismatches among interacting species. Soil pathogens and arbuscular mycorrhizal (AM) fungi shape plant success, so the spread of plants could be facilitated by a lack of pathogens or limited by a lack of mutualistic AM fungi. With two global datasets of soil fungal DNA sequences (which we have matched with known taxa using molecular markers), we examine relative colonization success of plant pathogens and AM fungi. As a proxy for colonization success, we use community completeness, that is, the proportion of present species out of all species (present and absent) that could potentially inhabit an area. This metric is derived from actual presence data and estimates of dark diversity, the set of species that could live in an area but are currently absent. We calculate dark diversity using an established method based on species co-occurrences indicating habitat suitability. We expect soil fungal community completeness to decline toward higher latitudes due to poleward areas becoming newly suitable after post-glacial and contemporary warming. However, this relationship may differ between plant pathogens and AM fungi, reflecting potential differences in their ability to disperse and establish in new areas. Additionally, if range expansions lag behind warming, we expect this to be reflected in lower community completeness in faster-warming regions of the world. We present our results and discuss their implications for plant-fungal interactions.

## MON P52 Fungal community shifts across Scots pine stand development: from early succession to maturity

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Root samples of Scots pine (*Pinus sylvestris*), lingonberry (*Vaccinium vitis-idaea*), bilberry (*Vaccinium myrtillus*), and heather (*Calluna vulgaris*) were collected from sites with different age classes: 2-year-old, 14-year-old, and mature Scots pine stands. Sequencing of fungal ITS2 regions revealed both shared and unique fungal compositions among species and sites. This was further confirmed with fungal isolation and identification of ITS region. The dark septate endophyte (*Phialocephala fortinii*) was the most common fungus observed in all roots. Selected DSE isolates were re-inoculated into Scots pine roots and tested for their ability to grow under drought conditions (low water potential). Inoculations confirmed the endophytic status of the DSE. There were differences among endophytes in their tolerance to drought conditions.

## MON P53 Climate effects on microbial communities across mountain forest ecosystems

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Microbial communities in forest ecosystems play crucial roles in biogeochemical cycling and ecosystem functioning, yet our understanding of how these communities respond to climate change remains limited. In this study, the effects of climate variables on bacterial and fungal communities in soil and litter across European mountain systems were examined. Samples were collected from 17 mountain sites representing diverse elevational and latitudinal gradients, with both soil and litter analyzed from each location. Microbial community composition in these samples was characterized through high-throughput Illumina MiSeq sequencing of bacterial 16S rRNA and fungal ITS2 regions. Through multivariate statistical approaches, the contributions of multiple climate variables (including mean annual temperature, precipitation, and seasonality, among others), soil physicochemical properties (pH, nutrients such as carbon, nitrogen, phosphorus), and vegetation characteristics to microbial community structure were assessed. Our research provides insight into distinct response patterns between habitats (soil versus litter) and taxonomic groups (bacteria versus fungi) to environmental variables, while also identifying key drivers of microbial community composition. This advances our knowledge of the complex interactions between climate, soil properties, and microbial communities in mountain forests, providing critical insights into how these key biogeochemical agents may respond to ongoing climate change.

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## MON P54 Forest management effects on the ericoid mycorrhizal fungal community in bilberry (*Vaccinium myrtillus*) roots

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Stand-based forest management with clear-cut harvesting has transformed boreal forests in Northern Europe into mosaics of homogeneous forest stands of different age classes. The understory vegetation in these forests is dominated by bilberry (*Vaccinium myrtillus*), which forms symbiotic relationships with ericoid mycorrhizal (ErM) fungi. Together, they influence carbon and nutrient dynamics in boreal forest soil. Previous studies have shown that bilberry cover in northern European spruce forests is decreasing due to clear-cut forestry, with potential, but so far unstudied, cascading effects on their mycorrhizal fungal symbionts. In this study, we first analyzed how the abundance of bilberry in spruce forests is influenced by previous clear-cutting. We then examined fungi colonizing bilberry hair roots and assessed how clear-cutting, along with other environmental factors, affects the diversity and composition of ErM communities. Vegetation surveys were conducted, and bilberry hair roots were sampled in twelve pairs of (i) previously clear-cut, mature forests, and (ii) never clear-cut near-natural forests, in South-Eastern Norway. Fungal communities were identified through ITS2 metabarcoding of cleaned bilberry hair roots. The vegetation surveys revealed a reduction in bilberry cover in the previously clear-cut forests compared to near-natural forests. Previously known ErM fungi were detected among the most abundant taxa in bilberry hair roots, but we also recovered saprotrophic and ectomycorrhizal fungi. Temperature and soil pH were significantly associated with fungal community composition. Our results indicate that clear-cut forestry has a significant but moderate effect on the ErM fungal diversity and composition.

## TUE P1 The impacts of sewage sludge fertilization on soil resistome

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Replacing inorganic fertilizers with sewage sludge has the potential to transform agricultural practices by promoting nutrient recycling and enhancing soil health. Sewage sludge, a by-product of wastewater treatment, is rich in organic matter and essential nutrients like nitrogen and phosphorus, making it an effective alternative to synthetic fertilizers. Utilizing sludge for soil fertilization can reduce dependency on chemical inputs, lower production costs for farmers, and mitigate environmental impacts associated with the manufacture and use of synthetic fertilizers, such as greenhouse gas emissions and soil degradation. However, sewage sludge contains contaminants, including heavy metals and antibiotic-resistant bacteria, which can pose long-term threats to soil health and human safety. Furthermore, the accumulation of toxic substances can adversely affect crop safety and ecosystem functioning. In this work we used metagenomic sequencing to determine the antibiotic resistance genes in sewage sludge. In addition, we studied how long-term application of sewage sludge on farmlands affects the concentration of antibiotics and heavy metals in soil and whether antibiotic resistance genes would accumulate in soil microbiome. Our results show that sewage treatment decreases the overall antibiotic resistance gene load in sewage sludge, but there are still antibiotic resistance genes of concern present. The long-term sludge application did not enrich antibiotic resistant bacteria or antibiotic resistance genes in farmland. However, the study was conducted in northern Europe, where antibiotic use is relatively low and colder climate might affect the survival of pathogenic bacteria, so further studies are needed in more diverse settings.

## TUE P2 Impact of herbicides and fungicides on soil bacteria: unveiling neutral to positive dynamics based on the soil and active substance

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Pesticides are essential for crop protection, but their adverse effects on beneficial soil microorganisms undermine the plants' natural defenses and disrupt crucial functions like nutrient cycling and soil fertility. Despite ongoing research, our understanding of the specific impacts of individual pesticides on microorganisms remains insufficient due to the many active ingredients on the market that frequently change. Here, we tested the immediate direct effects of three fungicides and five herbicides on the diversity, total abundance, and community composition of bacteria. We applied pesticides at concentrations recommended by manufacturers to three soils differing in pH, which had not been treated with pesticides for 10 years. To identify communities of bacteria, we used Illumina pair-end amplicon sequencing. To evaluate the total abundance of bacteria, we employed real-time PCR. We recorded positive, negative, and neutral effects of pesticides on the diversity and the total abundance of bacteria, depending on the active ingredient and soil used. As pH varied among the soils used, was influenced by pesticides, and in turn affected both total bacterial abundance and bacterial community composition, it can be concluded that the impact of pesticides on bacteria was at least partially indirect, mediated through changes in soil pH. Therefore, when selecting active ingredients, it is crucial to account for specific environmental conditions to minimize negative impacts on soil microbial communities and promote sustainable agriculture.

## TUE P3 The effect of pesticides on fungal diversity and abundance varies across soils

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Pesticides play a crucial role in controlling pests and diseases in agriculture, but their unintended effects on non-target organisms cannot be neglected, as they impact ecosystem functions and crop quality in agroecosystems. This study examined the effects of three fungicides and five herbicides on fungal diversity, total abundance, and community composition in soils from three farmlands with different pH levels, untreated with pesticides for 10 years. Soils were treated with pesticides according to manufacturer recommendations. Fungal communities were analyzed using Illumina sequencing and real-time PCR (qPCR). Our results revealed that the three tested soils had distinct fungal communities. Depending on the specific pesticide and soil used, pesticides influenced fungal diversity, composition, and abundance. Fungal diversity and total abundance were correlated with pH, which also affected fungal community composition. However, the impact of pesticides on pH did not always correspond with their effect on fungi. Some pesticides that affected fungal communities or total fungal abundance did not alter soil pH, while others that changed pH had no impact on fungal communities. This suggests that pH was not the sole factor driving the effect of pesticides, and the sensitivity of distinct fungal communities in different soils, or other untested soil factors, may contribute to the variability in pesticide effects. These findings highlight that uniform pesticide responses across soils cannot be assumed due to complex and context-dependent interactions between soil properties, pesticides, and fungal communities. This complexity must be carefully considered when selecting pesticides to ensure their effectiveness and minimize unintended ecological consequences.

## TUE P4 Diversity and seasonal variation of soil microbial communities in response to different agricultural practices

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Changes in climatic conditions and land-use are major drivers of global change and affect the functioning of soil ecosystems worldwide, with profound consequences for soil microbial communities. A large field experiment in central Germany – the Global Change Experimental Facility (GCEF) – was established in 2013 to investigate the consequences of a future climate scenario on ecosystem processes under different land-use regimes. Two farming and three grassland systems, differing in their land-use intensity, were subjected to ambient and projected future climate conditions. In the context of the GCEF, the present study investigated the responses and adaptations of soil bacterial and fungal communities to the implemented agricultural practices under the different climate scenarios and the potential interactive effects of both global change drivers. In addition, a seasonal soil sampling regime aimed at exploring inter-seasonal changes within the soil microbial communities. Sampling was conducted from June 2019 to March 2020, during a multi-annual period of drought. The study revealed that land-use type (farming vs. grassland) and an increasing land-use intensification significantly shaped the microbial community structure, which was more pronounced for fungi. Fungal alpha diversity decreased with higher intensification, especially in grassland, whereas bacterial alpha diversity was not influenced by land-use. Climate treatment had only a weak effect on microbial communities during the period of the study. In contrast, a strong seasonality of bacterial and fungal abundance was observed, leading to different seasonal patterns depending on individual taxa and land-use. Seasonal variations in the community structures could be explained by soil parameters.

## TUE P5 Linking agricultural management to soil microbial dynamics: how organic matter, biocontrol, and crop management shape soil ecology

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Understanding the influence of agricultural practices on the interactions between plants and soil microorganisms is crucial for developing new approaches that support the agroecological transition. In this context, farmers from the Carbon 'N' Caux group in Normandy are exploring innovative ways to manage their farms effectively while promoting agricultural practices that improve soil health. Three farm platforms were established across three sites to assess the impact of alternative farming systems on soil biological functioning: (1) the application of exogenous organic matter (livestock manure and green waste compost), (2) methods of cover crop destruction (chemical destruction using glyphosate and mechanical destruction using a harrow), and (3) the reduction in the use of phytosanitary products (comparison between phytosanitary products and biocontrol). Multi-year monitoring (2020–2023) was conducted using a range of bioindicators, including fungal and bacterial abundance, enzyme activities ( $\beta$ -glucosidase, alkaline phosphatase, N-acetyl-glucosaminidase) and mycorrhizal symbiosis (spores abundance and mycorrhizal colonization). The results showed that organic matter inputs positively influenced soil microbial communities, enhancing enzymatic activities and mycorrhizal colonization, with a continuous increase in these bioindicators observed since 2021. Biocontrol products demonstrated beneficial effects on microbial communities, significantly increasing spore abundance and mycorrhizal colonization from 2021 to 2023. In contrast, cover crop destruction methods negatively impacted fungal and bacterial abundance in the soil, although glyphosate showed a more positive effect on mycorrhizal colonization compared to harrowing. This study provides farmers and agricultural advisors with valuable insights into soil biological functioning, encouraging the adoption of sustainable farming practices to maintain soil health and productivity.

## TUE P6 Microbial response to fertilization intensity and cropping systems: insights from a 42-year-old long-term experiment

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Agricultural intensification has significantly increased food production at the expense of soil biodiversity and ecosystem services. Organic fertilization can enhance soil quality but also poses environmental risks. Reduced stocking density, and consequently lowering farmyard manure inputs (FYM), may further impact soil microbial communities, yet research on these effects remains limited. Furthermore, while taxonomic shifts in microbial communities due to different cropping systems are relatively well characterized, knowledge of how cropping systems influence soil metabolic potential is scarce. We present findings from the 42-year-old DOK long-term experiment, investigating (1) the impact of FYM input levels on microbial community structure using amplicon sequencing and (2) the effect of different cropping systems on soil metabolic potential using shotgun metagenome sequencing. We found that a decrease in livestock density with associated reduced levels of FYM inputs in organic and integrated cropping systems alters soil habitat quality and microbial communities. The reduced nutrient availability under low-input selects for more oligotrophic microbiomes which are more efficient in obtaining nutrients from various carbon sources - a potentially beneficial trait considering future agroecosystems. We also find that organic and conventional cropping systems distinctively shape the soil metabolic potential: Organic systems enriched genes involved in organic phosphorus acquisition, nitrate transformation, and complex carbon degradation, while in contrast, conventional systems favored genes associated with inorganic nutrient uptake and transcriptional activity, indicating distinct microbial strategies for nutrient cycling and survival. Consequently, cropping systems can be utilized to steer the regulating potential of agricultural soils, potentially lowering the environmental impact of food systems.

## TUE P7 Bio-based fertilizers and antibiotic-producing bacteria in the ecology of antibiotic resistance in Finnish agricultural soils

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The use of bio-based fertilizers is promoted due to sustainability goals, yet these materials may contain bacteria carrying antibiotic resistance genes as well as antibiotic producers. The role of antibiotic-producing bacteria in the ecology of antibiotic resistance has not been extensively studied and is, therefore, not fully understood. This study explores the role of antibiotic-producing bacteria in the dissemination and maintenance of antibiotic resistance in agricultural environments through bio-based fertilizers. Bacterial isolates from two bio-based fertilizers, the fertilizers, and soil samples collected before, immediately, and six weeks after fertilization were investigated. Metagenomic and whole genome sequencing were performed, and data was analyzed using bioinformatic tools. The highest abundance and diversity of antibiotic resistance genes and mobile genetic elements were detected in the bio-based fertilizers, followed by the soils immediately after fertilization, with a decrease in the soils six weeks post-application, returning to resemble pre-fertilization levels. The isolates, classified as *Streptomyces* spp., harbored putative resistance genes, various mobile genetic element components, and secondary metabolite gene clusters with antibiotic activities. Preliminary results suggest that antibiotic-producing bacteria may contribute to the maintenance and possibly even transmission of antibiotic resistance genes in composted biosolids, influencing the dissemination and evolution of antibiotic resistance. By examining the genetic environment of the antibiotic resistance genes – particularly their association with mobile genetic elements and/or antibiotic-producing gene clusters – we could assess their potential mobility and determine whether they are maintained due to antibiotic production.

## TUE P8 Is a dual-plant system more efficient in nitrogen cycle closure? An Italian study on clover-wheat intercropping

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Diverse agricultural systems, like intercropping, promote ecosystem services, including pest management, climate resistance, soil vitality, and water retention. Functional diversity creates biological synergies that improve nutrient utilization and pest and disease control, increasing system stability and reducing external inputs. Nitrogen is critical for plant growth. Examining its cycle provides insights into soil and vegetation health. This research investigates how co-cultivating wheat, and clover affects soil properties and microbes involved in nitrogen cycling. Study focuses on the first year to evaluate the immediate consequences of intercropping under two ammonium nitrate fertilizer regimens: standard application and a 30% reduced rate. qPCR was used to evaluate the abundance of various phylogenetic groups, potential microbial functionality of nitrogen cycle genes, and observe differences in plant cover pattern. The abundance of total bacterial and archaeal genes was not significantly affected by intercropping and nitrogen fertilization regimes. However, intercropping increased the abundance of fungal ITS genes under both fertilization levels. In intercropping with reduced nitrogen fertilization, an increase was observed in the abundance of genes associated with denitrification (*nirS*, *norB*, *nosZ*) and nitrification (archaeal *amoA*). Urease activity was elevated in soil under reduced fertilized intercropping. Both factors and their interaction did not significantly impact SOC, NT, and C:N ratios. Our research suggests that archaea may be the primary factor in activating denitrification processes, and intercropping could influence nitrogen cycle. Fertilization and intercropping strategies significantly affect the nitrogen cycle, with improved system performance observed in intercropping with reduced fertilization, indicating interspecific complementarity between wheat and clover.

## TUE P9 Preliminary results on bacterial and fungal microbiome transfer to wheat roots and rhizosphere in legume-cereal intercropping

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Legume-cereal intercropping is one of several approaches to supporting resilient climate, sustainable agriculture, and food production. It can also reverse biodiversity loss and soil degradation and contribute to reduced fertilization. Moreover, intercropping systems reduce interspecific competition by enhancing complementarity processes, thus improving resource exploitation. This causes plant production to increase, corresponding to the agroecosystem's greater efficiency. However, there is still a knowledge gap in recognising soil-plant-microbe interactions, including bacterial and fungal transfer among different ecological niches of plant holobionts. Therefore, the study aimed to assess the transfer of micro- and myco-biomes from tested plants (wheat, clover, grasses) shoots, roots, rhizosphere, and bulk soil to wheat roots and rhizosphere. The study was based on a long-term experiment in Poland (Osiny, N: 51°28', E: 22°4'). The organic intercropping system included Harenda variety spring wheat (*Triticum aestivum* L.) with a mixture of Dajana variety red clover (*Trifolium pratense* L.), perennial ryegrass (*Lolium perenne* L.) and meadow fescue (*Festuca pratensis* Huds.) grasses. Samples of plant and soil compartments were collected in 2023, separately for each plant species. After DNA extraction, next-generation sequencing of bacterial and fungal marker genes was performed on the MiSeq Illumina platform. After bioinformatics analysis, amplicon sequence variants (ASVs) were analysed using Source Tracker Software. The results allowed for the tracking of the source of microbes between ecological niches, especially highlighting the transfer of rhizosphere-roots and shoots-roots fungal and bacterial microbiomes, respectively.

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## TUE P10 Effects of different agroforestry systems on soil microbial communities

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Agroforestry has gained a lot of attention in recent years. Trees and shrubs in agroforestry systems (AFS) can influence soil organisms through their root systems, leaf litter, shading, etc. A number of studies have looked at effects on soil microbial communities. However, these studies are not easily comparable because of different environmental factors (climate, soil type, etc.). At the University of Hohenheim research station "Ihinger Hof" a test site was established in 2008 consisting of 3 different AFS: willow, walnut with grass undergrowth, and a natural hedge row. We studied the effects of these systems on soil microbial communities and arbuscular mycorrhiza fungi (AMF) in particular. In spring 2024, "in-growth containers" with a 500 µm mesh and filled with sterilized soil from the site were buried right below the soil surface within the different tree/hedge rows, and at 1 m and 12 m into the arable field. In autumn 2024, containers were dug out. Further, soil surrounding the containers were sampled. Soil microbial community structure was compared by phospholipid fatty acid (PLFA) analysis. The neutral fatty acid (NLFA) 16:1ω5 was used as a marker for AMF. Preliminary data shows that total PLFA are significantly higher in all tree/hedge rows compared to the arable field. Within the hedge/tree rows, fungal PLFAs are higher in the natural hedge compared to walnut and willow rows. AMF are also highest in the natural hedge. However, no eminent differences between the different AFS were found further within the arable field.

## TUE P11 Microbial metagenomic study of the soil vertical profile under different land use and agricultural soil management

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Land use and agricultural soil management affect soil microbial communities which play a part in nutrient and carbon cycling and ultimately impact soil health. Although up to half of the C and more than two-thirds of the nutrient stocks in arable fields may be confined to the subsoil layers, microbial analyses are typically restricted to the topsoil and the impacts of soil management on subsoil bacterial communities are poorly understood. Metagenomic analyses enable the simultaneous study of microbial taxonomic and functional diversity and so can provide important insights into potential biogeochemical processes contributing to nutrient and C cycling. To study the subsoil microbial communities and their functional potential under different land use and agricultural soil management, we analyzed shotgun metagenomic sequences from the vertical profile of four boreal soil treatments: long-term (24 years) organic and conventional crop rotation, permanent meadow, and forest. Samples span from topsoil, 0–10 cm, to the deepest layer, 40–80 cm. After quality filtering, we obtained on average 6M reads per sample in the 140 samples. Filtered reads were assembled into contigs (>1000bp) and subsequently used in functional and taxonomic annotation, and to obtain metagenome assembled genomes (MAGs). Preliminary results with read based taxonomic analysis recovered over 1100 bacterial genera and bacterial communities were affected by land use and agricultural soil management, soil depth and their interaction. Results from the ongoing MAG-based and functional analyses will be presented.

## TUE P12 Rhizodeposition-driven assembly of PGP taxa in the rhizosphere and plant endosphere

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Endophytic mutualists improve plant health and crop yields by providing numerous benefits to their host plants. A substantial part of endophytic diversity arises from the horizontal transfer of microorganisms, particularly those originating from the rhizosphere – the soil zone influenced by root-secreted primary and secondary metabolites. This study tests the hypothesis that rhizodeposition is key to recruiting beneficial microorganisms from the rhizosphere for endophytic mutualism. Three physiologically and phenologically distinct plant species were cultivated in two soil types with varying carbon content in the rhizobox experiment. By using 16S rRNA and ITS amplicon sequencing, we assess the abundance and phylogenetic diversity of the endophytic communities associated with the plants, i.e., *Glycine max*, *Hordeum vulgare* and *Salix alba*, as well as the microbial communities present in soil layers at increasing distances from the plant roots, i.e., in the direction of decreasing rhizodeposition concentration. We also demonstrate the plant growth-promoting activity of these communities in relation to their distance from the root and the influence of soil type and plant species. In addition, we obtained over seventy isolates from these communities, some of which tested positive for their ability to promote plant growth through phosphate solubilization, indoleacetic acid production, or 1-aminocyclopropane-1-carboxylate deaminase activity. Overall, our data deepen our knowledge of the influence of rhizodeposition and soil type on the selection of microorganisms for endophytic mutualism.

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## TUE P13 Nature-based solutions for plant health management – the NaBaSolu project

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Climate change presents new challenges for agriculture and food production. Crops face threats from new plant diseases, pests, and variable weather. Heavy rains during the growing season increase root-damaging diseases and toxigenic molds. Mild winters allow pathogens to survive in soil and plant residues, raising disease risk in subsequent harvests. Long-term monoculture and pesticide use in conventional farming deplete soil biodiversity, negatively affecting crop yield and health. Pesticides can also alter the soil microbiome, favoring resistant microbes or hindering beneficial ones. Enhancing the soil microbiome's natural disease-suppressing capabilities is seen as a promising preventive measure in Integrated Pest Management (IPM) for both conventional and organic farming. The soil microbiome plays a vital role in maintaining soil health, promoting plant growth, and protecting crops from pathogens. Various farming techniques and soil amendments can affect the microbiome composition. The potential of using the microbiome and other nature-based solutions for plant health management is underexplored, especially in Northern regions. The poster introduces the NaBaSolu project which has received funding from the Ministry of Agriculture and Forestry, Finland (Makera, VN/9109/2023) aiming to gather and share information on new sustainable, nature-based solutions to promote plant health. This enhances human and animal health, manages food safety risks, and reduces agriculture's environmental impact. The hypothesis is that utilizing the microbiome and strengthening plants' stress tolerance and defense mechanisms can improve plant health by preventing harmful plant pathogens' growth and spread and increasing plant resilience to changing climatic conditions.

## TUE P14 Undersown cover crop diversity impact on microbial carbon use efficiency in bulk soil

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Carbon use efficiency (CUE) refers to the proportion of carbon absorbed by microbial cells and retained in biomass relative to the amount lost through respiration. CUE is a vital microbial property influencing soil organic carbon (SOC) sequestration and nutrient cycling. Polyculture farming, which utilizes diverse cover crops (CC) may offer improved farming practices which are essential for increasing biodiversity and soil SOC sequestration. However, their effects on soil microbial community CUE in agricultural soils remain uncertain. We investigated the effect of CC diversity on bulk soil microbial community CUE. We used an experimental field established in 2019 in Finland where barley is undersown with 1, 2, 4 and 8 CC species. The rooting depth and nitrogen (N)-fixing ability of CC were combined to form four functional groups: shallow root Nfix and noNfix and deep root Nfix and noNfix. We found increase in microbial biomass carbon with CC richness. The two components of CUE, respiration and growth showed different response to CC richness. Microbial growth increased significantly with CC richness whereas microbial respiration showed no response. Additionally, there was no effect of CC richness on CUE. Results suggest that CC richness may lead to faster rate of microbial growth and turnover likely due to increased plant productivity. This in turn may result in increased microbial biomass and necromass leading to SOC accumulation. Additional results on microbial analyses will be discussed.

## TUE P15 Metagenomic insight into the nitrogen cycle of northern agricultural soil

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Nitrous oxide ( $\text{N}_2\text{O}$ ) is a potent greenhouse gas and an intermediate in the nitrogen cycle, released into the atmosphere primarily through microbial activity. Agricultural soils are major global sources of  $\text{N}_2\text{O}$ , with emissions influenced by various environmental factors. Understanding the microbial processes that drive  $\text{N}_2\text{O}$  production and consumption is essential for predicting emissions and for mitigating their environmental impacts. In this study, soil samples were collected from three horizons (top: 0–18 cm, middle: 32–70 cm, and bottom: 98–135 cm) at the SMEAR-Agri Viikki site in Helsinki, Finland, known for episodic  $\text{N}_2\text{O}$  emission peaks. DNA extraction from the middle and bottom layers proved challenging; however, the addition of milk powder as a competitive agent binding positively charged surfaces significantly improved DNA yields. Nitrogen cycling genes were profiled from Illumina shotgun metagenomic sequences using the NCycDB database. Our findings show that the top soil layer, which contains higher concentrations of nitrogen substrates (organic N,  $\text{NH}_4^+$ ,  $\text{NO}_3^-$ ), is associated with a greater abundance of genes related to nitrification and denitrification. Notably, ammonia-oxidizing archaea (AOA), still often an overlooked contributor to  $\text{N}_2\text{O}$  emissions from agricultural fields, were more abundant in the top layer, while ammonia-oxidizing bacteria (AOB) dominated in deeper horizons. Although our approach does not distinguish between active and relic DNA, these results suggest that the top soil layer plays a critical role in the nitrogen cycle and  $\text{N}_2\text{O}$  dynamics in the agricultural soils.

## TUE P16 Understanding mycorrhizal dynamics in alfalfa cultivation: influence of plant age and soil tillage

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This study explores the dynamics of mycorrhization in response to alfalfa age and tillage practices. Over two consecutive autumns (2022 and 2023), root samples from alfalfa plants aged between 1 and 5 years were collected in northeastern France from 10 farmers' fields, including five managed with conventional plowing and five using simplified cultivation techniques (SCT). In each field, six subplots covering a total of 1.35 m<sup>2</sup> were selected to measure taproot biomass, alfalfa density and root mycorrhization rate. The results indicate that both alfalfa age and tillage practices significantly influence mycorrhizal symbiosis. The mycorrhizal intensity increased with alfalfa age, peaking at 5 years. Under conventional plowing, it ranged from 3% (at 1 year) to 17% (at 5 years), whereas under SCT, it reached 40% at 5 years for this study. The abundance of arbuscules followed a similar trend, being higher under SCT (12%) compared to conventional plowing (3%). These findings suggest that reduced tillage helps preserve mycelial networks, thereby facilitating more effective mycorrhizal colonization in alfalfa. In SCT fields, alfalfa density accounted for 19% of the variation in mycorrhization in 2022 and 40% in 2023, suggesting a positive impact of this practice on mycorrhizal dynamics and the importance of roots characteristics in enhancing mycorrhizal network efficiency. This study highlights the importance of sustainable agricultural practices in preserving mycorrhizal networks in alfalfa, emphasizing their key role in mycorrhizal dynamics and soil biological quality.

## TUE P17 The role of different soil microbiota fractions in plant nitrogen uptake

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Soil microorganisms play a fundamental role in nitrogen (N) cycling and its availability for plant uptake. Bacteria contribute directly to N transformations, including ammonification, nitrification, and nitrogen fixation (e.g., by rhizobia). Additionally, some bacteria enhance plant growth through phytohormone production, promoting lateral root formation and thereby improving N acquisition. Beyond the bacterial level, protists – key predators of bacteria – have been shown to influence N availability not only by remobilizing nutrients through the microbial loop but also by altering bacterial community composition, with potential implications for plant performance. This raises the question of whether a natural microbial community in agricultural soils is essential for efficient N uptake by plants beyond direct N transformations, and what role bacterial predators play in this process. In a re-inoculation experiment using *Arabidopsis thaliana* grown in loamy agricultural soil from Cologne, we found that N fertilization enhanced plant growth only in the presence of a microbial community. Further experiments, in which maize plants were inoculated with a bacterial soil wash and additionally with different protist species, suggest that certain protists may influence N uptake efficiency. These preliminary findings highlight a microbe-dependent fertilization effect, prompting further investigation into the specific microbial fractions and their functional roles in the rhizosphere. Understanding these interactions will deepen our knowledge of plant-microbe dynamics and may contribute to the development of more sustainable agricultural practices.

## TUE P18 Potential risk of spreading antibiotic-resistant genes from biosolids

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Understanding the potential for the spread of antibiotic-resistant genes (ARGs) from biosolids to soil and the surrounding environment by viable microbiomes signifies differentiating intracellular ARGs (in live cells) from extracellular ARGs (from dead cells). The former is more likely to spread ARGs to other soil microbes and plants. The results indicated that most of rhizosphere microbiome consisted of live cells and ARGs were intracellular. Over 200 ARGs were found inside the microbiomes. Soil mixed with chemical fertiliser (NEG: negative control), stabilised biosolids (BIO) and untreated primary sludge (POS: positive control) were seeded with oat and plants grown for two months. Soil samples were collected at time-zero as bulk-soil (before seedling) and at the end of incubation from the rhizosphere. Samples were treated without (PMA-) and with propidium monoazide (PMA+) to differentiate cellular localization of the DNA. The DNA extracts were processed with normal shotgun and enriched for ARGs sequencing. Almost all ARGs in all treatments were intracellular. From an enrichment, over 200 ARGs were detected, whereas, in shotgun, the ARGs reads were significantly lower by approximately 3-order of magnitudes, and several ARGs could not be reliably detected due to low number of reads. Moreover, both ARGs and ARGs families identified by the two methods resulted in distinct disagreement. All three soil treatments resulted in distinct rhizosphere microbiomes; all were largely unaffected by DNA from dead cells, suggesting that microbes from the biosolids survived and influenced the rhizosphere microbiome.

## TUE P19 Land use has a greater impact than seasonality on soil bacterial and *phoD*-harboring communities in a Mediterranean ecosystem.

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Soil microbial communities are key indicators of soil health, playing a fundamental role in nutrient cycling and ecosystem balance. It is well known that land use is a key factor influencing soil microbiomes, as well as other soil physical and chemical properties. However, the interaction of land use and seasonality in shaping bacterial communities, including those involved in phosphorus cycling like *phoD*-harboring bacteria, is poorly understood in semi-arid Mediterranean climates. To fill this knowledge gap, we here studied physicochemical properties, enzyme activities, microbial abundances, and diversity of bacterial communities (16S rRNA gene metabarcoding) and *phoD*-harboring bacterial communities (metabarcoding) in soils from four land uses (forest, grassland, extensively managed nectarine orchard, and intensively managed almond orchard) in two different seasons (spring and autumn). Nutrient contents, enzyme activities, and microbial abundances decreased with land use in the following order: forest > nectarine orchard > grassland > almond orchard, with seasonality leading to increased contents of labile forms of certain nutrients and higher abundances of bacteria and fungi in autumn compared to spring. Land use was a key factor shaping the diversity and community structure of both bacterial and *phoD*-harboring bacterial communities; however, the influence of season was rather subtler. Furthermore, our results suggest that the impact of agricultural land use on microbial communities is driven by the effects of agricultural practices on soil organic matter content. In the studied Mediterranean ecosystem, the indicator potential of microbiomes for soil quality is not greatly challenged by the variations associated to seasonality.

## TUE P20 Does annual legume planting benefit soil microbial diversity and activity across Europe?

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Legumes in agriculture can deliver multiple ecosystem services and yet are under-represented in Europe. Enhanced nutrient supply, reduced nitrogen leaching or greenhouse gas emissions, and enhanced carbon sequestration have been associated with legume crops, and these are all processes which are mediated by soil microorganisms. Therefore, we hypothesised that legumes planted alone and in mixture would be beneficial for soil microbial biomass, diversity and activity. To test this hypothesis, we sampled soil in seven countries and within the European Horizon project LEGENDARY, which has established identical field experiments for 4 legume crops (lupins, lentils, field peas and faba beans) alone and in mixture with a companion cereal crop (barley or oats) and compared this to the cereal alone. We assessed soil microbial biomass, extracellular enzyme activity (B-glucosidase, N-acetyl-glucosidase, phosphatase) and stoichiometry as well as bacterial and fungal community structure with metabarcoding. Our preliminary results for biomass and enzyme activity indicate that there are no consistent treatment effects across sites or crops, instead there are clear site differences and interactions between treatment, sites and crops in response to local soil properties. Field peas and lentils are associated with higher water-extractable organic carbon, across all sites, but this did not influence biomass or enzyme stoichiometry. Community analysis is pending. Our preliminary conclusion is that one year of legume planting is insufficient to shift microbial community biomass and activity. Our follow-up analysis will test the same hypothesis in a perennial legume crop in the second year after sowing.

## TUE P21 Strategic tillage methods and crop type impact the soil food web in a Chromosol soil

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Conservation agriculture has resulted in improved soil health, however with time new agronomic issues have emerged. These include stratification of nutrients, compaction, water repellence and increased disease and pest problems. Many farmers are now considering strategic tillage, an as-needed, occasional application of tillage to rectify production constraints, though appropriate machinery choice is crucial to ensure constraints are ameliorated. A Chromosol soil was assessed in a field experiment for the combined effects of tillage and crop type on the soil food web, soil physico-chemical properties and yield. Crop treatments of barley, serradella, canola, and lupin were grown for two years before strategic tillage was applied. The different tillage treatments were mixing by ploughing, inversion by mouldboard ploughing, deep ripping or no-till (nil). Plots were then sown to barley for two years after tillage and assessed at different depths at the start and end of each production season. The strategic tillage increased barley yields only in the first year, compared to the nil treatment and were significantly affected by the previous crop. Mouldboard inversion resulted in increased phosphorus, organic carbon and total nitrogen at depth. Free-living and parasitic nematodes abundance and communities changed over the two years, with tillage not reducing sensitive higher level trophic groups such as omnivores and predator nematodes. Nematode-based indices showed that strategic tillage improved soil health over time with more mature and structured samples. Bacterial and fungal abundance was driven by different treatment factors and was strongly linked to nematode trophic groups. Long term, strategic tillage did not negatively affect the soil food web or soil health.

## TUE P22 The ecological drivers of organic matter temperature sensitivity in forest soils across Europe

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Despite microbial communities being key drivers of soil organic matter decomposition, their explicit inclusion in soil C biogeochemical cycling models remains debated. The high diversity of microbial communities makes their effects challenging to detect compared to larger drivers such as soil C inputs or climate. To address this, we evaluated multiple drivers of soil organic matter decomposition in forests across Spain, France, and Romania, focusing on climate, soil C inputs (via management approaches), and microbial communities (species diversity and enzymatic activities). By repeatedly measuring soil respiration across seasons and modeling temperature sensitivity of decomposition under different treatments and locations, we related these findings to microbial and ecological data. Our results show that canopy disturbances, influencing soil C inputs, are the primary driver of decomposition, followed by climate, particularly temperature. After accounting for these factors in a parametric model, site-specific temperature sensitivity of organic matter decomposition was best explained by the fungi:bacteria ratio and actinobacteria biomass, while other ecological site characteristics had minimal impact. Thus, management practices, especially adding fresh organic material, play a critical role in driving decomposition, but this is not just a pure substrate effect. The fungi and actinobacteria emerges as a pivotal microbial communities in explaining decomposition patterns. This underscores the importance of microbial community composition in understanding soil organic matter decomposition and its temperature sensitivity.

## TUE P23 Wheat-faba bean intercropping can sustain soil nutrients and C cycles under different N fertilization levels

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Legume-cereal intercropping systems are expected to play a significant role in promoting the sustainable enhancement of crop yield per hectare with reduced synthetic inputs. However, the effects on soil nutrients and C biogeochemical cycles in this multi-cropping system are not fully elucidated. In this study, wheat-faba bean intercropping effects on soil nutrients and C cycles were investigated under field conditions. The underlying hypothesis is that the more diversified rhizodeposition in intercropping may sustain nutrient and C cycling in soil more effectively than the respective sole crops. To test this hypothesis, soil and plant Total N and C (TN and TC) and their stable isotopic compositions ( $\delta^{15}\text{N}$  and  $\delta^{13}\text{C}$ ) were quantified, along with plant-available N forms in soil (ammonium and nitrate). Furthermore, the variations in soil Microbial Biomass N and C (MBN and MBC) and nutrients (P, K and micronutrients) were measured. Net Ecosystem Production (NEP) was also determined at crops flowering stage. Results are currently under statistical analysis. It is anticipated that intercropping may have led to a higher NEP, resulting in increased soil TC stocks. Moreover, N retention and availability for plants are expected to be higher in intercropping. It is also hypothesized that intercropping may have mediated a higher mobilization of P, K and micronutrients. The lower C:N ratio of rhizodeposits compared to sole wheat is predicted to facilitate microbial growth, ultimately sustaining MBN and MBC accumulation. Overall, it is expected that co-cultivating wheat and faba bean could lead to an improved Plant-Soil Feedback.

## TUE P24 Organic and inorganic carbon storage in Dutch agricultural systems

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Soil carbon is critical for feeding the global population and for mitigating climate change, yet agricultural intensification is leading to significant losses. Despite the need to stop agricultural soil carbon depletion and promote its restoration, uncertainties persist regarding agricultural practices that can enhance carbon accumulation. Although soil carbon encompasses both inorganic and organic components, research has focused on the effect of agricultural management on organic carbon. However, agricultural activities can cause irrevocable losses of inorganic carbon, which may be detrimental for soil health and contribute to climate change. It is therefore crucial to study the response of both inorganic and organic carbon to agricultural management. However, agricultural management includes a variety of practices that can be combined in different ways. This constitutes an obstacle in defining which agricultural practices can promote soil carbon retention. This project investigates how soil agricultural management influences soil carbon storage across diverse pedological conditions. Briefly, a total of 956 grasslands and arable soil samples from a wide range of agricultural management and pedological conditions were collected in the Netherlands. Detailed information on agricultural management was gathered using questionnaires and organic and inorganic carbon content were determined. In addition, chemical, physical and biological explanatory variables such aluminium and iron oxides content, pH, nutrient availability, soil texture and microbial biomass were measured. Here, we will identify agricultural practice combinations which promote soil carbon storage and how this varies with pedological conditions. These findings will help develop targeted management practices to stop soil carbon depletion and promote restoration.

## TUE P25 Rhizosphere metatranscriptomics of microbiome functions in carbon turnover assessed by a novel approach

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Soil organic carbon (SOC) is continuously transformed by soil microorganisms, determining its stability and quality in soils. Eroded soils have a particularly high potential for carbon sequestration, with the rhizosphere and its associated microbiome playing a crucial role in belowground carbon turnover. However, our understanding of the microbial metabolic processes contributing to SOC formation in the dynamic rhizosphere remains limited. We developed and employed an mRNA-targeted metatranscriptomic approach to identify specific metabolic pathways in the rhizosphere microbiome of *Brassica napus* L. at two growth stages under simulated erosion conditions. Our analysis revealed an increase in transcripts encoding chitin degradation and synthesis-related genes, polysaccharide-binding proteins, extracellular polymeric substance producing enzymes, as well as pectin- and xylan-degrading enzymes at the flowering stage. While erosion had a minor but modulatory effect on transcript profiles, it specifically decreased bacterial chemotaxis transcripts of *motB* and *rbsB* with increasing erosion intensity. Taxonomic analysis of functional genes indicated limited taxonomic shifts for transcripts of *motB*, *murL*, chitin synthase, and chitinase. Our study demonstrates the utility of mRNA-targeted metatranscriptomics for investigating carbon turnover processes in dynamic soil compartments like the rhizosphere. This tailored approach identified potential pathways relevant to both the buildup of microbe-derived SOC and the utilization of plant-derived and existing SOC stocks. Advancing soil microbiology research requires the integration of functional gene analyses to enhance our understanding of microbial contributions to SOC formation, stability, and carbon sequestration in soils.

## TUE P26 Soil carbon accumulation is enhanced by phosphorus limitation under long-term nitrogen fertilisation in a boreal forest

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Boreal forests represent a major sink for atmospheric CO<sub>2</sub>, but their carbon storage capacity is often constrained by nutrient limitations. In a 60-year study conducted in a *Pinus sylvestris*-dominated boreal forest, we examined the impacts of long-term nutrient inputs – specifically nitrogen, phosphorus, and calcium – on tree productivity and soil carbon dynamics. Our findings reveal that nitrogen fertilization, whether applied alone or in combination with phosphorus and calcium, boosted tree biomass by approximately 50% and increased soil carbon storage by 65% compared to unfertilized plots. However, the nonlinear relationship between primary production and soil carbon stocks suggests that microbial processes mediated carbon accumulation. When phosphorus was co-applied with nitrogen, soil acidification, shifts in fungal community composition, and enhanced degradation of biopolymers limited soil carbon sequestration. In contrast, nitrogen fertilization without phosphorus resulted in greater soil carbon storage, likely due to phosphorus-limited microbial activity. These results underscore that the climate mitigation potential of nitrogen fertilization in boreal forests is strongly modulated by phosphorus availability.

## TUE P27 Using SIP-metagenomics to characterise the microbial taxa responsible for transforming carbon compounds in arctic soil

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The arctic is particularly vulnerable to warming due to climate change. Warming increases the rates of microbial activity and the decomposition of stored carbon. Arctic microbes release stored carbon as carbon dioxide and methane, potentially resulting in a positive feedback loop. These processes cannot be accurately modelled without a solid understanding of the microbes involved and how they are affected by temperature. We characterised the microbial sub-populations involved in the transformation of carbon compounds (glucose, cellulose and acetate) in an incubation experiment using Greenland tundra soils collected from control (ambient) and warmed (open top chambers and snow fences-treated) plots. We have generated a dataset of metagenome assembled genomes labelled with <sup>12</sup>C and <sup>13</sup>C-carbon from the three carbon compounds after 28 days of incubation. This study will develop an understanding of the functional genes and pathways involved in carbon consumption in arctic soils as well as how these processes are affected by a warming climate. We will identify how different taxa use different functional genes and what this means for carbon cycling in the arctic ecosystem. Although microbes play a crucial role in the impacts of climate change, they are seldom considered in policy development. Our results will provide details which will allow microbial carbon cycling to be integrated into global models of climate change, improving the quality of their predictions.

## TUE P28 Stable isotope probing to disentangle carbon for nitrogen trading in mycorrhizal hyphosphere

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There is experimental evidence for the key role of hyphosphere microbiomes in releasing mineral nutrients such as nitrogen (N) from organic moieties in soil to be accessible for the arbuscular mycorrhizal (AM) fungi and their host plants, in consequence. Yet whether and how the N (or access to it) is exchanged by the hyphosphere microorganisms for reduced carbon (C) supplied by the AM fungus remains unclear. To disentangle whether and which microbes involved in organic N (chitin) degradation are reciprocally rewarded by fungal C, we undertook several stable isotope probing experiments, labeling both the AM fungus or the chitin with  $^{13}\text{C}$ , or chitin only with  $^{15}\text{N}$ . We followed the incorporation of the heavy isotopes into the microbial RNA in microbially complex microcosms. Our results so far indicate that microbes could utilize the chitin as sources of both N and C, not necessarily relying on the fungus to supply the energy/carbon. On the other hand, evidence was obtained for specific microbial communities to be established in AM fungal hyphosphere – whether these taxa specifically occupy the hyphoplane or are more loosely associated with the fungus still needs to be addressed.

## TUE P29 Spatial variation of soil nitrogen and carbon in Norway spruce-dominated stands with grey alder or birch admixture

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Norway spruce (*Picea abies*) can reduce soil fertility by producing low-nutrient needle litter that decreases soil pH. Broadleaved species, such as grey alder (*Alnus incana*) and birch (*Betula pendula*, *B. pubescens*), may improve soil by promoting microbial activity and increasing nutrient availability. The symbiotic relationship between grey alder and N<sub>2</sub>-fixing Frankia bacteria further enhances N inputs, potentially increasing soil organic carbon (SOC) accumulation. We examined the effects of broadleaf admixture on N availability and SOC stocks in spruce stands at varying distances from alder and birch. The study was conducted at three 40–56-year-old spruce-dominated stands, located in eastern and southern Finland and representing middle-fertile sites (*Vaccinium myrtillus* site type). Soil samples were collected from the organic horizon and 0–10 cm or 0–5 cm mineral soil. In the first site, systematic sampling (N = 56) was conducted on a spruce plot with 20% birch admixture and along transects adjacent to a grey alder (N = 21). In the second site, samples were collected along a transect between two alders (N = 6), and in the third site, samples were taken close to alder, birch, and spruce stems (N = 8 for each species). Diffusive fluxes of soil N were determined with microdialysis technique, while SOC and N stocks, C mineralization rates, and NH<sub>4</sub>-N and NO<sub>3</sub>-N concentrations were measured from soil cores. Some soil properties showed a response to the distance from a broadleaved tree, but most properties showed no response, indicating that litter and roots distribute widely in mixed stands.

## TUE P30 Long-term fertilization drives distinct nutrient dynamics and microbial activities in wheat rhizosphere and hyphosphere

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The rhizosphere (RH) and hyphosphere (HS) are important root-associated soil niches, but comparisons of how increased fertilization affects nutrient cycling in these two soil compartments are rare. We conducted a greenhouse experiment with wheat until seed maturity using soils from the Static Fertilization Experiment in Bad Lauchstädt, a long-term fertilization trial, at six fertilization levels: NONE, NK, PK and NPK, as well as organic farmyard manure (FYM) and combined fertilization (FYM\_NPK). FYM and FYM\_NPK increased wheat shoot biomass and photosynthesis, but reduced mycorrhizal colonization. Dissolved organic carbon and available N and P showed distinct fertilizer-related patterns and differences between RH and HS. Microbial biomass carbon and nitrogen increased with increasing fertilization and showed differences between RH and HS. C-, N- and P-cycling enzyme activities increased with fertilization and were mostly higher in RH than in HS, and showed fertilization-specific differences between RH and HS. Fertilization explained 79% of the variation in enzyme activities in RH, but 91% in HS. Redundancy analyses indicated a stronger influence of organic matter and C/N ratio, and piece-wise structural equation models revealed a stronger, direct and positive plant influence on enzyme activities in RH than in HS. Our study demonstrates how long-term fertilization alters nutrient availability, microbial biomass, and enzyme activities in root-associated soil niches and highlights distinct functional differences between the rhizosphere and hyphosphere. These findings improve our understanding of nutrient cycling processes in these niches and provide new insights into plant-microbe-soil interactions and their role in shaping biogeochemical functions in fertilized agroecosystems.

## TUE P31 Belowground nutrient transfer between Scots pine and bilberry mediated by ectomycorrhizas

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Ectomycorrhizal fungi (EMF) are essential for plant-soil nutrient cycling in forest ecosystems, forming symbiotic relationships with plant roots. They receive 10–30% host plant photosynthate and in return improve plant nutrient acquisition. EMF symbiosis can establish common mycorrhizal networks (CMNs), connecting multiple plant hosts from the same or different species. CMNs have been found to enhance plant productivity and crucial in carbon sequestration. However, the quantity of the resources exchanged between plants and who manipulates the exchanges remain unanswered. Therefore, it's significant to investigate CMNs role in belowground nutrient cycling and how it relates to the host species identity. This study aims to assess 1) the significance of carbon and nitrogen transfer through CMNs between pine and bilberry, 2) whether the interaction of different plant species affect their growth performance. One-year-old seedlings of Scots pine (*Pinus sylvestris* L.) and bilberry (*Vaccinium myrtillus*) were planted in the custom-made pots, which were divided equally with three types of barriers: solid barrier (no connection), 50µm mesh (roots blocked) and no-barrier (full connection). The seedlings were planted from October 2023 to October 2024 in three combinations: pine-bilberry, pine-pine, bilberry-bilberry. Labelling with <sup>13</sup>CO<sub>2</sub> and <sup>15</sup>N-needle-litter were performed for tracing the nutrient cycling. To quantify the carbon transferred by fungal hyphae, soil microbial biomass total C and <sup>13</sup>C were measured, alongside the plant photosynthesis and <sup>13</sup>C in needles/leaves. Plant productivity was evaluated through shoot and roots biomass. Microbial carbon use efficiency was analyzed using <sup>18</sup>O-H<sub>2</sub>O to determine SOC stabilization. Preliminary results will be presented through poster.

## TUE P32 Effects of forest management and microbial diversity and community composition on soil respiration

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Forest management and natural disturbances influence soil microbial communities, potentially altering carbon (C) turnover through changes in microbial functions such as decomposition. However, the specific role of microbial community composition in regulating C dynamics remains unclear. While laboratory studies indicate that microbial biomass improves model predictions for C turnover, and theoretical work highlights the potential importance of microbial functional diversity, empirical evidence from natural systems remains ambiguous. We hypothesize that uncertainties partly derive from the large heterogeneity of microbial communities, where different functional groups contribute differently to decomposition and have different sensitivity to environmental change. This study aims to disentangle the relative contribution of microclimate (i.e. soil temperature and soil moisture) and microbial community composition on decomposition rates in managed forests. We use empirical data from multiple forest management experiments across Europe collected by the HoliSoils consortium (Holistic management practices, modelling and monitoring for European forest soils; <https://holisoils.eu/>), and examine the link between microbial diversity and soil respiration. Preliminary results indicate a significant correlation between microbial diversity and soil respiration, but with significant differences between fungi and bacteria. This suggests that identifying appropriate diversity indicators could improve microbially explicit C turnover models and inform forest management practices of the role of microbial diversity in decomposition processes in forest soils.

## TUE P33 Biochar affects extracellular enzyme activity and soil microbiome after 8 years

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Biochar enhances physico-chemical properties of agricultural soils and is reported to promote microbial diversity in the short term. However, its long-term effects on microbiomes and soil health remain poorly understood. This study aimed to assess the effects of 8-year field-aged biochar on microbiomes from a loamy sandy soil and a coarse sandy soil under temperate climate conditions. We hypothesize biochar increases extracellular enzyme activity (EEA) and changes the structure of soil microbiomes. In June 2015, the soils (top 0–20 cm) were amended with 2% wt straw biochar in field lysimeters (cylindrical polyester tanks, 1.03 m diameter, 1.5 m depth). Soils were collected in August 2023 for EEA measurement, qPCR analysis of N cycling genes, and 16S rRNA and ITS2 amplicon sequencing. Biochar significantly increased the activity of  $\alpha$ -glucosidase,  $\beta$ -galactosidase, cellobioidase, phosphomonoesterase and arylsulfatase in both soils. Biochar significantly increased the abundance of the nitrite reductase (NirS) gene in both soils and the abundance of prokaryotes (16S rRNA), ammonia-oxidizing archaea (AOA AmoA), and ammonia-oxidizing bacteria (AOB AmoA) genes in the coarse sandy soil. In both soils, which harbored different prokaryotic and fungal communities (PERMANOVA;  $p < 0.001$ ), biochar affected the structure of prokaryotic communities ( $p < 0.05$ ) while the fungal communities were unchanged. The relative abundance of an unclassified genus (ammonia-oxidizing archaeon) member of the family *Nitrosphaeraceae*, increased significantly in both soils. We conclude that the effects of biochar manifest over eight years, increasing EEA and enriching taxa involved in N-cycling. These findings provide insights for assessing the long-term impact of biochar on soil health.

## TUE P34 Soil amino sugar measurement by high performance liquid chromatography – faster measurements and higher sensitivity compared to the gas chromatography method

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The research of soil carbon stocks has increased in recent years as their importance to climate change has been more thoroughly understood. It is important that more rapid and sensitive analysis methods are developed to assist in this research. A large proportion of soil carbon stocks have been proposed to be dead microbial residues, which are determined through formula proposed by Appuhn and Joergensen in 2006 based on measured fungal and bacterial cell wall amino sugar concentrations in the soil. The measurement of these amino sugars is frequently performed by a gas chromatography method initially published by Zhang and Amelung in 1996. The method reliably measures amino sugar concentrations but requires a lengthy pre-treatment and derivatization procedure in the laboratory. We have developed an alternative ultra high performance liquid chromatography method for amino sugars based on the method published by Indorf et al. in 2011. In our developed method, smaller concentrations can be reliably measured, and it is possible to measure a dataset of 140 samples in ten days, while the same sample amount with the gas chromatography method would have required three and a half months to measure.

## TUE P35 Carbon released from thawing palsamire and peatland is processed within site in a small Arctic catchment

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Climate change is altering biogeochemical cycling of carbon and nutrients in the northern peatlands and permafrost mires. Lateral transfer of carbon needs to be more widely studied, especially in smaller streams and catchments, as they receive high loading of carbon and nutrient from the soils and are hotspots of carbon degradation. In this study we combined measurements of dissolved organic matter (DOM) quality and quantity with microbial community data from a small Arctic catchment. Our aim was to understand how the catchment is affected by degrading palsamire as well as peatland thawing in spring. The small thaw ponds in the palsamire were distinct from the rest of the catchment. Palsa ponds had higher amount of DOM with more refractory properties and distinct microbial communities. Our results point towards low export rates of organic matter from the permafrost mire and peatland to the receiving small streams. Instead, our results point towards DOM being retained and metabolised within the small ponds in both palsamire and peatland. We were also able to detect high abundances of ultra-small Patescibacteria, dominating the community composition along the entire catchment.

## TUE P36 Linking microbial demand for limiting resources with microbial use of soil organic matter: insights from a 67-year field experiment

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Microbial growth is often found to be limited by carbon (C), but nitrogen (N) and phosphorus (P) can also be limiting. Microbial resource limitation is interlinked with soil organic matter (SOM) decomposition, where microorganisms may selectively mineralize specific components of SOM to acquire growth-limiting nutrients. However, the underlying mechanisms remain poorly understood. Long-term fertilization experiments provide a unique opportunity to study these mechanisms, as the history of nutrient inputs is expected to shift microbial resource limitations. We collected soils from a long-term fertilization experiment in Sweden, where mineral N and P and potassium (K) have been applied since 1957. To determine the limiting factor for microbial growth, we conducted a limiting factor assay by factorially adding C, N and P to soils and measuring microbial growth responses. We also assessed the effect of nutrient availability on SOM mineralization, measuring C and gross N mineralization rates. To assess microbial C use, we compared the <sup>13</sup>C signatures of respired CO<sub>2</sub> and soil-C. Microbial growth was C-limited in all soils, although the C-limitation was weaker in fertilized soils. Despite low N and PK availability in unfertilised soils, microbial growth increased up to four-fold in response to C addition, suggesting that microbes accessed nutrients beyond those dissolved in soil solution. N-fertilisation shaped the microbial community composition towards microorganisms mineralizing less soil-C and incorporating C more efficiently into their biomass. Overall, our results emphasise the role of nutrient availability in controlling microbial responses.

## TUE P37 Long-term potential for saprotrophic decomposition of humus following mycorrhizal removal in boreal forest

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Boreal forest soils are dominated by three fungal guilds; free-living saprotrophic decomposers, ectomycorrhizal fungi forming symbioses with canopy trees, and ericoid mycorrhizal fungi associated with the dense shrub understory. Previous work has suggested that soil carbon storage is linked to nutrient availability and that different fungi have different abilities to access carbon and nitrogen in organic matter. The goal of our research is to understand the long-term drivers of belowground organic matter accumulation and stabilization, particularly the role of interactions between ecto- and ericoid mycorrhizal fungi and plants in the boreal forest. We used a unique field experiment consisting of plots exposed to 7 years of factorial pine root trenching and shrubs removal. We investigated how the presence of pines and ericaceous shrubs influences carbon and nitrogen stocks and stability, litter and humus decomposition, enzymatic activities, fungal biomass and fungal community composition. Removal of single mycorrhizal guilds had effects on carbon and nitrogen stocks, but combined removal of both ecto- and ericoid mycorrhiza resulted in larger reductions of 29% and 20% for carbon and nitrogen, respectively. The absence of both mycorrhizal guilds led to community changes and a competitive release for saprotrophic fungi in the soil organic layer and decomposing litter, as evidenced by increased fungal biomass and hydrolytic and oxidative enzymatic activities. These results highlight the importance of interactions and the balance between fungal guilds for the stability of organic matter stocks in the boreal forest.

## TUE P38 Heterologous manganese-peroxidase from ectomycorrhizal fungus *Cortinarius aurae* and its role in nitrogen mobilisation

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Ectomycorrhizal fungi are fundamental nutrient cyclers in nitrogen-limited boreal forests and can have a direct role in the decomposition of soil organic matter. Some ectomycorrhizal fungi, particularly from the genus *Cortinarius*, have retained genes for potent oxidative enzymes, such as manganese-peroxidases, from their saprotrophic ancestors. Manganese-peroxidases oxidise divalent manganese to trivalent manganese, which is highly reactive and oxidises a range of organic compounds in an unspecific manner. Yet, unlike saprotrophs, ectomycorrhizal fungi do not utilize carbon from decomposition, rather their degradative capacity is likely to increase access to organic nitrogen from recalcitrant sources. The manganese-peroxidase genes from *Cortinarius*, as well as those from related saprotrophic fungi in the Strophariaceae and Hymenogastraceae families, have predicted functional sites that vary from “white-rot” saprotrophic fungi and are comparatively understudied. Here we aimed to confirm that the manganese-peroxidases from *Cortinarius* are capable of producing trivalent manganese and to characterise their activity. Because *Cortinarius* species are generally not amenable to laboratory cultures, we heterologously expressed manganese-peroxidases from *Cortinarius aurae* in *Pichia pastoris*. The heterologous enzyme was functional, yet, in contrast to manganese-peroxidases from *Phanerochaete chrysosporium*, it could also oxidise phenolic substrates in the absence of manganese. This could indicate that this type of manganese-peroxidase may have an unexpected alternate mechanism for oxidising organic matter, of which the implications for carbon and nitrogen dynamics are unknown. Furthermore, we aim to test the degree to which these enzymes can decompose organic compounds and release nitrogen from recalcitrant organic matter, such as proteins complexed with condensed tannins.

## TUE P40 Impact of shrub clearing or burning as restoration strategies of encroached mountain grasslands on soil C and microbial functions

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Reduced intensity of land use in mountain areas over the last decades has led to an expansion of woody species in open areas of many temperate mountain ranges, causing a loss of pasturelands, which is having consequences on biodiversity and C and nutrient cycling. In the Pyrenees, some restoration initiatives are being carried out to recover shrub-encroached grasslands. The objective here is to analyse the impact on soil carbon and microbial functions of two restoration strategies: mechanical clearing of shrub patches (and leaving the masticated debris on the floor) or prescribed shrub burning. With this purpose we experimentally carried out both treatments in several shrub (*Juniperus communis* L.) patches growing in a mesic subalpine grassland (1900–1950 m a.s.l.) at the *Alt Pirineu* Natural Park. Four years later, we estimated the impact of treatments on the C stocks in the upper soil layer and determined the community-level physiological profiles (CLPP) and functional diversity in mineral soils obtained from both cleared and burned shrub patches. Similarly, we determined the C stocks and CLPP under untouched shrubs (shrub control) and in open grassland (without shrubs, grassland control). The CLPP were performed using the Microresp™ technique, which is based on 6h-incubations of whole soil in the lab and the determination of the substrate-induced respiration (SIR) after the addition several sole carbon sources. The results will allow to discuss the impact of the different grassland restoration treatments on soil C stocks and on the catabolic capacities of the soil microbial community.

## TUE P41 Plant diversity drives carbon retention in soils through root-driven microbial carbon processes

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Long-term global warming and climate change induced droughts can trigger negative effects such as biodiversity loss and increased soil carbon (C) loss from ecosystems. Species diversity can increase soil C storage, yet the precise contributions and mechanisms of SOC stocks accumulation through species diversity compared to monoculture are still unclear. First, we conduct a second-order meta-analysis of 17 meta-analyses, encompassing originally 1592 original studies with 11,514 paired observations to examine species diversification practices in cropping systems and their impact on SOC stock. Overall, species diversification increased SOC stocks by 14% [confidence interval (CI): 7%–21%,  $P < 0.0001$ ]. Second, we propose that species diversity can better enhance soil C sink and mitigate climate change via root-driven ecological niche differentiation in microbial-mediated soil C transformation and stabilization processes. We further analyze the key pathways that species-diversified systems function through root-driven, microbe-mediated soil C processes to mitigate the effect of climate change (warming and drought) on soil C sequestration. Understanding these mechanisms will provide precise management of species diversity in agroecosystems to better combat climate change.

## TUE P42 Grassland management intensity affects nutrient limitation of soil microorganisms – two different analytical approaches reveal similar results

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Soil microbial growth and activity are typically limited by the availability of carbon (C) but also depend on additional nutrients such as nitrogen (N) and phosphorus (P). Various methods exist to assess microbial nutrient limitations, yet it remains unclear whether different methods yield consistent results. Grassland management intensity influences soil nutrient status through mineral or organic fertilization and grazing or mowing intensity, potentially altering microbial nutrient constraints. We examined microbial nutrient limitations in 50 grassland soils from the Schwäbische Alb (southwestern Germany), part of the German Biodiversity Exploratories, spanning a gradient of long-term land-use intensity (LUI). Two independent methods were compared: (1) respiration responses to N and/or P additions alongside glucose, indicating microbial growth limitations, and (2) the stoichiometry of C, N, and P cycling enzyme activities assessed via vector analysis. Microbial growth was most pronounced when both N and P were supplied in addition to C. Growth responses to the combined nutrient addition, as well as vector lengths (reflecting relative C vs. nutrient limitation), were positively correlated with LUI. Both methods consistently indicated increasing microbial nutrient limitation with decreasing LUI, with P being the most limiting nutrient in low-intensity grasslands. Despite assessing distinct microbial parameters (microbial respiration during growth and enzyme activities), both approaches revealed similar patterns of microbial nutrient limitation across land-use intensity gradients in grassland soils.

## TUE P43 Interplay of taxonomy, ecological guilds, and nitrogen availability in shaping fungal biomass composition

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Fungi play a crucial role in nitrogen (N) and phosphorus (P) cycling, influencing biomass decomposition and plant nutrition. The nutrient content of fungal biomass varies across habitats and ecological guilds, reflecting both environmental availability and phylogenetic constraints. This study integrates two complementary approaches to assess fungal nutrient economy. First, we analyzed the carbon (C), nitrogen (N), and phosphorus (P) content of fruiting bodies of 214 fungal species. Soil saprotrophs exhibited significantly higher N and P contents than wood saprotrophs and ectomycorrhizal fungi. A significant correlation between N and P content was observed, with a notable phylogenetic signal. However, the correlation between N content and chitin – a key fungal biopolymer containing N – was weak, suggesting that fungal lifestyle and phylogenetic relations shape macronutrient composition. Next, we examined how N availability affects fungal growth and biomass composition by culturing selected strains under varying N concentrations. Plant pathogens and soil saprotrophs increased biomass production with higher N availability, while wood-decomposing saprotrophs responded less. The C:N ratio of fungal biomass decreased with increasing N availability, with Ascomycetes showing the highest responsiveness similarly like following Mucoromycetes. Basidiomycetes maintained more tightly regulated C:N ratio. Together, these findings highlight the interplay between fungal taxonomy, ecological function, and environmental N availability in shaping fungal biomass composition. Nutrient dynamics in fungal biomass are governed by both phylogenetic constraints and external nutrient supply, with potential implications for ecosystem nutrient cycling.

## TUE P44 Effect of fungal necromass chemical quality and mean annual temperatures on its degradation rate

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In recent years, soil microbial necromass has been found to play a central role in SOM formation and the soil stable C pool accumulation. The magnitude of the soil C accumulation as microbial necromass depends on multiple factors, such as the soil chemical composition and chemical composition of the fungal necromass. The chemical quality of fungal necromass is proposed to be one of the central factors determining the fungal necromass decomposition rate. Fungal necromass with high N-content has been observed to decay faster than necromass with lower N-content. Also, the more melanin the fungal biomass has, i.e. the more pigmented it is, the lower degradation rate it has. Moreover, the initial decomposer community may affect the fungal necromass decomposition rate. To investigate this, we established a field experiment along a latitudinal gradient in boreal spruce and pine dominated forests with differing mean annual temperatures, growing season lengths, and soil chemical properties. We buried two types of fungal necromass, less and more pigmented, in mesh bags (50µm mesh size) between organic and mineral soil horizons and collected one set of bags after 2 and 4 months. One additional set will be collected after 12 months. We hypothesize that i) the less pigmented fungal necromass has higher degradation rate than the more pigmented one, and ii) necromass degradation rate is slower in colder climate. Additionally, we speculated that the initial decomposer community and soil C:N ratio may affect the fungal necromass decomposition rate. Our initial results partly support our original hypotheses.

## TUE P45 Methane cycling in boreal upland and peat soils – Links between functional gene composition, potential CH<sub>4</sub> production/oxidation and CH<sub>4</sub> fluxes

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Boreal terrestrial environments serve a double role in the cycling of methane (CH<sub>4</sub>): While well-aerated forest soil is often a significant CH<sub>4</sub> sink, submerged peatlands can act as large sources. Ongoing climate change is estimated to increase extreme weather events, such as high precipitation and droughts, thus potentially changing these dynamics. To predict the future CH<sub>4</sub> balance, related microbes and their controlling factors need better characterization especially in upland and forestry-drained peatland areas. We evaluated CH<sub>4</sub> cycling on an upland-peatland gradient within a large boreal catchment in Northern Finland (Pallaslompola, 67° 59'N, 24°13'E), and in an upland forest in Southern Finland (Hyytiälä, 61°51'N, 24°17'E). For a detailed view, we used probe-capture-metagenomics targeting the functional CH<sub>4</sub>-genes, coupled with CH<sub>4</sub> fluxes/process potentials and soil chemistry. As expected, both methanogens (*mcrA*) and methanotrophs (*pmoA*, *mmoX*) were most diverse in pristine peat, reflecting measured high potential for both CH<sub>4</sub> production and low-affinity oxidation. In the drained/upland soil, *mcrA* reads were detected in lower numbers and were mainly related to *Methanobacterium* and *Methanoregula*, but also to Bathyarchaeota. Consistent with high-affinity oxidation potential and the measured *in situ* CH<sub>4</sub> sink, methanotrophs in drained/upland soils were mainly related to the USC-alpha-cluster, while detection of the *pxmABC*-cluster and the "intra-aerobic" NC10-phylum indicated adaptability to oxygen-limited conditions. Additionally, simultaneous sequencing of nitrogen-cycling genes allowed assessing connections between the CH<sub>4</sub>- and nitrogen-cycles. By including all dominant forest soil types, results can be utilized in estimating the CH<sub>4</sub> cycling capacity even in the wider ecosystem-scale.

## TUE P46 Long-term effects of clear-cut forestry on fungal litter decomposer communities in boreal forests

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Boreal forest soils contain a major pool of terrestrial organic carbon, with plant litter as one major input source. Litter decomposition, mediated largely by saprotrophic fungi and invertebrates, is an important process regulating the accumulation of carbon in forest soils. Stand-based forest management with clear-cut forestry has transformed wide boreal forests areas into mosaics of homogenous forest stands in different age classes. In this study we investigate the long-term effects of clear-cut forestry on litter decomposition. Litter mesh bags with Norway spruce needles were distributed in ten forest pairs, each pair including one previously clear-cut but now mature forest, and one near-natural forest not impacted by clear-cutting. Bags of different mesh sizes were used to exclude or allow access of invertebrates. After two years of incubation, mass loss was determined, and we conducted quantitative and qualitative analyses of the fungal decomposer communities through ergosterol quantification and DNA metabarcoding. Preliminary analyses indicate no long-term effects of clear-cut forestry or presence/absence of invertebrates on decomposition rates of spruce litter, as well as no effect on fungal biomass (ergosterol) in the litter. There was a small but significant effect of clear-cut forestry on the fungal decomposer communities in the mesh bags, but no effect of invertebrate exclusion. Our preliminary results indicate no strong long-term effects of clear-cut forestry on spruce litter decomposition and the associated decomposer communities.

## TUE P47 Microbial responses in bulk soil and rhizosphere to cereal-legume intercropping: implications for soil health and carbon dynamics

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Intercropping, particularly cereal-legume associations, is a promising strategy for enhancing soil fertility and nutrient cycling in semiarid agroecosystems, where soil degradation and low organic matter content limit productivity. Legumes contribute to these benefits by fixing atmospheric N and stimulating plant-microbial synergies. However, the response of microbial communities in the rhizosphere and bulk soil to intercropping remains underexplored. This study investigated the effects of cereal-legume intercropping on microbial biomass (C and N), microbial community composition (PLFAs), enzymatic activities (C, N, and P cycles), and C dynamics (CO<sub>2</sub> emissions, CUE) in the rhizosphere and bulk soil. The experiment was conducted in a randomized field trial established in 2022 in semiarid central Spain, comparing alfalfa monoculture, barley monoculture, and their intercropping. Cereal-legume intercropping affected microbial communities in both the rhizosphere and bulk soil, increasing microbial biomass C and N, enhancing enzymatic activities, and inducing shifts in microbial community composition. Notably, intercropping promoted mycorrhizal associations in both soil fractions, suggesting improvements in nutrient cycling and overall soil health. The reduction in SOC-normalized respiration ( $q_M$ ) and microbial biomass C-normalized respiration ( $q_{CO_2}$ ) under intercropping indicated more efficient microbial C use and enhanced C stabilization compared to monocropping, which showed higher C losses. These findings highlight intercropping as a viable strategy for improving nutrient cycling and promoting beneficial plant-microbial interactions in soil, ultimately enhancing C storage in semiarid agroecosystems. Acknowledgments: This research was supported by the LEGUMINOSE project (grant ref. 101082289).

TUE P48 Molecular characterization and infection stability of a novel ormycovirus infecting mycorrhizal fungi  
*Lactarius tabidus*

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Ectomycorrhizal (ECM) mutualists and plant pathogens are intimately associated with living plants and, along with saprotrophs, represent the most abundant ecological guilds of soil fungi. Despite their crucial role in essential soil ecosystem processes, our understanding of the viral communities hosted by saprotrophic or mutualistic fungi lags behind the extensively studied viromes of plant pathogens. All major fungal taxa, including those forming mycorrhizal symbioses, harbor viruses with single- or double-stranded RNA genomes. These fungal viruses (mycoviruses) lack an extracellular phase in their lifecycle and are transmitted via hyphal contacts or spores. We have been investigating the diversity and population structure of mycoviruses hosted by long-living clonal individuals using high-throughput and Sanger sequencing. From the ECM fungus *Lactarius tabidus*, we have detected a novel single-stranded RNA (ssRNA) virus that is distantly related to recently discovered ormycoviruses. The genomes of ormycoviruses consist of two monocistronic ssRNA segments encoding RNA-directed RNA polymerase (RdRP) and a hypothetical protein. Here, we present the genomic structure of *Lactarius tabidus* ormycovirus 1 and show the stability of the infection in a boreal forest site.

## WED P1 A world beyond peat: how microbial and ecological engineering can reduce agricultural peat consumption

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Peatlands cover 3% of global landmasses and sequester more than one third of terrestrial carbon. Peat excavation cause aeration and release of CO<sub>2</sub> therefore accelerating global warming with adverse worldwide consequences. Besides land reclamation and energetic utilization, peat is exploited as ideal culture substrate for agriculture due to its water holding capacity, chemical adjustability and stability. Alternatives are available, but often insufficient for mimicking peat-based substrates. Thus, we evaluated microbial and physico-chemical properties of peat-free & peat-reduced substrates and their impact on plant growth. Correlation of 16S rRNA gene amplicon sequencing based microbiome analyses of substrates and components together with China cale (*Brassica pekinensis*) growth assays provided insights into potential plant growth anta- and protagonistic bacterial taxa. Agricultural pesticides including *dirty dozen* chemicals were below the detection limit, suggesting that observed plant growth inhibition was not pesticide residue-based in substrates. Non-targeted exometabolomics via LC-MS should identify chemical compounds on top of pesticides which could affect plant growth indicated eleven potential target compounds. Target compounds such as phenylacetic acid or ethane sulfonic acid were examined for garden cress (*Lepidium sativum*) growth assay as biotoxicity indicator to verify effects indicated by exometabolomics. Overall, this study provides broad insights into the microbial community of peat-free & peat-reduced substrates and provide promising candidate taxa as well as metabolites for developing quality control measures. Subsequently, the data provides a basis for the production of high quality peat-free substrates, resulting in a larger market cap and protecting valuable peatlands carbon sinks for a decarbonized society.

## WED P2 Exploiting the potential of soil microbiomes to control *Klebsiella pneumoniae* in arable ecosystems

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*Klebsiella pneumoniae* is the leading cause of infections associated with healthcare institutions worldwide. According to ECDC data, *K. pneumoniae* is the third most common pathogen associated with pneumonia, urinary tract infections and bloodstream infections. Classified as an ESKAPE pathogen, it has been designated as critical category pathogen by WHO due to resistance developed by it even to last resort antibiotics. Beyond clinical settings, it is ubiquitous in the environment, inhabiting soil, water, plants and even raw produce such as cucumber, tomato, lettuce, cabbage, and sprouts. However, surveillance of this notorious human pathogen in Indian agricultural scenario remains largely unexplored. The objective of the current study is to monitor the prevalence of *K. pneumoniae* species complex (KpSc) in Indian arable land and its mitigation using bottom up approach of rhizosphere engineering. In this context, KpSc was isolated from soil and compost samples from 15 different sites across India. In addition, bacterial strains with antagonistic activity against *K. pneumoniae* were isolated and evaluated for plant growth promoting properties. Shortlisted bacterial strains were strategically assembled into synthetic microbial communities (SMCs) after analysing their interactions. Efficacy of these SMCs was tested through *in vitro* and *in planta* experiments for plant growth promotion and biocontrol. Mechanism of action of biocontrol is being investigated. This study will not only generate knowledge on the surveillance of *K. pneumoniae* species complex in Indian arable land but will also bring forth a sustainable strategy for its mitigation.

## WED P3 Soil microbial populations under different land uses at the Eastern Plains of Uruguay, from natural grasslands to rice fields

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The natural grasslands (NGs) located in the Eastern Plains (EPs) of Uruguay hold unique botanical communities with low anthropological impact. However, it has been estimated that only 20% of the EPs are occupied by natural grasslands. Most of the EPs have been converted to rice fields (RFs) that in many cases are under regular rotation with sown pastures (SPs) for cattle grazing, following sustainability policies. Pressure to transform land for rice cultivation implies a threat to biodiversity. In this study, we analyzed the impact of the transition of NGs into RFs and SPs on soil prokaryotic and fungal communities using 16S rRNA and ITS amplicon sequencing. Estimated fungal and prokaryotic richness (Chao1) was higher in NGs than in RFs and SPs. PERMANOVA analysis showed that both fungal and prokaryotic communities differed between NGs and both RF and SP plots. The fungi classes Endonogomycetes and Zoopagomycetes were significantly more abundant in SPs plots compared to RF and NG plots. Regarding prokaryotic taxa, Anaerolineaceae (bacteria) and Methanocellaceae (archaea) were more abundant in RF and SP plots than in NG plots. Taken together, taxa related to methanogenesis and methylotrophy were more abundant in RF and SP plots than in NGs. This agrees with the fact that anaerobic conditions in rice promote the production of methane, a potent greenhouse gas. These preliminary results show that the conversion of NGs to rice and pasture cultivation can have effects on the microbial communities of the soil, affecting local and global key steps in soil nutrient cycling.

## WED P4 Evaluation of an innovative microorganism-enriched organic fertilizer on crop yield and microbiological activity of substrate

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Soil microbiological activity is crucial for driving processes that support plant growth and soil health. Soil microorganisms break down organic matter, releasing nutrients that plants need to thrive. Microorganisms also help improve soil structure and enhance water retention, contributing to overall ecosystem resilience and productivity. Fertilizers used in plant cultivation can significantly alter soil properties and impact the environment. Therefore, the issue of plant fertilization is becoming increasingly important in the context of environmental sustainability. The aim of research was to develop organic fertilizers that promote plant growth and productivity. These fertilizers are composed of composted cattle, pig, or poultry manure, along with peat and ash. Two forms of organic fertilizers were tested – non-granulated and granulated. Additionally, a microbial consortium, developed by microbiologists from the University of Latvia, was incorporated into fertilizers. To evaluate the effects of the fertilizers on the growth and yield of cucumbers, basil, and barley, trials were conducted in vegetation containers. All trial variants were balanced in terms of nitrogen, but the ratios of nitrogen, phosphorus, and potassium varied. A mineral fertilizer was used as the control. At the end of the experiment, substrate respiration and FDA hydrolysis intensity were measured. The results showed that soil microbiological activity depends on the cultivated crop. A trend was observed where higher yields were associated with lower microbiological activity. Higher FDA activity was found in the substrate where granulated fertilizer was used.

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## WED P5 Harnessing rhizosphere microbes for the optimization of Zn remediation by hemp

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Anthropogenic activities have caused widespread soil contamination with pollutants such as heavy metals, rendering soils unsuitable for agriculture and posing environmental and human health risks. To address this, soil remediation is crucial, with phytoremediation offering a sustainable solution. Hemp, with its high biomass and capacity for heavy metal uptake, is a promising candidate for this purpose. Microbes can enhance phytoremediation by improving the overall plant health, increasing the plant's tolerance to heavy metals and facilitating metal uptake. In this research, a rhizosphere start suspension (RSS) from a Belgian hemp field was isolated and serially transferred under laboratory conditions in zinc-contaminated soils with hemp plants. Rhizosphere samples were collected and stored as potential pools of microorganisms that might enhance zinc uptake by hemp. A total of 177 bacterial isolates were screened for zinc tolerance, siderophore production, and swimming motility. The best isolates were further assessed for organic acid and indole-3-acetic acid production, zinc solubilization, and biofilm formation. The impact of three isolates (*Pseudomonas*, *Enterobacter* and *Stenotrophomonas*) on hemp's zinc uptake was investigated through a pot experiment. Multi- and hyperspectral imaging techniques were used to evaluate the impact of these isolates on hemp growth under both optimal and zinc-contaminated conditions. Chemical analysis of shoots, roots, and soil material was performed to assess their potential to enhance zinc phytoremediation. Preliminary data indicate that microbial inoculation increased plant height in heavily Zn-contaminated soil, and ongoing analysis may reveal additional insights into microbial effects on hemp phenotype and phytoremediation.

## WED P6 Can cover crops limit the spread of antibiotic resistance in agricultural soil microbiomes?

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Agricultural production relies heavily on fertilizers to promote crop growth and often includes the application of livestock manure. Besides many positive impacts of organic fertilizer, it introduces contaminants such as antibiotics, antibiotic-resistant bacteria, and their genes into agricultural soils. If taken up and translocated to edible tissues in crops, this can pose a risk to food safety. Cover crops are known to provide a range of agronomic benefits, such as increasing organic matter content and improving soil moisture retention, next to supporting beneficial microorganisms in the soil. However, the potential of cover crops to reduce the spread of antibiotic resistance, has not yet been extensively studied. We expect that cover crops can reduce the spread of antibiotic resistance in the agricultural soil microbiome. By diversifying the soil microbiome, available niches are occupied more effectively, thereby limiting species invasion from manure. To investigate this, an outdoor mesocosm experiment was conducted to compare the effects of two different cover crop mixtures on the soil microbiome compared to microbiome dynamics in an unplanted control. Manure, likely contaminated with antibiotics and antibiotic-resistant bacteria, was applied to the soils in autumn and spring. By analyzing the transient dynamics of the microbiome composition and antibiotic resistance genes, we assessed the impacts of both cover crop mixtures to reduce the spread of antibiotic resistance in the agricultural soil microbiome. By integrating cover crops into manure management practices, we contribute to the development of sustainable agricultural practices that improve soil health, reduce environmental pollution, and promote food safety.

## WED P7 Granular organic fertilizers composed from multiple agri-food side flows impact soil microbial communities

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Stimulating microbial life in the rhizosphere by applying organic inputs have been suggested to lead to healthier root environments and increased crop resilience. However, the effects of fertilizer types on soil microbial communities remains poorly understood, especially considering the wide array of possible inputs. DCM produces ultrafine organic granules that can be composed of over thirty different high quality ingredients, sourced from side flows of the food processing and agricultural industry. Examples are cocoa shells, horn meal, bone meal, or vegetal residues. Each source material displays a unique nutrient composition and release pattern, leading to specific compositions of fertilizer formulas. Each granule is homogeneously composed of selected ingredients, allowing for fine and uniform distribution in the soil or substrate, where the complex blend acts as food source. These organic ingredients are being studied for their impact on soil microbiome and plant growth. The effects of diverse inputs, including chemical fertilizers, animal manures, and organic blends were assessed. Results indicate that fertilizer type significantly influences soil microbial life. Increased microbial biomass and activity were observed when using organic granules. Moreover, shifts in microbial community composition were noted and communities displayed dissimilar abilities to metabolize different carbon sources, indicating more functional diversity after application of organic fertilizers. Overall, our research underscores the potential of utilizing ultrafine, specifically composed organic fertilizers to enhance soil microbial life. Further investigations into optimal composition of blends are warranted to develop tailored practices to influence the soil microbiome leading to improved plant resilience and enhanced crop performance.

## WED P8 Quantitative insights into soil bacterial and fungal populations under conventional farming practices

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Soil microbiomes are crucial in maintaining the soil nutrient cycle as they play a key role in the decomposition and formation of humus and thus release nutrients for the crops. Conventional agricultural practices can affect the balance of soil microbiomes critical to soil health. This research aimed to study the abundance of microscopic filamentous fungi and bacteria in agricultural soil and a control site represented by soil with natural vegetation without any intervention. Microscopic fungi were isolated using the serial dilution plating method. One milliliter of the diluted sample (e.g.,  $10^{-4}$  dilution) was plated on MEA (Malt Extract Agar Base-w/Mycological Peptone), SDA (Sabouraud Dextrose Agar), PDA (Potato Dextrose Agar) and RBA (Rose Bengal Agar) to enumerate filamentous fungi, with results expressed as CFU (Colony Forming Units) per 10 g of dry sample. The same method was used to cultivate bacteria on MPA (Meat Peptone Agar). A higher abundance of microscopic fungi was observed in control soil samples compared to agricultural soil, where the abundance was 62% lower. That may signal that intensive agriculture negatively affects the fungal community. A higher number of sporulating bacterial colonies (32–64%) were detected in agricultural soil, while in the control sample, non-sporulating bacteria dominated (71–91%). Sporulation is often a defense mechanism for bacteria to survive adverse conditions; therefore, it may be a response to stressful conditions. These findings indicate that conventional agriculture is leading to a shift in soil microbial composition that may negatively affect soil quality and ecosystem function.

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## WED P9 Protist-mediated control of enteric bacteria in agricultural soils irrigated with treated wastewater

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Treated wastewater (TWW) irrigation is a sustainable practice but raises concerns about introducing human pathogens into agricultural soils and crops. While mitigation efforts have traditionally focused on water treatment, recent attention has shifted to the role of soil microbial food webs in pathogen control. This study examines how soil protists regulate enteric bacteria introduced via TWW and how environmental factors influence predation efficiency. We hypothesized that enteric bacteria, such as *Escherichia coli*, are susceptible to predation by indigenous protists and that environmental conditions modulate this interaction. To test this, we conducted soil microcosm experiments using two management strategies – organic and conventional – on an identical soil type, as management influences microbial communities. Soils were irrigated with synthetic TWW supplemented with *E. coli* and an inhibitor to protist activity. Inhibition significantly enhanced *E. coli* survival in both treatments, confirming the regulatory role of protists. Taxonomic analysis identified key bacterivorous protists, including *Poteriospumella* and *Pseudodendromonadales* in organic, and *Rosculus* and *Vahlkampfia* in conventional soil. Despite taxonomic differences, predation pressure remained consistent across soil treatments. To further assess environmental influences, we isolated 12 soil amoebae and tested predation efficiency of three enteric bacteria under varying temperatures (20–30°C) and salinities (2–30 mM NaCl), as TWW is more saline than freshwater. Predation increased significantly at lower temperatures and higher salinities ( $p < 0.01$ ), suggesting that irrigation salinity may benefit micropredators, while rising temperatures may promote bacterial resistance. Our findings feature protists' role in mitigating introduced enteric bacteria, offering new insights into soil food web resilience.

## WED P10 Harnessing adaptive soil microbiomes for dryland cultivation of tomato

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Dry spells are becoming more frequent and severe across the world, and farmers can no longer rely on climate predictability. With the global population projected to exceed 9.7 billion by 2050, agricultural output in the 21st century is threatened by record-high temperatures. Although leading to increased crop production, the Green Revolution also mainstreamed the use of synthetic fertilizers and pesticides, which resulted in the degradation of soil quality. Drought limits the availability of soil moisture and impairs the ability of root systems to absorb vital nutrients, thereby endangering plant viability. Conventional bioinoculants, such as plant growth-promoting rhizobacteria, offer environmentally favorable options; however their efficacy in agricultural soils can be compromised due to localized competition with native microorganisms. Microbiome engineering is a more systematic and novel strategy in this regard since it focuses on the entire microbial population, allowing for more persistent modifications. In this study, the tomato rhizosphere microbiome was adapted to induced drought stress through host-mediated indirect selection using a multiple-passaging approach. Tracking plant phenotypic indicators and biochemical stress markers revealed that the microbiome acclimatized over consecutive growth cycles and enhanced plant fitness through improvements in plant-soil feedback. Shifts in the soil physicochemical profile were also observed via significant augmentation of soil aggregate stability, saturated hydraulic conductivity, total porosity, and organic carbon content, which further correlated with changing microbial community composition across passages. This work emphasized the importance of indigenous soil microbial communities in fostering climate-resilient, sustainable food production systems and leveraged their innate capacity to improve drought tolerance.

## WED P11 Effects of prebiotics on *Zea mays* L. growth and rhizosphere microbial communities in drought stress: to understanding and beyond

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Facing declining crop yields and reduced soil fertility, biostimulants such as soil-applied prebiotics are designed to promote soil health and plant growth. Nevertheless, their mechanisms of action remain poorly understood. This study investigates the effects of the prebiotic Nutrigeo L<sup>®</sup> on *Zea mays* L. under severe drought (SD) conditions where soil water holding capacity (WHC) was maintained at 30%, compared to a well-watered (WW) control at 70% WHC. After 10 weeks of greenhouse cultivation in an agricultural soil, we observed significant differences in prebiotic-treated plants. Several phenotypic traits were measured, including plant height, which significantly increased by 18.70% under SD conditions and 20.57% under WW conditions. We explored rhizosphere's microbial responses by assessing bacterial and fungal abundances, as well as metabolic analysis using BIOLOG<sup>®</sup> Ecoplates. The latter revealed a significant increase in average well color development (17.78% under SD and 16.35% under WW). Additionally, we analyzed seven soil enzymatic activities related to different nutrient cycles to assess microbial functionality. Our results revealed a significant increase in the geometric mean of these enzymes and a significant decrease in the soil's alteration index. Prebiotic's effects and the resulting plant stress responses will be analyzed through proline content quantification, phytohormonal profiling, and metabarcoding analysis. To our knowledge, this study is the first to provide such a comprehensive analysis of prebiotic effects on both plant physiology and rhizosphere microbial communities. This provides critical insights into the mechanisms by which prebiotics enhance plant stress tolerance and soil functionality, paving the way for sustainable agricultural applications.

## WED P13 Soil microbial diversity, structure and interactions under conventional and conversion-to-organic agricultural systems in Québec

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From nutrient cycling to aggregate formation and greenhouse gas regulation, a myriad of biogeochemical processes take place in soils, largely driven by microorganisms. As such, soil biodiversity and microbiota structure contribute to soil multifunctionality. Pesticides, widely used in conventional agriculture, can reduce soil microbial biodiversity and alter community composition. Glyphosate, for instance, has been shown to negatively affect plant-beneficial microorganisms such as *Burkholderia* spp., *Pseudomonas* spp., nitrogen-fixing *Rhizobium* spp., and arbuscular mycorrhizal fungi communities, while favouring certain pathogens such as *Fusarium*. Most studies on pesticide impacts focus on individual compounds, whereas in practice, pesticides are applied in mixtures throughout the growing season. Here, we sampled twelve agricultural fields three times a year over three years. Half of the fields were conventionally managed and received a variety of pesticides, while the other half were transitioning to organic management, progressively reducing pesticide applications. We sequenced both bacterial and fungal communities in the soils and compared their composition between management practices. Our results showed that, while biodiversity remained similar between practices, microbial community structure differed significantly. Interestingly, network analyses also revealed distinct microbial interactions between conventional and transitioning fields. These findings provide valuable insights for both growers and scientists on the impact of pesticides on soil biodiversity and, ultimately, soil multifunctionality.

## WED P14 Transforming agro-industrial waste into fertilizer: assessing the short-term effects on the rhizosphere microbial biodiversity of hazelnut saplings via a metagenomic approach

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Soil microorganisms are fundamental for nutrient cycling and plant health, yet excessive synthetic fertilization depletes biodiversity. This study examines the short-term effects of different fertilization strategies—including synthetic NPK, composted olive pomace (OP), and a sulfur-bentonite-based fertilizer (SBOP)—on the rhizosphere microbiome of *Tonda di Giffoni* hazelnut saplings using metagenomic sequencing. The results indicate that adding just 5% organic material to sulfur-based fertilizers significantly enhanced alpha-diversity, as measured by the Chao1 index. Microbial richness increased by up to 22% in SBOP-treated soils compared to unfertilized controls, demonstrating the role of organic amendments in fostering microbial abundance. Beneficial bacterial genera such as *Thiobacillus*, involved in sulfur oxidation, and *Pseudoxanthomonas*, key in organic matter decomposition, were notably enriched in SBOP treatments. Likewise, the fungal genus *Thermomyces*, which plays a crucial role in carbon and nitrogen cycling, thrived in organic-enriched conditions. In addition, organic amendments also influenced beta-diversity, as revealed by Bray–Curtis dissimilarity analysis. SBOP treatments led to significant shifts in microbial community composition, differentiating them from NPK and unfertilized soils. The introduction of organic matter reshaped the soil microbiome, favoring taxa associated with improved nutrient cycling and soil health. These findings highlight the potential of integrating organic and mineral fertilizers to enhance soil microbial diversity, promote sustainable nutrient cycling, and mitigate biodiversity loss. The study underscores the viability of agro-industrial waste reuse as an eco-friendly fertilization strategy to improve soil health and optimize hazelnut productivity. Further research is needed to assess the long-term impact of these amendments on soil sustainability.

## WED P15 Distinct functional responses of root and rhizosphere microbial communities in intercropping systems under arid conditions

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Intercropping enhances soil nutrient availability and positively regulates soil microbiota, therefore improving crop yields in intensive agroecosystems. We conducted field experiments under arid conditions using intercropping with key crops (i.e., barley, mustard, alfalfa, broad beans, wheat yokara, and Egyptian wheat) and collected soil and root samples from amplicon sequencing and also isolated bacteria. We evaluated multiple PGPR tests in-vitro conditions under salinity and drought stress. Most exhibited PGP traits, enzymatic activity, and the ability to survive under osmotic stress (-132.0 MPa), high temperatures (45°C), and 5% NaCl. Rhizosphere bacterial isolates were more drought-tolerant and produced more EPS in the presence of glucose, while endophytic communities produced EPS with sucrose and more indole acetic acid. The functionality of endophyte and rhizosphere bacterial communities varied but was not dependent on the intercrop type. The 16S rRNA analysis revealed that mainly root endophytic isolates were *Proteobacteria*, *Bacillota*, *Pseudomonadota*, *Bacteroidota*, and *Actinomycetota*. While the rhizosphere isolates were *Proteobacteria*, followed by *Bacillota*, *Actinomycetota*, and *Bacteroidota*. The compatible strains were used to construct synthetic bacterial communities (SynComs). The results demonstrated that the eight root isolates were compatible, with seven SynComs consisting of two isolates and four SynComs comprising three isolates. Results suggest that bacterial strains could serve as plant probiotics, promoting growth and enhancing plant health under climate change, particularly in dryland areas.

## WED P16 Arbuscular mycorrhizal dependency in barley: the roles of variety age, agricultural management and fungal community composition

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Global food production faces the challenge of feeding more people with less energy and chemical inputs. Enhancing arbuscular mycorrhizal (AM) symbiosis in crops appears as a promising way to increase agricultural sustainability, as AM fungi can aid their host plants in nutrient uptake and protect them from pathogens and environmental stresses. However, crop domestication and breeding have produced less AM-dependent crop varieties, which may only benefit from AM symbiosis in nutrient-limited conditions. Furthermore, high fertilizer inputs can reduce the AM benefit for the crop and the amount of edaphophilic in relation to rhizophilic AM taxa. As these groups allocate differently to extra- versus intraradical hyphae, variation in their ratio can affect plant AM fungal benefit. However, whether a mutualistic AM symbiosis can be attained with crop variety selection, adjusted agricultural management, and optimized soil AM fungal community structure, remain unclear. I present root AM fungal colonization and community data from a field experiment in central Estonia, comparing thirteen barley varieties bred in different years and growing either under organic or intensive management. We hypothesize (1) that the mycorrhizal root colonization rate, a proxy of mycorrhizal dependency, decreases with variety age, (2) that the roots of plants growing in organic soil and of older varieties harbor more edaphophilic and non-cultured fungal taxa, and (3) that the root AM fungal community composition and diversity depend on the type of management but do not differ between varieties.

## WED P17 Rootstock genetic background influences microbial community composition and enrichment of taxa associated with plant defense and nutrient availability

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Beneficial root microorganisms play a crucial role in influencing key agronomic traits in rootstocks. However, little is known about the microbial communities naturally associated with almond rootstocks in Spain. To address this gap, we sampled roots of six *Prunus* rootstocks in a 15-year-old almond orchard representing two different genetic backgrounds: *P. cerasifera* background (PCB) with Rootpac 20, and Rootpac 40, and *Prunus persica* background (PPB), with Cadaman, Garnem, GF677, and Rootpac R. Root-associated bacterial, fungal, and arbuscular mycorrhizal fungi communities were evaluated using a high-throughput amplicon sequencing approach. PCB rootstocks were significantly enriched with *Streptomyces* amplicon sequence variants (ASVs), which contain bacterial species known as biocontrol agents. In contrast, PPB rootstocks were significantly enriched with ASVs of *Hyalorbilia* and *Rhizophagus*, the former being an ascomycete known for its nematophagous activity, and the latter for its role as a mycorrhizal fungus. Interestingly, taxa including known plant pathogens were significantly enriched in PCB rootstocks, namely ASVs from Venturiales and Nectriaceae. Moreover, in PCB rootstocks we identified bacterial and fungal ASVs that were positively correlated with N and P soil concentrations, respectively, suggesting their potential role in enhancing nutrient availability for plants. Similarly, certain bacterial and fungal ASVs were positively and highly correlated with Na concentration among PPB plants, suggesting a potential role in plant salinity tolerance. These results suggest that the genetic background of the rootstock influences bacterial and fungal taxa recruitment in field conditions, thus potentially affecting nutrient cycling, plant defense, and offering microbiome markers for plant resilience.

## WED P18 Limited and idiosyncratic thermal acclimation in soil saprotrophic fungi

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Increased soil microbial activity due to higher temperatures caused by heatwaves could lead to higher carbon losses from soil into the atmosphere, further accelerating climate change. Hence, knowing how soil microbes respond to higher temperatures is crucial for improving soil-atmosphere carbon circulation models in the context of climate change. Thermal acclimation may reduce carbon losses from soils by retarding increases of microbial activity in response to higher temperatures. However, the capability of soil microbes to acclimate and our possibilities to predict this capability, remain unexplored. Here we tested how submission to two environmental histories affected subsequent growth at two exposure temperatures, for seven widespread soil saprotrophic fungi. We hypothesised that (1) soil fungi would have higher intrinsic growth and weaker self-limitation after being exposed to a colder environmental history, and (2) the response of fungal eco-physiological traits (pigmentation and spore load) to heatwave exposure could predict fungal acclimation in terms of growth. Our results showed that environmental history temperatures had limited impact on the tested fungi, and trait responses to environmental history temperatures did not predict fungal growth after treatment with both environmental history and exposure temperatures. We conclude that the phenomenon of fungi thermal acclimation is limited and idiosyncratic.

## WED P19 Life cycle dynamics as a trait of arbuscular mycorrhizal fungi species

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Arbuscular mycorrhizal fungi (AMF) are obligatory plants symbionts, assisting the host with nutrient uptake, stress resistance and promoting ecosystem stability in soils. AMF culturing is a laborious process, with highly variable results shaped by fungal identity, host plant interaction, soil properties and growth conditions. Our goal is to determine the temporal dynamics of AMF species and families, comparing the life cycle rate among them. We hypothesize that some AMF species develop slower than others, thus needing more time or more suitable conditions to complete their life cycles. To investigate this, we've established a greenhouse experiment with 16 monospecific AMF treatments and one non-mycorrhizal control, with 6 replicates each. *Inula salicina* subsp. *salicina*, a perennial herb, was chosen as host plant. The analyzed variables were AMF root colonization (hyphae, arbuscules and vesicles) and number of living spores per gram of soil, future analysis also include extraradical mycelium density. Ten harvests are planned across two years. Preliminary results indicate an earlier investment in hyphal and arbuscules development by *Scutellospora calospora*, *Gigaspora rosea*, *Claroideoglossum etunicatum*, *Septoglossum deserticola*, *Rhizophagus manihotis* and *Rhizophagus intraradices*, while a preceding development of vesicles was found only in *Paraglossum brasilianum*. Species with the earliest onset of sporulation were *Diversispora spurca*, *C. claroideum*, *C. etunicatum* and *S. deserticola*. Further harvests and data analysis are still ongoing and are fundamental to elucidate the temporal dynamics of each species and families.

## WED P20 *Pseudomonas veronii* and a bacterial consortium as Sb(V)-reducing bacteria: unlocking bioremediation potential

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Microbes from mining-contaminated sites play an important role in metal(loid) transformation, which enables their use as environmental tools for the removal of contaminants. We isolated and characterized microbes from Finnish mine sites which were able to tolerate (and potentially metabolize) a priority pollutant and critical raw material, antimony (Sb). The present study focused on identifying potential genes involved in the anaerobic reduction of Sb(V) by the bacterium *Pseudomonas veronii* as well as changes in the relative contribution of different species in a microbial consortium depending on the offered electron acceptor. To accomplish this, bacterial isolates and consortia were grown anaerobically with either Sb(V) or NO<sub>3</sub><sup>-</sup> as terminal electron acceptors. Differential gene expression via transcriptomic analyses of *P. veronii* as well as taxonomic changes of the consortia were assessed via metagenomic analyses in the exponential growth phase. Results from the transcriptome of *P. veronii* indicated that several genes encoding for reductases, such as those belonging to the DMSO family as well *ssuE* and *sfnF* reductases presented potential in the anaerobic respiration of Sb(V). Metagenomic analyses revealed that the consortium was formed by members of *Mesorhizobium*, *Sphingomonas*, *Bradyrhizobium* and *Carnobacterium*, being the first one the dominant genus in the Sb(V) samples while the two latest the dominant genus in the NO<sub>3</sub><sup>-</sup> samples. Findings improve understanding of bacterial Sb(V)-reduction using (meta-)genomics and (meta-)transcriptomics approaches. Future work will focus on testing the feasibility of the bacteria at a larger scale for its implementation in bioremediation.

## WED P21 Arctic seabird-affected soils as a source of microbial N<sub>2</sub>O emissions

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Nitrous oxide (N<sub>2</sub>O) is a potent greenhouse gas with a higher global warming potential than carbon dioxide and methane and is primarily produced by microbial processes. Recent studies have reported N<sub>2</sub>O fluxes from selected polar ecosystems at levels comparable to tropical forests, a major natural source. This study aimed to identify new hot spots of N<sub>2</sub>O emissions in the Arctic and investigate the microbial mechanisms driving its production. To achieve this, geomicrobiological characterization of diverse terrestrial habitats in the Arctic (Hornsund area, Spitsbergen) was performed. Bird-affected soils, under the influence of planktivorous little auk (*Alle alle*) colony, showed the highest potential for N-turnover and N<sub>2</sub>O production. This potential was further investigated using metagenomics and microcosms experiment assessing also the impact of nutrients input and temperature rise. Results showed that bird-affected soils harbored the highest concentrations of nitrate, total C, N and the lowest C:N ratio from studies soils, which are all factors predicting high N<sub>2</sub>O emissions. The soil microbial community possessed the capacity to utilize a broad range of substrates, high ammonification capacity and abundant N-cycling pathways. These microbial communities produced N<sub>2</sub>O after substrate addition in anoxic conditions, in which denitrification is the dominant pathway. Two new species of bacteria belonging to genus *Herminiimonas*, capable of N<sub>2</sub>-fixation and denitrification were discovered. These findings highlight seabird-affected soils as unique nitrogen-rich environments and potential N<sub>2</sub>O emission hotspots in the Arctic, emphasizing the need for further ecosystem screening to quantify the polar regions' contribution to global greenhouse gas budgets.

## WED P22 Microbial community dynamics and functioning under three common plants encroaching the Canadian tundra

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Rapid expansion of shrubs and trees into the Arctic tundra could lead to changes in soil microbial communities, consequently affecting belowground ecosystem processes and potentially resulting in a large loss of soil organic carbon in northern ecosystems. Therefore, we investigated the impact of encroaching plant species on the composition and functioning of soil microbial communities using molecular and isotopic methods. Dwarf shrubs (*Betula glandulosa*) allocated relatively more photosynthates belowground than tall shrubs (*Alnus viridis*) and black spruces (*Picea Mariana*) during a <sup>13</sup>CO<sub>2</sub> pulse-chase experiment in Inuvik, Canada. During this presentation, we will present data that disentangle the impact of the plant-specific differences on microbial functioning and the potential for rhizosphere priming of native soil organic matter. Firstly, we will show how the deposition of <sup>13</sup>C decreases with soil depth and compare the turnover rates of these rhizodeposits by microbial communities in bulk soils across depth. Secondly, we discuss the drivers of microbial community assembly below the encroaching plant species by characterizing fungal and bacterial communities across root proximity and soil depth. We compare the influence of the three plant species on microbial community assembly both under field conditions and in controlled laboratory conditions (where starting soils were homogenous for all groups) to separate plant and soil characteristics. Overall, this work suggests that changes in vegetation play a crucial role in the structuring and functioning of soil microbial communities of the Arctic tundra and highlights the importance of plant-soil interactions in the permafrost feedback to climate change.

## WED P23 An endohyphal bacterium contributes to light dependent metabolism and growth in the ubiquitous soil fungus *Trichoderma reesei*

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In nature, complex organismic communities have evolved for optimal colonization of habitats. Interkingdom interactions between fungi and bacteria can be mutualistic, but also parasitic. Fungi inhabited by bacteria may change their behaviour in the ecosystem in terms of growth or efficiency of substrate degradation. Therefore, we were interested, how widespread the presence of endofungal bacteria is in strains of the genus *Trichoderma*, comprising species with a variety of ecological functions – from beneficial plant interaction and mycoparasitism on pathogenic fungi to degradation of cellulosic litter. Endohyphal bacteria of different species inhabit the majority of *Trichoderma* strains tested. In the saprophyte *Trichoderma reesei*, we confirmed the presence of a *Methylobacterium* which influences growth and cellulase production of its host. Moreover, it impacts growth of *T. reesei* differently in light and darkness on several carbon sources, particularly on xylitol and mannitol. The transcriptome of *T. reesei* changes significantly in the absence of the bacterium in light and darkness, including multiple Czyme encoding genes. Genome analyses showed that the metabolic capacities of *T. reesei* and *Methylobacterium* complement each other and that the latter comprises multiple genes with light response associated characteristics, hence explaining the light dependent impact on its host. In summary, we show that the interkingdom interaction of endohyphal bacteria with their host is not limited to metabolic capacities, but can also extend to a specific contribution to adaptation to light on certain substrates, hence enhancing competitiveness and ecological services in their habitat.

## WED P24 Soil microbial diversity in Mediterranean oak forest ecosystems subjected to ungulate grazing and forest management

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The soil microbial community (SMC) is essential in supporting life on Earth's ecosystems. It contributes to nutrient cycling, organic matter dynamics, carbon transformations and sequestration, and biogeochemical cycling of elements such as nitrogen, phosphorus, and sulphur. While several studies have addressed the impact of flora and ecological constraints on SMC composition and functionality, the effect of long-term animal grazing has been largely overlooked. Animal grazing can affect soil nutrient turnover by altering C and N allocation between soil layers, plant biodiversity, and forest regeneration. With this in mind, we studied the long-term effects of animal grazing on SMC composition and functionality in Campo di Rota (CPR), a 24-ha deciduous oak forest inside the Presidential estate of Castelporziano (Rome, Italy). Since 2013, an area of 12 ha inside CPR has been fenced to exclude ungulates and subjected to silvicultural activities to help forest regeneration. The fenced area makes it possible to study the SMC in the presence and absence of ungulates, thus measuring the effect of long-term ungulate grazing on SMC composition and functionality. Targeted and genome-centric metagenomic analysis, combined with chemical-physical and biochemical characterisation of soil samples at different depths (core sampling at 0–10 cm, 10–30 cm, and 30–50 cm), suggests that long-term ungulate exclusion has minimal impact on SMC composition and functionality, with vegetation and soil chemical-physical properties being the primary influencing factors.

## WED P25 Linking CO<sub>2</sub> and CH<sub>4</sub> emission rates to microbial diversity in semi-natural and agricultural grasslands in Eastern Germany

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Natural or semi-natural grasslands represent some of the most diverse terrestrial habitats and are central elements of terrestrial carbon (C) cycling. Soils under (semi-)natural grasslands are able to sequester more C than their counterparts in intensively managed systems. In Central Europe, remaining (semi-)natural grasslands are threatened by over-fertilization, fragmentation and land use change in favor of intensively managed agricultural land. This is especially true for Eastern Germany, where few semi-natural grasslands remain due to historical development with possibly large effects for C cycling and sequestration. In our study focusing on the comparison of semi-natural and intensively managed grasslands in the border region of Germany and the Czech Republic, our goal is to use Next Generation Sequencing to characterize below-ground diversities of fungi, bacteria and archaea and link them to emissions of methane (CH<sub>4</sub>) and carbon dioxide (CO<sub>2</sub>). Preliminary results show highly significant increases in emissions of both CH<sub>4</sub> and CO<sub>2</sub> in agricultural grassland compared to semi-natural grassland, but no differences between patches in semi-natural grassland differing in plant species richness.

## WED P26 Impact of small-scale spatial heterogeneities on methane-cycling microorganisms in semi-permanently flooded kettle holes

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Wetlands are the main terrestrial source of the greenhouse gas methane. Kettle holes, which are typically small (< 1 ha) wetlands characterized by a highly dynamic hydrology, spatial heterogeneities and location often within agricultural fields, are hypothesized to emit substantial amounts of methane. Nonetheless they are typically not considered in regional and global emission estimates. They are subject of matter input from their surroundings, which includes fertilizers as well as soil material. The resulting irregular horizonation with colluvial horizons over peat impacts on the microbiota composition. Thus, together with their often frequent dry-wet cycles, kettle holes likely also provide unique and dynamic conditions for methane-cycling microorganisms. We sampled three kettle holes with similar colluvial horizon structure to a depth of 1 m, capturing heterogeneities within each kettle hole by targeting 4 locations from the kettle hole edge to its center with different moisture, horizon and vegetation compositions. The cores were dissected into 4–5 horizons. Differences between kettle holes were significant for soil pH, sulfate content and abundances of methanogens, atmospheric methane consuming and anaerobic methanotrophs. However, trends by core position were also apparent and sometimes significant. PCA revealed a grouping of samples according to horizon characteristics (mineral, boggy, peat). These results suggest some individuality among kettle holes, but they also show the expected impact of vertical and horizontal spatial heterogeneities. Incorporating methane oxidation and production rates and microbiota composition data will identify shared vertical and horizontal patterns and thus will allow to identify soil-associated determinants of methane-cycling microorganism in kettle holes.

## WED P27 Relating fundamental to realized niches of arbuscular fungi along a temperature gradient

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While the realized niche can be derived from a species' distribution in different habitats, the fundamental niche is approached more difficultly – it requires experimental investigation of responses to environmental gradients. Knowing parameters of fundamental niches of arbuscular mycorrhizal species, however, would be a valuable tool for predictions of species' responses to changing abiotic environments, important e.g. in relation to expected climate change. As temperature was recently identified as one of the most important abiotic predictors of the distribution of arbuscular mycorrhizal fungi (AMF), we conducted growth chamber experiments with four plant species and eleven AMF isolates to assess their fundamental niche along a temperature gradient. The GlobalAMFungi database was used to preselect the AMF based on their putative preference for colder or warmer environments. Development of their intraradical and extraradical phase along a gradient of temperature was scored after two months of cultivation. We observed clear differentiation of AMF in sensitivity to increasing temperature: e.g. *Gigaspora rosea*, *Rhizophagus manihotis* and *Racocetra fulgida* had higher intraradical colonization in 40°C, whereas it was much lower in 25°C and they did not establish at all in 5°C. In contrast, e.g. *Diversispora epigagea*, *Claroideoglossum claroideum* or *Archaeospora schenkii* displayed very low colonization in 5°C, proliferated best in 25°C, while had lower or even zero root colonization in 40°C. Fundamental niche assessment in AMF is new to science and our results hint that different AMF species will respond very differently to global changes, which could influence their future distribution.

## WED P28 Recovery of soil fungal communities after clearcutting in previously fertilized and unfertilized forests

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Forests in northern Europe are intensively managed, including the use of nitrogen fertilizers and clearcut harvesting. The severe disturbance of clearcutting means that carbon supply to ectomycorrhizal fungi (EcMF) is cut off and they largely disappear from the stand. Because of the Gadgil effect, we expect saprotrophic fungi to increase at first, followed by a decrease as EcMF reestablish. Due to differences in dispersal capacity and ecological niches, EcMF vary widely in their propensity to (re)colonize regenerating forests. As forest fertilization during the previous rotation period can affect soil conditions after clearcutting, it could also affect EcMF recovery. Here, we used a space-for-time approach to study soil fungal communities in the first 13 years after clearcutting. We collected soil samples in 48 clearcuts of previously fertilized and unfertilized forests. By combining ITS2 metabarcoding and qPCR, we were able to semi-quantitatively determine soil fungal communities. In the first year after clearcutting EcMF abundance was low and their communities were clearly distinct from the ones in older clearcuts, being dominated by *Russula*, *Cenococcum* and *Cortinarius*. EcMF abundance subsequently linearly increased while saprotrophic agaricomycetes abundance showed a hump-shaped relationship with time since clearcutting. In the 4–6, 7–9 and 10–13 year old clearcuts, respectively *Thelephora*, *Suillus* and *Piloderma* were the most abundant EcMF genera. *Piloderma* showed a stronger increase in abundance in clearcuts of unfertilized forests compared to fertilized forests. Overall, we found that despite the intense disturbance of clearcutting, fertilization effects on soil fungal communities linger on into the next rotation period.

## WED P29 Exploring climate-independent factors driving *Pinus sylvestris* root traits and bacterial endophyte communities in a common garden experiment

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Plant adaptation to diverse climatic conditions across their distribution range involves the differentiation of root traits and associations with below-ground bacteria. These bacterial communities are directly influenced by plant root traits; however, their relationship is not fully understood. We hypothesized that some root traits of Scots pine (*Pinus sylvestris*) would emerge from genetic differences among populations and vary according to provenance, even under common garden conditions, in turn influencing the bacterial root endophyte community. We selected trees from ten provenances across Europe, ranging from Russia to France, grown in a IUFRO 1982 common garden experimental setting in Poland. Roots were sampled separately in spring and autumn to address the seasonal variability of the studied communities. The bacterial root endophytes were characterized using Illumina MiSeq sequencing of the 16S rRNA gene. As hypothesized, tree provenance significantly influenced the variability of root traits and differentiated the root endophytic bacterial communities in terms of both quantitative and qualitative diversity. Furthermore, the effects of tree provenance on bacterial communities fluctuated between seasons, being more pronounced in spring. The abundance of several bacterial groups showed a significant correlation with the root traits that differed among provenances. Our results shed light on the mechanisms structuring the communities of root endophytic bacteria, highlighting climate-independent factors. Gaining a better understanding of this aspect would allow for more accurate predictions of how below-ground bacterial community structure shifts under a changing climate.

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## WED P30 Conjugative gene transfer: advancing bioremediation of polyaromatic hydrocarbons in soils

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Microbial communities play a central role in biodegradation processes, yet their ability to degrade persistent pollutants like polyaromatic hydrocarbons (PAHs) can be limited. Bioaugmentation, introducing microorganisms capable of degrading specific contaminants, is a promising strategy; however, colonization resistance can hinder the establishment of allochthonous strains. Plasmid-mediated bioaugmentation offers an alternative, using conjugative plasmids to transfer catabolic genes to indigenous microbes, enhancing degradation capacity. This study explores the spread of the *tod* (toluene dioxygenase) gene cluster from *Pseudomonas putida* F1, a proficient PAH degrader, via the RP4-derived conjugative plasmid pMATING $\alpha$ -msfGFP in pristine and PAH-contaminated soil microcosms. Horizontal gene transfer was tracked using a dual fluorescence reporter system combined with an expression/repression mechanism. The donor strain, a *P. putida* derivative chromosomally tagged with the *mCherry* gene and expressing the *lacIq* repressor, carried the pMATING $\alpha$ -msfGFP-*tod* plasmid. Donor cells were mCherry-positive/GFP-negative, while transconjugants, upon acquiring the plasmid and lacking *lacIq*, expressed GFP. Transconjugants will be sorted via flow cytometry, characterized through 16S rRNA metabarcoding, and assessed for their PAH degradation ability in degradation assays using model pollutants. This approach highlights the potential of plasmid-mediated gene transfer to enhance environmental restoration and provides insights into microbial ecology and evolution in contaminated soils.

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## WED P31 Influence of rock phosphate application rates on soil bacterial density and community composition

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Phosphorus availability in agricultural soils is often limited due to the low solubility of phosphate compounds, prompting farmers to use inorganic and organic fertilizers. Fertilization influences bacterial community abundance and diversity, with chemical fertilizers having a well-documented impact on soil microbes. This study evaluated the effects of different Rock Phosphate application rates on soil bacterial communities in Man, western Côte d'Ivoire. A three-year field experiment was conducted in maize cropping systems, where four bio-phospho-compost fertilizers were applied during the first cultivation cycle. Soil samples were collected after each cycle to quantify total and cultivable phosphate-solubilizing bacteria (PSB) and to analyze bacterial community structure and  $\alpha$ -diversity (Shannon, Evenness, and Chao1 indices). The results revealed a stable bacterial community composition across treatments, dominated by Firmicutes, Actinobacteria, Proteobacteria, Halobacterota, and Chloroflexia. Regardless of the Natural Rock Phosphate dose applied, bacterial community composition remained unchanged. However, Rock Phosphate application significantly increased both total aerobic bacteria and phosphate-solubilizing bacteria (PSB) populations. Notably, the highest bacterial abundance was observed at 450 kg RPM/ha, surpassing the lower doses of 150 and 300 kg RPM/ha. These findings suggest that applying 450 kg RPM/ha is optimal for enhancing soil bacterial communities and improving acidic soil fertility.

## WED P32 Soil microbiological activity in differently managed urban meadows

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Urban environments are increasingly introducing meadows, replacing intensively maintained lawns or previously industrial areas. Urban areas, especially city centres, are major contributors to atmospheric CO<sub>2</sub>. Expanding green spaces helps reduce atmospheric pollution. Plant growth is significantly affected by soil quality, which is also influenced by the microbiological processes in the soil. Urbanization leads to the creation of soils, which are influenced by human activity and may contain significant amounts of contaminants. There is a critical need to understand urban soil's role in ecosystem services. The research project aimed to enhance the sustainability of the city's green area. The project assessed soil microbiological activity in eight Jelgava city meadows, which differed in their botanical composition and mowing intensity. Three of the meadows were newly established during the project. Soil microbiological activity was assessed by soil respiration intensity and soil enzymatic activity was determined by (i) dehydrogenase activity, (ii) urease and (iii) the activity of hydrolytic enzymes assessed by the intensity of fluorescein diacetate hydrolysis. The obtained results show that soil microbiological activity depends on soil management. The newly established meadow exhibited reduced microbiological activity, which varied depending on soil and meteorological conditions as well as the botanical composition of the plants

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## WED P33 Successional dynamics of arbuscular mycorrhizal fungal communities in remediated soils after the removal of metal contaminants

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The finite resource of fertile soil is a slow-building medium that takes millennia to develop. Soils contaminated with non-degradable toxic metals, known as heavy metals, pose a significant risk due to their longevity in the environment. Soil washing with EDTA (ethylenediaminetetraacetic acid), a chelating agent, has been shown to remove toxic metals (Pb, Zn, Cd), but this process can also have a significant impact on soil microbial diversity, particularly on fungal communities. In this study, we investigated the development of the arbuscular mycorrhizal fungal (AMF) community in the roots of *Lolium perenne* using molecular methods (18S rRNA amplicon sequencing). Plants were grown on two soil types (calcareous and acidic) in remediated soils after EDTA wash treatment and with or without addition of a local environmental inoculum. The EDTA washing and inoculation affected the development and composition of AMF communities in the two soil types in different ways, resulting in different AMF communities. Soil inoculation increased taxa richness and evenness in remediated and contaminated soils in all soil types, with diversity increasing with increasing time after remediation. Disturbance (remediation) leads to a shift in dominant taxa in the communities, reflecting different traits of AMF in remediated soils. This study is a crucial step towards understanding the recovery of AMF communities in remediated soils and steps that can enhance them (e.g. inoculation with indigenous fungi) and highlights the importance of AMF for sustainable soil management practices and the restoration of soil diversity in contaminated and remediated sites.

## WED P34 Opposite effects on plants of mycorrhiza establishment and soil microbial community manipulation with biocides

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Soil harbors extraordinary diversity of soil microbes. Simplification of soil microbial communities thus may compromise ecosystem processes and stability. To test how changes in soil microbial diversity affect such processes, we devised a two-stage experiment manipulating microbial communities through application of biocides (four antibiotics and four fungicides) to suppress specific microbial guilds. The first stage aimed at imposing a short-term biocide stress on a complex microbial community derived from soil, and measuring their population size and metabolic activity (respiration of  $^{13}\text{C}$ -glucose) upon incubation in closed vessels. The emission of  $^{13}\text{CO}_2$  revealed that antibiotic treatments caused generally a higher disturbance to the soil microbes as compared to fungicides. The qPCR showed that biocides affected mostly bacterial and protistan, but not fungal communities. On the basis of microbial abundance data, ceftazidime was found less effective than other biocides. The second stage of the experiment utilized the microbial communities derived from the first stage in a plant biotest, assessing growth of mycorrhizal and non-mycorrhizal chicory in the different pre-incubated soils. Mycorrhiza systematically suppressed plant biomass production, but biocides generally increased plant biomass production. Both chitinase and acid phosphatase activities were higher in mycorrhizal pots. Besides, chitinase activity was positively affected by pre-treatment of microbes with fungicide cycloheximide. Interestingly, alkaline phosphatase activity was higher when microbes were pre-treated with some of the fungicides. These findings indicate that the biocide pre-treatments significantly influenced the structure of soil microbial communities, resulting in changes in plant biomass promotion and soil enzymatic activities.

## WED P35 Mitigating short-term response of fungal communities in temperate forest soils to tree harvesting

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Crucial to the global economy, forestry's impact on ecosystems, especially with rising CO<sub>2</sub> emissions and climate change concerns, prompts exploration of the effects of various methods of tree harvesting. Here we compared the effects of clearcutting (removal of all trees) and retention harvesting (distributed removal of 25% of trees) on fungal communities in a tree species-rich temperate forest with the special emphasis on the response of communities of root-symbiotic ectomycorrhizal (ECM) and arbuscular mycorrhizal (AM) fungi. Fungal biomass and community composition were followed over four years before and after harvesting (clearcutting, retention harvesting, and control without tree harvesting). Fungal biomass exhibited dynamic fluctuations over the observed years, with ergosterol levels further declining in clearcut sites, in contrast to retention harvesting and control sites. Clearcutting had a strong negative impact on the proportion of ECM fungi within the fungal community compared to the alternative harvesting practices. We observed a fivefold decrease in ECM fungi after clearcutting, whereas an almost twofold decrease was noted after alternative harvesting. The latter drop was likely caused by soil disturbance, but ECM fungi recovered relatively quickly in the following years and became comparable with our control plots. The most noticeable change in soil properties occurred in clearcut sites, revealing a significant twofold increase in soil moisture content compared to the other two treatments. It is evident from the findings that retention harvesting causes negligible disturbance and should be prioritized for future forest management practices.

## WED P36 Abiotic reactions drive post-wetting soil emissions of N<sub>2</sub>O and NO, but partially contribute to CO<sub>2</sub> emissions

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Pulse emissions of soil trace gases (carbon dioxide: CO<sub>2</sub>, nitrous oxide: N<sub>2</sub>O, and nitric oxide: NO) following the wetting of dry soils may contribute disproportionately to total annual trace gas emissions in drylands. These pulses are driven by coupled biotic–abiotic processes that are challenging to partition. To address this, we measured the immediate pulse of soil trace gases emissions after the wetting of  $\gamma$ -irradiated and live intact cores of soils with different soil C and N pools, exchangeable cations, and microbial activity. For all soils, the immediate emissions pulse of CO<sub>2</sub> and N-oxides was measured within 5 min of wetting. Post-wetting CO<sub>2</sub> emission pulses from the live soils were approximately twice as large as those from the  $\gamma$ -irradiated soils and were correlated with soil C content. However, the  $\gamma$ -irradiated soil emitted up to 5 times more N<sub>2</sub>O and up to 13 times more NO compared with the live soil and emissions were correlated with soil N content. After normalization against the soil inorganic N content, the immediate post-wetting N<sub>2</sub>O and NO emissions were the same from the live and  $\gamma$ -irradiated soils. The dependence of the post-wetting N<sub>2</sub>O and NO burst on substrate pools, regardless of the presence of live microbes, suggests an abiotic origin of immediate post-wetting fluxes.

## WED P37 Active and total prokaryotic communities in arctic-alpine soils are shaped by temperature and soil moisture along elevational and microtopographical gradients

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The soil microbiota in arctic-alpine ecosystems changes in relation to elevation and microtopography, with individual taxa responding to temperature and soil moisture regimes. While former research has mainly focused on DNA to study these influences, our aim was to assess whether active prokaryotic communities respond more strongly especially to the highly dynamic influence factors than the total community does. To address this, samples were taken from two mountains in the Norwegian Scandes in June 2023. We covered seven elevational levels above the treeline, with four microtopographic positions at each level. All study sites were equipped with permanent data loggers to document temperature and soil moisture. Prokaryotic communities were analyzed by amplicon sequencing, targeting the 16S rRNA gene for the total prokaryotic community and the 16S rRNA to cover the potentially active community. Active ASVs made up 35 to 60% of the total ASVs in the samples, and the community composition differed significantly between active and total communities. While the active communities had greater relative abundances of *Frankiales* and *Solibacterales*, the total featured more *Acidobacterales* and *Acidobacteriota* of Subgroup 2. Although elevation and microtopography significantly influenced the community composition of both fractions, their explanatory power remained rather low. Evaluation of the effect of long-term temperature and soil moisture dynamics on the detected taxa through partial least square regression will give us insight into the underlying drivers and will help to explain observed differences in the active and total communities.

## WED P38 Assessing heavy metal resistance and plant growth-promoting capabilities of earthworm's associated bacteria

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Earthworms serve as a rich microhabitat that supports a wide variety of soil microorganisms. Consequently, bacteria associated with earthworms have attracted attention for their high metabolic activity and their positive impacts on soil fertility and plant growth. In this study, we isolated, for the first time, aerobic bacteria from the chloragogenous tissue of the earthworm *Apporectodea molleri* and assessed their Plant Growth-Promoting (PGP) potential as well as their resistance to heavy metals (Mn, Zn, Cu, Cd, and Ni). Sequencing of the 16S rRNA gene revealed that the fifteen isolates belonged to six key bacterial genera: *Enterobacter*, *Citrobacter*, *Aeromonas*, *Pseudomonas*, *Bacillus*, and *Terribacillus*. These strains exhibited various PGP traits, such as the production of indole-3-acetic acid (IAA), siderophores, nitrogen fixation, and phosphate and potassium solubilization. Additionally, they showed varying degrees of resistance to the tested heavy metals. Among them, *Bacillus* strains, specifically *B. subtilis* strain TC34, *B. circulans* strain TC7, and *Bacillus sp.* strain TC10, demonstrated all PGP traits and resistance to all heavy metals. This study underscores the potential of bacteria from the chloragogenous tissue to display multiple beneficial characteristics, likely related to the tissue's role in storing metabolites and neutralizing toxic elements

## WED P39 Local microbial yield-associating signatures largely extend to global differences in plant growth

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Rapid advancements in high-throughput DNA sequencing have enabled microbiome-based machine learning approaches to model and predict agricultural productivity and sustainability. Although previous studies have attempted to link soil microbial communities with crop yields and soil health indicators, the generalizability of locally identified microbial signatures for global agricultural predictions remained uncertain. In this study, we initially characterized the soil bacterial microbiome in a maize field located in Grabko, northeastern Germany, employing high-resolution spatial sampling. The bacterial community composition was correlated with precise, volume flow-based maize yield measurements. Applying machine learning through least absolute shrinkage and selection operator (LASSO) regression, our local model successfully predicted approximately 65% of yield variability via cross-validation. To evaluate the broader applicability of this locally derived model, we validated predictions against seven independent global datasets. Remarkably, the model, comprising 26 bacterial genera, correlated significantly with diverse global yield and plant growth metrics, explaining up to 37% of variation in global vegetation as measured by the normalized difference vegetation index (NDVI). Further examination identified *Hyphomicrobium*, *Luedemannella*, *Reyranella*, *JGI.0001001.H03*, *Aeromicrobium*, *Flavitalea*, and *Ellin6055* as the genera consistently associated with plant growth predictions across distinct geographical regions. Optimizing the LASSO regression approach improved global vegetation prediction capability, accounting for up to 50% of variation in plant growth worldwide. Collectively, our findings demonstrate that the microbial patterns initially observed at a single site in northeastern Germany represent globally conserved bacterial signatures. Future validation through extensive field trials assessing actual crop yields will further establish the practical utility of microbial-based models for enhancing agricultural productivity globally.

## WED P40 Long-term effects of clear-cut forestry on soil fungi and soil properties

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Clear-cut forestry has been applied in North-European boreal forests for more than 70 years. Here we investigate long-term effects of clear-cut forestry on boreal forests soils, focusing on soil fungal communities as well as carbon fluxes and stocks. A paired plot study design set up in southeastern Norway, including twelve forest pairs of (a) previously clear-cut, now mature forest plots, and (b) not clear-cut, near-natural forest plots, were used to infer influences of clear-cut forestry. Only a minor effect of clear-cutting on the overall fungal community composition was observed, but certain groups – such as the widespread Archaeorhizomycetes, were associated more strongly with near-natural forests, while others were more abundant in previously clear-cut plots. Carbon stocks, as well as fungal biomass (ergosterol), were higher in the top LFH layer in near-natural forests, while a generally higher level of respiration was observed in the previously clear-cut plots. Our results indicate so far that carbon-demanding fungi adapted to high carbon turnover are more prevalent in the previously clear-cut forests, while more slow-growing fungi are relatively more prevalent in near-natural forests.

## WED P41 Conversion of methane to organic acids by aerobic methanotrophic bacteria

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Gamma- and alphaproteobacterial aerobic methanotrophic bacteria (MOB) play an important role in regulating methane emissions at the oxic-anoxic interfaces of various methanogenic soil and aquatic ecosystems, such as wetlands, peatlands, freshwater lake water columns and sediments. Under oxygen limitation, MOB potentially shift from aerobic metabolism to fermentation, resulting in secretion of organic acids, which could then serve as carbon and energy sources for non-methanotrophic microbes. To find out whether wetland and lake MOB convert methane to organic acids, we subjected two arctic wetland MOB strains, i.e., gammaproteobacterial *Methylobacter tundripaludum* SV96<sup>T</sup> and alphaproteobacterial *Methylocystis rosea* SV97<sup>T</sup>, as well as three boreal lake MOB strains, i.e., gammaproteobacterial *Methylobacter* sp. S3L5C, *Methylomonas paludis* S2AM, and *Methylovulum psychrotolerans* S1L, to laboratory experiments and genomic analyses. The isolates converted methane to organic acids, including acetate, formate, lactate, malate, succinate, and propionate with differences in production spectrum between species. The efficiency in methane conversion to organic acids varied from 0.9% to 7.0% (of consumed methane-carbon) showing also differences between species. Moreover, genes linked to organic acid production were found in the genomes of the isolates as well as in the dataset of metagenome-assembled genomes representing MOB in lake ecosystems. In conclusion, our results suggest that the conversion of methane to organic acids is a common trait among MOB in wetlands and lakes, emphasizing their significant role in channeling methane-carbon into the microbial food chains of these ecosystems.

## WED P42 Effects of bacterial nitrogen transfer on fungal growth in nitrogen-deficient environments

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While a growing number of studies have addressed the promoting role of fungal mycelia in bacterial activity and contaminant turnover, less is known about bacterial effects that may assist fungi during contaminant biodegradation in the soil mycosphere (the zone surrounding and influenced by hyphae). Here, we hypothesise that nitrogen-fixing-bacteria in the mycosphere provide nitrogen to fungi to support growth and may potentially facilitate the biotransformation/degradation of organic contaminants in nitrogen-deficient environments. To challenge our assumption, we tested the impact of Nitrogen-fixing soil bacteria (i.e. PAH-degrading *Pseudomonas chengduensis*, and non-PAH degrading *Azotobacter vinelandii*) on growth of contaminant degrading basidiomycetes *Coprinopsis cinerea* and *Pleurotus ostreatus* in N-deficient and C-rich laboratory microbial ecosystems. Compared to bacteria-free controls, *C. cinerea* showed significant growth in the presence of *A. vinelandii*, but not *P. chengduensis* while *P. ostreatus* grew in presence of both bacteria. We further analysed fungal growth on heat-deactivated bacterial biomass in N-deficient or N- and C-deficient habitats to distinguish between utilization of bacterial metabolites or bacterial biomass. *P. ostreatus* and *C. cinerea* did not grow on *A. vinelandii* necromass but were able to utilize *P. chengduensis* suggesting preferential utilization of bacterial biomass. Using metabolomic and stable isotope probing approaches, current work aims to identify and quantify possible metabolites responsible for the observed dynamic fungal biomass development in the presence of metabolically active bacteria, the associated N and C fluxes, and the beneficial role of bacterial-fungal interactions for the biotransformation of soil contaminants such as PAHs.

## WED P43 Clearing the air: harnessing plant microbiomes for better malodor elimination

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Indoor air quality has been identified as a severe health concern by the World Health Organization (WHO). With people spending up to 90% of their time indoors the problem of indoor air pollution presses concern. Bad indoor air harbors toxic and malodorous compounds from various sources, including living organisms and chemical releases from household materials. While several technologies exist to combat malodors, they often come with limitations. Innovative botanical biofiltration systems are a promising tool in cleaning indoor air and were the starting point for this research. We explored the potential of rhizosphere microbiomes of household plants to enhance the degradation of malodorous volatile organic compounds (VOCs). The rhizosphere of plants from different households, located in various areas such as bathrooms, bedrooms and kitchens was sampled and used as a starting point (rhizosphere start suspension, RSS) for a plant based-enrichment of VOC-degrading bacteria. *Arabidopsis* plants were inoculated with the RSS and subsequently exposed to sublethal concentrations of VOCs such as hexanoic acid or isovaleric acid. Through this process, we successfully selected bacterial strains that combine malodor metabolization capacity with plant compatibility and the ability to thrive in an indoor environment. Using multispectral imaging techniques, precision phenotypic responses to the imposed stress were monitored. After only one enrichment cycle, plants were already able to cope better with stress induced by VOCs. Using a metabarcoding approach, the initial rhizosphere flora and enriched microbial populations were uncovered and compared to a standard *in vitro* enrichment method.

## WED P44 Cross-kingdom interactions within arbuscular mycorrhizal fungi (AMF) hyphosphere

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Arbuscular mycorrhizal fungi (AMF) are crucial symbionts playing a significant role in plant acquisition of nutrients, e.g., nitrogen and phosphorus from soil. These organisms can provide access to remote nutrient sources. Yet, they cannot utilize nutrients bound in organic compounds, such as chitin or phytate, alone. This is due to their limited exoenzymatic repertoire. And this is why they team with other microorganisms in the immediate surroundings of their hyphae, the hyphosphere, to facilitate access to organic nutrient. Despite their key role in mycorrhizal functioning, the knowledge about hyphospheric microorganisms, their interactions with AMF, and their contribution to soil-plant nutrient fluxes is still limited. To better comprehend this subject, few dozens of bacterial strains from AMF hyphosphere have been isolated and identified by 16S sequencing. They have been screened for their capacity to degrade chitin, phytate, and/or proteins, and 24 non-redundant taxa were tested for their interaction with actively growing AMF hyphae under monoxenic culture conditions. Most of the tested strains belonged to genera of *Streptomyces*, *Pseudomonas*, and *Sphingobium*. Pairwise interaction assays indicated a lack of strong antibiosis. Out of 24 tested strains, 11 demonstrated the ability to move along the AMF hyphae. Five of them exhibited the capacity to induce fungal sporulation, suggesting bacterial production of bioactive compounds, the analyses of which are in progress. Both mentioned effects were proven to be statistically significant.

## WED P45 Response of soil microbial enzymatic activities to climate change and different tree species

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Climate change alters microbial communities and their ecosystem functions, ultimately affecting microbial contributions to forest biogeochemistry. One of the key functions affected by climate change are potential extracellular enzyme activities, which play a crucial role in forest nutrient cycling. Despite their importance, few studies have investigated how multiple, concurrent elements of climate changes affect microbial extracellular enzyme activities, particularly in forest environments comprised of different tree species. In this study, we assessed potential extracellular enzyme activities involved in carbon, nitrogen and phosphorus cycling, including cellulose, hemi-cellulose, and lignin degradation, to understand how experimental climate change (warming and drought) affect them and how these activities differed in relation to different native and non-native tree species. The experiment is located in Switzerland and includes three sites with different climatic and environmental characteristics. Enzymatic activities were measured using standardized assays and soil samples from control and treatment plots. Preliminary results indicate that warming significantly affects certain enzyme activities, particularly  $\beta$ -cellobiohydrolase (CBH) and chitinase (NAG) activities. Drought conditions seem to have a slight synergistic effect with warming, further reducing activity of CBH and NAG. However, enzyme activities varied considerably between tree species, due to species-specific and site-dependent responses to climate treatments. This study highlights how future climate conditions may alter key players in forest nutrient cycles, potentially altering forest soil biogeochemistry. Understanding these mechanisms is essential for predicting forest resilience and developing mitigation strategies to maintain ecosystem functionality under changing environmental conditions.

## WED P46 Aerobic bacteria in the sulfidic sediments of a marine hypoxic zone: sustenance and biogeochemical potentials

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Aerobic microorganisms are never explored in the marine oxygen minimum zone (OMZ) sediments, though their presence and activity can have significant impact on carbon-sulfur cycling within these highly-sulfidic (anoxic) complex organic matter sinks. Our group first discovered metabolically active aerobic communities of chemolithoautotrophs and chemoorganoheterotrophs, in the eastern Arabian Sea OMZ sediment using metagenomics and metatranscriptomics. Genes for diverse aerobic metabolisms were detected in the metagenomes explored at 15-30 cm intervals along ~3-m sediment-cores retrieved from 530 and 580 meters beneath the sea-level, off the west coast of India. Several obligately aerobic bacteria were isolated, across the sediment-cores. High levels of sequence correspondence between the isolates' genomes and the habitat's metagenomes and metatranscriptomes illustrated that, strains were widespread and active *in situ*. The isolated sulfur-chemolithotrophs and chemoorganotrophs could grow on reduced sulfur compounds and simple/complex organic compounds, only when O<sub>2</sub> is present. However, few could grow anaerobically on yeast extract/acetate by reducing nitrate and/or nitrite. Fermentation did not support growth but enabled some strains to survive amidst prolonged anoxia. Under extreme oligotrophy, robust growth followed by protracted stationary phase was observed for all the isolates at low cell density, under only aerobic conditions. While metabolic deceleration was apparently central to the strains' adaptation to dwindling organic carbon, metagenomic exploration revealed possibility of anoxia being surmounted via potential supply of cryptic biogenic O<sub>2</sub>. These findings hold critical implications for remineralization/sequestration of buried organic matter within anoxic marine sediments and illustrate the possibilities of sulfide back-flux *in situ*.

## WED P47 Diversity and function of novel members of the genera *Mucilaginibacter* and *Janthinobacterium* in Arctic tundra soils

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Approximately one-third of the global soil carbon pool is stored in Arctic soil ecosystems, which are permanently frozen or only experience thaws briefly. Microbes play essential roles in nutrient cycling as they decompose soil organic matter (SOM), including plant litter and microbial necromass. As polar soils warm due to climate change, it is of concern that enhanced microbial activity will increase the rate of SOM degradation and, consequently, greenhouse gas emissions. Delineating the diversity and activity of Arctic tundra microbial communities is thus of keen interest. In this study, cold-adapted bacteria belonging to the genus *Mucilaginibacter* and *Janthinobacterium* were isolated from Arctic tundra soils in Finland. These isolates are aerobic chemoorganotrophs and appear well adapted to the low-temperature soil environment, where they are also exposed to desiccation and a wide regime of annual temperature variation. Phylogenomic and average nucleotide identity analyses indicated that the strains represented novel species. Comparative genome analysis showed their potential in complex carbon degradation, nitrogen assimilation and polyphenol degradation. Further, a pangenome analysis of the newly described species with known members of their respective genera from different habitats provided insight into the differential features of the tundra strains. Unique genes involved in energy generation, nitrogen assimilation, adaptation, and secondary metabolite synthesis may be beneficial for growth and explain their abundance and distribution in tundra soil. By uncovering novel bacterial species, we aim to enhance our understanding of microbial processes in soil and elucidate how environmental fluctuations shape microbial functionality and interactions in Arctic tundra ecosystems.

## WED P48 Linking genomic traits to carbon necromass prediction in soil: a step-by-step guide for the soil ecology community

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There is growing interest in applying genomic traits to explain microbially mediated processes, including the formation, stabilization and persistence of soil organic carbon (SOC). However, it remains unclear which microbial traits consistently predict SOC pools, particularly those formed by microbial necromass (responsible for ~50% of SOC), and how they can be estimated from genomic data. To address these gaps, we developed a step-by-step guide by aggregating publicly available bacterial reference genomes (e.g., MAGs, SAGs, and isolate genomes from IMG/JGI) and with previously published bioinformatic tools we estimated traits related to microbial growth (necromass producers) and resource acquisition (necromass consumers). Next, we applied this structure to over 300 16S rRNA gene-based samples from an agricultural land survey in Luxembourg. As a result, we successfully integrated predictions of dozens of genomic traits (including discrete and continuous ones, such as growth rates, genome size, and CAZyme traits), supported by the literature, with a potential link to microbial necromass C turnover. In addition to providing a novel approach for the soil ecology community to leverage microbial traits, our guide paves the way for the development and improvement of next-generation SOC models based on microbial processes, with the potential to predict responses of microbial-derived C to changing environment.

## WED P49 SoWaFUN - Assessing fungal richness at the soil-water interface

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Terrestrial fungi enter the aquatic ecosystem as airborne spores, and together with decomposing plant and animal organic matter or attached to soil particles and soil aggregates. However, their further role in C and nutrient cycling and their interactions with other microorganisms, including fungi adapted for the aquatic lifestyle, in the aquatic ecosystems is still unclear. Here, we present the results of culture-based approach to characterize the fungal diversity and interactions in the temperate lentic waterbodies of varying trophic. Sampled potential niches for aquatic fungi include macrophyte surfaces, the water column of hypertrophic shallow lakes, reservoir inflow, epilimnion, hypolimnion, and sediment, as well as biofilms, sedimented plant litter and fungal traps. Hundreds of different strains were isolated using serial dilution, solid media inoculation, and baiting methods, and characterized by sequencing. Their presence and relative abundance was compared to NGS sequencing datasets. Overall, Ascomycota dominated among the isolated strains, followed by isolates belonging to Mucoromycota and Basidiomycota. The most abundant genera in all samples were *Trichoderma*, *Cladosporium*, followed by *Penicillium* and *Fusarium*. We have also isolated several strains belonging to the Oomycota, namely from the following genera: *Phytophthora*, *Phytophthora*, and *Globisporangium*. Oomycota antagonistic bacteria were isolated along some of the strains. The collection is currently used to conduct manipulative experiments on the ecophysiology and interactions at the assemblage level.

## WED P50 The contribution of rare fungi to soil functioning

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Fungi are ubiquitous microorganisms and represent the second-largest group of species in soil ecosystems, where both abundant and rare taxa coexist. Despite their ecological importance, rare fungal species, due to their low numerical abundance, sparse distribution, and limited biomass, are often assumed to contribute minimally to key ecosystem functions. In this study, we designed synthetic communities comprising rare and abundant fungal taxa to investigate their roles in plant biomass production and litter decomposition using experimental microcosms. Additionally, we assessed the functional diversity of these taxa using Biolog FF™ MicroPlate assays. Our results revealed that microcosms inoculated with rare fungal taxa exhibited significantly higher litter decomposition (46.7±3.0% litter lost) compared to uninoculated controls (30.9±2.9%) or those inoculated solely with abundant taxa (41.9±8.2%). Combined inoculations of rare and abundant taxa demonstrated significantly higher litter decomposition relative to microcosms inoculated with only abundant taxa. While fungal inoculations positively impacted plant biomass relative to uninoculated controls, no significant differences were observed among the rare, abundant, and combined inoculation groups. Carbon substrate utilization analysis revealed a broad range of substrates used, up to 30 for abundant taxa and up to 35 for rare taxa. Organic acids (i.e., carboxylic and amino acids) were found to be the preferred substrates by both abundant and rare taxa. These findings highlight the role of rare fungal taxa on litter decomposition and plant biomass production, and reveal their functional contribution to carbon cycling, challenging the assumption of their limited role in soil ecosystems.

## WED P51 Salinity limits of photosynthesis, respiration, sulfate reduction and methanogenesis in microbial mats thriving at salt saturation in a salt flat from Oman

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Limits of microbial metabolism due to salt stress have been investigated mainly by cultivation-based experiments and theoretical extrapolations. We tested the susceptibility of the key processes for ecosystem functioning to extreme salinities in salt crust covered microbial mats from a coastal sabkha in Oman with a combination of geochemical and molecular ecology methods, including microsensor profiles, hyperspectral imaging, pigment extraction, and fluorescence microscopy combined with 16S rRNA gene amplicon sequencing. While the salt crust did not reduce light or heat fluxes, several major processes persisted. Sulfate reduction, aerobic respiration and anoxygenic photosynthesis could be measured at saturation-level salinity (40%). However, oxygenic photosynthesis was completely inhibited under saturated salt concentrations and only resumed two days after inundation of the mats with seawater leading to dissolution of the salt crust and dilution of the salt down to 12% in upper mat layers. Although very low, some photosynthesis was measurable at  $\leq 30\%$  salinity. Methanogenesis was still detectable at salinities between 25% and 35%, and the rate of the process increased in the presence of molybdate, a selective inhibitor of sulfate reduction. Our study describes a microbial community adapted to exist near salt-saturation and reveals a salinity limit for primary production via oxygenic photosynthesis at around 30% salinity. Thus, ecosystems under or in a salt crust ultimately depend on temporary salt dilution by tides or floods to be self-sustaining.

## WED P52 Dynamic in situ detection in iRhizo-Chip reveals diurnal fluctuations of *Bacillus subtilis* in the rhizosphere

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Effective colonization by microbe in the rhizosphere is critical for establishing a beneficial symbiotic relationship with the host plant. *Bacillus subtilis*, a soil-dwelling bacterium that is commonly found in association with plants and their rhizosphere, has garnered interest for its potential to enhance plant growth, suppress pathogens, and contribute to sustainable agricultural practices. However, research on the dynamic distribution of *B. subtilis* within the rhizosphere and its interaction mechanisms with plant roots remains insufficient due to limitations in existing in situ detection methodologies. To achieve dynamic in situ detection of the rhizosphere environment, we established iRhizo-Chip, a microfluidics-based platform. Using this device to investigate microbial behavior within the rhizosphere, we found obvious diurnal fluctuations in the growth of *B. subtilis* in the rhizosphere. Temporal dynamic analysis of rhizosphere dissolved oxygen (DO), pH, dissolved organic carbon, and reactive oxygen species showed that diurnal fluctuations in the growth of *B. subtilis* are potentially related to a variety of environmental factors. Spatial dynamic analysis also showed that the spatial distribution changes of *B. subtilis* and DO and pH were similar. Subsequently, through in vitro control experiments, we proved that rhizosphere DO and pH are the main driving forces for diurnal fluctuations in the growth of *B. subtilis*. Our results show that the growth of *B. subtilis* is driven by rhizosphere DO and pH, resulting in diurnal fluctuations, and iRhizo-Chip is a valuable tool for studying plant rhizosphere dynamics.

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