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Effects of softwood biochars on soil biota in medium-term field experiments in Finland

Zrim, Jure

2018-06-17

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Natural resources and
bioeconomy
studies 29/2018

3rd Conference
Ecology of Soil ganisms

17–21 June 2018, Helsinki, Finland

Effects of softwood biochars on soil biota in medium-term field experiments in Finland

Krista Kettunen & Oili Kiikkilä (Eds.)

NATURAL RESOURCES
INSTITUTE FINLAND

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Natural Resources Institute Finland, Helsinki 2018

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2018

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Welcome to ESM2018!

We are pleased to welcome you to the 3rd conference on the Ecology of Soil Microorganisms in Helsinki, Finland. The two previous meetings were organized in Prague in 2011 and 2015 by Petr Baldrian. We are delighted to see that as many participants, 400 are joining us also under the midnight sun.

During the meeting, soil science will be linked with traditional microbiology and modern genomic, transcriptomic and proteomic analysis tools, extending from the soil-microbe interphase to their interactions with plants. Indeed, one important goal of the conference is to inspire us to bring forward new dimensions in the characterization of the interplay between soil microbial ecology and larger-scale processes in various ecosystems. In this meeting we will cover not only the role of soil microbiota but also their viruses. We hope that you take a moment to think of recent studies that have begun to unearth relationships found between soil microbes, plant performance and even human health. Sustainability of soils and their role in mitigation of climate change are key challenges for preserving life on Earth. As microbes are living functional components of soils, our focus during the week could not be timelier.

The organizers and the host organization Natural Resources Institute Finland wish you a fruitful and invigorating conference. We are excited that you have joined us here in Helsinki to promote state-of-the-art research in soil ecology under the northern midsummer madness!

Taina Pennanen and Hannu Fritze

Chairs of the Organizing Committee

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British Mycological Society promoting fungal science

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INSTRUMENTS
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Image Analysis for Plant Science

Suomen Metsätieteellinen Seura

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SOIL FOOD

Looking for Root and Seedling Image Analysis Tools?
Here is an overview of our four automatic systems and our two interactive software

WinRHIZO™ 2018

Basic, Regular & Pro
Systems Designed for Automatic Washed Root Analysis

Scan washed roots easily and rapidly with Regent's scanners and root positioning systems.

See analysis results summarized on screen automatically after scanning.

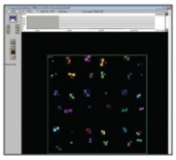
√ Root morphology in function of root diameter and color: length, area, volume and number of tips
√ Number of forks and crossings
√ Root overlap detection for accurate measurement
√ Topology, link and architecture with fractals
√ Developmental classification
*** Available measurements and features vary according to WinRHIZO's version. See our website for details.

Arabidopsis
Automatic Analysis System for Washed Roots and Seedlings in Petri Dish

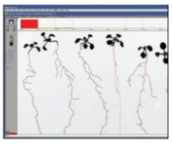
Analyse seedlings and leaves:

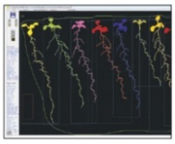
Globally
one analysis per image

Individually
multiple analyses per image

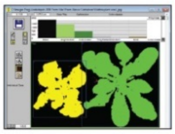


√ Leaf area of seedlings grown in Petri dish
√ Germination Count





√ Leaf area - leaf/hypocotyl distinction
√ Root morphology
√ Topology and developmental analysis



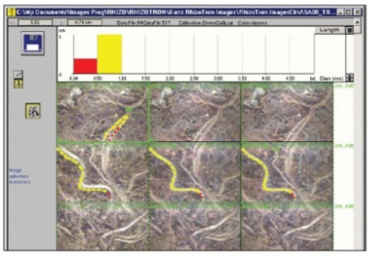
√ Leaf area, length and width of plants in soil
*** All measurements and features of the WinRHIZO Pro version are included.

WinRHIZO™ Tron 2018

Tron & Tron MF
Software Programs for Interactive Analysis of Images of Roots in Soil and Rhizotron

Trace roots manually with a mouse or by touching the screen of all-in-one or tablet computers.

Monitor root growth by analysing Multiple Frames (images) of a root system taken at different times.



√ Root morphology in function of root diameter and color: length, area, volume and number of tips
√ Topology and developmental analysis
√ Data retrievable from file names using the ICAP naming scheme
√ Previous analysis can be retrieved to resume analysis of the same location at a later time simply by adding new or dead roots since the last analysis.

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PROGRAM

17.6.2018 | SUNDAY

DAY 1

13:00-19:00 **Doors open, registeration & speakers service open**

16:00-16:15	**OPENING OF THE ESM2018 CONFERENCE** **Chairs:** ***Taina Pennanen, Hannu Fritze*** • Music by a Quintet from the Academic Choral Society (Akateeminen laulu) • Opening Words, **Mari Walls**, President and CEO, Luke • Music by a Quintet from the Academic Choral Society (Akateeminen laulu)

MICROORGANISMS IN ECOSYSTEM FUNCTIONS AND HUMAN HEALTH

16:15-17:00	Starvation amidst plenty: microbes, soil organic matter, and the role of water in regulating them, **Joshua Schimel**
17:00-17:30	Linking microbial belowground diversity and plant health, **Gabriele Berg**
17:30-18:00	The environment-microbiota-health axis:At the interface between soil and human microbiota, **Lasse Ruokolainen**
18:05-20:00	**GET TOGETHER**

18.6.2018 | MONDAY

DAY 2

08:00-18:00 **Registeration & speakers service open**

MICROBES IN COLD ENVIRONMENTS

Chairs: ***Sara Hallin, Krista Peltoniemi, lightning talks Sannakajsa Velmala***

08:30-09:00	Planctomycetes in boreal and subarctic peatlands: diversity patterns and potential functions, **Svetlana Dedysh**
09:00-09:15	Microbial activity along a climate gradient in the arctic, **Jenni Hultman**
09:15-09:30	Co-occurrence networks show response of microbial communities to warming in tundra soils, **Mathilde Jeanbille**
09:30-09:45	Geomicrobiology of glacier basal ice: a frozen or future soil? **Robin Sen**
09:45-10:00	Soil carbon and nitrogen cycling along a natural environmental gradient in Subarctic Mountain Birch forest: the fungal decoupling, **Jeppe Aagaard Kristensen**
10:00-10:30	**COFFEE**
10:30-11:00	Importance of methanotrophy in the C and N cycle, **Hannu Fritze**
11:00-11:20	Unususal acid-tolerant denitrifiers of permafrost affected peatlands drive massive N2O emissions, **Marcus A. Horn**
11:20-11:35	An experimental roadmap for in-depth proteome analysis of the methane-oxidizing Methylocystis sp. strain SC2, **Anna Hakobyan**
11:35-11:50	Permafrost peatlands plants and their bacterial rhizobiome: stronger plant species-specific effects in permafrost than in active layer peat, **Sylvain Monteux**
11:50-11:55	Bacterial and fungal community composition but not richness or biomass follows plant primary succession in arctic inland sand dunes, **Heli Juottonen**
11:55-12:00	Patterns and predictors of methane production and methanogen community composition across peatlands globally, **Michael Carson**
12:00-12:05	Climate change in subarctic tundra - responses of microbial communities to changes in snow accumulation and soil temperature, **Minna Männistö**
12:05-12:10	Predominance of methanogens over methanotrophs contributes to high methane emissions in rewetted fens, **Viktoria Unger**
12:10-14:45	**LUNCH**
12:45-14:00	**POSTER SESSION 1**

MICROBES IN STRESSED ENVIRONMENTS

Chairs: ***Anders Tunlid, Leho Tedersoo, lightning talks Sannakajsa Velmala***

14:05-14:20	Circumpolar microbiome pattern as determinant of subducted carbon vulnerability in Arctic permafrost soils, **Jiří Bárta**
14:20-14:35	Fine scale niche differentiation among amoebal communities of dark-spored myxomycetes determined by landscape structures as well as biotic factors, **Mathilde Borg Dahl**
14:35-14:50	Permafrost as an active microbial ecosystem: pushing up against the thermodynamic limits of life, **Mary-Cathrine Leewis**
14:50-15:05	Stable Isotope Probing Reveals a Subzero-Active Bacterial Community in Arctic Tundra Soils, **Preshita Gadkari**
15:05-15:10	Time to Wake Up! - Mycelia Enable Bacterial Activity in Dry and Oligotrophic Environments, **Anja Worrich**
15:10-15:15	Insights into long-term drought, storms and rewetting effects on streambed microbial diversity, **Giulia Gionchetta**
15:15-15:20	Secret collaborations: plant-associated Archaea and their interaction with their hosts, **Julian Taffner**
15:20-15:25	Role of secondary plant metabolites in the ecology of soil microorganisms, **Ondrej Uhlik**
15:25-15:55	**COFFEE**

NEW METHODOLOGICAL APPROACHES

15:55-16:15	Soil microbial responses to drought and exotic plants shift carbon metabolism in a semiarid ecosystem, **David Lipson**
16:15-16:30	Legacy of drought affects microbial community composition and activity induced by root exudation, **Angela Straathof**
16:30-17:00	The known and the unknown in soil microbial ecology, **Petr Baldrian**
17:00-17:20	Information in droplets - towards single-cell sequencing in microbiology%M-CEPASTEBIN%, **Marja Tiirola**
17:20-17:35	Methods, Measurements, and Models of In Situ pH of the Soils of Wisconsin, **Michael Braus**
17:35-17:40	Drought and climate change induced shifts in the plant community favor specific soil bacterial communities with contrasting functional characteristics, **Mika Tarkka**
17:40-17:45	Micro-RIP: Functional analysis of uncultivated microbes using radioisotope probing, **David Hopkins**
17:45-17:50	Plant growth stage drives microbiome community assembly, interaction patterns and functionality, **Jie Hu**
17:50-17:55	Performance of plant-microbial-soil system as affected by plant species and N availability, **Eva Kastovska**
17:55-18:00	The evolutionary legacy of microbial taxa impacts ecosystem functioning, **Marta Goberna**
19:00-20:30	**HELSINKI CITY RECEPTION,** City Hall, address Pohjoisesplanadi 11-13

19.6.2018 | TUESDAY

DAY 3

08:00-17:00 Registeration & speakers service open

INTERACTIONS OF MICROORGANISMS WITH BIOTIC AND ABIOTIC ENVIRONMENT

Chairs: *Peter Baldrian, Aurélie Deveau*

08:30-09:00	Plant-microorganism interactions under climate warming-induced range shifts: consequences for ecosystem functioning, **Wim van der Putten**
09:00-09:20	Impacts of long term rice cultivation on soil microbial diversity: A synthesis, **Yong-Guan Zhu**
09:20-09:35	Soil legacy effects on plant endophytes and plant-feeding caterpillars, **S. Emilia Hannula**
09:35-09:55	Bacterial War on Fungi, **Wietse de Boer**
09:55-10:10	Volatile organic compounds link distant microbial community composition to plant growth and health, **Raza Waseem**
10:10-10:40	**COFFEE**
10:40-11:10	Soil microbial community analyses - From habitat filtering to interactions, **Christoph C. Tebbe**
11:10-11:25	How does spatial heterogeneity affect decomposition dynamics? **Arjun Chakrawal**
11:25-11:40	Utilization of soil organic nitrogen by arbuscular mycorrhizal fungi - mechanisms and players, **Jan Jansa**
11:40-11:55	Interactions between grassland plants and arbuscular mycorrhizal fungi are selective, **Maarja Öpik**
11:55-12:10	Distinct fungal guilds respond differently to the availability and diversification of plant and carbon resources, **Rasmus Kjøller**
12:10-12:45	**LUNCH**
12:45-14:00	**POSTER SESSION 2**

FUNGI AND THEIR FUNCTIONS IN SOIL

Chairs: *David Myrold, Jenni Hultman, lightning talks Sannakajsa Velmala*

14:05-14:35	Using genomics to understand the role of soil fungi in forest ecosystems, **Annegret Kohler**
14:35-14:50	Spectroscopy and transcriptomics provide novel insights into the decomposition of soil organic matter by fungi, **Anders Tunlid**
14:50-15:05	Mycorrhizal types differ in ecophysiology and ecosystem functioning, **Leho Tedersoo**
15:05-15:20	Macroecology analyses of millions of fruit body records: Environmental drivers of phenology and species assemblies across Europe, **Håvard Kauserud**
15:20-15:25	Tree-to-Maize Nutrient Transfer via Mycorrhizal Networks in Low-Input Maize Cropping Systems?, **Janina Dierks**
15:25-15:30	Soil fungal communities in paddy soils after carbon amendment at blooming stage, **Vanessa Otero Jiménez**
15:30-15:35	Nutrient demand as dominant driver of resource allocation into extracellular enzyme synthesis in soil, **Svenja Stock**
15:35-15:40	Compositional changes through repeated years of summer drought in fungi (non-ECM) associated with roots of beech and spruce, **Fabian Weikl**
15:40-15:45	Fine root foraging strategies of Norway spruce seedlings with contrasting future phenotypes in response to nutrient-rich patches, **Sannakajsa Velmala**
15:45-15:50	Cover crop mixtures increase microbial functional diversity during decomposition, **Sytske Drost**
15:50-16:20	**COFFEE**
16:20-16:35	Contribution of saprotrophic and ectomycorrhizal fungi to organic P mobilization in forest soils, **Ellen Kandeler**
16:35:16:50	Changes of ectomycorrhizal communities along a nitrogen deposition gradient and with soil depth, **Lucienne de Witte**
16:50-17:10	The mycorrhiza-root interphase of spruce is under genetic control of the host and adaptive to soil characteristics, **Taina Pennanen**
17:10-17:15	Suppression of mycorrhizal fungi (AMF) mycelium by soil microbiota, **Carla Cruz-Paredes**
17:15-17:20	Arbuscular mycorrhizal fungi stimulate organic phosphate mobilization by changing bacterial community structure under field conditions, **Gu Feng**
17:20-17:25	Bacteria in ericoid roots and mycospheres, **Sari Timonen**
17:25-17:30	May Matsutake mycorrhiza-associated Streptomycetes distinguish friend and foe in shiro, the evidences from in vitro studies, **Lu Min Vaario**
18:15-24:00	**BOAT TRANSPORT TO ISLAND KLIPPAN,** boat leaves from address Ehrenströmintie 14
19:00-23:30	**CONFERENCE DINNER,** Restaurant Saaristo

45 min opening lecture (45min)

30 min presentation (25min)

20 min presentation (15min)

15 min presentation (12min)

5 min lightning talk (4min)

Poster Session

Social Program or Meal

20.6.2018 | WEDNESDAY DAY 4

08:00-17:00 Registeration & speakers service open

MICROBES AND PROCESSING OF SOIL ORGANIC MATTER

Chairs: *Aino Smolander, Sue Grayston, lightning talks Sannakajsa Velmala*

09:00-09:30	Microbial hotspots and hot moments in soil, **Yakov Kuzyakov**
09:30-10:00	Microbial Carbon Pump and its Significance for Carbon Sequestration in Soils, **Chao Liang**
10:00-10:15	The fate of carbon in hot spots: linking decomposition processes to microbial key players, **Karolin Müller**
10:15-10:30	Increased activity of surviving bacteria facilitate functional resistance to recurrent disturbances: a modelling study, **Sara König**
10:30-10:45	Global distribution of mycorrhizal host plants explained by climate and soil properties, **Milagros Barcelo**
10:45-11:15	**COFFEE**
11:15-11:35	Linking biogeographical patterns of microbial distributions to the modelling of soil functions and associated ecosystem services, **Nadia Soudzilovskaia**
11:35-11:50	Depolymerization of organic matter as a bottleneck for carbon cycling, **Delphine Derrien**
11:50-12:05	The plant-microbial impacts on soil processes with direct climate feedbacks: conclusions from studies on CO2, CH4, N2O, VOCs and amines, **Jussi Heinonsalo**
12:05-12:10	What controls the response of N2O and CH4 fluxes to warming: Changes in microbiological or physical soil properties?, **Sven Marhan**
12:10-12:15	Glucose induced priming effect of soil organic matter decomposition in boreal forest soils with different C:N ratios, **Kristiina Karhu**
12:15-12:20	Bacterial and fungal turnover of litter-derived DOC in top- and subsoil of a beech forest, **Sebastian Preusser**
12:20-12:25	Does the distribution of the functions of microbial community in soil particles follow the pattern of organic C turnover?, **Lingling Shi**
12:25-12:30	The impact of restriction of photosynthetic carbon flow on fungal and bacterial communities in boreal forest soils, **Outi-Maaria Sietiö**
12:30-12:35	Sticky Dead Microbes, **Kate M. Buckeridge**
12:35-13:10	**LUNCH**
13:10-14:25	**POSTER SESSION 3**
14:30-14:45	Soil C/N and legacy effects of fertilization controls denitrifying and DNRA bacteria affecting N retention, loss and N2O emissions, **Sara Hallin**
14:45-15:00	The effect of plants on methane flux of upland soils and methanogenic and methanotrophic microorganisms in the rhizosphere, **Nadine Praeg**
15:00-15:15	Bacterial synthesis of storage compounds - a neglected dimension of the carbon cycle, **Kyle Mason-Jones**
15:15-15:30	Coupled metagenomic-chemical analyses of degrading fungal necromass and its contribution to soil organic carbon, **Louise Egerton-Warburton**
15:30-15:45	Nutrient content affects the turnover of fungal biomass in forest topsoil and the composition of associated microbial communities, **Vendula Brabcová**
15:45-16:00	Deciphering the structure of decomposer food web and functional relevance of microbial communities in the C flow in forest soil, **Rubén López -Mondéjar**
16:00-16:30	**COFFEE**

REGULATORY MECHANISMS OF MICROBES BY VIRUSES AND ANTAGONISM

Chairs: *Wietse de Boer, Jarkko Hantula, lightning talks Sannakajsa Velmala*

16:30-17:00	Complex fungal communities in 3-dimensional space: emergent properties in antagonistic mechanisms, **Lynne Boddy**
17:00-17:20	Virus communities of forest fungi inhabiting decomposing wood and tree roots, **Eeva Vainio**
17:20-17:50	Major genetic elements that spur horizontal gene transfers across bacteria in the mycosphere, **Jan Dirk van Elsas**
17:50-18:05	Multiple phages therapy agents keeps pathogens in check by generating disproportional resistance costs, **Xiaofang Wang**
18:05-18:10	Functional characterization of bacteria associated with dead wood based on genome and metagenome annotation, **Vojtěch Tláskal**
18:10-18:15	New biocontrol applications against Heterobasidion spp, **Jarkko Hantula**
18:15-18:20	Interactions of Polyporales fungi: enzyme activities, release of VOCs and progress of spruce wood decomposition upon three-species cohabitation experiments, **Tuulia Mali**
18:20-18:25	Fungal growth, lethal to solitary bee Osmia bicornis larvae, is inhibited by soil bacteria isolated from the species' nests, **Anna Voulgari Kokota**
18:25-18:30	ACC deaminase positive bacteria - Serving dual role of Protector and Benefactor for plants under salinity stress, **Gautam Anand**

21.6.2018 | THURSDAY DAY 5

08:00-14:00 Registeration & speakers service open

SUSTAINABILITY OF SOILS

Chairs: *Cindy Prescott, Katri Rankinen*

08:35-09:05	Introduction to Sustainable Deveopment Goals by using soil-human microbiota as a case, **Eeva Furman**
09:05-09:50	What do we demand from our soils?, **Rachel Creamer**
09:50-10:10	Connecting Microbial Communities to Soil Health, **David Myrold**
10:10-10:25	Integrating diverse environmental microbiota into everyday life of urban dwellers, **Aki Sinkkonen**
10:25-10:55	**COFFEE (WITH SANDWICHES)**

Chairs: *Jussi Heinonsalo, Pekka Vanhala, lightning talks Sannakajsa Velmala*

10:55-11:25	Where has our scientific tea break brought us? Overview of recent TBI developments, **Judith Sarneel**
11:25-11:30	Termites, teabags and tropical savannahs, **Stuart W. Smith**
11:30-11:35	Long-term climate regime modulates the impact of short-term climate variability on decomposition in alpine grassland soils, **Inge Althuizen**
11:35-11:40	TeaTime4Schools: How to put decomposition into practice, **Taru Sandén**
11:40-11:45	Global change effects on litter breakdown in tidal wetlands: implications from a global survey using the Tea Bag Index, **Peter Mueller**
11:45-11:50	Occurrence of plant growth promoting Ochrobactrum and Bacillus sp. in the nodules of Vigna radiata, **Mohsin Tariq**
11:50-11:55	Exploring microbial functional resilience in a Canadian agricultural system using dry soil archives, **Lori Phillips**
11:55-12:10	Carbon and nutrient cycling in organic agriculture: a chronosequence approach, **Sophie Q. van Rijssel**
12:10-12:25	The role of fungi in restoring old fields, **Elly Morriën**
12:25-13:00	**CLOSING CEREMONY**

POSTERS PROGRAM

Posters Monday 12:45-14:00

Lynette Abbott	P1 | How influential is the common mycorrhizal network in nutrient transfer?
Sylwia Adamczyk	P4 | The potential role of plant secondary metabolites in carbon and nitrogen cycling in boreal forest soils
Saija Ahonen	P7 | Soil microbial communities in subarctic mountain birch forests in two reindeer grazing regimes recovering from a severe moth herbivory
Dalia Ambrazaitienė	P10 | Microbial activity in relation to changing soil chemical and physical properties
Wassila Riah-Anglet	P13 | Introduce grassland in crop rotation, a way to restore microbiodiversity and soil function
O. Oluranti Babalola	P16 | Some vast assemblage of archaea in termiteria
L. Carrasco-Barea	P22 | Litter decomposition of three halophytic species in a Mediterranean salt marsh: influence of leaf chemical quality and edaphic heterogeneity
Arifa Beddiar	P25 | Arbuscular mycorrhizal fungi enhance industrial tomato growth and production and compensate reduced fertilization levels in an Algerian field soil
Rebecca Bevans	P28 | The Microbial Mediation Model: linking microbial communities, litter traits, and soil carbon cycling via community-level physiology.
Ewa Błońska	P31 | The C:N:P stoichiometry of deadwood of different decomposition rate and tree species
S. Zechmeister-Boltenste	P34 | Nitrogen addition to temperate forests lead to changes in microbial community structure and function
Andreas Breidenbach	P37 | Impact of pasture degradation on the structure and function of microbial communities on the Tibetan Plateau
Michael Carson	P40 | Culturing techniques in the age of omics: Strategies for obtaining uncultured soil microorganisms and genomes from environmental samples
Dorkrak Chaisarn	P43 | Effect of Plant Growth Promoting Endophytic Bacteria on Riceberry Rice
Alica Chroňáková	P46 | Increasing bacterial contribution in the nitrification following turf disturbances of the translocated wet meadows
Irene Cordero	P49 | Strong legacy effects of intense and frequent droughts on soil microbial community structure and function
Evi Deltedesco	P52 | Increases in temperature and atmospheric CO2 can induce shifts in soil microbial communities
Laila Dubova	P55 | Soil microbiological activity in differently cultivated Faba bean (Vicia faba L.) fields
Lill Eilertsen	P58 | Defining sustainable and economic forestry practices with minimal impact on soil biodiversity and maximum benefits for tree growth
Á. Prieto-Fernández	P61 | Assisted phytostabilization of Cu- contaminated mine-soil using combinations of soil amendments and bioinoculants
Hanna Friberg	P64 | Fungal communities in winter wheat – effects of cropping practices
Talia Gabay	P67 | Bacterial communities of rehabilitated biological soil crusts in desert phosphate mines
Carlos Garbisu	P70 | Rhizoremediation of mixed contaminated soil using Brassica napus and a bacterial consortium
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ORAL ABSTRACTS

O1 Starvation amidst plenty: microbes, soil organic matter, and the role of water in regulating them

Joshua Schimel

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Five thousand: the number (roughly) of microbial taxa, the ^{14}C age (in years) of soil carbon deep in the profile, the number of distinct chemical structures identifiable, and even the total concentration (in ppm) of that C. These numbers define the grand challenges in soil science: understanding how such diversity of starving microorganisms can exist amidst a potential wealth of resources. Yet, maintaining the health and function of the soil is essential to feeding the growing human population and increasing soil C has been identified as a tool for limiting climate change—the 4-per-mil initiative. Achieving these goals requires that we understand the links among microbes, minerals, and soil organic matter. Although microorganisms ultimately metabolize organic matter, whether specific compounds are bioavailable is regulated by minerals and interactions with water, which controls substrate solubility and mobility. One aspect of SOM dynamics that is increasingly important is the role of dry/wet cycles in regulating SOM dynamics. Moisture pulses can directly stress microbes but can also mobilize soil organic matter and stimulate respiration, yet the source of the CO_2 has been unclear: is it a release of microbial constituents such as osmolytes that microbes must get rid of upon rewetting? Or is it C that was mobilized by moving water? Increasingly it appears that the loss of microbial C on drying and rewetting is at most ca. 20% of the microbial C, and that the major source is from mobilizing mineral-associated C. These patterns highlight our uncertainties about the mechanisms that limit microbial use of soil C. I will discuss evolving ideas about the interactions of microbes with the soil physical matrix and water in regulating soil C dynamics.

O2 Linking microbial belowground diversity and plant health

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The microbiome of soil and plants plays a crucial role in plant and ecosystem health. Plants and their associated microorganisms form a holobiont and have to be considered as co-evolved species assemblages. The microbiomes associated with plants form tight networks, which revealed strong species and niche specialization. Soil-borne diseases are microbiome diseases; they are the result of a microbial imbalance in soil and consequently in the rhizosphere and endosphere of plants. Structural and especially functional microbial diversity is suggested as a key factor in preventing plant diseases. Here, examples will be presented from soil - seed – rhizosphere microbiomes. Interestingly, antibiotic resistances (resistome), the most urgent drug resistance trend according to the global action plan on antimicrobial resistance (WHO 2015) is strongly connected with microbiome diversity. The plant-associated microbial diversity is interconnected with other microbiomes, e.g. indoors. It can be also transferred to the gut microbiome because fruits and vegetables are the major component of a healthy diet. Increasing chronic diseases in children can be explained by the “theory of disappearing microbiota” published by Blaser. These novel insights will lead to a paradigm shift regarding the microbiome and health issues.

O3 Environment-microbiota-health axis: at the interface between soil and human microbiota

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Humans in western societies are losing their ancient connection with soil micro-organisms. Lack of exposure to these “old friends”is likely to be one reason behind the rising epidemic of inflammatory disorders. Microbes encountered in early life have an important role in inducing the development of immune structures in the body and educating the immune system to differentiate between harmful and harmless invaders. Several lines of evidence suggest that lack of immune tolerance is associated with a reduced contact with natural environments, which is in turn associated with urbanisation and the loss and fragmentation of natural ecosystems, as well as abandonment of traditional lifestyles. We have shown that increasing proportion of green space in the living environment is associated with reduced risk of allergic sensitisation. More broadly, urban environment and lifestyle tend to increase the prevalence and severity of allergies in both humans and their companion dogs. Differences in living environment and lifestyle can also be associated with patterns in the composition of host microbial communities. Local exposure to specific microbes via the skin, airways, and gut have been shown to exert systemic effects in the host to prevent inflammatory responses, by interacting with the host immune cells. A picture is emerging that to promote health, we need to preserve biodiversity in the environment and make sure a microbial part of this diversity, colonises our bodies. This also bares consequences to, e.g., urban planning, agricultural practices, and child care.

O4 Planctomycetes in boreal and subarctic peatlands: diversity patterns and potential functions

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Members of the phylum *Planctomycetes* are common inhabitants of boreal *Sphagnum*-dominated peat bogs and lichen-dominated tundra peatlands. The 16S rRNA gene fragments from these bacteria comprise one of the major groups of reads retrieved from oxic and anoxic peat in cultivation-independent studies. Despite their wide distribution, the functional role of planctomycetes in peatlands remains poorly understood. We used metatranscriptomics to assess the activity response of peat-inhabiting planctomycetes to biopolymers abundantly present in these habitats, i.e. cellulose, xylan, pectin and chitin. Each of the four polymers induced specific planctomycete responses, suggesting the presence of hydrolytic capabilities in these bacteria. The strongest substrate-induced response was detected on chitin. Given that most conventional tests used for assessing hydrolytic capabilities are not fully suitable for slow-growing planctomycetes, the comparative genomic approach was applied to unveil the hidden potential of these bacteria. The genomes of two peat-inhabiting planctomycetes, *Paludisphaera borealis* PX4^T and *Fimbriiglobus ruber* SP5^T, were sequenced and analyzed. The genomes encode wide repertoires of carbohydrate-active enzymes including many unclassified putative glycoside hydrolases, which suggests the presence of extremely high but partly hidden glycolytic potential in planctomycetes. We were also able to prove the presence of chitinolytic capability in *Fimbriiglobus ruber* SP5^T, which showed the specific response to chitin availability in our metatranscriptomic study. This is the first member of the order *Planctomycetales* with confirmed chitinolytic capability. In summary, these results suggest participation of peat-inhabiting planctomycetes in degradation of plant-derived polymers, exoskeletons of peat-inhabiting arthropods as well as exopolysaccharides produced by other bacteria.

O5 Microbial activity along a climate gradient in the arctic

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Climate change is affecting the arctic dramatically as the warming is fastest in higher latitudes. Previously frozen ground is thawing and releasing substantial quantities of carbon which microbes can decompose. Microbes mineralize the carbon fraction and convert it to carbon dioxide and methane. Climate change models estimate that C released from thawing arctic permafrost can represent the largest future transfer of C from the biosphere to the atmosphere. In addition to temperature, also oxygen and moisture, among many others, affect the microbial activity. Understanding the drivers of arctic soil communities and especially how the microbial activity changes with warming and resulting changes in soil characteristics is needed. However, this kind of information in lacking for the arctic soil microbial communities. We have analyzed over 100 soil plots from a large field site in Scandinavian low arctic with environmental gradient of microclimatic conditions. Metagenomic approach has been used to create a database of microbial genes and metagenome assembled genomes (MAGs) found within this gradient. As DNA can originate from dead or dormant cells, we utilized RNA sequencing to create comprehensive understanding on the metabolic activities of microbes within this fine-scale climatic variation. The metatranscriptomic results show activity of genes involved in carbon, iron, sulfate and nitrogen cycles. In addition, stress related functions were actively expressed in these harsh arctic conditions. As both organic and mineral layer were analyzed we could compare active functions. In upper organic layer ammonia assimilation, carbohydrate and phosphate metabolism were active, whereas in mineral soil methane oxidation and CO2 fixing reaction were more active. On phylum level Actinobacteria and Acidobacteria were the most active bacterial taxa but also activity of fungi was observed.

O6 Co-occurrence networks show response of microbial communities to warming in tundra soils

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The arctic tundra is experiencing dramatic changes due to global warming. The directional changes in vegetation cover are expected to impact the soil microbial communities, with consequences for overall ecosystem functioning. Samples were collected from 19 warming experiments within the International Tundra Experiment (ITEX) across 13 sites, each with 4 control plots and 4 open-top chambers per site. We used metabarcoding of the ITS region and 16S rRNA gene to describe the fungal and prokaryotic communities, and quantified the genes involved in the nitrogen cycling. Our aim was to investigate if the co-occurrence networks were modified by warming, by comparing the topologies of the “small-world” networks, typical of microbial systems. The fungal network was reorganized in the warming experiment, with a strong increase of the length of the paths between nodes and a modification of most of the modules. Those modules, indicating fungal consortia sharing the same ecological niche, were related individually to sites and vegetation, suggesting a site-dependent response to experimental warming. For prokaryotes, the modules were preserved between the control and the treatment and harbored similar relationships with soil nutrients and N-cycling genes, but a turnover of putative keystone species was observed between conditions. The negative co-occurrences between prokaryotic members was denser in the warming treatment compared to the control. This expansion of negative links is indicative of disturbance as they typically increase stability of complex networks under perturbation. In conclusion, warming resulted in disturbances on the interactions within the microbial communities, which potentially impact nutrient cycling and above- and belowground interactions.

O7 Geomicrobiology of glacier basal ice: a frozen or future soil?

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Under current Arctic and sub-Arctic warming, glaciers are predominantly in recession leading to enhanced input of subglacial debris into the forefield. Glacier basal ice forms through interactions between the glacier and its substrate, which imparts physical and chemical characteristics that differ markedly from atmospherically-derived firnified englacial ice. Most obviously, basal ice is sediment-rich. Upon release at the glacier margin as tills and moraines, sediment entrained in basal ice provides minerals essential for the development of proglacial soils. As late as the 1990s, the subglacial environment was regarded as sterile and even today subglacial microbiota remain poorly characterised. Basal ice sediment from our target glacier (Svínafellsjökull, S.E. Iceland) exhibited low C and N status but was rich in Fe, a growth-limiting nutrient. We have estimated basal ice releases 1016 microbial cells year-1 to the glacier margin. Culture-dependent (classical and iChip) and -independent ribosomal rRNA gene sequence based microbiome analyses confirmed bacterial and fungal viability and diversity. A high abundance of bacterial chemolithotroph-associated sequences, particularly affiliated with iron oxidising bacteria, indicating potential for subglacial carbon cycling, supports proliferation of identified soil and aquatic heterotrophic bacteria and fungi in the basal ice microbiome. Basal ice microbiota able to survive and proliferate, both within and external to the ice matrix, transform entrained sediment into an organo-mineral complex. Bacterial and fungal communities associated with the basal ice-mineral matrix appear likely to play crucial roles in soil formation in situ and following glacial recession, associated melt, and sediment-microbe release from basal ice into the forefield.

O8 Soil carbon and nitrogen cycling along a natural environmental gradient in subarctic mountain birch forest: the fungal decoupling

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High-latitude forests are key ecosystems for understanding responses to climate change due to their relatively high productivity. Although birch forests cover extensive areas of the Eurasian Subarctic, their climate change responses are understudied. Increasing temperatures generally increase process rates, including belowground organic matter turnover, but indirect consequences, such as increased labile organic matter input to soils, are equally important to consider. Currently our understanding of above-belowground interaction is incomplete, and the biogeochemical outcome of this balance remains highly uncertain. Recent studies have revealed that soil carbon (C) and nitrogen (N) mineralisation in boreal forests and heath tundra are decoupled; an effect that grows stronger with higher abundance of inorganic N and labile substrates, and which seems to be primarily correlated with the level of fungal dominance of decomposition. These studies were done in experimental systems, but we hypothesised that this fungal driven decoupling of C and N cycling could be observed along natural environmental gradients. We present a unique dataset collected along a natural environmental gradient in Subarctic Sweden, spanning 2.5 °C mean annual temperature and 1000 mm mean annual precipitation. We assessed key soil microbial processes including bacterial and fungal growth along with rates of biogeochemistry, proxied by respiration and gross N-mineralisation, as well as a wide range of potential abiotic and biotic drivers of these. Our results broadly confirm a decoupling of C and gross N-mineralisation linked to a fungal dominance of decomposition, suggesting that observations previously made in smaller experimental setups can be extended to hold also on natural ecosystem scale. This represents a potential climate mitigation effect, as less C is respired per unit mineralised N when primary productivity increases.

O9 Importance of methanotrophy in the C and N cycle

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Peatlands store 1/3 of the terrestrial C. Peat is formed and C sequestered due to the slow anaerobic microbial decomposition ending in CH4 formation in these waterlogged ecosystems. This methane ends up in the peatland characterizing GHG fluxes but before being released into the atmosphere much of it becomes oxidized through methanotrophic bacteria (MOB). Sphagnum mosses are the most important peat forming plants. Up to 30 % of the moss biomass originates from CH4. Sphagnum mosses are associated with methanotrophs (SAM) under peatland flooding conditions. This association enables the moss to use the CO2 produced during CH4 oxidation in its photosynthetic machinery and SAM operates only under water logged conditions. The MOB diversity associated to the process is broad. While SAM is operating another benefit is guaranteed to the peatland ecosystem. MOB fix N2 which is delivered to the moss and thus into peat. In mineral soil ecosystems moss associated N2 fixation has not been associated to MOB but there might operate another system involving MOB. During wood decay fungal OTUs proliferate and N accumulates. As mycorrhizal fungi dominate the late decay stages it has been suggested that they import N from the mineral soil into the wood. But wood decaying fungi produce methane in low concentrations. Could this attract MOB? Analyzing the N2-fixing community through the nifH gene of decaying wood revealed MOB to be involved in the process. Wood associated methanotrophs thus could play a role in the decay N budget and thus to the whole forest ecosystem.

O10 Unususal acid-tolerant denitrifiers of permafrost affected peatlands drive massive N2O emissions

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Peatlands represent hitherto under-appreciated sources of the greenhouse gas nitrous oxide (N2O). Indeed, pristine permafrost-affected acidic peat circles emit N2O in the range of fertilized agricultural soils. The main process yielding N2O under anoxic conditions is denitrification, i.e. the sequential reduction of nitrate to N2O and N2. Active key denitrifiers of peatlands are important but hitherto unknown. Thus, it is hypothesized that acid tolerant peat circle denitrifiers are new, impaired by pH and unable to reduce N2O. Microcosm studies, RNA stable isotope probing, functional gene sequencing and expression analyses, as well as isolation campaigns demonstrated that acidic peatlands host acid-tolerant new denitrifiers capable of N2O reduction at low pH, prone to respond to temperature increase, a correlation of in situ N2O emissions with denitrifier community structure. Burkholderiaceae, other Proteo-, and Actinobacteria as well as Verrucomicrobia were identified as key acetate assimilating denitrifiers. Complete denitrifies operate under substrate limitation in peat circles and thus produce large amounts of nitrate derived N2O. Consequently, peatland denitrifiers might be more important for climate change than previously thought.

O11 An experimental roadmap for in-depth proteome analysis of the methane-oxidizing *Methylocystis* sp. strain SC2

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Microbial methane oxidation is one of the fundamental processes in biological mitigation of greenhouse gases. Among the well-described methane-oxidizers, type II methanotrophs of the genus *Methylocystis* are known to be both most oligotrophic and most widespread in nature. Using recent developments in sample preparation strategies and improvements in mass spectrometry (MS), an optimized procedure was developed to characterize the proteome of *Methylocystis* sp. strain SC2. The major challenge for developing an efficient analytical proteomics workflow for methanotrophic bacteria is their high amount of membrane-associated proteins that need to be efficiently solubilized and digested for downstream analysis. Therefore, each step of the workflow, including cell lysis, protein solubilization and digestion, and MS peptide quantification, was assessed and optimized. We show that detergent-based procedures are more efficient in extracting and solubilizing SC2 proteins than chaotropic strategies. Using an uncommon crude-MS approach, we assessed how sample preparation strategies contribute to quantification biases, in particular for membrane-associated sub-proteomes within whole-cell proteomics. Our new workflow proved to increase protein quantification accuracy and proteome coverage of strain SC2. It captured 62% of the predicted SC2 proteome, with 10-fold increase in membrane-associated proteins relative to less effective conditions. To further validate the workflow efficiency, we analyzed the response of the SC2 proteome to low and high nitrogen conditions, with a focus on the differential expression of proteins involved in methane and nitrogen metabolism. Upon exposure to high ammonium, we observed a good correlation between differential protein expression and previously reported mRNA transcript levels.

O12 Permafrost peatlands plants and their bacterial rhizobiome: stronger plant species-specific effects in permafrost than in active layer peat

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Soil carbon and nitrogen cycles in northern ecosystems are sensitive to climate change due to the vulnerability of permafrost soils to thawing. An important aspect of this phenomenon is the potential role for plant roots and their possibly distinct rhizosphere communities (rhizobiome) in influencing subsoil biogeochemistry. Such influences might be plant species-specific because only certain plant species can grow roots deep enough to reach the newly-thawed soil layers. In peatlands, the strong chemical constraints exerted by *Sphagnum* mosses (pH, phenolics) could mask rhizosphere effects, particularly on rhizobiome composition. Whether bacterial rhizobiomes differ from the surrounding *Sphagnum* peat or between plant species, and whether such differences persist in permafrost soils, is still unclear. We characterized the bacterial rhizobiome of five plant species representative of the main functional types found in sub-arctic peatlands (*Andromeda polifolia, Betula nana, Empetrum nigrum, Eriophorum vaginatum, Rubus chamaemorus*). We grew the plants in rhizobox-like microcosms filled with peat or permafrost soil, and compared the bacterial rhizobiome with communities found in no-plant controls, using RNA and DNA co-extraction and 16S amplicon sequencing. Bacterial rhizobiomes differed from the no-plant control in both soils, but only in RNA-based profiles. The species-specific effects were weaker in peat than in permafrost-soil microcosms where *E.vaginatum, R. chamaemorus, A. polifolia,* and *B. nana* strongly differed from the controls. Since *E. vaginatum* and *R. chamaemorus* roots can reach the permafrost table, their distinct bacterial rhizobiome should be more closely investigated to determine possible impacts on carbon and nitrogen cycling in the subsoil of permafrost peatlands.

O13 Bacterial and fungal community composition but not richness or biomass follows plant primary succession in arctic inland sand dunes

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Microbes contribute to establishment of vegetation by shaping soil chemistry and colonizing plants, but it remains unclear whether microbes show predictable trajectories in primary succession. To clarify the drivers of soil microbial communities, we sampled six succession stages in subarctic sand dunes which wind has eroded into deflation basins. The stages were based on vegetation: bare sand, sand with grass or moss, lichen crust, ericoid heath, and mountain birch forest. Bacterial (16S rRNA gene sequencing) and fungal (ITS2) communities followed a gradient of increasing organic matter and decreasing pH from sandy to vegetated stages. Richness and biomass diverged from this gradient: Bacterial richness peaked in the heath, but fungi were most diverse in sand. Bacterial biomass (PLFA) was lowest in sand and highest in forest, whereas fungal biomass was highest in the heath, where an ericoid mycorrhizal OTU dominated. A distinctive group for the sandy stages was candidate phylum WPS-2, which as proposed autotrophs could promote carbon accumulation. Acidobacteria increased with succession, but several subgroups preferred the earlier stages. In bare sand, 35% of fungi belonged to unclassified clusters. Late succession fungi included Agaricomycetes, Eurotiomycetes, and Zygomycota. Soil chemistry explained a smaller portion of community variation in sandy than vegetated stages, suggesting a larger role of stochasticity in early succession. Our results indicate that the formation of lichen crust created a main shift in microbial community composition. Bacterial and fungal richness followed different trajectories. Community succession in deflation basins can serve as a revegetation model for eroded arctic soils.

O14 Patterns and predictors of methane production and methanogen community composition across peatlands globally

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Methane is a potent greenhouse gas and while peatlands cover little global surface area, their soils produce disproportionately large amounts of methane. In this study, we evaluated global potential methane production and associated methanogen community composition by assessing 423 peat samples from all 7 continents and 105 distinct site locations. A standardized methodology was employed, and peat was incubated over an 80-day period, with methane measurements taken at regular intervals. DNA was extracted and amplicons sequenced on the MiSeq platform. Metadata including temperature, pH, water table position, latitude and longitude, total elements, structural chemistry (FTIR), and von post as well as broad plant communities were used to determine if there is a “universal control” or predictor of methane production and community composition in peatlands globally. Results indicate that methane production is increased with peat chemistry low in complex organic acids and other aromatic compounds, and high in carbohydrates as well as in sites with more neutral pH and *Carex* and *Cyperaceae* plant communities present. Only five percent of samples had a disproportionately high production of methane compared to anaerobic CO_2-C, highlighting the important role of anaerobic CO_2 production in the microbial greenhouse gas burden of peatlands. Methanogen community composition data are currently being analyzed. For the first time, this study uses common methods across a globally distributed set of samples to show that peatland type, pH, and vegetation are the drivers of broad scale methane production.

O15 Climate change in subarctic tundra – responses of microbial communities to changes in snow accumulation and soil temperature

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Northern regions are experiencing considerable changes in winter climate leading to alterations in the amount and quality of snow. The timing and extent of snow cover is a major controller of soil temperature and hence winter-time microbial activities. To obtain a deeper understanding on how changes in winter-time conditions affect carbon and nutrient cycling in northern ecosystems, we compared microbial communities under contrasting snow accumulation in shrub dominated tundra heaths. Compared to snow-accumulating tundra, wind-swept tundra heaths were characterized by extremely low and fluctuating winter soil temperatures, higher number of freeze-thaw cycles and lower availability of labile C and N. Despite these differences, bacterial 16S rRNA gene and fungal ITS region amplicon sequencing data indicated surprisingly similar microbial communities under both habitats. To elucidate the role of different taxa active in winter-time litter degradation we conducted a laboratory incubation at -5, -1 and +2°C. Litter addition resulted in a rapid CO_2 pulse down to -1°C followed by decomposition of mainly water soluble compounds of the added litter. Litter amendment resulted in rapid shifts of the active microbial community indicating a dynamic response of the community to increased labile C even at sub-zero temperatures. Overall the data indicated that soil microbial communities under shrub dominated tundra heaths are not sensitive to changes in winter-time soil temperatures but activities are controlled by the availability of labile C and N. Long-term shifts in vegetation with changes in labile C and N will likely have important consequences to the microbial community structure and functioning.

O16 Predominance of methanogens over methanotrophs contributes to high methane emissions in rewetted fens

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The rewetting of drained peatlands alters peat geochemistry and often leads to sustained elevated methane emission. Although this methane is produced entirely by microbial activity, the distribution and abundance of methane-cycling microbes in rewetted peatlands, especially in fens, is rarely described. In this study, we compare the community composition and abundance of methane-cycling microbes in relation to peat porewater geochemistry in two rewetted fens in northeastern Germany, a coastal brackish fen and a freshwater riparian fen, with known high methane fluxes. We utilized 16S rDNA high-throughput sequencing and quantitative polymerase chain reaction on 16S rDNA, *mcrA*, and *pmoA* genes to determine microbial community composition and the abundance of total bacteria, methanogens, and methanotrophs. Electrical conductivity was more than three times higher in the coastal fen than in the riparian fen, averaging 5.3 and 1.5 mS cm^{-1}, respectively. Porewater concentrations of terminal electron acceptors varied within and among the fens. This was also reflected in similarly high intra- and inter-site variations of microbial community composition. Despite these differences in environmental conditions and electron acceptor availability, we found a low abundance of methanotrophs and a high abundance of methanogens, represented in particular by Methanosaetaceae, in both fens. This suggests that rapid re/establishment of methanogens and slow re/establishment of methanotrophs contributes to prolonged increased methane emissions following rewetting.

O17 Circumpolar microbiome pattern as determinant of subducted carbon vulnerability in Arctic permafrost soils

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Arctic permafrost soils contain about half of the global soil organic C (approx. 1300 Pg). One third of this C is stored in subducted organic matter (cryoOM) by the cryoturbation processes. We here present results from the Arctic project that aimed at identifying the role of microbial functioning for OM decomposition in cryoturbated soils (Siberia, Greenland, Canada) and at assessing the potential vulnerability of this OM in a future climate. Our main findings were: 1) Abundance of bacteria and fungi closely correlates with carbon loss. Low fungal to bacterial ratio may be one of the reasons of slow decomposition of cryoOM and can be used as cryoOM vulnerability predictor. The microbial community is distinctly different from topsoil and more similar to surrounding subsoil communities. There is, therefore, a mismatch between microbial community composition and OM quality that added to the retarded decomposition of cryoOM. 2) OM availability is reduced and N cycling decelerated. In several incubation experiments including experiments with labelled substrates we demonstrated different nutrient limitations of the microbial communities in cryoOM. The N-containing substrates led to a significant priming effect, indicating a strong N limitation of the microbial community. High portion of crypOM is bound to clay minerals which may contribute to lower availability for microbial decomposition and lower vulnerability of cryoOM. In summary, we demonstrate that, in addition to unfavorable environmental conditions, decomposition processes in cryoturbated arctic soils are retarded by a combination of changes in microbial community composition, reduced OM availability and decelerated N cycling.

O18 Fine scale niche differentiation among amoebal communities of dark-spored myxomycetes determined by landscape structures as well as biotic factors.

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Myxomycetes (Myxogastria, Amoebozoa) also known as 'slime molds' have historically been described as fungi, due to their macroscopically visible fructifications which, though considerably smaller, resemble those of fungi. These fruit bodies provide enough morphological traits to support a morphological species concept with currently ca. 1000 species described. Therefore diversity studies of myxomycetes have been conducted for over 200 years and a substantial body of data on ecology and distribution of these fructifications exist. In the study presented we ask: 'do myxomycetes show broader realized niches as soil amoebae than as fructifications?' and 'is the myxamoebae distributions correlated to potential prey organisms (fungi and/or bacteria)?'. To answer these questions parallel metabarcoding of bacteria, fungi and dark-spored myxomycete was used in a combined approach to analyse the communities from an elevational transect in the northern limestone German Alps (48 soil samples). Potential interactions between the three target organisms were analysed by integrating community composition and phylogenetic diversity with environmental parameters. We identified niche differentiation for all three communities (bacteria, fungi and myxamoebae) which was strongly driven by the vegetation. Bacteria and fungi displayed similar community responses, driven by symbiont species and plant substrate quality. Myxamoebae showed a more patchy distribution, though still clearly stratified among genera, which seemed to be a response to both structural properties of the habitat and specific bacterial taxa. In addition we find an altitudinal species turn-over for all three communities, most likely explained by adaptation to harsh environmental conditions.

O19 Permafrost as an active microbial ecosystem: pushing up against the thermodynamic limits of life

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Permafrost is an extreme habitat with low water and substrate availability, yet it hosts microbial populations that remain active over geologic timescales. Using permafrost collected from a Pleistocene chronosequence (19 ka to 33 ka), we hypothesized that increasing age and associated stressors drive adaptive changes in microbial community function and composition, and that functional changes in the metagenome would be related to changes in the chemistry of permafrost carbon (C). Examinations of water-soluble organic carbon (OC) by Fourier-transform ion-cyclotron-resonance mass spectrometry (FT-ICR-MS), quantification of total anions, and metagenomic sequencing were combined to better understand the relationships between microbial populations, the molecular-level composition of potentially bioavailable organic matter (OM), and age. We found that age had a marked effect on both the molecular composition of dissolved OM and the microbial community. Diversity of the total microbial community, the relative abundance of carbohydrate active enzyme families, and the nominal oxidation state of C (NOSC) all significantly decreased as soils became older. In contrast, the concentration of low molecular weight organic acids and ammonia significantly increased with age. Both our chemical data and functional gene data supported the hypothesis of a shift from sugar to amino acid metabolism over geologic time. To this end, we present a conceptual model of microbial metabolism in permafrost based on fermentation of OC, changing metabolic pathways, loss of methanogenic activity, and the buildup of organic acids that helps to explain the unique chemistry and high C lability of ancient permafrost soils.

O20 Stable Isotope Probing Reveals a Subzero-Active a Bacterial Community in Arctic Tundra Soils

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Global climate change, with variation in the timing and extent of snow cover and soil temperatures, is having a major impact Arctic tundra soils. In turn, these changes may also impact soil microbial activities and geochemical cycling of stored carbon. While there are numerous studies investigating the impact of thaw on soil microbial processes, very little is known about the role of temperature changes within subzero-active microbiomes of frozen Arctic soils. To discern how subzero-temperature impacts active bacteria, we used a stable isotope probing (SIP) and 16S rRNA amplicon sequencing approach with tundra soils from Kilpisjärvi, Finland. Soil microcosms were amended with ^{13}cellobiose and incubated at 0, -5, and -16°C for 5-40 weeks. The relative abundances of subzero-active taxa, such as members of the *Caulobacteraceae*, Candidatus Brocadiaceae, *Pelobacteraceae*, *Acetobacteraceae*, *Armatimonadaceae*, *Desulfobacteraceae*, *Anaerolineae*, *Verrucomicrobiaceae*, *Planctomycetaceae*, and *Melioribacteraceae*, increased at -16°C from the initial resident soil community. Members of the bacterial families of *Prochloroccoceae*, *Thermaceae*, *Rubrobacteracae*, *Rhizobiaceae,* and *Nocardiae* were detected and active at 0°C, but not at -5°C or -16°C. This study reveals that subzero temperatures impact bacterial community composition and activity, which in turn may affect global biogeochemical cycles of carbon. Understanding the factors that control subzero-active microbial community composition is important, since despite slower rates, winter-time biodegradation can account for significant quantities of the annual carbon mineralization.

O21 Time to Wake Up! - Mycelia Enable Bacterial Activity in Dry and Oligotrophic Environments

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Bacterial-fungal interactions contribute to many ecosystem processes in natural and constructed environments. However, their emergence and benefit under environmental stress conditions remains elusive. Here we used a spatially explicit synthetic microbial ecosystem to elucidate whether mycelia reduce bacterial water and nutrient stress in a dry and oligotrophic microhabitat. We found that mycelia enabled dormant bacteria to regain activity despite the absence of water and nutrients in their direct environment. We observed germination and subsequent growth of bacterial spores (*Bacillus subtilis*) in the vicinity of the hyphae of different fungi (*Fusarium oxysporum*, *Lyophyllum* sp. strain Karsten) and the mycelium-like networks formed by the oomycete *Pythium ultimum*. Using a unique approach combining Time of Flight- and nanoscale Secondary Ion Mass Spectrometry (ToF- and nanoSIMS) coupled with stable isotope (^{13}C,^{15}N,^{18}O) labeling, we could demonstrate that spore germination is accompanied by hyphal transfer of water, carbon and nitrogen. This work provides for the first time direct experimental evidence for the stimulation of bacterial activity by mycelial supply of scarce resources in dry and nutrient-free environments. We propose that mycelia may stimulate bacterial activity and thus contribute to the stability of ecosystem functioning in environments exposed to stress.

O22 Insights into long-term drought, storms and rewetting effects on streambed microbial diversity

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Intensified droughts and floods are growing stressors worldwide. Microbial sediment communities inhabiting intermittent streams are expected to undergo longer and more frequent droughts leading to changes in diversity. Here, bacteria, fungi and archaea diversity were tracked over a 157-days experiment in sediment column microcosms. We examined the effects of long-term drought, storms and rewetting on microbial communities from two sediment depths (surface and hyporheic) and buried leaves under three conditions: water saturated (Control), dried for 5 months (Dry), and dried for 5 months interrupted by two flash storms (Dry-Storm). The effect of storms and rewetting was greater than that of long-term drought in bacterial and archaeal communities' diversity, while fungi remained insensitive. Bacterial and archaeal OTUs richness in surface sediment and leaves was reduced by the wet conditions, while effects in the hyporheic were more attenuated probably because of the lower decrease in water content. Sequences affiliation revealed that storms limited the increase of *Thermoplasmata* and favoured the recovery of *Nitrosopumilales* abundance in the archaeal community of the hyporheic, thus facilitating a complete recovery of this community during rewetting. Water resumption did not modify bacterial diversity from the hyporheic, whereas flash storms kept *Actinobacteria* abundances low in surface sediment permitting a complete recovery of the community. Fungi revealed overall the lowest diversity with high species variability among treatments and substrata. Our findings revealed the remarkable sensitivity of the archaeal community to hydrological intermittency as well as the influence of flash storms in favouring microbial communities recovery once rewetted.

O23 ACC deaminase positive bacteria - Serving dual role of Protector and Benefactor for plants under salinity stress

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The misuse of chemicals as fertilizers and pesticides for increasing productivity in agriculture has led to ecological and human health hazards. Bioinoculants as plant growth promoting rhizobacteria present an eco-friendly, long term and sustainable alternative to these chemicals. ACC deaminase production is a nodal plant growth promoting property that protects the plant from all biotic and abiotic stresses that a plant encounters. Salinity and drought are the major factors impacting Indian agriculture and worldwide. Plant growth experiment was setup in natural conditions using *Cajanus cajan* as the model crop with simulated salinity and drought conditions. The objective of the experiment was enumeration, diversity analysis and isolation of potent ACC deaminase producers along with other desirable PGP properties for amelioration of stress in fields. High salt and natural drought conditions increased the abundance of probable ACC deaminase positive bacteria. Isolates obtained were screened for ACC deaminase activity and other PGP properties including salt tolerance; subsequently plant growth experiment was set up with the most potent isolate in controlled condition and field conditions for validation of plant growth promotion. Further, denaturing gel gradient electrophoresis and Illumina sequencing was performed for analysis of its impact on the rhizospheric community structure and function. Generation of *acdS* negative mutants and subsequent plant growth experiment with it further confirmed ACC deaminase role in amelioration of stress and plant growth promotion. ACC deaminase producers was thus found to serve dual function: protecting the plant from stress conditions and also promoting plant growth and productivity.

O24 Secret collaborations: plant-associated *Archaea* and their interaction with their hosts

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Plant holobionts are known to harbour a wide diversity of microorganisms, such as bacteria and fungi, influencing plant nutrition, resistance to stress and fitness. Furthermore recent studies showed that actually *Archaea* also shape the microbiome of plants, but their functions and interactions with their hosts remained mostly unclear. To get a broader insight into the community structure, habitat preferences and functions of plant-associated *Archaea*, we compared 41 different agriculturally used plant-species from the mediterranean area, Austria and Eastern Africa as well as the vegetation of alpine raised bogs from upper Styria (Austria). Therefore we used a combined approach including 16S rRNA amplicon sequencing, whole metagenome shotgun sequencing and fluorescence *in situ* hybridization confocal laser scanning microscopy (FISH-CLSM). The highest relative abundances of *Archaea* were detected in the endosphere of olive trees (*Olea europaea* L.), with up to 67.3% of total reads, in dwarf shrubs (*Vaccinium myrthillus* and *V. oxycoccus*, with 33.0% and 31.7% respectively), and in the rhizosphere of sugar beets (*Beta vulgaris* L.) with 20.0%. Across all habitats the archaeal community structure was clearly dominated by *Euryarchaeota*, followed by the less abundant phylum of *Crenarchaeota* and *Thaumarchaeota*, except in *O. europaea*, where *Thaumarchaeota* were predominant. On plants, we observed signatures for putative adaptation mechanisms of *Archaea* for their hosts, including those for higher chemotaxis, nutrient cycling like CO_2 fixation, stress response, especially against oxidative stress, archaeon stability, and possible plant growth promotion through auxin. These findings reveal a so far unobserved role of *Archaea* for plant holobionts.

O25 Role of secondary plant metabolites in the ecology of soil microorganisms

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Among the plant-derived organic matter, secondary plant metabolites (SPMEs) seem to be of outstanding importance in controlling soil ecology: not only can SPMEs serve as carbon and/or energy sources for bacteria but they often have antimicrobial activity or ability to disrupt bacterial quorum sensing and some SPMEs have been predicated of regulating the decomposition of organic matter. SPMEs are likely to have evolved to assist the plant in tolerating frost, storing nutrients, reinforcing structurally, signaling to mutualists, as well as acting as allelopathic chemicals and chemicals protecting the plant from herbivory. Because insects and other herbivores are continually developing mechanisms of resistance to SPMEs, plants are driven to modify and develop new mechanisms of protection, including modification of SPMEs. These changes in plant SPME content and composition in turn affect soil microbial communities which has resulted in the establishment of detoxifying enzymes with broad substrate specificity in soil bacteria. This all leads to the hypotheses (i) that SPMEs are among key features controlling soil microbial community structure; and (ii) that enzymes originally evolutionarily developed for the detoxification and/or degradation of SPMEs are also fortuitously involved in the degradation of anthropogenic pollutants. In order to test our hypotheses, we conducted a series of experiments in which we screened the ability of selected SPMEs to induce the expression of ring-hydroxylating dioxygenases in soil bacteria. Furthermore, we investigated how plants with different amount and composition of SPMEs influence the structure of microbial communities in soil. Overall, this presented work help us understand the role of SPMEs in the ecology of soil microorganisms and provide a more specific link between SPMEs and biodegradative genes, with potential implications for both bioremediation and agriculture.

O26 Soil microbial responses to drought and exotic plants shift carbon metabolism in a semiarid ecosystem

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We investigated the effects of extreme drought and exotic plants on soil microbial community composition and carbon metabolic genes within a four-year field rainfall manipulation experiment in a semiarid shrub ecosystem. We combined measurements of bulk microbial and soil properties with high-throughput microbial community analyses to elucidate microbial responses and microbial-mediated alterations to carbon cycling. While microbial responses to experimental droughts were weak, scant rainfall periods resulted in decreased microbial biomass and activity, and an altered bacterial community composition. There was a striking commonality between the impacts of wet vs. dry years and the influence of native vs. exotic plant communities on the microbial community structure. Exotic plots and the driest years were overrepresented by Actinobacteria, Chloroflexi, Cyanobacteria, Deinococcus-Thermus and Firmicutes, and these phyla were positively correlated with genes for aminosugars and sugar alcohols, possibly indicating osmotic stress life-strategies. Native plots and the most mesic year were represented by Acidobacteria, Bacteroidetes, Planctomycetes, Proteobacteria and Verrucomicrobia, which were mostly positive correlated with polysaccharides and glycoside hydrolases. Compared to native plots, soils under exotic plants had more seasonally variable microbial activity, along with more stressful and dynamic conditions: lower soluble carbon, higher daytime temperatures, and enhanced infiltration but decreased soil water retention after rainfall events. Drought and exotic plants could potentially impact ecosystem C storage by producing a smaller, more vulnerable C pool of microbial biomass that is prone to increased pulses of heterotrophic respiration. Increased frequency of extreme weather events might exacerbate the influence of plant invasion on soil C storage.

O27 Legacy of drought affects microbial community composition and activity induced by root exudation

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Occurrences of drought are projected to increase in temperate grasslands, leaving these ecosystems susceptible to environmental stress and altering plant-soil-microbe feedback. One critical mechanism in this feedback is root exudation; these compounds released by plant roots are a major source of substrate (C) for the soil microbial community. Soil C-cycling and microbial community composition are changed under conditions plant stress, but it remained unknown how root exudates played a role in mediating these changes. In a controlled environment using a sandy loam soil, we subjected two common grassland species (*Holcus lanatus*, a grass, and *Rumex acetosa*, a broad-leaved forb) to a two week long drought. Root exudates were collected from individual plants and added back to soil in a substrate-induced respiration experiment. Rates of soil microbial activity were found to be significantly increased when droughted soil was exposed to exudates from droughted plants (instead of control plants), even after a two week recovery period, and even independently of exudation rates. Root exudation rates were relatively independent of measured root traits, except for root biomass. Phospholipid fatty acid analysis of the soil microbial community indicated shifts that may explain the substrate preference and are associated with plant type. This study illustrates how even short periods of drought can result in a soil microbial community with altered substrate preference that may amplify effects root exudates have on the global C cycle.

O28 The known and the unknown in soil microbial ecology

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The methodical developments in the fields of molecular biology and analytical chemistry significantly increased the level of detail that we are able to achieve when exploring soils and their microbial inhabitants. High-resolution description of microbial communities, detection of bacterial and fungal taxa with minor abundances, screening of gene expression or the detailed information on the composition of soil metabolomes are nowadays technically feasible. Despite these apparently unlimited possibilities, our understanding of soil is limited in many ways. The uncertain definition of fungal and bacterial species make it difficult to determine basic ecological entities and variation in marker genes hampers both relative and absolute quantification. The size of samples that we are able to analyse do not allow us to study microbial interactions at a relevant scale. The quantification of metabolite content brings little information without the information on metabolite fluxes – production and consumption – and the in situ enzyme activities is impossible if fine chemical properties and substrate availability are not known. In the future, it is important to look at soil at a finer detail to obtain a better picture on the properties of individual microbes, their in situ interactions, metabolic rates and activity at a small, spatially relevant scale. It will be necessary to develop techniques to track the flux of organic compounds and other nutrients. On the other side, the exploration of soil ecology should move towards scaling up to get answers at a large-scale ecosystem or even biome levels instead of sample or site levels.

O29 Information in droplets – towards single-cell sequencing in microbiology

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Emulsion PCR enabled the first applications in next-generation sequencing, but further advances in sample preparation in emulsion droplets allow high-throughput single-cell approaches. Recent technologies for single-cell transcriptomics and genetics are already widely used in cell biology, but utilization of the technology for microbial samples meets several obstacles that retard the use of the technology for characterizing prokaryotic communities. First, prokaryotic messenger RNAs lack the polyA-tail, important for the amplification of gene transcripts in the cells. Secondly, many prokaryotic cells are hard to lyse, therefore one has to optimize the cell lysis step after droplet generation. I will present the advances in the current microfluidic and droplet technology and their microbiological perspective. EpicPCR is a protocol that is based on the PCR-amplification of chimeric sequences in emulsion droplets. These chimeras are then sequenced to link sequences of functional genes to the phylogenetic groups. This method introduced by Spencer, Tamminen, et al. (ISME J [2016] 10, 427–436) will enable huge numbers of applications to study microscopic organisms from viruses to small eukaryotic cells. Sample encapsulation protocol has been simplified in our laboratory to allow a simple workflow by exploiting the droplet generator by Bio-Rad. The new tool is especially useful in analyzing the physiology of uncultured microbes, analyzing microbial food chains and symbiotic/spatial relations in the microbial communities. Eventually the tool will help us to proceed to a new era where hypotheses generated by metagenome explorations can be tested in real experimental conditions.

O30 Methods, measurements, and models of *in situ* pH of the soils of Wisconsin

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Soil pH has long been considered a “master variable” in soil microbial ecology, but growing evidence suggests standard soil pH—widely measured by soil scientists with a glass pH electrode in a 1:1 soil:water slurry—is very likely dissimilar to *in situ* soil pH as experienced by soil microbes. *In situ* soil pH requires more precise measurements because bacteria regulate cytosolic pH to ensure the prevention of denaturing of DNA and intracellular proteins outside a narrow, neutral range and rely heavily on the pH of the external environment being low enough to generate sufficient protonmotive force (PMF) to survive. Additionally, biogeochemical analyses of soil pH require accounting for heterogeneity among microhabitats, and the standard method may therefore reduce the applicability of pH values to the investigation of the physiological ecology of soil bacteria. We are testing a range of methods to better measure *in situ* soil pH across the microhabitats of the diverse soils of Wisconsin, USA: (1) glass pH microelectrode, (2) ion-sensitive field effect transistor (ISFET), and (3) ratiometric fluorometry using confocal laser scanning microscopy or soil solution extract in a plate reader. The novel methods developed and models created from the dataset will enable both the investigation of interactions of bacterial cell envelopes and membranes with soil solution and particles, as well as an estimated net magnitude of net proton activity in soil hydrofilms of thin but variable thicknesses in which soil bacteria survive and reproduce.

O31 Drought and climate change induced shifts in the plant community favor specific soil bacterial communities with contrasting functional characteristics

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Soil properties and plant community composition (PCC) shape the structure and function of soil microbial consortia. We performed a common garden experiment in order to study the combined effects of climate (ambient/drought) and PCC (current northwestern /predicted southwestern European) on the rhizosphere microbiome. Soil enzyme activity measurements indicated resilience of microbial functions. Functional properties of cultivable bacteria were maintained in drought by specialized taxa, including cellulose decomposing (CD) *Arthrobacter* and *Streptomyces,* and phosphate solubilising (PS) *Phyllobacterium* isolates. Amplicon sequencing detected increased numbers of *Streptomyces* and *Arthrobacter* reads upon drought. The number of total PS bacterial colonies reduced but fungal ones increased in drought, suggesting functional redundancy. CD and PS microorganisms were most strongly affected by drought when associated with the future PCC. The proportion and phylogenetic composition of nutrient-releasing *Pseudomonas* community were affected by drought and in a minor extent by changes in PCC, with some concordance between the metabolic activities and 16S phylogeny. The drought induced shifts of the *Pseudomonas* community and of corresponding functional traits, specifically P and K solubilization and siderophore production. Whereas decreased soil moisture induced a highly active phosphate-solubilizing community, the siderophore-producing community showed the opposite response, and K solubilization was not affected. The observed functional shifts of the *Pseudomonas* community were correlated with abiotic soil parameters. These results suggest that microbial community quickly responds to drought, the response is based on the metabolic potentials of the isolates, and the level of the response is affected by plant community composition.

O32 Micro-RIP: Functional analysis of uncultivated microbes using radioisotope probing

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Despite the wealth of big data (genomic, transcriptomic, metabolomic) that can now be obtained from environmental samples, it has proven fiendishly difficult to analyse soil and water microbiomes beyond simple descriptions of their community diversity. Firstly, it is often difficult to directly link microbes to their functions, especially in samples from complex environments with large numbers of genera. Secondly, environmental samples often contain significant quantities of relic DNA from deceased organisms appearing in results, but not affecting the functions of the systems. Micro-RIP *(radioisotope probing of microbes*) is an ambitious project to address both these problems by re-purposing Ion Torrent next generation sequencing chips to measure radioactivity in the molecular level. In the RIP analyse we can record the genetic identity of the microbiome members (via standard PGM sequencing) and measure the radiolabelling of the original DNA/RNA molecules, essentially giving the information of both identity and function of each taxa within a given microbiome. This tool would allow classical radioisotope experiments designed to determine microbial function to do so on the genetic scale, as long as the radioisotope used (such as ^{14}C or ^{3}H) is easily incorporated into the DNA or RNA. This would reveal the role of thousands of coexisting microbial genera in different ecosystem processes, in just one analysis. The Micro-RIP technique is currently being optimised, so in this talk will cover the development process and how the technique could eventually help lift the lid off the ecosystems function 'black box' that exists for many microbiota.

O33 Plant growth stage drives microbiome community assembly, interaction patterns and functionality

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Rhizosphere communities are very dynamic, starting from a virtually sterile seedling that will be progressively colonised by surrounding taxa. Despite of the recent tremendous researches and progresses in sequencing technology, our understanding on rhizosphere community assembly is still very limited. In this study, bacterial isolates are randomly selected from different growth stage rhizosphere. Bacterial identity information was collected *in vitro*, for instance microbial resource utilization ability, plant growth promotion trait production, pairwise interactions among bacteria inside a community were tested. The traits-based experiments gave us more details to know the interactions among the bacteria in rhizosphere microbiome. We found that flowering stage is a critical moment for microbial assembly, the microbiome changed tempestuously at flowering stage. Further, the functional diversity, plant growth promotion trait production and cooperation density of rhizosphere microbiome reached highest level at flowering stage. We investigated how rhizosphere communities assemble in growing plants, starting from a sterile seedling until a mature plant, providing the base for informed bio-engineering strategies to optimize the functionality of the rhizosphere microbiome serve for plant health and sustainable agriculture.

O34 Performance of plant-microbial-soil system as affected by plant species and N availability

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Rhizodeposits, which are highly contributed by low molecular weight root exudates, continually supply soil microbial communities with carbon, nutrients and energy. The exudation flux, its molecular composition and C:N stoichiometry are important factors shaping composition of soil microbial community and its performance in soil organic matter (SOM) cycling (priming effect). We aimed to shift the flux and quality of root exudates by plant foliar N fertilization with ^{15}N–urea in concentrations of 0, 0.3 and 1% and study how these changes impact composition and activity of soil microbial communities formed under two different plant species, *Glyceria maxima* and *Carex acuta*. This design affected soil microbial processes only through the root–derived inputs. The plant were continually labeled using CO_2 with d^{13}C of -30 ‰ to separate the root– from soil–derived C in the soil CO_2 efflux. After 10 weeks, plant biomass and its C:N, exudation flux and quality, microbial community structure, exoenzymatic activities, gross N transformation rates and CO_2 efflux were measured. The foliar N fertilization significantly increased ^{15}N abundance in biomass of fertilized plants but decreased only the C/N ratio of shoots in both species. The flux and composition of root exudates were highly species–specific and significantly responded to fertilization. Soil bacterial and fungal communities did not reflect the changes in exudation quality. Activity of living roots stimulated decomposition of pre-existing soil organic matter, with roots of fertilized plants inducing stronger positive priming effect. In summary, species effect exceeded that of fertilization, which significantly impacted only exudation flux and composition, decreased gross N mineralization and mildly increased SOM decomposition. Other characteristics were predominantly controlled by plant species.

O35 The evolutionary legacy of microbial taxa impacts ecosystem functioning

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Microbial regulation of ecosystem functions (EF) depends on a wealth of taxa, whose individual contribution to the overall function depends on complex combinations of functional traits. Microbial traits that impact EF show phylogenetic conservatism (closely-related taxa have more similar traits), suggesting that the historical conditions under which lineages evolved might have long lasting effects determining ecosystem performance. Such evolutionary legacies can be tracked based on the phylogeny, which may predict species contribution to EF. Bacterial communities can deliver high EF rates at: i) high phylogenetic diversity, when functionally distant lineages coexist, ii) low phylogenetic diversity, when a productive lineage outcompetes distant clades. These scenarios are modulated by community composition: the effects of anciently-divergent lineages, whose deeply-conserved traits determine the occupancy of major niches, may differ from those of recently-divergent lineages showing adaptations to current conditions. We speculated that, in our model Mediterranean ecosystem, microbially-driven EF can be explained by the concurring competitive superiority of ancient lineages and the functional complementarity of recent lineages. We sequenced the bacterial 16S rRNA gene across 28 soil plots, and reconstructed dated phylogenies. We quantified ecosystem properties related to pools of materials (microbial biomass carbon and ATP) and process rates (decomposition, and organic C, N and P hydrolysis). Most EF showed the highest rates in plots accumulating recently-divergent lineages at low levels of anciently-divergent lineages. This pattern suggests that, in productive communities, competitive ancient clades prevail and are composed by recent specialized taxa showing high niche complementarity. Our results indicate that the phylogenetic scale matters when addressing the diversity-ecosystem functioning relationship.

O36 Plant-microorganism interactions under climate warming-induced range shifts: consequences for ecosystem functioning

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Current climate warming enables range shifts of many plant and animal species to higher latitudes and altitudes. Although initial concerns pointed at species that could not keep up with their moving abiotic climate envelop, an increasing number of examples shows that many species do migrate, which gives rise to another question: how will new biotic interactions be established in the novel range? In order to address this question for plants, we have compared range-expanders with congeneric-related species that are native in both the original and new range of the range expanders. In addition, we also included range-expanding plant species that do not have such close relatives in the new range. We analyzed the soil- and plant-related microbiome of 12 plant species, from each group 4 species. Our results show that there are indeed differences in belowground microbomes among the three species groups, however, when we carried out further tests, it appeared that plant origin is affecting microbiome composition less than is done by plant relatedness. Then, we grew the natives and range-expanding plant species in outdoor mesocosms in soil from the novel and native range, under normal and extreme weather conditions. We determined resistance and resilience of soil functions depending on plant-soil combinations and found interesting differences between range expanders and natives, which will be explained in more detail during the presentation. We conclude that that consequences of plant range expansion under climate warming will depend on relatedness with the native flora, and on exposure to environmental stress.

O37 Impacts of long term rice cultivation on soil microbial diversity: A synthesis

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Rice is the major staple food for Southeast Asia and feeds half of the world population. In this presentation, we use three studies to illustrate how long-term rice cultivation has been influencing soil microbial diversity and functions. First, we compared a currently cultivated soil with adjacent buried Neolithic paddy soil from an archeological site in China, and found the currently cultivated paddy soil contained 10-fold more microbial biomass. Results also revealed the currently cultivated soil had significantly higher phylogenetic diversity, but less functional diversity. Second, a 2000-year chronosequence of paddy soil was studied to investigate influences of continuous rice cultivation on soil bacterial diversity. We revealed an orderly shift of bacterial communities towards higher productivity along with paddy soil development at a long-time scale after wetland reclamations, associating with soil physicochemical alterations, especially changes of cation exchange capacity and pH. Lastly, we used a long-term field-experiment to explore the impact of chemical fertilization on soil microbial diversity and functions. Long-term chemical fertilization showed little effect on bacterial phylogenetic diversity and composition; however, it significantly changed the microbial functional gene structure. Most functional genes involved in C, N, P cycling were significantly stimulated. Significant correlations were found among functional genes, related soil enzymatic activities and rice yield, suggesting a fertilizer-induced shift in the microbial community may accelerate the nutrient turnover, in turn influencing rice growth. These results indicate agricultural cultivation has driven soil microbial community to “work” on few functions to effectively improve productivity with intensive inputs.

O38 Soil legacy effects on plant endophytes and plant-feeding caterpillars

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Plant communities change the soil microbiome, and this will have feedback effects on the following plant community. Here, we wanted to expand this concept and investigate whether legacies could affect plant-feeding herbivores via a transfer of functional microbiota from soils to roots, shoots and the herbivores. We created specific soil legacies by growing different communities consisting of forbs, grasses or grass-forb mixtures in the field. Soil was collected from these plots, and clonal dandelions were grown on it. We evaluated soil legacy effects on microbial community in the rhizosphere, endosphere of the roots and shoots as well as in the caterpillars that were placed either directly on the plant or on detached leaves (with no soil contact). We expected to find largest effect of soil legacy on the microbial community in the rhizosphere soils followed by root endophytes, and eventually indirect effects on microbial communities in leaves and in guts of caterpillars. We found that soil legacies had a significant effect on the rhizosphere microbiome but no effect on the endophytes of roots or leaves. Surprisingly, we found a significant effect of soil legacy on the community composition of both bacteria and fungi in the caterpillars that were kept in contact with plants and soil but not on the caterpillars that were fed with detached leaves. We show that the caterpillars acquire their microbiome, at least partly, from the soil. This opens a new area of research in soil-plant-insect interactions and shows that direct soil effects should not be ignored.

O39 Bacterial War on Fungi

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Competition for organic energy sources is a common type of interaction between bacteria and fungi in soils. Once microbes have access to an energy source an important aspect of successful competition is the ability to prevent other microbes from getting also access. In unsaturated soils, fungi have an advantage over bacteria in crossing air-filled pores and can, therefore, explore a bigger soil volume than bacteria for energy sources. Hence, substrates that have been accessed by nearby occurring bacteria can still be reached by fungi occurring at a wider distance. There is increasing evidence that volatile organic compounds (VOCs) produced by soil bacteria may play an important role in restricting growth of fungi. Hence, bacterial VOCs may increase the chance for bacteria to monopolize decomposition of “occupied” substrates. Here we examined whether VOC-mediated inhibition of fungi in soil may be a collective activity of bacteria present in soil bacterial communities. To this end we followed the growth dynamics of fungi and bacteria colonizing sterilized soils during exposure to VOCs produced by soil bacterial communities growing on different media. There was a clear negative effect of exposure to bacterial VOCs on the growth of fungi whereas that of bacteria was not affected. Furthermore, strong effects of bacterial VOCs on the composition of fungi were observed. Our results are in support of a collective VOC-mediated antagonism of soil bacteria against fungi. This VOC-mediated warfare of bacteria against fungi may also play an important role in the widespread occurring soil fungistasis.

O40 Volatile organic compounds link distant microbial community composition to plant growth and health

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Plant roots are in tight association with a myriad of microorganisms that provide essential services to the plant, including growth stimulation and pathogen inhibition. Microbiome species diversity and composition in the direct vicinity of the roots is a major determinant of its functioning. Here we show that distant soil microbiota without direct contact with roots provides similar services to the host via volatile organic compound (VOCs) production. We grew the plant and pathogen without contact, but with a gas exchange with constructed microbial communities of varying diversity and composition. We followed two representative functions, plant growth stimulation, and pathogen inhibition. Distant communities affected plant and pathogen growth in a genotypic diversity-dependent way. The increase in genotypic richness increased the production of antibacterial VOCs up to intermediate richness level and then a drastic decrease in VOCs mediated antibacterial activity was found. On the other hand, the increase in genotypic richness reduced the VOCs mediated plant growth promoting activity consistently. We link this variation to changes in the composition and abundance of VOCs. The VOC profiles showed that production of plant growth promoting VOCs was shifted to antibacterial VOCs with the increase in genotypic richness, which revealed the strong antagonistic interactions in the microbial community. This study demonstrates that the effective plant microbiome affecting growth and health may be much larger than previously assumed encompasses not only species in contact with the host but a large pool from the distant bulk soil.

O41 Soil microbial community analyses - From habitat filtering to interactions

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Studies analyzing soil DNA by PCR amplicon sequencing provided ample evidence that the diversity of soil microorganisms is high and site-specific, yet the same phylogenetic groups emerge across soils even from contrasting climatic regions and land use types. Typically, such studies seek to explain the microbial community structure and presence of specific taxonomic groups by correlations with physicochemical soil properties, e.g., pH or soil organic carbon (SOC). While the structure of the microbial community can be regarded as a result of habitat filtering, this approach is highly problematic because it disregards spatial scale and is biased by the selection of explanatory parameters. Our studies indicated that the importance of SOC as a selective factor is equal to pH when it is qualitatively and not only quantitatively analyzed. Particulate organic matter was associated with more bacterial OTUs than any other SOC fraction. Previously we demonstrated that the majority of dominant bacterial, but not archaeal, taxa were preferentially associated with specific soil particle size fractions (PSF), and that the impact of SOC on bacterial diversity declined with decreasing particle sizes. This highlights the importance of microscale interactions for shaping microbial community structure and dynamics. While soil particles provide the surfaces for microbial attachment, the living conditions of soil microorganisms are mainly defined at larger scales, i.e. soil aggregates. To approach the aggregate-level for microbial community analyses (*Aggregatomics*), we extract DNA from small amounts of soil. Our results demonstrate that bacterial community patterns from small soil samples display lower taxonomic richness and higher heterogeneity between samples. Increasing the spatial resolution of soil sampling will allow us to detect ecologically meaningful microbial interactions.

O42 How does spatial heterogeneity affect decomposition dynamics?

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In soils, organic matter (OM) is partly protected in micro-pores within aggregates, making it physically unavailable to microbes. The occurrence of high-OM patches creates a spatially heterogeneous distribution of OM and therefore microbial activity. Most soil carbon cycling models do not account for this micro-scale heterogeneity, which may lead to unrealistic predictions of carbon stocks in Earth system models (ESMs). Here, we hypothesize that the rate of microbial decomposition (DEC) 1) is affected by the pore-scale spatial heterogeneity of substrate and microbes and 2) depends upon the degree of heterogeneity. We assumed that DEC is not limited by environmental factors and microbial cells are lumped into a functionally (but not spatially) homogeneous pool. We start with a 2D domain characterized by a heterogeneous substrate and simulate with a two-pool model the dynamics of OM in each cell of the domain. Then a spatial averaging scheme is applied to evaluate the mean behavior of the system as a function of the degree of spatial heterogeneity. Further, we propose a first-order spatial moment approximation for DEC that accounts for the micro-scale heterogeneities. The results obtained from a spatially homogeneous model are compared with the spatially averaged results of the heterogeneous model, showing that the DEC increases or decreases with heterogeneity depending upon the sign of spatial covariance between OM and microbes. This study highlights the inadequacies of DEC models at different scales and proposes that upscaling using spatial moment methodology could offer insights on how to capture macro-scale dynamics in ESMs.

O43 Utilization of soil organic nitrogen by arbuscular mycorrhizal fungi – mechanisms and players

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Nitrogen (N) availability is arguably one of the most widespread limitations of plant growth and ecosystem productivity. Science already achieved deep understanding of the mechanisms and pathways of N transformations in soil-plant systems. However, we are still only scratching surface in understanding the exact mechanisms of organic N utilization by arbuscular mycorrhizal fungi, widespread root symbionts with very limited production of lytic exoenzymes. It seems that complex microbial interactions are involved in releasing and capture of N by these mycorrhizal fungi from biomolecules like proteins and chitin. Our recent research (using ^{15}N-labelled soil organic amendments and molecular community profiling) indicated very efficient utilization of organic N by the hyphae and concommitant decrease of at least some saprotrophic microorganisms in organic soil patches. Further, we established clear competitive interactions for free ammonia ions between the mycorrhizal hyphae and ammonia oxidizers, and suggest an important role of soil protists (soil microbial loop) in releasing and making the N available from the biomolecules for the mycorrhizal hyphae. We still do not know, however, whether this is because the N has been preferentially cleaved off the biomolecules and moved away from the point of mineralization by the mzcorrhizal hyphae, eventually stabilizing organic carbon in soil, or whether the entire biomolecules were actually mineralized on spot. Using RNA-stable isotope probing and deep community sequencing approaches allowed identification of prokaryotes that were likely receiving carbon from the mycorrhizal hyphae, but releasing N from the organic soil amendments, fulfilling the definition of hyper-symbionts.

O44 Interactions between grassland plants and arbuscular mycorrhizal fungi are selective

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Arbuscular mycorrhizal (AM) fungi form symbiosis with most land plants. Among temperate ecosystems, grasslands are particularly dependent on the mycorrhizal symbiosis, but community-level understanding about the dynamics of plant-AM fungal interactions is still missing. Here, we described AM fungal diversity in the roots of all locally co-occurring plant species from a dry calcareous grassland site in Western Estonia. AM fungi were identified by SSU rDNA sequencing, showing clear patterns in richness and community composition among plant species and sampling times. Furthermore, network analysis revealed partner selectivity in the case of both partners: there were less links per species in the observed plant-AM fungal networks than randomly expected. These results highlight that grassland plant diversity is highly interconnected with root symbiotic AM fungal diversity. I will discuss these results in the context of a large-scale grassland restoration effort in the same system and experimental testing of target whole-community AM fungal inoculation to direct grassland recovery after re-introduction of suitable management regimes.

O45 Distinct fungal guilds respond differently to the availability and diversification of plant and carbon resources

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Despite great advances in the molecular description of diversity from environmental samples, knowledge on how soil organisms are distributed at the landscape level is still patchy compared to that of above-ground macro-organisms. On top of this, groups of soil organisms e.g. eubacteria or fungi are often treated as one response variable even though they each encompass several distinct nutritional modes or guilds. This is problematic as richness and community composition of distinct guilds may not respond similarly, not even in the same direction, to underlying biotic or abiotic factors. Specifically, one would expect biotrophic and saprotrophic microorganisms to respond in contrasted ways. Biotrophic microorganisms should primarily reflect availability and phylogenetic diversity of hosts, while saprotrophs, on top of abiotic factors, would be expected to respond to the amount and diversification of dead carbon resources. Here we tested these hypotheses focusing on fungi by using an unprecedented broad sampling of 130 plots across Danish ecosystems. Fungi were amplified and deep sequenced from 81 pooled soil samples from each plot. Plots were stratified regionally along three main environmental gradients: soil fertility, water availability and openness of vegetation and thus included the broadest range of terrestrial nature types found in Denmark e.g. sand dunes, old growth forests, peat bogs, agricultural fields etc. The analysis is the first census of fungal guilds across such a diverse set of nature types.

O46 Using genomics to understand the role of soil fungi in forest ecosystems

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Forest soils host microbial communities that impact tree health and productivity, and play pivotal roles in carbon sequestration and biogeochemical cycles. Soil fungi, displaying different lifestyles as leaf litter-decomposers, humus saprobes, white- and brown-rot wood decayers and mycorrhizal symbionts, are important players among these communities. Our comparative genomic studies revealed adaptations that seem to be fundamental to the convergent evolution of ectomycorrhizal fungi from saprotrophic ancestors, including the loss of some metabolic functions and the acquisition of effectors that facilitate mutualistic interactions. The loss of some decay functions was probably a major step towards symbiosis, but due to the polyphyletic origin of ectomycorrhizal fungi, the retained sets of degrading enzymes are highly diverse and reflect variation in capabilities for decay and therefore, probably different roles in the ecosystem. Large-scale genome sequencing projects of soil fungi represent also the basis for functional studies. Genomes from cultured fungi are essential references to identify expressed functions (e.g. degrading enzymes) from metatranscriptome studies. We performed a high-throughput analysis of soil eukaryotic metatranscriptomes sampled in French forests during different seasons characterized by contrasted photosynthetic activities and variations of plant carbon allocation to the associated eukaryotic microbiote. Interestingly, the analysis revealed a primary impact of soil horizon, and secondly a significant season influence on fungal functions, independently of spatial taxonomic heterogeneity. Moreover, specific Carbohydrate-Active Enzyme families, Glycosyl Transferases and Glycoside Hydrolases were differentially regulated between these seasons. All these results confirm the determinant contribution of soil fungi to carbon cycling and to soil organic carbon pools.

O47 Spectroscopy and transcriptomics provide novel insights into the decomposition of soil organic matter by fungi

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Filamentous fungi are thought to have a key role in the decomposition of soil organic matter (SOM). During the last decade, novel insights into the activity of these organisms have become available using genomics and transcriptomics. To interpret these data, homologs to genes known to be involved in the decomposition of lignocellulose by wood-decaying fungi are usually identified and their expression levels are used as markers for SOM decomposition. However, such approaches might reveal only part of the functional diversity of soil residing filamentous fungi (free-living or symbiotic). First, SOM is a complex mixture of plant- and microbial derived material, vertically and spatially heterogeneous, with chemical composition and structure that are very different from plant cell wall material. Second, our knowledge on wood-decaying mechanisms is based on the study of a limited number of fungal species of biotechnological importance. Comparison of the genomes of these fungi with those of e.g. litter-decomposing and ectomycorrhizal fungi have revealed large variation in the gene contents of enzymes associated with lignocellulose degradation. The functional implications of this variation are largely unknown. To link genes to decomposition activities in various saprotrophic and ectomycorrhizal fungi we are analyzing in detail the processing of SOM using spectroscopic methods such as FTIR, Raman spectroscopy, pyrolysis GC/MS and X-ray absorption spectroscopy. In parallel, the genes expressed are examined using transcriptomics. Combining data from spectroscopy and transcriptomics have provided novel insights into the mechanisms of SOM decomposition in saprotrophic and ectomycorrhizal fungi.

O48 Mycorrhizal types differ in ecophysiology and ecosystem functioning

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Mycorrhizal fungi benefit plants by improved mineral nutrition and protection against stress, but little is known about the fundamental functional differences among mycorrhizal types in fungi and plants and their relative importance in biogeochemical processes. We test differences in genomes and critically review the ecophysiological differences in mycorrhizal fungal guilds and mycorrhizal types of plants on other plant traits, ecosystem properties and global nutrient cycles. Mycorrhizal fungi display fundamental differences in genomic capacity for mineral nutrition, particularly oxidative degradation of carbohydrates and releasing nitrogen and phosphorus from organic material. Mycorrhizal associations modulate the trade-off between allocation to roots or mycelium, ecophysiological traits such as root exudation, weathering, enzyme production, plant protection, community assembly as well as response to climate change. Mycorrhizal types exhibit differential effects on ecosystem nutrient cycling that may affect global nutrient flux and drive functional shifts in response to global change impacts. The heavy temperate sampling bias associated with differential nutrient limitation and soil processes across biomes insists caution in global modelling and interpretation. Combining controlled carefully replicated experiments with –omics techniques will offer great promise in understanding differences in ecophysiology and ecosystem services among mycorrhizal types.

O49 Macroecology analyses of millions of fruit body records: Environmental drivers of phenology and species assemblies across Europe

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Fungal species occurrence observations are increasingly available for scientific analyses through citizen science projects and digitization of museum records. When combined with open-source data, there is unparalleled potential for addressing new questions in fungal macroecology and global change biology. We have assembled a pan-European database of ~6 million fungal records of ~10,000 species and integrated this with open-source environmental data. We identify the major geographical and environmental gradients structuring fungal assemblages throughout Europe for two main nutritional modes, saprotrophic and ectomycorrhizal fungi. For both nutritional modes, mean annual temperature correlated most with the first gradient identified that structured assemblages. Soil organic carbon was the highest correlate of the second compositional gradient for ectomycorrhizal fungi, likely an indicator of vegetative- and pH-related covariance. In contrast, a pollution gradient was of secondary importance for saprotrophic fungi, reflected in a high correlation with nitrogen deposition. The highest rates of compositional change in fungal assemblages by time (1970–1990 versus 1991–2010) suggest targeting higher latitudes and altitudes for a better understanding of fungal dynamics related to climate change. We also assess the phenology of fungal fruiting at a European scale and relates the phenology to climate variability and the seasonality of fungal fruiting. Mean annual temperature is ubiquitously important, and more so for autumnal fruiting fungi. Spring fruiting fungi, especially ectomycorrhizal fungi, are additionally responsive to primary productivity. There is significant likelihood that further climatic change, especially in temperature, will impact fungal fruiting patterns at large spatial scales.

O50 Tree-to-maize nutrient transfer via mycorrhizal networks in low-input maize cropping systems?

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Common mycorrhizal networks (CMN) may play a key role in low-input agricultural systems because they can facilitate interplant nutrient exchange and enhance nutrient access for seedlings. Trees can maintain CMN across cropping seasons but whether these CMN are crop-enhancing is unknown. While a tree-to-grass nitrogen (N) transfer has been demonstrated, it remains unclear whether this can be extrapolated to crops. We assessed whether maize seedlings connect into tree-maintained CMN. *Mangifera indica* and *Faidherbia albida*, trees commonly found in farmers' fields in Africa, were grown in mesocosms for two years. Maize was sown in root-free in-growth cores between the trees. We used ^{15}N and ^{33}P tracing to assess i) tree-to-maize transfer of N and P via CMN and ii) N and P uptake from soil by tree-facilitated CMN. We applied three treatments: isotopic labeling of trees via stem injection (1), labeling via root-free soil compartments with trees present (2) and trees absent (3). We found no ^{15}N and ^{33}P in maize with tree stem injection. When tracers were applied to the soil compartments, the same amounts of ^{15}N and ^{33}P were obtained in maize grown with versus without trees. We conclude that young trees do not enhance nutrient uptake of maize. We are currently investigating the potential of well-established trees to facilitate N transfer to maize via CMN in farmers' fields. Results from this field experiment are expected in May and will provide insight into the potential of CMN in low-input agroforestry systems to improve crop establishment.

O51 Soil fungal communities in paddy soils after carbon amendment at blooming stage

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Soil fungal communities play major roles in soil organic matter cycling and have an important impact on the decomposition of straw in soil. However, knowledge about fungal ecology in paddy soils is smaller compared to other environments. The aim of this study is to determine the effect of rice straw (RS) incorporation on the composition and function of fungal communities associated with rice after carbon amendment. We performed a field assay using different carbon amendments compared to a control treatment, as follows: 1. disposition of RS as mulch with addition of microorganisms, 2. incorporation of RS with microorganisms, 3. disposition of RS as mulch without microorganisms and 4. burning of RS. We collected samples from rhizosphere at four different time points during the grown of rice (i.e., before amendment, after incubation period for RS degradation, at blooming and before harvesting). To reach this aim we evaluated culture dependent fungal communities (total and cellulolytic) and enzyme activities (cellulase, β-1.4 glucosidase, xylosidase, and galactosidase) in four sampling points and community structure of culture-independent fungi at blooming. These statistical analyses were performed with R. Data revealed that treatment of mulch of RS with microorganisms had the highest cellulolytic´s counts. Besides, majority of taxa belongs to typical soil´s fungi, strongly dominated by Ascomycota genus, however, another important fraction belongs unidentified fungi. Despite that, there was no significant variation in microbial community composition among treatments. Most of the fungal taxa were assigned to different functional guilds like saprotrophs.

O52 Nutrient demand as dominant driver of resource allocation into extracellular enzyme synthesis in soil

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Soil organic matter decomposition is catalyzed by extracellular enzymes, originating largely from soil microorganisms. Extracellular enzyme production is primarily regulated by microbial economics as synthesis is energetically expensive and requires N. Substrate availability and nutrient demand are two dominant factors regulating microbial enzyme production. Nutrient demand initiates enzyme synthesis only if available substrate for acquisition is detected. To determine microbial nutrient demand and constrains on enzyme production, activities of seven hydrolyzing extracellular enzymes as well as C, N, and P contents were analyzed in three climatic regions: semiarid, Mediterranean, and humid temperate. Further, total fungal and bacterial abundance as well as the nitrogenase marker gene *nifH* were determined by qPCR. Proportional C:N:P enzyme activity ratios indicated N limitation in the semiarid site, whereas microbes in the Mediterranean and humid temperate sites were additionally P- and C-limited. Coinciding, *nifH* copy numbers and fungal/bacteria ratios increased from semiarid to humid, indicating greater relevance of N-fixation and fungal biomass as N sources in the humid site. Availability of organic substrate increased from semiarid to humid, indicated by microbial biomass abundance and nutrient contents. Greater resource allocation into C- and nutrient acquisition in the humid site, however, indicated high demands as consequence of stimulated microbial growth. In conclusion, resource allocation into enzyme production depended strongly on nutrient demand, regulated by substrate availability, microbial growth, and alternative acquisition pathways.

O53 Compositional changes through repeated years of summer drought in fungi (non-ECM) associated with roots of beech and spruce

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Repeated summer dry years are predicted to challenge Central European beech-spruce forests with increasing frequency and severity. By using a retractable roof system on plots with adult European beech and Norway spruce trees (Kranzberg roof experiment, KROOF), we recently showed that three consecutive years of summer drought lead to quantitative losses in ectomycorrhizal community responses at the ecosystem level that could not be compensated at the individual root level. For the current study, we analysed the community composition (ITS2 rDNA) of non-ectomycorrhizal (non-ECM) fungi associated with fine roots of beech and spruce in this experiment, and compared fungal communities under drought and ambient conditions. Derived from findings for ectomycorrhizae, we hypothesised a reduced potential in the general root-fungal community to exploit nutrients bound in complex forms such as phenolics, which is severe enough to be reflected in the root-fungal community composition. In a following step, these findings are compared to fungal community composition at sites from a natural precipitation gradient (360 – 780 mm during the growing season) along Bavaria, Germany. As secondary mission, our study is reporting on the distribution of scarcely documented fungal groups such as the Archaeorhizomycetes.

O54 Fine root foraging strategies of Norway spruce seedlings with contrasting future phenotypes in response to nutrient-rich patches

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Spatial heterogeneity and low availability of nutrients in boreal forest soils highlight the importance of tree root architecture, but there is a need to better understand the within species heterogeneity of fine-roots and their effects on soil processes. The explorative growth of lateral roots seems pivotal in seeking for nutrient-rich patches in soil. Norway spruce (Picea abies) has high adaptability of coarse root architecture in response to the environment. Furthermore, we have found differences in the fine root architecture of spruce seedlings representing contrasting long-term growth phenotypes in a homogeneous growth substrate. Thus, we have investigated the nutrient foraging patterns by Norway spruce seedlings of contrasting future growth phenotypes. Our central goal was to determine the extent to which nutrient exploitation of a humus patch is related future growth phenotype or to root growth parameters. Ten replicate seedlings from ten spruce families (five fast- and five slow-growing) were grown for ten months in growth chambers in flat transparent Perspex microcosms filled with sand-vermiculite-peat with a humus patch placed in the middle. Photosynthesis rate, dark respiration and leaf water potential were measured from these seedlings, and root characteristics were documented with WinRhizo® Pro-image analysis tool. Our results do not support the hypothesis that future growth performance affects root growth or branching strategy in response to a nutrient spot. Nevertheless, the most vital seedlings showed higher potential of branching of functional roots.

O55 Cover crop mixtures increase microbial functional diversity during decomposition

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Due to common agricultural practices, biodiversity is lost, soil is degraded and nutrients are leached collectively leading to lower crop productivity. To increase sustainability in agricultural systems, farmers use cover crops to reduce nutrient losses, reduce pests, increase soil organic matter, increase soil biota, etc. The functional traits (C:N ratio, nitrogen fixing, rooting depth, microbial association) differ between cover crop species. It is hypothesized that combining plant species with different, complementary traits have a positive effect on soil functioning. Studies in natural ecosystems have shown that plant diversity improves soil microbial diversity leading to enhanced ecosystem functioning. In a pot experiment, residues of cover crop monocultures (three monocultures: radish, vetch and oat) and mixtures (three species mixture of radish, vetch and oat and a 15 species mixture) were mixed with soil. During cover crop decomposition, fungal biomass, microbial functional diversity, greenhouse gas emissions and soil nutrients were measured over time. C:N ratio of the cover crop (mixtures) is an important variable in explaining CO_2 and N_2O emissions. Mixtures of cover crops only showed reduced N_2O and CO_2 emissions compared to monocultures at the start of the experiment. Adding nitrogen to the cover crop treatment with the highest C:N ratio (oat) did increase N_2O emissions, but not CO_2 emissions. Nitrogen fertilization alone might be not sufficient to increase decomposition in oat. Fungal biomass increased for all treatments compared to a control without addition of cover crop residues but there were no additional effects of cover crop mixtures. Interestingly, soil microbial functional diversity, measured with Biolog ECO plates, was significantly higher in cover crop mixtures as compared to monocultures. Residue mixtures might increase niches for microbes in the soil by adding higher diversity of substrates or by changing soil physico-chemistry by different rooting patterns that can lead to increased functional diversity.

O56 Contribution of saprotrophic and ectomycorrhizal fungi to organic P mobilization in forest soils

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In the last decades, tree nutrition in European forest ecosystems deteriorated and phosphorus (P) concentrations in tree leaves decreased. To investigate the contribution of saprotrophic (SAP) and ectomycorrhizal (EMF) fungi to P mobilization and a possible antagonistic effect between both fungal guilds, we carried out a soil tube experiment at five beech (*Fagus sylvatica* L.) forests in Germany. The micromesh windows of the open ingrowth tubes (IGTs) allowed EMF to grow into the tubes, while the re-growth of EMF hyphae into the closed ITGs was inhibited. A reduced relative abundance of EMF in closed tubes after 18 months of exposure was mainly due to the loss of *Russula* and *Craterellus* species. In contrast, we observed a higher presence of SAP (mainly *Mortierella* and *Solicocozyma*) in closed compared to open IGTs. Thus, we found a competitive relationship between EMF and SAP fungi. The reduction of EMF in closed tubes was mirrored in diminished fungal phospholipid fatty acid (PLFA) content and phosphodiesterase activities (PDA). However, there were no significant differences in acid phosphomonoesterase activity (PMA), plant-available P (P_{resin}) and microbial P content (P_{mic}) between treatments. Since phosphomonoesterases cleave P from monoester forms, such as phospholipids or nucleotides, and phosphodiesterases release P from compounds like nucleic acids, we suggest that the experimental shift in fungal community composition modified the balance between the decomposition of different organic P substrates (mono- and di-esters). Shifts in fungal community composition between treatments at a steady PMA gave indication for functional redundancy of P cycling fungi in forest ecosystems.

O57 Changes of ectomycorrhizal communities along a nitrogen deposition gradient and with soil depth

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Climate change and atmospheric pollution have implications for forest ecosystem health and diversity. We monitor tree performance in Switzerland since 33 years and investigated ectomycorrhizal communities in 15 European beech plots along a nitrogen deposition gradient ranging between 16 and 33 kg N ha^{-1} a^{-1}. Drought stress, warmer winter temperatures, nitrogen deposition above 25 kg N ha^{-1} a^{-1}, soil acidification and ozone were found to negatively affect beech performance and nutrient levels. Phosphorus nutrition declined by 25%. Most important factors explaining variation in EMF composition were increased N deposition and base saturation. Root length, EMF diversity, root colonization, and production of extramatrical mycelium in soil and the abundance of the important species *Cenococcum geophilum* decreased strongly with increasing N deposition. Meanwhile, foliar K and P were positively associated with increasing EMF diversity and we found EMF composition to be associated with foliar N and P. These results support the hypothesis that the decrease in nutrient uptake in beech forests across Europe is related to changes in EMF communities and suggests that continued high N deposition may change soil carbon and nutrient cycles, thereby affecting forest ecosystem health. In Swiss beech forests, soils are often deep and base saturation varies strongly due to calcareous bedrock. In a new study we dig deeper to see whether ectomycorrhizal fungi can support trees with nutrients and water from deep soil layers. Preliminary results suggest that forests on deep soils can benefit under continued environmental pollution and future climate change.

O58 The mycorrhiza-root interphase of spruce is under genetic control of the host and adaptive to soil characteristics

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A key mechanism of the long-lived coniferous forest trees in enhancing their resource acquisition in nutrient poor forest soil is efficient soil exploration by the means of formation of roots and symbiosis with ectomycorrhizal fungi (EMF). Contributions of soil EMF diversity and variation in functional characteristics of fungal species for the performance of the host are however better acknowledged than the role of intraspecific variation or adaptation of the host tree roots to the soil environment. Therefore we focus on the relationship between EMF and genetically determined growth of Norway spruce (*Picea abies*). A long-term field experiment revealed that high EMF species diversity was associated with fast growth of spruce. In contrast to our hypothesis, the underlying mechanism behind variation in ECM fungal diversity was not the genetic difference in the susceptibility to EMF symbiosis formation in the host. Instead, we found systematic, genetically controlled variation in root characteristics between the variable growing spruce phenotypes. Still even-sized but in future fast-growing seedlings showed a higher number of root tips, more frequent branching of roots as well as allocation of root tips further away from the base of the seedling compared to slow-growing seedlings. We suggest that this provides an advantage in nutrient limited, heterogeneous forest soil by enhancing exploration and contact with the soil microbiota. Furthermore, root architecture showed intraspecific diversity as an adaptive response to changing soil quality and temperature. Over time, small differences in these specific allocation patterns of root growth may create positive self-reinforcing mechanisms that can be the underlying factor behind the higher EMF fungal diversity and long-term growth performance of certain spruce origins.

O59 Suppression of mycorrhizal fungi (AMF) mycelium by soil microbiota

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The activity of AMF may be suppressed in non-sterile soils resembling the phenomenon of 'disease suppressive soils'. Microbial groups and microbial metabolites responsible for suppression of other fungi have been identified, while organisms and metabolites suppressive towards AMF are unknown. This study aims to assess whether suppression of the AMF by unsterile soil is common and if it can be ascribed to specific taxonomic groups of soil microorganisms. Suppression of AMF was investigated in a *Medicago truncatula* model system with ^{33}P-labelled patches of soil where the patches could be accessed by hyphae but not roots. ^{33}P uptake into shoots was used as a proxy for AMF activity. Different cultivated and non-cultivated soils were compared. For selected soils, effects of liming and pasteurization were evaluated. In addition, experiments on suppression transferability were performed. Data of ^{33}P uptake and hyphal growth were compared to microbiome profiles. We found a large variation in AMF suppression across soils and suppression was mitigated by soil pasteurization. Besides, suppression was greater at low than at high pH. We were able to transfer suppression by adding small amounts of suppressive soils to non-suppressive soils. Multivariate analysis of amplicon sequencing data revealed a clear separation between AMF suppressive and conducive soils. Acidobacteria subgroup 1 was more abundant in suppressive than in conducive soils and may constitute a potential AMF suppressor. Ongoing work aims to identify and isolate AMF suppressive microorganisms and to identify the metabolites responsible for suppression.

O60 Arbuscular mycorrhizal fungi stimulate organic phosphate mobilization by changing bacterial community structure under field conditions

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The extraradical hyphae of arbuscular mycorrhizal fungi (AMF) harbor and interact with a microbial community performing multiple functions. However, how the AMF-microbiome interaction influences the phosphorus (P) acquisition efficiency of the mycorrhizal pathway is unclear. Here we investigated whether AMF and their hyphal microbiome play a role in promoting organic phosphorus (P) mineralizing in situ and the mechanisms involved under field conditions. We developed a AMF hyphae in-growth core system for the field by using PVC tubes sealed with membrane with different size of pore (30 µm or 0.45 µm) to allow or deny AMF hyphae access to a patch of organic P (i.e., phytate) in root-free soil. AMF and their hyphae associated microbiome played a role in enhancing soil organic P mineralization in situ in the field, which was shown to be a function of the change of bacteria community on the hyphae surface. The bacterial communities attached to the AMF hyphae surface were significantly different from the bulk soil. Importantly, AMF hyphae recruited bacteria that produced alkaline phosphatase and provided a function that was absent in the hyphae. These results demonstrate the importance of understanding trophic interactions to be able to gain insight into the functional controls of nutrient cycles in the rhizosphere.

O61 Bacteria in ericoid roots and mycospheres

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Ericoid plants typically cover most of the forest floor in boreal forest. Ericoids have fine root systems and together with their mycorrhizal consortia they effectively colonize the upper layers of forest soil. Despite the importance of ericoid plants to local and global cycling of elements and their prevalence in boreal habitats, there is remarkably little information about their microbial partners. In this study the effect of the roots and mycorrhizal fungi of ericoid plants, heather (*Calluna vulgaris*), bilberry (*Vaccinium myrtillus*) and lingonberry (*Vaccinium vitis-idaea*) ericoids on soil bacteria were compared with the effect of pine roots and mycospheres. Bacterial numbers and community structures were studied by qPCR and Next Generation Sequencing (NGS). Colonization by mycorrhizal mycelia increased the total number of bacterial 16S rDNA gene copies in the soil, but decreased the number of different bacterial OTUs. Interestingly, bacteria in blueberry mycospheres were similar to those in pine mycospheres, but not to bacteria in heather and lingonberry supported mycospheres. In contrast, bacterial populations of ericoid roots were more similar to each other than to those of pine roots. Sequences belonging to classes Alphaproteobacteria and Acidobacteria were the most frequent in all sample types. Soil samples contained more Actinobacteria, Deltaproteobacteria, Opitutae and Planctomycetia, whereas Armatimonadia, Betaproteobacteria, Gammaproteobacteria and Sphingobacteriia were more typical to roots. All mycospheres and roots contained unique sequences, which were only detected in this particular habitat. Thus it is likely that ericoid roots and associated mycorrhizal mycelia increase the overall diversity of bacteria in forest soil.

O62 May Matsutake mycorrhiza-associated Streptomycetes distinguish friend and foe in shiro, the evidences from in vitro studies

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We focused on an economic valuable ectomycorrhizal fungus – *Tricholoma matsutake*, which is a dominant fungus presenting in shiro soil (mycelium-soil aggregation). We hypothesize that the helper-neighbor organism may exist for shaping shiro ecosystem. Bacterial community of shiro soil, isolation of actinobacteria from matsutake mycorrhizas and evaluation of the bioactivities of the isolated strains were conducted in this study. The results show that actinobacterial phylum was the most frequent phylum in shiro soil, but no clear difference of DNA sequence reads between shiro and non-shiro was found. Several strains of Streptomyces were successfully isolated from matsutake mycorrhizas. Among them, B2 and FY4 strains exhibited substantial variation in inhibition of various pathogenic fungi. Extraction and culture medium significantly affected the antifungal activities. However, the extraction of B2 and FY4 both had no negative effect on the growth of ectomycorrhizal fungi on agar media, which are the general species in conifer forest. In contrast, B9 and B14 strains exhibited positive effects on *T. matsutake* growth on agar medium. The root elongation of *Pinus densiflora* seedling, a host tree of matsutake was slightly inhibited by B2, but not negatively affected by B9 and B14 strains. The potential of antioxidant activity of B2 and FY4 strains were indicated by ORAC and FRAP assays and total contents of phenolics. This study indicates that matsutake mycorrhiza-associated Streptomyces may take important roles in shiro, suppressing the growth of pathogenic fungi, but friendly living together with other ECM fungi in shiro ecosystem.

O63 Microbial hotspots and hot moments in soil

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Soils are the most heterogeneous parts of the biosphere, with an extremely high differentiation of properties and processes within nano- to macroscales. The spatial and temporal heterogeneity of labile C input creates microbial hotspots over short periods of time – the hot moments. Microbial hotspots are small soil volumes with much faster process rates and much more intensive interactions compared to the average soil conditions. Such hotspots are rhizosphere, detritusphere, biopores, aggregate surfaces. Hot moments are short-term events inducing accelerated process rates as compared to the average rates. Thus, hotspots and hot moments are defined by process rates. We reviewed and examined the localization and size of hotspots, their spatial distribution, lifetime and process intensities, with a special focus on process rates and microbial activities. The fraction of active microorganisms in hotspots is 2-20 times higher than in the bulk soil, and their specific activities (respiration, microbial growth, enzyme activities, RNA/DNA ratio) are also much higher. The duration of hot moments in the rhizosphere last a few hours up to a few days. Hot moments induce succession in microbial communities and intense intra- and interspecific competition affecting C use efficiency, microbial growth and turnover. The faster turnover and lower C use efficiency in hotspots counterbalances the high C inputs, leading to the absence of strong increases in C stocks. Consequently, the intensification of fluxes is much stronger than the increase of pools. By this review, we raised the importance of concepts and ecological theory of distribution and functioning of microorganisms in soil.

O64 Microbial Carbon Pump and its Significance for Carbon Sequestration in Soils

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Soil carbon transformation and stabilization have received significant interest in recent years due to a growing need for quantifying its role in mitigating climate change. While it is readily accepted that the magnitude of the belowground organic carbon reservoir in terrestrial ecosystem depends upon microbial involvement because soil carbon dynamics are ultimately the consequence of microbial growth and activity, it remains largely unknown how these microbe-mediated processes lead to soil carbon sequestration. In this talk, I will present the recently recognized notion on microbial necromass, a significant source for soil organic matter genesis. I will discuss two pathways, *ex vivo modification* and *in vivo turnover*, to jointly explain soil carbon dynamics driven by microbial catabolism and/or anabolism and provide a new conceptual framework, consisting of the raised concept of the soil "*microbial carbon pump*" (MCP), to describe how microbes act as an active player in soil carbon storage. The MCP couples microbial production of a set of organic compounds to their further stabilization, and this integration captures the cumulative long-term legacy of microbial assimilation on soil organic matter formation. Finally, I will propose the need for increased efforts to seek to inspire new studies that utilize the soil MCP as a conceptual guideline for advancing our fundamental knowledge that improves process-level understandings of the contributions of soil microbes in soil carbon dynamics under global environmental changes.

O65 The fate of carbon in hot spots: linking decomposition processes to microbial key players

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Linking carbon decomposition processes to different life strategies and substrate preferences of microbial key groups in soil microhabitats are particularly important for a better understanding and implementation of microbial driven processes in carbon turnover models. We set up a microcosm experiment to determine the turnover of microbial C recently assimilated from differently aged maize litter in the detritusphere. A short-term reciprocal transplantation of ^{13}C-labeled and unlabeled litter on soil cores pulse-labeled different components of the microbial food web during the decomposition process. Re-transplantation of unlabeled litter on top of soil cores that have been previously incubated with labeled litter allowed the quantification of the current depletion of the ^{13}C signal in different biotic and abiotic soil C pools while maintaining the specific habitat conditions of the detritusphere. Litter quality influenced the incorporation rate of C into bacteria and fungi as well as the subsequent C turnover in phospholipid fatty acid biomarkers. We calculated a faster C turnover in the fungal biomass than in the bacterial biomass for the early and intermediate decomposition stages, whereas bacterial turnover was faster in the later decomposition stage, which highlights the role of fungi in the rapid turnover process of plant residues. With quantitative DNA-SIP we identified copiotrophs (Proteobacteria, Firmicutes, Bacteroidetes, Actinobacteria) as active key players in the ^{13}C-utilizing bacterial community, whereas oligotrophic phyla (Acidobacteria, Nitrospirae) exhibited almost no ^{13}C-enrichment. While *Bacillus* was predominantly active in the early stage of decomposition, more actinobacterial genera were involved in the degradation in the later decomposition stage.

O66 Increased activity of surviving bacteria facilitates functional resistance to recurrent disturbances: a modelling study

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Bacterial degradation of organic compounds is an important ecosystem function with relevance for e.g., the cycling of elements or the degradation of organic contaminants. It remains an open question, however, to which extent ecosystems are able to maintain such biodegradation function under recurrent disturbances (functional resistance) and how this is related to the bacterial biomass abundance. In this study, we use a numerical simulation approach to systematically analyze the dynamic response of a microbial population to recurrent disturbances of different spatial distribution. The spatially explicit model considers microbial degradation, growth, dispersal, and spatial networks that facilitate bacterial dispersal mimicking effects of mycelial networks in nature. We find: (i) There is a certain capacity for high resistance of biodegradation performance to recurrent disturbances. (ii) If this resistance capacity is exceeded, spatial zones of different biodegradation performance develop, ranging from no or reduced to even increased performance. (iii) Bacterial biomass and biodegradation dynamics respond inversely to the spatial fragmentation of disturbances: overall biodegradation performance improves with increasing fragmentation, but bacterial biomass declines. (iv) Bacterial dispersal networks can enhance functional resistance against recurrent disturbances, mainly by reactivating zones in the core of disturbed areas, even though this leads to an overall reduction of bacterial biomass.

O67 Global distribution of mycorrhizal host plants explained by climate and soil properties

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It is widely recognized that mycorrhizal fungi have a massive impact on ecosystem functioning, however, the direction and magnitude of these impacts depend on the mycorrhizal type involved. Different types of mycorrhizas are recognized to predominate under different environmental and soil conditions. However, the role of climate and soil characteristics in shaping mycorrhizal global distribution is still unknown. Here, we presented for the first time, a comprehensive global analysis of the predictors of mycorrhizal plants distribution. We aim to identify the main climatic and edaphic factors that can explain the distribution patterns of the abundance of plants featuring arbuscular mycorrhiza (AM), ectomycorrhiza (EcM) and ericoid mycorrhiza (ER). A generalized additive model (GAM) was fitted to a large dataset containing relative coverage of plants featuring AM, EcM and ER associations and a set of 44 climatic and edaphic parameters. The best GAM models were able to explain, respectively, 58.6%, 41.9% and 54.1% of AM, EcM and ER distribution variance. Temperature and precipitation related- factors were the main predictors of the three different mycorrhizal types. pH, C/N and soil textural variables remained in AM and EcM models, which reflects the potential of soil conditions to affect or be affected by AM and EcM plants distribution. These results highlight climate as the main force shaping the distribution of AM, EcM and ER host plants at the global scale and suggest that climate change can significantly alter the global distribution of mycorrhizal host plants, with the subsequent impact on ecosystem functioning.

O68 Linking biogeographical patterns of microbial distributions to the modelling of soil functions and associated ecosystem services

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A large number of recent studies on the ecosystem services provided by soil has highlighted the role of soil biodiversity in maintaining soil functions underpinning existence of human society. Novel methods of molecular analysis such as high-throughput sequencing, digital droplet PCR, metabolomics and proteomics have enabled us to both describe soil community composition at great taxonomic resolution and get insights into the functioning of these communities. Accordingly it has advanced our knowledge on global disputation patterns of microorganisms. Modelling of soil-associated microbial ecosystem services across large geographical scales requires proper understanding of such geographical distribution patterns of soil microbes. I will highlight recent advances in our understanding of global distribution patterns of microorganisms, and their environmental drivers, with a particular focus on mycorrhizal fungi. Consequently I will discuss how models of soil-associated ecosystem services could and should make use of these recent advances, linking soil community composition to function across environmental gradients and allowing us to better understand contribution of microorganisms to ecosystem services and human well-being.

O69 Depolymerization of organic matter as a bottleneck for carbon cycling

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Enzyme activities play an undisputable role in soil carbon cycling. They catalyse the breakdown of organic substrates into small compounds before they can further be assimilated and respired or transformed into microbial metabolites. To account for this major process, a new generation of models has emerged during the past decade, reporting enzyme properties and decomposer physiology. However, these models are built on the premise that organic matter can be represented as one single entity or is divided only into a few pools, while organic matter exists as a continuum of many different forms. The key question thus still remains: how does enzyme functional diversity regulate the progressive depolymerization of organic matter and its turnover? We challenge this question with a new model based on substrate accessibility to the decomposers and to their enzymes. This model integrates the fact that a given substrate exists in many different forms, depending on its stage of polymerization or its interactions with other organic or mineral phases of the soil matrix. The model reports how the level of polymerization of the substrate evolves under enzyme action until a threshold value where the substrate becomes accessible for microbe uptake. Our simulations reveal how the lignolytic activity regulates the action of cellulolytic enzymes during the decomposition of woody litter. We also show how the breakdown of highly diverse plant substrate and microbial metabolites needs the successive action of different decomposer communities. We finally demonstrate that enzymes action strongly controls the amount and chemistry of soil carbon.

O70 The plant-microbial impacts on soil processes with direct climate feedbacks: conclusions from studies on CO_2, CH_4, N_2O, VOCs and amines

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We have conducted a series of experiments in boreal Scots pine forest ecosystem where the aim was to discover in which ways plants and their root-associated microbes affect the atmosphere through greenhouse gases (GHGs) or various volatile organic compounds (VOCs). In the laboratory, we identified VOCs produced and quantified the amine content of different soil-inhabiting fungi. We have mathematically estimated whether boreal soil is a source or sink of two amines that are known to affect aerosol and cloud formation processes. In the greenhouse experiments we studied how the roots and shoots of different boreal forest plant species, *Calluna vulgaris*, *Vaccinium myrtillus*, *V. vitis-idaea* and *Pinus sylvestris,* affect the CH_4 production or consumption, and how these plant species differ in their CO_2 dynamics. In the field, where the below-ground C allocation of plants was restricted using trenching and ground vegetation removal, we studied how C flow to soil affects soil CO_2 fluxes but also VOC, CH_4 and N_2O production or consumption. Finally, we studied if there are biogenic components in the atmospheric aerosols by quantifying their DNA content and performed qPCR to estimate fungal and bacterial presence. We have found several direct climate-feedback that are of plant-microbial origin. Soil fungi actively produce or their biomass contain climatically important volatile organic compounds. Below-ground C flux did not play a significant role in CH_4, N_2O or VOC fluxes whereas plant-derived C compounds affect soil processes through priming. Ground vegetation has also an important contribution to soil C cycling and CO_2 fluxes.

O71 What controls the response of N_2O and CH_4 fluxes to warming: Changes in microbiological or physical soil properties?

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Warming typically increases CO_2 emissions, while fluxes of N_2O and CH_4 were shown to be much less temperature sensitive. However, other factors like the amounts of N, C, O_2 and water in soil determine the activity of N_2O and CH_4 producing and consuming microorganisms and these factors are as well affected by warming and changed precipitation. Due to the application of N-fertilizers, soils of agroecosystems represent major sources for N_2O and at the same time reduced the sink capacity for CH_4. Within the Hohenheim Climate Change experiment (HoCC), we investigated the influence of elevated soil temperature (+ 2.5°C) and changed amount and frequency of precipitation on N_2O and CH_4 fluxes on an arable field over the duration of 9 years. With respect to the cumulative fluxes over this period, elevated soil temperature significantly increased N_2O emissions by 27%, while CH_4 uptake was also increased by 13%, indicating contrary effects with respect to the greenhouse gas balance of the ecosystem. The effects of changed precipitation were less clear and showed strong variations over time. The relation of N_2O and CH_4 fluxes with data on available C and N, soil moisture and temperature etc. will give information on the dependencies between fluxes and changed soil conditions due to climate change. We will discuss, to which degree the observed effects of climate change on N_2O and CH_4 fluxes can be explained by soil biological changes (e.g. abundance of N_2O producing microorganisms) or by changed physical soil properties (e.g. gas diffusion).

O72 Glucose induced priming effect of soil organic matter decomposition in boreal forest soils with different C:N ratios

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The controlling factors and role of different soil microorganisms in rhizosphere priming effects (PE) are not yet well understood. We hypothesized that the positive PE (enhanced SOM decomposition) results from microbes using the additional C/energy from added labile substrates to decompose recalcitrant materials to release N (“microbial N mining hypothesis”). To test this hypothesis we assessed PE along a boreal forest gradient ranging from Estonia to Northern Finland, with soil C:N ratios increasing towards north. The soils received daily additions of ^{13}C-labelled glucose during one week. Respiration of glucose and respiration of SOM were distinguished by continuously measuring $^{13}CO_2$ using a Picarro analyzer. Glucose additions induced PE (12-52% increase in SOM respiration) in all soils, but there was no linear relationship between PE and soil C:N ratio. Instead, cumulative PE (µg C g-1 SOM) and the relative magnitude of the PE (%) were positively correlated with the average C:N imbalance experienced by the microbes (calculated as soil C:N ratio/microbial biomass C:N ratio). Total oxidative enzyme activities, and the ratio between the activities of C and N acquiring enzymes were lower in soils with higher C:N ratios, but these findings could not be quantitatively linked to the observed PE. Glucose additions did not significantly affect enzymes activities. In general, the abundance of microbes growing on substrates of different decomposability was not correlated with soil C:N ratios and we could not find evidence to support the hypothesis that an unbalanced C to N supply increases the abundance of microbes decomposing complex SOM.

O73 Bacterial and fungal turnover of litter-derived DOC in top- and subsoil of a beech forest

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The fate of litter-derived dissolved organic carbon (DOC) from the soil surface to deep soil environments and its contribution to soil organic matter (SOM) pools and turnover with increasing soil depths are largely unknown. To trace the litter-derived DOC flow and to gain insights into the spatial and temporal patterns of microbial DOC processing, we conducted a field experiment with ^{13}C labelled leaf litter in a beech forest in Lower-Saxony, Germany. Starting in January 2015, labelled litter was applied on the soil surfaces of three observatories followed by continuous measurements of ^{13}C-DOC fluxes and habitat conditions (soil temperature and moisture) in different soil depths. Replacing the labelled litter by unlabelled litter after a period of almost two years allowed disentangling DOC turnover and storage in different organic and microbial C pools. Soil samples from 15 different depths from the soil surface to a depth of 180 cm were taken at three sampling campaigns until spring 2018. We followed the development of C flow into specific groups of soil microorganisms (^{13}C phospholipid fatty acids) to account for acclimation of soil microbial communities to different soil resources as well as abiotic and climatic conditions at different soil depths. Our results demonstrate to which extent bacteria and fungi in top- and subsoil environments made use of litter-derived DOC and provide the microbial components (pool and process rates) for C cycling modelling within a soil profile to accurately predict feedbacks between soil habitats and organic matter decomposition.

O74 Does the distribution of the functions of microbial community in soil particles follow the pattern of organic C turnover?

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Soil micro-habitat is important for soil organic carbon (SOC) stabilization, because of the physical isolation by soil aggregates and chemical sorption onto soil minerals. These mechanisms are responsible for SOC turnover times that vary significantly across soil particles. Although microbes mediate SOC turnover, it remains unclear how microbial communities vary among soil particles. In this study, we aim to quantify the distribution of the size and functions of microbial community in soil particles of different size. We hypothesize that (1) with decreasing soil particle size, as SOC becomes more stable, Cmic per soil particle generally decreases, C- and N-related enzyme activity decreases, and P- related enzyme activities increase, (2) the relative contributions of each soil particle to Cmic and enzyme activity of bulk soil would not follow the above patterns. We found 42 articles about Cmic and 65 articles about enzyme activity in different soil particles, and synthesized results from these studies. The preliminary results show that Cmic per soil particle reduced with decreasing soil particle size as predicted, but this pattern depends on land use and vegetation types. We also observed that P related enzyme activities increased with deceasing soil particle size, but C and N related enzyme activity did not follow the similar pattern. Our further analyses will quantify the relative contribution of soil particles to Cmic and enzyme activity of bulk soil across climate, land use, and soil types, and identify the controls of the relative contributions of soil particles.

O75 The impact of restriction of photosynthetic carbon flow on fungal and bacterial communities in boreal forest soils

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Saprotrophic and ectomycorrhizal fungi cohabit organic layers of boreal forest soils. However, some spatial separation between saprotrophic and ectomycorrhizal fungi is observed, probably due to different competitive abilities for the substrates. Exclusion of plant C-flow is proposed to favor saprotrophs over ectomycorrhizal fungi. Soil bacterial community structure in turn is hypothesized to fluctuate according to the shifts in fungal community. Here, we studied in a three-year field experiment in pine forest, the effect of restriction of the photosynthetic-C flow to the soil fungal and bacterial communities' composition and potential functionality. The photosynthetic-C flows were discriminated by filling mesh bags with three different pore sizes (1000µm, 50µm and 1µm) with homogenized and sieved (4 mm) but unsterilized humus and burying them between organic and mineral layers. The 1000µm mesh allowed penetration of both fungal hyphae and fine roots, 50µm allowed fungal hyphae to penetrate but restricted plant roots, and 1µm prevented the entrance of both fungal hyphae and plant roots. One set of bags (n=18) was harvested after 1st, 2nd and 3rd growing seasons. The restriction of direct C-flow caused changes in both bacterial and fungal community structures. However, our results indicate that the boreal forest soils´ microbial community is resilient and can adapt to rather short term environmental changes. We did not detect the restriction of photosynthetic-C flow to favor saprotrophs over mycorrhizal fungi in humus, indicating that the spatial separation of these two fungal guilds might not be due to antagonism but due to different substrate preferences.

O76 Sticky Dead Microbes

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Soil organic matter (SOM) stabilisation is critical to food security, global carbon cycles and policy (4‰), yet it is unclear mechanistically, with stabilisation a relative concept: no SOM molecule is absolutely stable but is more or less susceptible to microbial attack, with abiotic and biotic interactions protecting SOM. Recently, we have learned that microbial residues form 50-80% of mineral soil SOM, despite also being a potential microbial substrate. Therefore, do microbial residues benefit from enhanced abiotic protection and retention? We tested two hypotheses: 1) Abiotic retention of microbial residues in soil is larger than that of a simple C source, or than biotic retention: we incubated (1-3d) live and sterile grassland soils with ^{13}C-microbial residues and glucose, then analysed retention in the soil matrix vs. microbial biomass/CO_2, and 2) Existing microbial residues in soil promote the abiotic retention of new microbial residues: we augmented the soil with different microbial functional group necromass' and compared sterile- and live-soil retention of ^{13}C-microbial residues. The short-term retention of microbial residues in mineral soil was 3x larger than glucose and was much larger abiotically (25-75%) than microbially (1-2%). This abiotic retention of ^{13}C-necromass was enhanced with higher background fungal but not bacterial necromass. The rapid, abiotic retention of residues does not necessarily equate to persistent soil C. However, these experiments illustrate that abiotic mechanisms vastly increase the potential for persistent soil C, more than biotic mechanisms. We make a number of suggestions to further explore the abiotic retention of microbial residues.

O77 Soil C/N and legacy effects of fertilization controls denitrifying and DNRA bacteria affecting N retention, loss and N_2O emissions

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Arable soil is a major source of the greenhouse gas N_2O; ultimately controlled by microbial communities in N cycling. Under anoxic conditions, dissimilatory nitrate reduction to ammonium (DNRA) competes with denitrification for nitrate and result in N conservation, whereas denitrification leads to gaseous losses (N_2 or N_2O). Moreover, the reduction of N_2O in denitrifiers and non-denitrifying N_2O reducers is a biological sink for N_2O. Using a series of microcosm and long-term field experiments, we addressed if the proportion of these functional communities determines the net N_2O emission, and specifically we tested the hypotheses: i) nitrate and carbon replete conditions and long-term N fertilization promotes truncated denitrifiers terminating with N_2O and disfavors non-denitrifying N_2O reducers, and ii) management supporting accumulation of soil organic matter favors the abundance of DNRA bacteria and microorganisms with a higher capacity to reduce N_2O. We sequenced the 16S rRNA and N_2O reductase genes, quantified the abundance of N-cycling genes and determined denitrification, DNRA and N_2O production rates. Overall, we conclude that soil C/N ratios has consequences for the genetic potential of denitrifiers and DNRA bacteria, which is manifested in N_2O emissions. Nevertheless, site-specific conditions and legacy of fertilization also influences the effects of the electron donor/acceptor ratio. Although N_2O reduces are important, we conclude that the balance between DNRA and denitrification can be much more determinant for net N_2O emissions. Overall, conservation of soil N and mitigation of N_2O can be mediated by the soil microbiome by maintaining soil organic matter.

O78 The effect of plants on methane flux of upland soils and methanogenic and methanotrophic microorganisms in the rhizosphere

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Soils play an important role in cycling of methane (CH_4), a greenhouse gas contributing roughly 20% to the observed climate warming. Studies about the effects of plants to the global methane flux have focused quite intensively on wetland ecosystem while knowledge about the influence of plants on methane cycling of aerobic soils and on methanogenic and methanotrophic microorganisms is barely examined. Thus, the general objective of this study was to investigate the influence of plants on net CH_4 fluxes from forest and grassland soils. Within *lab-scale* approaches, we investigated whether and how i) bedrock type, ii) temperature, iii) plant species, and iv) light intensities influenced net methane balances of forest and grassland soils. Culture-independent and culture-based analyses were further used to determine if changes in CH_4 fluxes correspond with the activity and abundance of soil microorganisms engaged in methane cycle. To characterize the microbial community structure of bulk and rhizosphere soil, NGS (next-generation sequencing) was performed and ddPCR (droplet digital PCR) was conducted to quantify the abundances of methanogenic Archaea and methanotrophic Bacteria. Results showed that the studied forest and grassland soils had a high potential to consume methane under ambient conditions. Distinct differences depending on bedrock, plant species, and temperature were established. The studied site-specific grassland plants significantly increased methane balances whereas the studied forest plants significantly boosted methane consumption. Increased light intensity decreased the oxidation capacity of the forest soils. The effect of increased light intensity significantly influenced the abundance of methanotrophic and methanogenic microorganisms in the rhizosphere.

O79 Bacterial synthesis of storage compounds – a neglected dimension of the carbon cycle

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Many microorganisms are able to produce storage compounds under conditions of carbon (C) surplus. Some soil-derived strains can accumulate polyhydroxybutyrate (PHB) – a key bacterial storage polymer – to as much as 50% of their dry biomass. C and energy storage likely plays a central role in bacterial physiology and survival, community stoichiometry, and carbon use efficiency, yet its importance has been neglected in experimental and theoretical studies in soil. We applied a novel approach comprising polymer extraction, ethanolysis and GC-MS analysis to experimentally confirm the presence of native PHB in soil. We have also demonstrated for the first time that indigenous soil microorganisms synthesize PHB when supplied with additional carbon. Isotopic labelling of added glucose unambiguously revealed the source of C for PHB biosynthesis. We provide a comparison between two strongly contrasting soils, one agricultural and one under deciduous forest, to test the generality of our results and explore the diversity of microbial responses to enhanced C supply. Our findings bring to light an exciting new dimension of soil bacterial capabilities, with broad implications for how microbial life histories in soil are conceptualized.

O80 Coupled metagenomic-chemical analyses of degrading fungal necromass and its contribution to soil organic carbon

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Fungi comprise a significant portion of total soil biomass, the turnover of which must represent a dominant flux within the soil carbon cycle. Fungal organic carbon (OC) can turn over on time scales of days to months, but this process is poorly understood. We examined the temporal changes in tissue mass, chemistry (FTIR, GC-MS) and microbial community composition (high throughput sequencing) during a 2-month decomposition experiment. We found a dynamic two-pool system. Most of the necromass (74- 80%) was degraded after one week in the soil (labile pool; turnover time ~6 days) while the residuum (recalcitrant pool) remained relatively constant in mass over the temporal sequence (turnover time >50 days). FTIR spectroscopy and thermochemolysis-GCMS showed complex patterns of chemical change over time. Certain lipids ($n\mathrm{C}_{16}$, $n\mathrm{C}_{18:1}$) degraded in a similar exponential curve to the bulk fungal tissue, while others ($n\mathrm{C}_{24}$, $n\mathrm{C}_{18}$) were unchanged or increased in concentration over time. Chitin from fungal cell walls was lost in the first week of degradation based on both FTIR (glucosamine peak at ~971cm^{-1}) and GCMS analyses for glucosamine monomers. High throughput sequencing showed the presence of 305 fungal taxa on the necromass. The genus *Mortierella* (Zygomycota) was abundant throughout the degradation sequence, but especially prominent during the first week of degradation. Other taxa were abundant early (Pleisporaceae), late (Corticiaceae, Tremellaceae), or in relatively constant abundance across the degradation sequence (Peniophoraceae). An increasing abundance of *Mortierella* was correlated with the loss of chitin glucosamine monomers, and increased levels of ergosterol, peptidoglycans and *n*-acetyl-glucosaminidase. Overall, necromass degradation is a highly dynamic process driven by a diverse and temporally structured fungal community, and fungal macromolecules may contribute to both fast (chitin) and slow turnover pools (lipids, ergosterol, peptidoglycans).

O81 Nutrient content affects the turnover of fungal biomass in forest topsoil and the composition of associated microbial communities

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Due to the standing biomass and turnover of fungal biomass in forest topsoils, decomposition of fungal biomass represents an important process. Within plant litter, dead fungal biomass represents a unique typically nitrogen(N)-rich substrate and is assumed to be rapidly decomposed. However, our current knowledge of mycelial decomposition has been largely derived from short-term studies, often limited to a single mycelia type, and the guilds of microbial mycelium decomposers have not yet been described. Furthermore, nutrient content may vary largely in fungal mycelia, and the consequences of this variation are unknown. Here, we followed the decomposition of dead biomass of 12 ectomycorrhizal and saprotrophic fungi of temperate forest using mycobags incubated in litter for 3 and 9 weeks. Loss of substrate dry mass, microbial biomass content, community composition and the activity of extracellular enzymes reflecting microbial activity were followed. Decomposition rates of mycelia were typically high (0.13-0.30 week^{-1}), yet variable. Rapid initial phase was followed by a slower turnover of remaining biomass. The initial N content (1.5% to 10%) appeared to be the most important factor that affected colonization of dead mycelia and their decomposition. The relatively high content of N makes fungal mycelia an attractive resource in the N-poor habitat of plant litter. Decomposition of mycelia was performed by a guild of specialist decomposers showing rather low abundance in surrounding litter and changed during decomposition. Bacteria were much more abundant on dead fungal biomass than in the surrounding litter and appeared to play an important role in decomposition. Fungi associated with dead mycelia were mainly represented by yeasts and moulds. Although the importance of fungal mycelia for nutrient cycling in forests is not yet clear, the fact that they are turned over rapidly suggests that they may represent an important and dynamic pool of carbon and nitrogen.

O82 Deciphering the structure of decomposer food web and functional relevance of microbial communities in the C flow in forest soil

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Forest soils represent important carbon (C) pool in the terrestrial biosphere with the potential to influence the feedback between climate and the global C cycle. Soil microorganisms are the main drivers of the C flow, playing critical roles in the C balance through the decomposition of plant and microbial biomass and the turnover of organic matter. Thus, a better understanding of C fluxes in these ecosystems is essential for incorporating the microbial dynamics into C cycle models. Here we have tracked the flow of C originating from various biomass types (plant, fungal, bacterial) in the microbial decomposer food web in a temperate forest soil. We followed the path of C by using stable isotope probing (SIP) coupled with amplicon and shotgun metagenomics in soil microcosms upon addition of ^{13}C-labelled biomass. We demonstrate that both fungi and bacteria are involved in the assimilation and mineralization of C from the major complex sources existing in soil. Decomposer fungi are, however, better suited to utilize plant biomass compounds, while the ability to utilize fungal and bacterial biomass is more frequent among bacteria. In addition, both fungi and bacteria encode a diverse and distinct pool of carbohydrate-active genes specialized in the degradation of a specific type of dead biomass. Our results indicate that decomposer food webs are networks with a high level of recycling of the microbial biomass pool, rather than hierarchical structures with unidirectional flow of C. These findings reveal new insights into the complex structure of the soil food web and into the microbial taxa and functional genes involved in the decomposition process.

O83 Complex fungal communities in 3-dimensional space: emergent properties in antagonistic mechanisms

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Wood decomposition is brought about by communities of wood decay fungi interacting in 3-dimensional space. Intense competition for space and resources occurs, and fungi fight with one another to obtain these, using antagonistic chemical weaponry. Fungi ‘attack’ and ‘defend’ their territory using a variety of mechanisms including deploying a chemical arsenal of enzymes, volatile organic compounds (VOCs) and diffusible organic compounds (DOCs). During interactions, the complement of intercellular metabolites (metabolome) which function in the biosynthesis and/or detoxification pathways of the fungal chemical arsenal, changes. Most studies have used simplistic pairwise interactions in a 2-dimensional plane, and while these have formed a solid basis for our understanding of the way in which fungi interact with each other, they do not mimic well the complexities of the real-world situation. Here, we review interspecific interactions amongst wood decay fungi. We then compare the metabolome of a three-species community, in environmentally realistic 3-dimensional systems of different species-distribution patterns, with simple 2-dimensional wood systems. Emergent properties arose with increased spatial heterogeneity: greater coexistence occurred in 3-D systems where territory was less fragmented, and production of metabolites involved in the biosynthesis pathways of antagonistic chemicals changed.

O84 Virus communities of forest fungi inhabiting decomposing wood and tree roots

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Fungal viruses (mycoviruses) occur commonly in all major fungal taxa and some of them are capable of altering the phenotype of their hosts. Hence, this poorly known group of microbes may play an important role in regulating the ecology of their host fungi and associated plants. We have addressed the diversity and community structure of mycoviruses infecting fungi of the boreal forest ecosystem, focusing on ecologically and economically important species, such as root rot pathogens (*Heterobasidion* spp.) and ectomycorrhizal fungi (*Lactarius* spp.). The characterization of dsRNA elements has led to the discovery of several novel virus species, and the use of high throughput sequencing has revealed the presence of cryptic viruses that are difficult to detect by traditional methods. Virus screening at single forest sites showed the diverse and dynamic nature of virus communities infecting *Heterobasidion* wood decay fungi and elucidated possible mechanisms of virus dispersal via contacting mycelia and aerial spores. We also obtained evidence of interspecies virus transmission between pathogenic, saprotrophic and mycorrhizal fungi inhabiting the same forest stand, which may possibly have an important effect on fungal interactions due to differences in virus tolerance.

O85 Major genetic elements that spur horizontal gene transfers across bacteria in the mycosphere

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In the microhabitat that surrounds fungal hyphae in soil, coined the mycosphere, carbonaceous compounds released by fungal cells stimulate the growth of soil bacteria. Thus, interactions between active cells in biofilms, in which locally-selective genes may be swapped, were hypothesized to be fostered. In a series of studies on the mycospheres of ectomycorrhizal fungi sampled in a Noordlaren forest, we found *Paraburkholderia* as well as *Variovorax* species to prevail. In terms of the proneness of these, as well as other mycosphere bacteria, to horizontal gene transfers, we so far identified two major (broad host range) plasmid classes, i.e. IncP-1 and PromA, to dominate in the mycosphere. We obtained the full sequences of two IncP-1 plasmids, allowing us to predict, and subsequently experimentally show, their ecological role with respect to iron acquisition and bacitracin resistance. Moreover, recent genome-based data on the presence of bacteriophages in *Paraburkholderia* types points to clear roles of these as agents that modulate the structure of the host genome, and by inference, its evolution, in the mycosphere. Experimental evidence for all of these contentions will be presented.

O86 Multiple phages therapy agents keep pathogens in check by generating disproportional resistance costs

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The emerging multiple antibiotics-resistant bacteria necessitate the development of novel approaches to combat bacterial infection in both clinical and agricultural contexts. Bacterial viruses (phage), especially the lytic phages that are obligate killers of host bacteria with less disturbance to natural community represent one potential avenue of the investigation. While it is established that multiphage therapy is typically more effective than the application of a single phage type, the potential mechanisms behind improved suppression have not yet been addressed. We used the experimental evolution approach to study how a panel of lytic bacteriophages assemblages suppress a focal host- *Ralstonia solanacearum* (the causal driver of global bacterial wilt epidemics) both in vitro (in simple micro-well plate) and in vivo (in complex tomato rhizosphere). We showed that multi-parasite agents performed better in planta environment rather than in vitro. Phage resistance increased with the increasing of phages richness and was higher evolved in vitro. We also found that pathogen evolved specific resistance to local parasites, regardless of whether they were in single or multiple-phage environments. However, there were high context-dependent costs associated with phage-resistance which positively correlated with resistance. The trade-offs between phage-resistance and bacterial growth might further alter the pathogen virulence which explained the diversity effect of phages cocktail. Given that in nature host populations face selection pressures from multiple parasite strains and species, our results suggest that costs may be even more critical in shaping the pathogen behaviors. In our case, multi-phages treatments “fail” in preventing pathogenic bacteria evolve resistance to phages, but it is likely to decrease the fitness of host or more readily dealt with by the plant immune system or other control agents.

O87 Functional characterization of bacteria associated with dead wood based on genome and metagenome annotation

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The decomposition of dead wood substantially contributes to the carbon cycling in temperate forests. Dead trees at various decomposition stages differ in their properties and can thus harbour diverse communities of bacteria adapted to these specific conditions, strongly influenced by fungal wood decay. Our aim was to identify potential ecosystem services provided by bacteria inhabiting the dead wood of *Fagus sylvatica* during different stages of wood decay in the temperate mixed natural forest in Central Europe. Metagenome of coarse woody debris decomposing for a time range of 5 up to more than 40 years was sequenced and its annotation was improved by combining with genomes of several bacterial taxa which were isolated from dead wood. The presence of genes encoding glycoside hydrolases (GH) involved in the decomposition of cellulose, such as the genes from GH5 and GH6 families encoding cellulases were found in genomes of isolates (present in *Pseudomonas*, *Mucilaginibacter*, *Burkholderia*) as well as the genes from families GH18 and GH20 involved in the degradation of chitin, the component of fungal biomass (*Terriglobus*, *Edaphobacter*, *Luteibacter*). During the succession of bacterial community on decomposing wood, genes for N fixation were identified in the metagenome of fresh, nitrogen limited wood and genes for methylotrophy were observed as well. The ability to degrade chitin and other compounds of fungal origin as a convenient source of nutrients was widespread as was also the ability to degrade cellulose. Although the rate of bacterial contribution to dead wood turnover remains unclear, characterization of bacterial members of dead wood community indicates their active involvement in decomposition processes and N cycling.

O88 New biocontrol applications against *Heterobasidion* spp.

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Root rot pathogens of the genus *Heterobasidion* are the most detrimental fungal disease agents of boreal conifer forests. They are currently controlled by preventive chemical (urea) or biological (*Phlebiopsis gigantea*) stump treatments, which are, however, of almost no use in already infected forest sites. We have shown that *Heterobasidion* spp. host a number of viruses, some of which are promising virocontrol agents. We showed that one of them, HetPV13-an1, reduces growth of its fungal host considerably on both artificial and natural substrate, and affects the expression of 683 host genes. Furthermore, pre-existing viral infections have variable effects on the transmission of other mycoviruses depending on the virus strain, which should be considered in possible virocontrol applications. We also tested a new type of *P. gigantea* usage in restricting the spread of prevailing *H. annosum* infection in pine forests i.e. treating the healthy root systems of pines surrounding the infected spot by the biocontrol agent supplemented with the treatment of infected stumps with HetPV13-an1. Preliminary results have shown that the fungal biocontrol agent grows efficiently to the root systems whereas evidence for the pathogen spread was not observed.

O89 Interactions of Polyporales fungi: enzyme activities, release of VOCs and progress of spruce wood decomposition upon three-species cohabitation experiments

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Fungal communities are under constant transformation in nature. Interactions of fungal species may vary from tolerant and mutualistic to opposing and antagonistic relationships. The influence of *Fomitopsis pinicola*, a common brown rot Polyporales species encountered in boreal and temperate forests, on the white rot Polyporales species *Phlebia radiata* and *Trichaptum abietinum*, was studied in co-cultures of species combinations on Norway spruce wood. Activities of lignocellulose-decomposing enzymes - CAZymes and lignin-modifying oxidoreductases - were followed together with protease and chitinase activities, along with oxalic acid production and Fenton chemistry indicating iron(III) reduction capacity. Volatile organic compounds (VOCs) were quantified and fungal growth was followed by ergosterol analysis. Apparent wood carbohydrate consumption and mass loss occurred within three months in fungal co-cultures including the brown rot species *F. pinicola*. Increasing amounts of reducing sugars from the wood substrate were accumulating with production of cellulolytic and hemicellulolytic activities, and promotion of Fenton reaction, thus pointing to aggressive non-enzymatic and enzymatic decomposition of wood polysaccharides by the brown rot fungus. The white rot species *T. abietinum* and *P. radiata* secreted an array of enzyme activities including lignin-modifying oxidoreductases (laccase and manganese peroxidase). Two and three species co-cultures showed increase in enzyme activities for hyphal decomposition and recycling of organic nitrogen. Preliminary analysis on VOCs created in the wood-substrate cultivations indicate the dominant effect of mainly non-enzymatic lignocellulose-degrading approach of *F. pinicola*. Our results point to the significance of fungal species-species interactions for wood-decomposition processes and carbon cycling in the forest ecosystems.

O90 Fungal growth, lethal to solitary bee *Osmia bicornis* larvae, is inhibited by soil bacteria isolated from the species' nests

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The red mason bee *Osmia bicornis* is a solitary bee species valued for its services as a generalist pollinator. During early spring, the females choose natural cavities and divide them with soil, in order to form cells to lay their eggs in. When one nest is complete, the bee seals the entrance and leaves, providing no additional maternal nursing. Contrary to the enclosed structure of social bee hives, where the natural microbiome is driven by controlled selection processes and active bacterial transmission, solitary bees rely on the microbiome of the environmental material initially introduced into the nests to overcome challenges such as pollen bioconversion and defense against microbial pathogens. We collected nests from diverse localities and sequenced soil specimens from a total of 99 nest chambers using Illumina next generation sequencing of 16S ribosomal DNA, in order to investigate soil contribution to the overall nest microbiome. Results showed high biodiversity, with many bacteria originating from soils present within the nest chambers. Especially, members of *Paenibacillus* potentially obtained from soil materials caught our attention: We designed functional bioassays to check culture-isolated bacterial strains from the same soil specimens to detect possible antifungal abilities. Two *Paenibacillus* strains showed strong fungal inhibition properties against mould found in nests with deceased larvae. Future research will focus on further inhibition bioassays against common bacterial and fungal pathogens and on the investigation of genomes of microbes possibly undertaking services of organism immunity.

O91 Introduction to Sustainable Deveopment Goals by using soil-human microbiota as a case

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There is a growing interest on the interlinkages between soil and human microbiota. A healthy environmental microbiome supports a healthy commensal microbiome and strengthens human immune-tolerance against illnesses such as allergies and other inflammatory deceases that are typical for modern societies. This is called the biodiversity hypothesis. What does this mean to human health and wellbeing, to food quality and security, to poverty, urbanization and their management, and to the need to maintain and foster healthy terrestrial ecosystems - the building blocks of the SDG framework locally, nationally and globally? In my presentation, I will give a general introduction of the UN Agenda2030, its 17 sustainable development goals and its overarching principles. I will then move on to discuss the challenges of reaching the goals and the pathways for transformation towards sustainable development. Understanding these pathways helps countries and various institutions to plan how they will implement the Agenda2030 and its SDG framework. In addition, it elucidates what kind of roles various societal actors, including the research community, could and should take in the implementation of the SDGs. I will finish my talk by returning to the biodiversity hypothesis. What role does the soil-human microbiota-relationship play in sustainable development? What kind of systemic changes are needed to ensure that humans are better exposed to a rich soil microbiota and thus enhance human health and wellbeing through the entire framework of the SDGs.

O92 What do we demand from our soils?

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In recent years, sustainable food production has risen to the top of the EU policy agenda. Europe's land is now expected to provide multiple ecosystem services (soil functions) for society. These include: i) food production, ii) carbon storage, iii) the provision of clean water, iv) habitats for biodiversity and v) nutrient cycling. However, we must balance the demand for these soil functions (by society), with the intrinsic capacity of the soil to supply, under different landscapes, climates and management systems. All soils are capable of delivering these five soil functions individually, but our management defines the capacity of the soil to deliver multiple functions at once. Many synergies exist between soil functions and so it is probable under the right management system to supply multiple functions in harmony, but we also must consider potential conflicts that exist between some functions and therefore supply of all five functions may not be possible. Every day, farmers make decisions on how they manage their land and soil. At the same time, national and European policy makers make long-term decisions on how to manage their soil resources at larger scales. Therefore, the contemporary challenge for researchers and stakeholders is to link the decision making on land management across scales, so that the practicalities of how farmers make decisions is reflected in policy formation and that policies enable farmers to make decisions that meet EU policy objectives. This is currently the topic of a H2020 project: LANDMARK, which will form the basis of this presentation.

O93 Connecting Microbial Communities to Soil Health

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Soil health can be defined as the continued capacity of soil to function as a vital living ecosystem that sustains plants, animals, and humans. Yet, most indicators of soil health measure physical or chemical soil properties and represent biology indirectly (e.g., short-term soil respiration). Our goal was to test the hypothesis that direct measures of microbial community structure will enhance our ability to determine the status of a soils health. We sampled more than 100 soils across the state of Oregon in the US that represented a wide range of land-use and productivity. For each soil, an onsite evaluation of soil condition was done and microbial communities were assessed by sequencing the 16S rRNA gene (bacteria) and ribosomal ITS region (fungi) of DNA. For cropland sites, we found a positive correlation between bacterial diversity and the in-field soil health. Soil health was also significantly related to both bacterial and fungal community structure. These findings suggest that direct measures of the microbial community, in conjunction with physical and chemical soil properties, will improve assessments of soil health.

O94 Integrating diverse environmental microbiota into everyday life of urban dwellers

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The incidence of immune mediated diseases has rapidly increased in western urbanized societies. Nowadays the costs of the diseases are more than one billion euros annually in the U.S. The main reason for the diseases is generally thought to be the lack of exposure to diverse environmental microbiota among urban dwellers. We identified how land use modified the quality and quantity of environmental microbiota transferred indoors by urban dwellers. We tested how pollution alters the quality and quantity of environmental microbiota in urban areas. We added green elements to outdoor environments to increase the environmental microbial diversity that urban dwellers are exposed to. Finally, we brought diverse environmental microbiota indoors, in order to modify skin and gut microbiota and change immune modulation among urban dwellers. The results show how the proportion of built environment is inversely related to the diversity of key phyla in environmental microbiota. Pollution altered the composition of the key phyla. Studies related to modifying kindergarten yards gave promising results. Most importantly, indoor exposure trials showed marked differences between intervention and control groups. The changes covered both skin and stool microbiota and immunoregulatory cytokines in blood samples. We conclude that in the future it might be possible to reduce the incidence of immune mediated diseases by integrating diverse environmental microbiota into outdoor and indoor environments in urbanized societies.

O95 Where has our scientific tea break brought us? Overview of recent TBI developments

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Decomposition is an important process in the global carbon cycle. Since decomposition is labor and time consuming to measure, we have limited understanding of the complex interactions between factors that drive decomposition. We developed a simple and cheap method to measure decay rate of plant material. The method consists of burying commercial tea bags (Green tea and Rooibos tea in plastic triangle mesh) and digging them up ca. three months later. From the weight loss of Rooibos and Green tea we obtain two parameters that are indicative of two different phases of the decay curve, being, initial decomposition rate and later stabilization. The simplicity of the method allowed crowdsourcing methods and in the past years, many researchers, school children, farmer, gardeners and other interested people have buried tea bags and shared their data with us. This provided thorough field experience and validation of the method. With this, global maps are created and analyzed. Together with the ICOS network, we have buried tea and local litter and compared local litter decay curves and the decomposition parameters based on tea. This showed that the tea bag index is sensitive to environmental parameters, but its predictive power for decay curves of local litter is low, as probably local interactions with liter quality such as homefield advantages interfere. We further ran comparisons between the non-woven (new) and the woven (old) tea bags and will discuss methodological developments. In short, this talk will summarize the latest developments on the tea bag method.

O96 Termites, teabags and tropical savannahs

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Change from wildlife to human-dominated land-uses can potentially alter the balance between microbial and soil fauna regulation of litter decomposition. Using the Tea Bag Index (TBI) we investigated the impact of land-use on microbial and termite decomposition in savannah ecosystems surrounding the Serengeti National Park, Tanzania. We buried over 1700 teabags across three land-uses (wildlife management, pasture and agricultural land) and a spatial and temporal climate gradient (wet and dry region and season) as well as permitting or excluding termite access to litter. Overall, we found that rooibos was strongly preferred by termites compared to green tea. Moreover, the contribution of termites to decomposition varied across land-uses with the highest mass loss in wildlife management areas followed by pasture and agricultural land. However, for green tea and rooibos excluding termites the trend reversed with higher decomposition rates in agricultural land, intermediate in pastureland and lowest in wildlife management areas. By modifying the TBI approach, we demonstrated that the strength of the additive effect of termites on litter decomposition rates was dependent on litter type and land-use. Furthermore, greater human alteration of savannah land-uses is likely to lead to more microbial rather than termite-based litter decomposition with important implications for decomposition of recalcitrant litter types and nutrient cycling.

O97 Long-term climate regime modulates the impact of short-term climate variability on decomposition in alpine grassland soils

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Decomposition of plant litter is an important process in the terrestrial carbon cycle and makes up ~70% of the global carbon flux from soils to the atmosphere. Climate change is expected to have significant direct and indirect effects on litter decomposition processes at various time-scales. Using tea bag index (TBI), we investigated the impact on decomposition of short-term direct effects of temperature and precipitation by comparing temporal variability over years, versus long-term climate impacts that incorporate indirect effects mediated through environmental changes by comparing sites along climatic gradients. We measured the initial decomposition rate (k) and stabilization factor (S; amount of labile litter stabilizing) across a climate grid combining three levels of summer temperature (6.5-10.5°C) with four levels of annual precipitation (600-2700mm) in three summers with varying temperature and precipitation. Several (a)biotic factors were measured to characterize environmental differences between sites. Increased temperatures enhanced k, whereas increased precipitation decreased k across years and climatic regimes. In contrast, S showed diverse responses to annual changes in temperature and precipitation between climate regimes. Stabilization of labile litter fractions increased with temperature only in boreal and sub-alpine sites, while it decreased with increasing precipitation only in sub-alpine and alpine sites. Environmental factors such as soil pH, soil C:N, litter C:N and plant diversity that are associated with long-term climate variation modulate the response of k and S. This highlights the importance of long-term climate in shaping the environmental conditions that influences the response of decomposition processes to climate change.

O98 TeaTime4Schools: How to put decomposition into practice

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Decomposition of organic material in soil is crucial for the global carbon cycle as well as for growth and metabolism of plants and microorganisms. Still, soil functions and processes are rarely a topic that students learn about in school. Therefore, it is essential to develop hands-on teaching activities that enable a better understanding and appreciation of soil functions. In the TeaTime4Schools project, students will study decomposition by burying tea bags under different land uses (Grassland, Maize field, Forest) near their schools in Austria. The tea bags will be recovered three months later, dried, weighed and the results recorded on a global map. The schools will also send soil samples for analysis of biochemical soil characteristics, enabling the correlation of their results to soil properties. One of the schools, the higher secondary school for Viticulture and Pomology Klosterneuburg, will additionally participate in DNA workshops. Students will extract and analyse the DNA of the buried tea bags and from soil samples and fresh tea bags as a reference. Thereby, the students will learn the basics of molecular biology and soil microbiology. The extracted DNA will be analysed in more detail using next generation sequencing analysis of 16S and 18S rRNA, eventually allowing the students to identify the microbial actors in decomposition. A final comparison for of the data from all participating schools to global datasets will raise the awareness of the students towards the importance of microbes and soil functions as well as show the connections to the global carbon cycle.

O99 Global change effects on litter break-down in tidal wetlands: implications from a global survey using the Tea Bag Index

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Tidal wetlands, such as tidal marshes and mangroves, are hotspots for carbon sequestration. The preservation of organic matter (OM) is a critical process by which tidal wetlands exert influence over the global carbon cycle and at the same time gain elevation to keep pace with sea-level rise (SLR). The present study provides the first global-scale field-based experimental evidence of temperature and relative sea level effects on the decomposition rate and stabilization of OM in tidal wetlands, utilizing commercially available standardized litter. While effects on decomposition rate per se were minor, we show unanticipated and combined negative effects of temperature and relative sea level on OM stabilization, as based on the fraction of labile, rapidly hydrolyzable litter that becomes stabilized during deployment. Across study sites, OM stabilization was 29% lower in low, more frequently flooded vs. high, less frequently flooded zones. OM stabilization declined by ~90% over the studied temperature gradient from 10.9 to 28.5°C. Additionally, data from the Plum Island long-term ecological research site in Massachusetts, US show a pronounced reduction in OM stabilization by >70% in response to simulated coastal eutrophication, confirming the potentially high sensitivity of OM stabilization to global change. We therefore provide evidence that rising temperature, accelerated SLR, and coastal eutrophication may decrease the future capacity of tidal wetlands to sequester carbon by affecting the initial transformations of recent OM inputs to soil organic matter.

O100 Occurrence of plant growth promoting *Ochrobactrum* and *Bacillus* sp. in the nodules of *Vigna radiata*

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Root nodules are small nitrogen fixing factories on the roots of legume plant and occupied by the bacteria, rhizobia. Nodules formation takes place by rigorous molecular crosstalk between legume plant and rhizobia. Nodule accommodates various non-nodulating bacteria that invade during nodule organogenesis. Non-rhizobial endophytic bacteria are unable to induce nodule, but have the ability to promote plant growth by phytohormone production, nutrient mobilization and pathogen destruction. In this study, we investigated the occurrence of non-rhizobial endophytes from *Vigna radiata* nodules and their plant growth promoting properties. Ten fast growing non-rhizobial endophytic bacteria were isolated from nodules of *Vigna radiata*. Their non-rhizobial nature was confirmed by the absence of nod genes and inability to induce nodules on *Vigna radiata* plant in nodulation assay. None of the bacterial isolate was able to fix nitrogen, however, NIB4, NIB6 and NIB10 showed the highest potential for *in vitro* plant growth promoting properties. Potential isolates were identified by sequencing 16S rRNA gene. NIB4 and NIB6 showed 100% similarity with *Bacillus* sp. while NIB10 showed 100% similarity with *Ochrobactrum oryzae.* This is the first report on the occurrence of *Ochrobactrum* in the nodules of *Vigna radiata.* Selected bacterial isolates could be used as Biofertilizer after field-testing.

O101 Exploring microbial functional resilience in a Canadian agricultural system using dry soil archives

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Soil microbial communities provide beneficial ecosystem services, such as nutrient cycling processes, which affect crop performance and soil health. Managing microbial communities and the services they provide is an increasingly important component of sustainable agricultural systems. Soil sample archives are a potentially valuable resource of in-depth historical information on microbial resilience to change. To assess the feasibility of using dried archive soils for this purpose, samples were obtained from a long-term Agriculture and Agri-Food Canada field trial, established in 1959 on a Brookston clay loam at Woodslee, Ontario, Canada. Trial treatments include a never cropped woodlot area, as well as fertilized and unfertilized phases of continuous bluegrass sod, monoculture corn, and a corn-oat-alfalfa-alfalfa rotation. Intact soil cores and grab samples were collected to a depth of up to 20 cm from 1994 to 2013. The cores were used to determine bulk density, air capacity, and plant available water capacity, and grab samples were air dried (20^oC and 50% humidity), crushed to 2mm, and archived in sealed containers at 20^oC. Carbon and nitrogen in the archived soils was determined by dry combustion. Microbial DNA was extracted using PowerSoil DNA extraction kits with a modified protocol to increase DNA recovery from air-dry soil. Changes to microbial communities that regulate different nitrogen cycling processes, including organic nitrogen mineralization, nitrification, and denitrification, were measured using quantitative PCR. Temporal trends in these functional communities were explored to provide insight into microbial resilience to climate and management changes.

O102 Carbon and nutrient cycling in organic agriculture: a chronosequence approach

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A key challenge is to increase sustainability in agriculture without yield loss. Organic agriculture uses no chemical fertilizers and pesticides. Instead, yield depends on nutrients released from organic inputs, and thereby on soil communities that drive soil carbon and nutrient cycling. However, these soil communities may need time to establish, resulting in lower yields during the beginning of this conversion. How carbon and nutrient cycling change during the conversion from conventional to organic agriculture is not well understood, but it may help us to understand, and eventually reduce, the yield gap. Here, we studied how carbon and nitrogen cycling change when converting conventional agricultural systems into organic agricultural systems. We used a chronosequence approach, where we collected soil samples from 37 organic fields, on both sand and clay soils, that have been converted from conventional to organic agriculture between 1 to 40 years ago and from neighboring conventional fields. Under controlled conditions we measured potential rates of carbon and nitrogen mineralization. Potential carbon mineralization and substrate induced respiration were higher in organic soils, but there was no effect of time since conversion. This might be explained by variation in abiotic factors such as soil organic matter content. We use our data to unravel how fast ecosystem processes change after the conversion of conventional into organic farming systems. Our findings will yield important insights how the performance of soil communities is changed during transition and this will help us to understand changes in crop yield.

O103 The role of fungi in restoring old fields

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Soil organisms have an important role in aboveground community dynamics and ecosystem functioning. However, most studies have considered soil biota as a black box or focussed on specific groups, whereas little is known about entire soil networks. Here we present results that during the course of nature restoration on abandoned arable land a compositional shift in soil biota, preceded by tightening of the belowground networks, corresponds with enhanced efficiency of carbon uptake. We discovered that although fungi represent a relative small amount of the total microbial biomass half the amount of carbon that flows from plants into soil is taken up by the soil fungi in early stages of succession. After 30 years, that share has risen to three quarters of the plant-derived carbon stored in the soil. By labelling the carbon atoms, we were able to follow the carbon flow into the soil food web. In this way, we could link the organisms to their corresponding functions in the community. Next to this we pioneered in looking into the mechanisms on how root exudation shapes soil communities with a focus on the fungal community. Recently photosynthesized carbon from the plants combined with secondary plant metabolites seems to shape soil communities. Some preliminary results on how the plant hormone group of strigolactones might be used to advance the restoration of old fields will be presented.

POSTER ABSTRACTS

P1 How influential is the common mycorrhizal network in nutrient transfer?

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Common mycorrhizal networks formed by arbuscular mycorrhizal fungi are claimed to facilitate direct transfer of nutrients between adjacent plants. A range of experimental protocols has been used to investigate this, including split-chamber microcosms, separation of plants using fine mesh that excludes roots, inclusion of hyphal chambers, severing of hyphal connections between plants, growth of plants in compartmented Petri dishes, and nutrient labelling. Such studies identified nutrient transfer between the same or different plant species. However, there can be both direct and indirect nutrient pathways between plants growing adjacent to one another in soil; previously used protocols do not clarify the relative contributions of these pathways. Therefore, we investigated a common mycorrhizal network and neighbour plant proximity in relation to nutrient acquisition by a legume and a C_4 grass under nutrient-limited soil conditions, with and without water stress. We included several different control treatments. Shoot growth of subterranean clover (*Trifolium subterraneum*) increased when grown in close proximity to the grass (*Panicum clandestinum*) when the only possible connection between the two was a common mycorrhizal network. Despite this, P transfer by subterranean clover, at a level sufficient to overcome P deficiency, may not have occurred directly via the common mycorrhizal network. On the contrary, there was evidence of indirect transfer of P to subterranean clover via hyphal scavenging from soil near the neighbouring grass roots. This indirect hyphal P transfer pathway was likely to be of greater physiological significance than direct P transfer via the common mycorrhizal network.

P2 How interaction between fungi and plant-derived polyphenolics contributes to soil carbon stabilization?

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Boreal forest ecosystems store globally significant amounts of C mainly in the plant biomass and in the soil organic matter (SOM). The role of boreal forest SOM in future C budget is uncertain as processes underlying SOM formation are largely unknown. Fungi are proposed to be the main drivers of SOM decomposition but they are also involved in SOM formation providing large input of C and nitrogen, which availability is limited in the boreal forest soil. Recent studies suggest that more than half of C stored in the soil originates from fungal mycelium and plant roots. Contradictory, fungal necromass (FNM) seems to decompose rather fast, indicating that the role of FNM in the soil organic matter formation is still unresolved. We combined laboratory and field experiments to demonstrate possible mechanism for enhanced stability of FNM. Taking into account that plant-derived polyphenolics (tannins) may form complexes with proteins and chitin, abundant fungal polymer, we propose that complexation of FNM with tannins is a mechanism stabilizing FNM-derived C in soil. Our laboratory study with pine seedling microcosm showed that decomposition of FNM and nitrogen uptake is significantly decelerated by formation of complexes with tannins. Our field study with FNM placed in mesh bags and buried in soil for up to three growing seasons proved that FNM-tannin complexes are created in natural conditions and confirmed that such transformation stabilizes FNM. Our results imply that interaction between tannins and FNM may be one of the hitherto overlooked mechanisms stabilizing microbial-derived C in soil.

P3 Plant-associated microbes use a different pathway to decompose soil organic matter than free-living saprotrophic microorganisms

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Boreal forests are one of the world's largest terrestrial carbon (C) sinks, storing high amounts of C in the soil organic matter (SOM). Global warming may switch this C sink into C source accelerating climate change. Therefore, we need mechanical understanding of the main processes steering SOM formation and decomposition to mitigate climate change. Recent advances underline the role of the microorganisms in SOM transformations, however, the underlying mechanisms and pathways of SOM decomposition remain not well-known. Here, using a three-year-long field experiment with humus filled mesh bags we compared decomposition of SOM driven by different decomposers: 1000µm mesh size allowed penetration of all organism having the same or smaller size as fungal hyphae and fine roots, 50µm restricted plant roots, but not other microorganisms and 1µm restricted also fungal hyphae, but not saprotrophic microorganisms. Our results suggest that plant associated microbes use a different pathway of SOM decomposition than small sized free-living microbial decomposers. SOM decomposition shaped by plant-associated microbes is more soil organic nitrogen (SON) orientated with slower mineralization, but also with higher recalcitrant-N pool due to the stabilization of microbial-N and SON with plant-derived N-binding tannins. On the other hand, SOM decomposition shaped by saprotrophs was orientated more into mineralization with no SOM building-up, however, due to lack of priming support from plants such decomposition was slower. In conclusion, these findings call for a change in paradigm from purely plant litter traits or only fungal traits to plant-microbe interaction traits in explaining the complexity of SOM transformations.

P4 The potential role of plant secondary metabolites in carbon and nitrogen cycling in boreal forest soils

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Studies over the last century clearly showed that plant secondary metabolites (PSM) play a major role in the adaptation of plants to their environment, making them crucial compounds in plants existence. These molecules largely contribute to plant fitness by interacting with the ecosystems. The main role of PSM is ascribed to defense against pathogens and herbivores, but they are also antioxidants and allelopathic agents and potential regulators of soil organic matter (SOM) decomposition. It has been suggested that PSM have potential to play significant roles in the carbon (C) and nitrogen (N) cycling of boreal forest soils. PSM are abundant in the litter. During decomposition of litter terpenes and other PSM are released into the soil and may modify N and C cycling by altering microbial processes and populations. Laboratory experiments showed that terpenes increased mineralization of carbon and inhibited net N mineralization and net nitrification. As decomposition is driven by multiple sets of enzymes, a possible influence of plant secondary compounds on enzyme activity appears to have a significant role in controlling this process. Terpenes showed inhibitory potential against enzymes, which are involved in C, N, P, S cycling. The mechanism of inhibition seems to be based at least partially on the ability of terpenes to bind enzymes. Also tannins affect soil processes in the boreal forest, however, their influence on plant N uptake and SOM decomposition appears highly complicated due to the high reactivity of tannins with different compounds.

P5 Bacterial genetic features determining the strain specificity of *Pisum sativum* line P61 interaction with *Rhizobium leguminosarum*

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Ability to assimilate nitrogen by forming symbioses with nitrogen-fixing bacteria developed in various plants. Fabaceae possess the ability to form nodules, specialised structures that house the symbiotic bacteria supplying the plant with fixed nitrogen. The development of this highly specialised organ is controlled both by plant and bacterial genetic programmes. In 1993 Sagan et al. produced the P61 pea line, mutant in the sym25, exhibiting the so-called fix- phenotype (nodules incapable of fixing nitrogen). They later discovered that phenotype to be strain-specific, but the strains were subsequently lost. Recently in our laboratory the ability of strain Rhizobium leguminsarum bv viciae RCAM102 to suppress the mutant phenotype of P61 line was discovered. The exact cause of the increased symbiotic prowess of RCAM1026 remained a mystery. The aim of this study was to uncover the genetic traits granting the strain RCAM1026 increased affinity to the line P61. In order to determine the exact genomic composition of the RCAM1026 it was sequenced using the MiniON sequencing platform. Using RNAseq on Illumina, the gene expression levels in the developed nodules of line P61 inoculated with the effective RCAM1026 and the ineffective 3841 strains were compared. The transcriptome profiles of effective and ineffective nodules varied drastically, with RCAM1026 showing higher levels of up-regulated genes when interacting with the mutant. Thus, we determined the set of unique genetic features probably involved in the process of mutant phenotype suppression.

P6 Peatland provides metal remediation by preserving microbial diversity and facilitating microbial Fe and S oxidation

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A peatland that has historically received acid mine drainage (AMD) from an abandoned metal mine at Parys Mountain (Anglesey, UK) has been shown to markedly reduce metal contamination of nearby coastal waters. Such natural bioremediation is a sustainable alternative to AMD chemical treatments but a better knowledge of the microbial-mediated processes is needed. By using a combination of microbial genomics and micro-XRF techniques we are beginning to understand the role of the plant-associated microbial community involved in the remediation of AMD in relation to metal distribution along the peatland. An integrative analysis was performed using soil metagenomics and high resolution X-ray fluorescence scans (ITRAX) to examine peat cores sampled at intervals along the peatland. The study reveals a selective mobilisation of metals, in which iron remains in the surface while trace metals migrate to deeper layers along the peatland. This occurs in locations where increased abundance of iron-oxidising bacteria and increased expression of sulphate-oxidation genes is observed. The microbial community and metal distribution vary according to plant species, organic matter and sulphur content. Taxonomic analysis and metabolic reconstruction of the surface microbiome shows that the peatland enhances microbial diversity in contrast to a region of the AMD-impacted river without vegetation, which has low microbial diversity and very distinct microbial-derived metabolic activity profile. We conclude that the peatland plays a key role in facilitating microbial-mediated Fe and S cycling and trace metal immobilisation by preserving the overall diversity and metabolic capacity of the soil microbiome.

P7 Soil microbial communities in subarctic mountain birch forests in two reindeer grazing regimes recovering from a severe moth herbivory

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Outbreaks of the foliage feeding autumnal moth Epirrita autumnata and winter moth Operophtera brumata may cause large-scale forest damages in subarctic mountain birch forests, while intensive reindeer (Rangifer tarandus) grazing can reduce birch regeneration after moth damage. This decreases carbon flow from plants to soil. On the other hand, herbivores increase soil nutrient availability, due to feces and urine. Together they can have a major impact on soil microbial communities, responsible for carbon and nutrient cycling in ecosystems. Here we studied how reindeer herbivory affects soil microbial communities in mountain birch forests recovering from moth outbreaks. To address this we selected study site at Polmak in the border of Finland and Norway. The area on the Finnish side of the border is grazed more intensively, i.e. both in summer and in winter, while the Norwegian side is grazed only in wintertime. We set fenced reindeer exclosures and unfenced control plots on the study area and collected soil samples four years after fencing. Ion Torrent sequencing was used to analyze fungal and bacterial communities in humus and mineral layers separately. Soil microbial communities in humus and mineral layers differed as expected. In addition, fungal communities in humus layer differed between grazing regimes, but not between fenced and unfenced plots. These results suggest that microbial communities are either resilient towards changes in grazing regime or changes are too slow in this environment to be seen in four years period.

P8 Determination of Changes in Soil Microbiota of Different Soil Genesis and of Long-Term Diverse Soil Use Intensity

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Recent studies have indicated that anthropogenic activities, such as agricultural intensification and land use change, is reducing soil microbial abundance and general diversity of soil organisms. The research was aimed to assess the impact on soil microbiota changes of different soil genesis due to long-term diverse soil use intensity. For that, the evaluation of soil microbiota diversity was performed respecting to land use (cropland and afforested sites), site management and soil properties under different soil genesis (according to WRB system referred as *Endocalcari-Endohypogleyic Cambisols*, *Calc(ar)i-Epihypogleyic Luvisols*, *Bathihypogleyi – Eutric Albeluvisols*, *Epieutric Endocalcaric Endogleyic Planosol*) in Lithuania. The results confirmed the key role impact of plant rhizosphere (up to 30 cm) and in some extent of mineral soil layer (30-50 cm in depth) to, especially, on organic matter decomposing bacteria's. Even though, the diversity was evaluated according the predominant bacteria classes (*Actinobacteria*, *Alphaproteobacteria, Bacteroidetes*, *Proteobacteria*, *Acidobacteria* and *Cyanobacteria*), the significantly expressed differences have been estimated in the diversity of *Actinobacteria* and *Bacteroidetes* classes, either in cropland and in forest sites. However, the diversity of mineral soil bacteria was decreasing with soil depth. Thus, if to compare with croplands it was by more than 2 times higher in afforested sites. It was evident, that afforestation considerably increased organic matter content in the studied sites. As well as soil development resulted in a high production of carbon and nitrogen pools under the forest stands, contrary to studied croplands. This altered the soil microbiological community structure and composition of the microbial communities below ground.

P9 Response of microbial growth to substrate complexity under different temperature regimes

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Soil microbial communities mediate soil feedbacks to climate change and a thorough understanding of their response to temperatures is central for predicting climate-induced changes in carbon fluxes. How microbial communities will change their structure and functions in response to temperature and organic C quality variations is still unclear. In our study, soil microbial communities from two different regions and land-uses were exposed to organic C of varying stabilities; cellobiose (CB), xylan or coniferyl alcohol (CA) and were incubated at 5, 15 or 25 °C. Increasing temperature stimulated cumulative respiration rates, but decreased total microbial biomass (total phospholipid fatty acids, PLFAs) in all treatments. Temperature response of fungi (fungal PLFAs, ergosterol and ITS fragment) depended upon substrate quality. Whereas, fungal biomass of CB amended soils decreased with increasing temperature from 5 to 25 °C, CA and xylan treated soils showed optimal abundance at 15 °C. These results gave first evidence that CA and xylan decomposing fungi have different life strategies and temperature optima than CB decomposing fungal communities. Gram-negative and gram-positive bacteria differ strongly in their capacity to decompose CB under different temperature regimes: whereas gram-positive bacteria showed highest PLFA abundance at 5°C, gram-negative bacteria were most abundant at 25°C. Therefore, microbial community composition at low taxonomical resolution might change their functional trait (carbon decomposition of different substrate qualities) in the context of climate change and this might have important implications for C cycling.

P10 Microbial activity in relation to changing soil chemical and physical properties

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In order to meet growing human food demands, scientists face new challenges that result from significant ongoing climate changes: mild winters, prolonged vegetation period, extreme temperatures and intense rain. These factors encourage to intensify current agricultural systems in order to increase their production volume and quality of the same unit area. The soil is considered to be non-renewable natural resource, which is characterized by high degradation level and extremely low regeneration degree, so anthropogenic activity has the negative impact on stability and long-term productivity. One of the most important indicators of soil quality is the accumulation of common biomass of microorganisms in the arable soil layer. The activity of soil microorganisms determines ecosystem stability, metabolism, and soil fertility. The aim of the study was to evaluate the influence of agro-techniques on the changes in soil chemical and physical properties and to determine the dynamics of microorganism communities in agroecosystems. Dystric Glossic Retisol was analysed, geographical coordinates 55°43'38″N, 21°27'43″E. According to the results of variation partitioning analysis of soil microorganism physiological groups under different soil properties, the 64% of the population of the physiological groups of soil microorganisms describing the data varies depending on soil chemistry and physical characteristics, and 36% of the data varies due to the influence of unanalyzed factors. Soil chemical properties influence the physiological groups of microorganisms more than their physical properties, respectively 22% and 14%. These two groups of indicators can produce a synergetic effect and explain 28% of the abundance of physiological groups of microorganisms.

P11 Degradation of azo dyes by fungi inhabiting contaminated soil: optimization of the degradation conditions with the view to bioremediation

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The wastewater from textile industry has polluted soils with complex mixtures of toxic and carcinogenic substances. Remediation of soil with biological methods would be more sustainable compared to chemical techniques. Although several microorganisms have been reported to degrade azo dyes, the toxicity of the contaminated soils forces to search specific resistant microorganism to be used in bioremediation. Moreover, the biodegradation conditions need optimization. We studied the biodegradation of five azo dyes (Congo red, Dispersed red, Reactive red, Basic blue, Acid blue) with four *Aspergillus* species that we had isolated from contaminated soil. We had selected these species as the most promising after a preliminary experiment. In the final *in vitro* experiment, we studied the effect of various carbon and nitrogen sources to find out an optimal co-substrate for remediation purposes. We also tested different pH values and temperatures to understand the factors affecting the degradation efficiency. The degradation of the dyes was assessed by measuring the color change (spectrophotometer) and the metabolites formed (HPLC and GC-MS) during seven-days incubations. The four *Aspergillus* species were efficient in degrading the azo dyes; fungi were able to degrade all five dyes more than 90 % in the best conditions. The best conditions varied between the dyes to some extent. The dyes were degraded 40 - 95 % depending on the pH, temperature, the substrates added and the original dye concentration. The study gives guidelines to *in situ* experiment of remediation.

P12 New insights into the origin and role of biological rock crusts in rock weathering processes

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Rock surfaces support microbial communities that may be involved in weathering processes. In arid and hyper-arid environments microbes colonise rock surfaces and were linked to weathering because the scarcity of water excludes classical mechanisms that erode rocks. We studied subaerial biofilms coating arid rocks, focusing on sedimentary rocks that feature comparable weathering morphologies but different lithologies. We hypothesized that weathering is fashioned by salt erosion and mediated by biofilms that play dual roles: stabilizing the rock surfaces by coating, and enhancing salt crystallization by preventing rapid desiccation (thus mitigating and facilitating erosion processes, respectively). We used a combination of microbial and geological techniques to characterize the rocks' morphologies and their subaerial biofilms. Deep sequencing and microscopy analyses suggest that bacterial diversity is low, dominated by Proteobacteria, Cyanobacteria and Actinobacteria. Together these phyla formed laminar biofilms that secrete extracellular polymeric substances to aggregate microfabrics and mitigate desiccation, reducing water loss by over 40%. The biofilm was detected only in rocks exposed to the atmosphere, present distinct architecture and burrowed up to 6 mm beneath the surface, protected by sedimentary deposits. A closer inspection revealed that the composition of the biofilm was tightly linked to dust bacterial communities but distinct from soil communities. Moreover, the biofilm composition changed according to the rock location rather than lithology, suggesting that microclimate (dew, relative humidity and radiation) play an important role in arid weathering. Our results contradict common dogmas that considered biofilms as degrading agents and propose their role as mitigators of geomorphic processes.

P13 Introduce grassland in crop rotation, a way to restore microbiodiversity and soil function

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Soils need to be recognized and valued for their productive capacities as well as their contribution to food security and the maintenance of key ecosystem services driven by soil biodiversity particularly microorganisms. Today, there is an urgent need to establish sustainable soil management systems. Adding grasslands within arable crop rotations may be away to reconcile agricultural productivity with concerns about environmental quality by integrating crop systems. The intimate connection between soil state, microbial communities and enzyme activities emphasizes the importance of considering the role of microbial communities during soil restoration by the introduction of grassland in crop rotations. Therefore, the objective of this study was to investigate the influence of ageing grassland in the recovery of soil state by the comparison of different grassland regimes (two restored grasslands and two temporary grasslands) between permanent grassland and conventional crop in a same pedoclimatic context. To achieve our aim, we analyze, physicochemical properties, microbial communities (indicators of abundance and diversity) and soil functions (fourteen enzyme activities) during the adding of grassland in crop rotations. The results indicate that the structure and the functions of microbial communities were strongly associated with soil physicochemical characteristics. The effect of different grassland regimes on soil microbial communities showed that a continuous crop regime has a stronger legacy on the structure of microbial communities. By contrast, the legacy of a grassland regime changes quickly when the grassland regime is interrupted by recent culture events. A grassland regime enables resiliency by the restoration of functions, but more than five cumulative years in the grassland regime are required to observe this resilience. Finally, including grasslands in crop rotations has strong consequences for the microbial communities and the sustainability of their functionality. Such biological studies could help to optimize crop rotations for both agricultural productivity and ecosystem services.

P14 The physiology of plant soil feedbacks in temperate tree species

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Plant traits influence how trees interact with their environment, and the diverse mycorrhizal fungal associations living within plants can influence tree morphology and physiology. We hypothesized that for a given tree species conspecific soils (“home”) would accumulate a larger proportion of host specialist ectomycorrhizal species in relation to heterospecific soils (“away”), and that this distinct community composition will influence tree physiological and morphological traits. We used soil cores from birch, larch and scots pine forests (three plots per forest type) in a greenhouse pot factorial experiment, in which we planted birch, larch and scots pine in “home” and “away” soils. We quantified the resource exchange between trees and mycorrhizal fungal communities during four days by reciprocal pulse-labelling of the experimental pots with ^{13}C and ^{15}N. In addition we measured ecosystem respiration and primary productivity, plant growth traits (height, branching, root:shoot, biomass), plant physiological traits (nutrient content) and fungal traits (number of colonized root tips, hyphal length, mycorrhizosphere respiration). Results to date show a greater aboveground biomass and height of birch trees in home and pine soils compared to larch soils. We also found a reduction in branching in pine trees grown on larch soils when compared to other soil origins. These results will be discussed in relation to the resource exchange between the tree species and their associated ectomycorrhizal fungal communities in home and away soils. Further work will include the characterization of the fungal associations in each of the soil cores at the beginning of the experiment and the realised fungal colonization of the tree root tips.

P15 Bioaugmentation with fluorene-degrading *Sphingobium* sp. strain LB126: role of biodiversity of resident communities on establishment and survival of the invader

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The present work focuses on guidance to strategies for optimizing bioaugmentation of sites contaminated by polycyclic aromatic hydrocarbons (PAHs). We targeted the factors that govern bioremediation success and enable successful establishment of metabolically-active, fluorene-degrading *Sphingobium* sp. strain LB126 in fluorene-contaminated sites in the context of biodiversity-ecosystem functioning experiments. In particular, we assessed the effect of biodiversity of resident microbial communities in contaminated site, on the establishment and survival of *Sphingobium* sp. strain LB126 in soil microcosms. The following hypothesis was tested: higher levels of resident microbial diversity reduce the ecological niche available to an invader via increased competitive interactions. Using a dilution-to-extinction approach, we constructed soil microcosms inoculated with a gradient of biodiversity implemented by serial dilution of contaminated soil samples. Afterwards, *Sphingobium* sp. strain LB126 was introduced as a beneficial invader for ecological restoration. The invasion success was monitored by qPCR analyses targeting a specific functional gene involved in fluorene biodegradation. Significant differences between treatments became evident from the second week after the invasion, and they increased until the end of the experiment. The invader survival was significantly higher in the more diluted soil treatments than in the less ones. The results obtained confirmed the coupling between biodiversity of the invaded community and invasion potential: the more diverse a community, the lower the invasion potential of strain LB126.

P16 Some vast assemblage of archaea in termiteria

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Archaea species contributes immensely to the ecosystem with regards to nutrient cycling within the soil. However, there is a paucity of information on these species with regards to their identities within microbial communities of the termiterium. In order to characterize these archaea, a high-throughput 16S rRNA sequencing techniques was utilized in this study using termiterium and its adjacent soil. This study revealed the identity of the unculturable as well as the culturable archaea with their species abundance. The methanogens identified in the samples were *Methanocuelleus bouurgenesis* and *Methanocuelleus marisnigri* both from the *Methanomicrobiacea* family, along with methanogenic prokaryotes that are not thoroughly characterized, but all of them contribute towards the total global methane production. Moreover, the most abundant phylum of archaea found in this study was Crenarchaeota with the class Thermprotei. There is a significant difference in the archaea diversity pattern of distribution in the termiterium and its adjacent soil. However, Thermprotei was more prevalent in the adjacent soil than the termiterium itself. These Thermprotei are sulphur oxidizers that can assist in global sulphur cycle, reducing most toxic compound detrimental to the nitrifier in the soil, indirectly improving the soil health and fertility towards food safety and security.

P17 The varied assemblages of fungi on termite mounds

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Most termite species depend on the cultivation of a specialized fungus, *termitomyces*, for food, contributing indirectly to nutrient cycling of the soil. Despite the discovery of the mutualistic relationship between termites and fungi, less studies have been on the varied assemblages of fungi found in termite's mounds. Thus, this study employed the 16S rRNA amplicons sequencing to detect the taxonomic classification of the fungi prevalent in the termite mounds resulting in the symbiotic relationship with the termites. This study reveals that phylum Ascomycota is the most predominant phylum, with the class *sordariomycetes*, genus *Verticillium* and species *dahllae* in the both termite and its adjacent soil. These Ascomycota will enhance the decomposition of lignocellose complex for termite to feed on. Moreover, all the fungi species discovered possessed the ability of converting complex substances into simpler ones, which is essential in the nutrient cycling for food safety and security.

P18 Impact of long-term farming practices on the rhizosphere microbiome and plant health

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Agricultural intensification due to raising food and energy demands during last decades has resulted in severe consequences for agricultural soils. In order to maintain soil quality and productivity, the development of sustainable farming strategies is needed. Soil and rhizosphere microbiomes play an integral role in virtually all soil processes and are intimately linked to plant performance. We hypothesize that the impact of agriculture is conveyed by the microbiome to the future plant generation. We used twelve differently managed soils from three long-term field trials established in 1978 (Therwil, Switzerland), 1992 (Bernburg, Germany) and 2006 (Thyrow, Germany). The model plant lettuce (*Lactuca sativa* L.) was cultivated for ten weeks under growth chamber conditions in these soils and the impact of various management strategies (crop rotation, fertilization, tillage) on soil and rhizosphere microbiomes under consideration of soil suppressiveness and plant performance was analyzed. High-throughput amplicon sequencing of bacterial 16S rRNA genes and fungal ITS fragments amplified from total community DNA of rhizosphere and soil samples showed significant differences in microbial community compositions between soils that originated from different field sites and long-term farming practices. Moreover, differences depending on agricultural management in microbial biomass, root exudation, plant productivity and health as measured by RT-qPCR of stress-related plant genes were observed. Agricultural management also affected soil suppressiveness to the soil-borne model pathogen *Rhizoctonia solani*. Our study under controlled growth chamber conditions suggests the legacy of long-term agricultural management practices on the establishment and performance of a subsequent plant generation and its associated rhizosphere microbiome.

P19 Soil microbial community in an ecosystem succession chronosequence of tropical riparian forests

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Soil microbial community characteristics provide information on ecosystem functioning since they are sensitive indicators of disturbances and land use changes. Here we evaluated whether the microbial community size, estimated by microbial biomass carbon (MBC) and the microbial activity, estimated by soil basal respiration (RBS), responded to soil properties in an ecosystem succession chronosequence. Soil samples were obtained from nine riparian areas (including undisturbed forests and recovering reforested areas) in SE Brazil. MBC and RBS were determined using the fumigation-extraction method and CO2 evolution, respectively. Soil properties analyzed were bulk density (Ds), moisture, C:N ratios, phosphorus (P), pH, soil organic matter (SOM) and cation exchange capacity (CTC). After a multicollinearity test, we selected P, Ds, pH, and C:N as predictive variables. MBC and RBS were not correlated (Pearson r = 0.198), so we expected that they were differently affected by soil properties. The relationships of MBC and RSB to soil properties were determined using stepwise multiple regression. The final models indicated that MBC was negatively related only with C:N ratio (adj-R^2 = 0.15, P = 0.018), whereas RBS was related negatively with Ds and positively with pH and C:N (adj-R^2 = 0.31, P = 0.002). The results suggest that MBC is mainly driven by the supply of C higher quality, whereas RBS is affected by chemical and physical soil properties that influence the microbial environment. In an ecological succession gradient, C inputs could be different, and the activity of the microbial community may not necessarily be proportional to such inputs.

P20 The characteristics of soybean (*Glycine max*) cultured soil with high microorganism activities on Saprolite soil

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Recently, the importance of microbial communities has paid attention to environment-friendly agriculture. Soil microorganism community is different and up to environment and crop varieties. Because crop can secrete various compounds through their roots, rhizosphere soil highly is affected by crop variety. In this study, we investigated characteristic of soil microorganism community with three crops-*Solanum tuberosum L* (potato)., *Glycine max*(soybean) and *Brassica compestris* ssp. *pekinensis* (kimchi cabbage). To demonstrate characteristics of soil microorganism, dehydrogenase activity analysis and denaturing gradient gel electrophoresis analysis were carried out. As a result, soybean cultivated soil showed highest microorganism activities than others over almost 4 months of growth period. Soil DNA was extracted every two weeks during plant growth period separated into bulk soil and rhizosphere soil. Overall DGGE profiles were similar but little different. While some DGGE bands of soybean-grown soil showed stronger intensity than the others, some were only shown in each crop. From sequence analysis of DNA fragments from DGGE bands, common soil bacteria-*alpha proteobacteria*, *actinobacteria*, *flavobacterium*, etc- were identified. In addition, the bacterium from chloroplast was shown in rhizosphere soil and root. However to find the reason of high microorganism activities in soybean cultured soil, more specific bacterial population analysis is needed.

P21 Shiga toxin producing stx I and II genes in *Escherichia Coli* O157: H7 from domesticated Cane Rat (*Thryonomys swinderianus*)

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Rodents have been reported as reservoir of *Enterobacteriaceace* especially *E coli.* Cane rat or grass cutter is an indigenous rodent, consumed for its tasty meat in sub Saharan West Africa. Cane rat (*Thryonomys swinderianus*) is one of the main sources of animal protein and most preferred meat in rural and peri-urban Sub Saharan, West Africa. Limited data exist for the presence of *E. coli O157. H7* in domesticated cane rat hence, this study is aimed at isolating and identifying shiga toxin producing genes in *E. coli* (STEC) O157:H7 from feed, faecal matter, soil and drinking water in cane rat pen. This was done so as to ascertain the possible route of transmission of STEC. Identified *E. coli* isolates were streaked and screened on Sorbitol MacConkey Agar (presumptive test). O157:H7 were serologically identified and confirmed by using latex agglutination reagent. Confirmed O157:H7 strains were subjected to antibiotics sensitivity using disc diffusion method. Shiga toxin genes were detected using Multiplex Polymerase Chain Reaction. *E. coli* was not isolated from water samples. Out of the *E. coli* isolates obtained, five were confirmed O157:H7 strains and were 100% resistant to the selected antibiotics used. Multiplex PCR analysis revealed *Stx* 1 gene at 400bp and *Stx* 2 gene was detected at 600bp from faecal matters. None of the Stx genes were detected from O157:H7 strains isolated from feed, soil and water samples. This study revealed that isolation of shiga toxin producing *E. coli* O157:H7 from faecal matters are of public health importance as the organism can cause food poisoning.

P22 Litter decomposition of three halophytic species in a Mediterranean salt marsh: influence of leaf chemical quality and edaphic heterogeneity

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Plant and soil in salt marshes are important carbon reservoirs, with litter decomposition contributing to soil carbon storage. Litter decomposition rates vary greatly depending on environmental conditions, soil microbial activity and the intrinsic characteristics of plant species. Hence, this study was focused on litter decomposition of three halophytic species (*Sarcocornia fruticosa, Atriplex portulacoides* and *Elymus phycnanthus*), with high morpho-biochemical differences, distributed in two areas of a Mediterranean salt marsh (NE of the Iberian Peninsula). For each area, several edaphic parameters were also monitored. For each species, litter content of cellulose and lignin was initially measured and litter decomposition rates, extracellular enzyme activities (β-glucosidase, β-xylosidase, leucine-aminopeptidase and phenol oxidase), and litter carbon and nitrogen concentrations were determined throughout the decomposition process. *E. pycnanthus* litter showed the lowest decomposition rates in accordance with its lowest extracellular enzyme efficiencies and its highest initial cellulose and lignin content. *S. fruticosa* litter had the highest nitrogen content throughout all the decomposition process. Nevertheless, decomposition parameters of *S. fruticosa* and *A. portulacoides* differed between zones within each area, according to different soil properties. Specifically, *A. portulacoides* litter showed different decomposition rates, enzyme efficiencies and nitrogen content (three months after experiment beginning) between zones. In the case of *S. fruticosa* and *E. pycnanthus*, edaphic heterogeneity affected decomposition rates of the former and carbon content of both species in the last stages of decomposition. Results indicate that, besides plant litter quality, microhabitat conditions can determine significantly microbial decomposition rates in typically heterogeneous habitats, such as salt marshes.

P23 Mycobacteria in the microbiomes of Hranice Abyss and Zbrasov Aragonite caves (Hranice Karst, Czech republic)

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The diversity of bacterial and archaeal community regarding specific cave environments was studied in the Hranice Abyss (HA), the deepest abyss in the world, and adjacent Zbrasov Aragonite Caves (ZAC). The microbiome was detected by next generation sequencing (NGS) and mycobacterial species were differentiated using culture and mycobacterial DNA (genes *hsp65* and *dnaA*) examinations. The phylum Proteobacteria was dominant in all samples from both HA and ZAC. The bacterial microbiome of the mineral water from HA water zone was similar in diversity to bacterial slimes and differed from the mineral water from ZAC. Despite the depth of sampling the large bacterial diversity of mineral water from HA originates from surface contamination. Nontuberculous mycobacteria (NTM) were cultured in 12.5% of the samples from photic and dry zone. The DNA examination has shown 25.0% of the samples, including the water zone, to be positive for mycobacteria. In the Hranice Abyss *M. florentinum* in soil were identified by culture. *M. arupense*, *M. mucogenicum*, and *M. sediminis* were determined by PCR methods in bacterial slimes. In Zbrasov Aragonite Caves, *M. intracellulare* was detected in residual sediments, and *M. avium* complex in fluvial sediments. All cultured mycobacterial species belong to slow-growing mycobacteria. The results obtained by both culturing and DNA examination indicate that presence of mycobacteria is more correlated to oxygen concentration than to the geochemical characteristics (pH, conductivity, oxidation-reduction potential, total organic carbon) in all the zones.

P24 The role of petrichor in desert soil microbial communities resuscitation during a rain event

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The infrequent and unpredictable desert rain events alleviate the soil from its main limiting factor water, and the microbial community resuscitates. The revival of the microbial community results in a distinct earthy smell called petrichor, that is mainly composed of the volatile geosmin. However, the justification for the costly production of copious amounts of geosmin by members of the soil microbial community is unclear. We hypothesized that geosmin is produced at the early stages of a rain event by the non-photosynthetic members of topsoil community to induce primary production by cyanobacteria residing in the biological soil crust (BSC). To test our prediction, we modeled rain events with and without geosmin and/or organic carbon source using intact desert soil columns (up to 10cm). Following these treatments, the mesocosms were distractively sampled for 24 hours at intervals monitoring ribosomes and geosmin content in BSC and topsoil.. Our results suggest that geosmin activate the BSC cyanobacteria, directly after the rain event, while in later samples the effect of the volatile on the active community was less apparent. Moreover, geosmin measurements suggested that 24 hours after hydration, geosmin treated samples showed the same volatile levels as untreated samples. The effect of carbon addition was more apparent at later stages of hydration. In contrast the changes in the topsoil community in response to geosmin application were less apparent. In summary, we suggest that the pleasant smell of rain after a long draught play an important role in enhancing primary productivity in desert BSC.

P25 Arbuscular mycorrhizal fungi enhance industrial tomato growth and production and compensate reduced fertilization levels in an Algerian field soil

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The effects of arbuscular mycorrhizal fungi (AMF) inoculum and fertilization on industrial tomato {*Lycopersicon esculentum* Mill. cv. Isma F1} cultivated in North-Eastern Algeria was evaluated under field conditions in a vertisol soil intended for the cultivation of industrial tomato. The commercial AMF inoculum was combined with three rates of chemical fertilizers used for the cultivation of industrial tomato (monoammonium phosphate, ammonium sulphate and NPK, applied at 0, 50 and 100% of the recommended dose). Plant growth and mycorrhizal root colonization levels were measured at the time of fruiting, and fruit yield and number were measured at harvest. The introduction of AMF significantly improved mycorrhizal root colonization rates, growth, yield and number of fruits as compared to the indigenous AMF alone. Lowest yields were obtained in treatments without fertilization and the highest yield was obtained with AMF inoculation combined with the recommended fertilizer doses. In addition, in the presence of the mycorrhizal inoculant, an application of 50% of recommended fertilizer doses provided the same yield as the full fertilizer doses without inoculation. Results clearly show that in the soil intended for commercial tomato production, plants needed both fertilization and AMF inoculation to achieve optimal growth and yield, and that the application of AMF can compensate for the reduction in chemical fertilizers, offering a more sustainable farming system that is respectful of the environment.

P26 Microbial Community Assembly Processes in a Grassland Undergoing Invasion

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Invasive species have severe impacts on the ecosystem, including drastically altering the plant community which can then have cascading effects on ecosystem functions. Despite an increasing knowledge of how invasive plants can change soil properties, little is known about how multiple invasive plants influence soil microbial community structure and function. To investigate the spatial and temporal dependency of how invasive species can alter soil microbial communities 20-26 soil cores were collected weekly for 26 weeks in a grassland undergoing invasion by smooth brome (*Bromus inermis)* and five other invasive species including Canada thistle, Kentucky bluegrass and Perrenial Sow Thistle*.* Greenhouse gas production, extracellular enzymes, and soil aggregate structure were measured for each sample, and plant and litter surveys were conducted in each plot. Smooth brome invaded plots had higher decomposition activity, elevated CO_2 production, increased nutrient cycling and significantly altered soil aggregate structure. These results suggest smooth brome is causing changes in the soil microbial community. Previous work has shown that smooth brome invasion increases bacterial diversity in the A horizon via litter inputs and in the B horizon through root exudation. This study examines microbial community assembly processes throughout the growing season and with distance from invasion. We hypothesize that microbial community assembly in smooth brome invaded plots will differ from native plots and will increase in differences throughout the growing season, but will decrease in differences with increasing sample distance.

P27 Consequences of climate change on PFLAs (Phospholipid Fatty Acids) in lysimeters of agricultural soils in the Pannonian area of Austria

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Regional climate change scenarios for 2050 predict fewer but heavier rainfall during the vegetation period without substantial changes in the total annual amount of rainfall for Eastern Austria (Pannonian region). An experiment was carried out at the lysimeter station of the Austrian Agency for Health and Food Safety (AGES), comprising the three main soil types of the pannonian agricultural area (Calcaric Phaeozem, Gleyic Phaeozem, Calcic Chernozem) with six replications of each (18 in total). The lysimeter station was covered by a greenhouse whose ventilation panels are automatically regulated in synchronization with rain, wind and temperature sensors. Precipitation rates have been modified according to the predicted scenario for the second half of this century in comparison to the current precipitation pattern. The overall aim of the project was to obtain more information on possible changes in the soil–plant system due to lasting droughts and heavy rain events. The analysis of Phospholipid Fatty Acids (PFLAs) should highlight possible responses of the microbial community. Already after the first few months, a response of the PLFA´s could be detected. Whereas at the beginning of our experiment (in May) no difference between the precipitation treatments occurred, only after 3 months higher biomass levels were measured following the change of precipitation. Across all three years the PLFA´s were more or less affected by the rainfall treatment and the soil type. There is a variability between the treatment, the soil types and the sampling dates (seasonal and annual).

P28 The Microbial Mediation Model: linking microbial communities, litter traits, and soil carbon cycling via community-level physiology

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Understanding the role microbial communities play in plant litter decomposition and soil carbon cycling requires studies that test explicit theories of microbial community functioning and carbon cycling at multiple scales. Through empirical research, from microcosms to field experiments, we seek to disentangle the influence of litter traits and microbial communities in driving variation in litter decomposition rates and subsequent soil carbon storage. We base this study on a conceptual model which uses a community-level, trait-based approach to link litter traits with variation in soil carbon storage via microbial community structure and function. We argue that the influence of litter traits on decomposition rates and subsequent distribution of organic carbon among soil fractions ranging from relatively protected and persistent (e.g. mineral-associated) to unprotected (e.g. free particulate matter) is mediated by microbial decomposer community activity. We predict that litter traits select for varying microbial communities with distinct physiological traits, including carbon-use efficiency (CUE), which in turn drive the fate of decomposition products within the soil. Here, we discuss specific predictions of the model and outline a set of mesocosm and field-level experiments designed to test these predictions at multiple scales, focusing on a ‘common garden’-type forestry plantation in the Netherlands with a relatively short history of tree-derived carbon input. We also discuss results from our initial field survey of surface litter testing whether the predicted relationship among litter traits, microbial CUE, and soil carbon distribution is present at the field scale, and discuss implications for further research.

P29 Single microbial population controls energy and carbon use efficiency during growth and starvation in soil

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Despite the metabolic pathways of labile substrates are well documented in pure cultures, the relationship between microbial growth and transformation of matter/ energy still remains uncertain under natural soil conditions. Here we compared an efficiency of energy (by isothermal calorimetry) and carbon (by 16S rRNA gene copy number and CO_2) metabolism during glucose decomposition by soil microbial community. Remarkably, the sole phylogenic group of *Bacillus* outcompeted the others responding to the glucose addition with a 400-fold increase in number and representing 38.4% of the bacterial community. Such *Bacillus* domination demonstrated tight synchrony of catabolic and anabolic processes during exponential phase of growth. At growth retardation, however, the rate of CO_2 emission decreased much slower as compared with sharp decline pattern of heat release. This study gives an alternative view on soil microbial community response to the batch supply of available substrate showing how microbial metabolism in soil can be linked with evolution of specific microbial group.

P30 Soil biochemical properties and stabilization soil organic matter in relation to deadwood of different tree species

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Dead trees are an important element of properly functioning forest ecosystem and they play a very important role in the maintenance of biodiversity, soil fertility and they alsoparticipate in hydrological processes. The aim of study was to estimate how the deadwood of different tree species in various stages of decomposition affected soil biochemical properties and stabilization of soil organic matter. The deadwood of four species (Common alder, Common aspen, Silver fir and Common hornbeam) was selected. Three logs from each species in the third, fourth and fifth decay classes were chosen for the analysis. We estimated and monitored the soil organic matter stabilization and biochemical properties of soil in different distances from decaying logs. The investigation was carried out in Czarna Rózga Reserve in Central Poland. The basic physical and chemical properties, respiration, microbial biomass C and N, enzyme activity of soil and wood were determined. Additionally, fractions of soil organic matter were estimated. The results confirmed the importance of the wood species and the stage of decomposition for the amount and quality of soil organic matter. Significant differences in the carbon stock between coniferous and deciduous species were noted. Studies have confirmed the importance of decomposition rate in the formation of fractional organic matter. With the advancement of the deadwood decomposition process, the microbial activity slightly increased. The highest carbon accumulation and microbial activity was determined in soil under deadwood and in its direct vicinity. At a 100 cm distance from the deadwood, the influence of logs was not visible.

P31 The C:N:P stoichiometry of deadwood of different decomposition rate and tree species

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Deadwood is a natural and indispensable component of forest ecosystems, it plays a very important role in biodiversity and soil fertility maintenance. The aim of study was to estimate the C:N:P stoichiometry of deadwood in different decay classes. The deadwood of four species (Common alder, Common aspen, Silver fir and Common hornbeam) was selected. In deadwood samples the carbon, nitrogen and phosphorous content were determined. Additionally, soil samples under deadwood were taken and fractions of soil organic matter - humin, humic acid, and fulvic acid were estimated. The stoichiometric trends identified in this work indicated the differences in rate of deadwood decomposition. The stoichiometric patterns established in this work provide a new quantitative framework for deadwood classification. Studies have confirmed the importance of deadwood rate decomposition and species in the formation of the fractional organic matter.

P32 Short-term changes in grassland soil microbial function and composition are explained by concurrent shifts in plant functional traits

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Soil microorganisms are key players in the nutrient cycles of grasslands. Nevertheless, we lack information on the speed by which changes in the land-use intensity (LUI) of grassland sites affect soil microbial function and community composition, and an understanding of the mechanisms through which these changes operate. Within the framework of the Biodiversity Exploratories project we investigated the drivers of changes in soil microbial biomass, function and community composition within three years on 150 agricultural grassland sites located in the South-West, Central and North-East of Germany (50 sites per region) and differing in their LUI. Topsoil samples (0–10 cm) were analyzed for microbial biomass (microbial C, N and P), function (enzyme activities of C, N, P cycles) and community composition (PLFA, ergosterol). We then related these properties to abiotic soil conditions, LUI, community abundance weighted means (CWM) of plant functional traits, and to plant biomass measures (mass, content of cellulose, hemicelluloses, lignin, N, P). Hierarchical modelling demonstrated that observed changes in microbial biomass, function and community composition were explained by both short-term changes in the environmental properties or by the history of these properties (legacy effect). It also revealed that changes in the CWMs of plant traits, particularly plant P content, were the best predictors of changes in soil microorganisms, and that changes in LUI were relatively unimportant. Additional structural equation models revealed that historic LUI partly affects changes in soil microorganism's function and community composition indirectly via long term changes of plant traits.

P33 Microbial colonization of organo-mineral complexes and microbial resource partitioning in grassland soils under different land-use intensities

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Colonization of minerals and organo-mineral complexes depends mainly on biotic and abiotic soil properties, but initial colonization processes of mineral surfaces under field conditions are poorly understood. Further, it is still debated whether archaea, bacteria or fungi start feeding on root litter resources in grassland soils simultaneously or whether their activity occurs at different successional stages, and whether this depends on land-use intensity (LUI). To fill these knowledge gaps, we established a field experiment on ten differently managed grasslands – five sites with low LUI and five sites with high LUI – located at the Swabian Alb, Germany, within the Biodiversity Exploratories project (*http://www.biodiversity-exploratories.de*). On each grassland site, PVC-containers (further “containers”) filled with a mixture of 71.4% illite, 9.6% goethite, 17% silt-sized and 2% sand-sized quartz, mimicking local soil texture, and labeled roots of *Dactylis glomerata* and *Lolium perenne* (13.1 atom% ^{13}C and 31.1 atom% ^{15}N) were buried in 5 cm depth in September 2014. The containers were sampled after 1, 2, 7, 12 and 31 months together with adjacent soil and plants. Compared to the surrounding soil, only 13% of microbial biomass carbon was detected within the exposed mineral mixtures after 31 months. Fungi (ITS) colonized the new surfaces faster than both, bacteria and archaea already after one month of exposure, supporting the view of preferential fungal hyphae growth towards new substrates. Bacterial attachment to soil particles is probably the cause for slow transport of bacteria within the top soil of different grassland ecosystems.

P34 Nitrogen addition to temperate forests lead to changes in microbial community structure and function

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Increased nitrogen (N) inputs from atmospheric deposition have been proposed to foster carbon (C) storage in forest soils. Here, we examine how two decades of N addition have affected belowground C and N pools, physicochemical soil properties, as well as microbial biomass, activities and community composition. The main questions asked were: (i) What is the effect of additional N input on the structure and function of microbial communities? (ii) Is microbial community structure and function related to soil C sequestration? Our two sites in Denmark and Switzerland received N fertilization of 30-35 kg N ha^{-1} y^{-1} and are dominated by Norway spruce. We found that chronic N addition resulted in similar vertical changes in soil C storage at both stands: Carbon accumulated in moderately decomposed organic horizons (Oe), while C pools of the first mineral horizon (Ah) were dramatically reduced. Rather unexpectedly, we did not find evidence for reduced microbial biomass, fungal biomass, soil respiration and oxidative enzyme activities in the N addition plots. However, we observed (i) shifts from Ascomycota to Basidiomycota with N addition (ii) changes in C pools were reflected by plant protein abundance, and also community function in terms of energy production and conversion, as well as microbial carbon use efficiency. Increasing SOC pools in O-horizon, decline in A-horizon, this could imply that N negatively affects long-term C sequestration in temperate forests by promoting C accumulation in the less stable organic layer at the expense of the more stable C pool in mineral soil.

P35 Ecological functions of two putative *Streptomyces* phosphinothricin N-acetyltransferases

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The antibiotic bialaphos is produced by two *Streptomyces* species and finds wide application as herbicide in agriculture. It inhibits prokaryotic and eukaryotic glutamine synthase, thereby interfering with the nitrogen metabolism of the cell causing a depletion of glutamine, followed by cell death. The bioactive conversion product of bialaphos, phosphinothricin (PPT), can be detoxified by a phosphinothricin N-acetyltransferase. Homologues of this enzyme are found in many soil bacteria. They are often also active against other glutamate analogues and oxidized forms of methionine, thereby contributing to the cell's general stress resistance. In the present study, two genes encoding putative phosphinothricin N-acetyltransferases of the soil isolate *Streptomyces mirabilis* P16 B-1, designated as *SmPat1* and *SmPat2*, were investigated. The aim was to determine the substrate spectrum of the enzymes to obtain hints as to why two similar genes are maintained within the same genome. This seems relevant since redundancy should lead to gene loss. Regarding their primary sequences, both proteins show high similarity to other well-described acetyltransferases. SmPat1 has a higher similarity to Pat and Bar, the streptomycete PPT acetyltransferases, while SmPat2 is more similar to YwnH of *Bacillus subtilis*, which acetylates PPT, methionine sulfoximine and methionine sulfone. *SmPat1* was inactivated in P16 B-1, which resulted in a decreased resistance to bialaphos on minimal medium. Concordantly, overexpression of *SmPat1* in *S. lividans* TK24 increased bialaphos resistance. Heterologous overexpression in *E. coli* lead to increased tolerance towards bialaphos, and the transformant showed better growth in presence of methionine sulfone. Overexpression of *SmPat2* had no influence on resistance to either substance. The investigation leads to the conclusion that the enzymes show different substrate spectra and therefore contribute to the response towards different stressors. From an evolutionary point of view, this can be seen as the reason for maintaining multiple genes with high sequence similarity.

P36 Microbial interactions in the avocado rhizosphere: pathogenic fungi and plant growth-promoting bacteria with antifungal activity

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Rhizosphere microorganisms actively interact with their host plant in beneficial, harmful, or neutral ways. Beneficial microorganisms include those with plant growth promoting activity or antagonistic effects against plant pathogens, which could enhance plant health and productivity. However, this productivity could be hindered by the occurrence of phytopathogens. It is therefore important to evaluate the plant growth promoting activity or the pathogenic effect of rhizosphere microorganisms, especially of those associated with economically important crops. We evaluated the plant growth promoting activity of 11 bacterial isolates that were obtained from the rhizosphere of healthy avocado trees and from that of avocado trees having survived root rot infestations. Moreover, we assessed the pathogenic activity of 10 fungal isolates obtained from the same trees. Seven bacterial isolates, identified as *Bacillus* spp., *Pseudomonas* sp. and *Arthrobacter* sp., promoted the growth of *Arabidopsis thaliana* in *in vitro* assays and were also tested for antagonistic activity against *Phytophthora cinnamomi*. Isolate A8a, a bacterium identified as *Bacillus acidiceler*, was able to inhibit the growth *P. cinnamomi* by 76% through the production of volatiles, which were found to be mainly composed of ketones, aldehydes, alkyls, sulfoxides, and pyrazines. Some of the detected volatile compounds were previously reported to present antifungal activity against other fungal pathogens. Molecular identity and phytopathological tests with fungal isolates evidenced at least 3 new fungal species potentially pathogens of avocado trees. These results confirm the importance of rhizobacteria for the control of soil-borne fungal pathogens.

P37 Impact of pasture degradation on the structure and function of microbial communities on the Tibetan Plateau

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The Tibetan Plateau hosts the world's largest alpine pasture ecosystem playing an important role in carbon storage. Large areas are dominated by *Kobresia pygmaea*, which is adapted to moderate grazing. However, recurrent frost impacts together with strong overgrazing have caused vast soil degradation. We aimed at identifying interactions between SOM quality/quantity and the microbial community along a degradation sequence. Activity of extracellular enzymes (C, N, P cycles), a t-RFLP analysis and MiSeq sequencing of the microbial community were performed. Increasing translocation of cutin-derived fatty acids and sugars to subsoil occurred with intensified degradation. Decreasing C contents and $\delta^{13}C$ values with increasing degradation reflect high SOC losses due to mineralization. In consequence, lignin relatively accumulates, inducing a higher phenol oxidase activity. Simultaneously, intensified degradation decreases all other enzyme activities, indicating a functional shift of the microbial community. This agrees with t-RFLP and MiSeq data, confirming changes within bacterial and fungal assemblages. These communities change significantly during degradation and are controlled by both lignin enrichment and a decrease in C, N and P contents: i.e. *Nitrosomonas* was increased, indicating a severe N loss. Furthermore, mycorrhiza composition also changes with degradation: VAM association with *Kobresia* disappears with increasing degradation and is replaced by ECM. ECM indicates the necessity of nutrient acquisition from complex SOM. When *Kobresia* meadows are fully degraded and other plant communities establish, VAM gets dominant again. These structural and functional changes of the microbial community on *Kobresia* grasslands may be irreversible as nutrient losses are likely to prevent recovery.

P38 Decomposition Parameters Using the TBI Method in Two Cerrado Environments in Southeast Brazil

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The decomposition consists in the gradual organic matter disintegration, controlled mainly by physical factors, residue quality and decomposers. To measure decomposition rates in different ecosystems, the Tea Bag Index (TBI) method is used worldwide, based on green and rooibos tea bags (Lypton®) use. Therefore, this study's objective was to verify the rate of decomposition using the TBI method in palm swamp and cerrado *sensu stricto* ecosystems in Bonito de Minas-MG, southeastern Brazil. In each environment, four transects of five meters with five units of each tea (green and rooibos) were delimited, totaling 80 samples. On October/2017 the tea bags were weighed and buried at 8cm deep, distant 15cm from each other and 100cm between the sets. After 90-day incubation, they were recovered, 48-hour oven-dried at 60ºC and weighed. The TBI calculations were made based on the decomposition rate (k), teas stabilization factor (S), proposed by Keuskamp et al. (2013) and analyzes in software R. There was significant relationship between S and the environments ($F=6.4408$, $P<0.017$), with highest values observed for the cerrado, while k had no difference ($F=3.9005$, $P<0.062$) between the areas. The mass lost percentage varied between the environments ($F=6.7454$, $P<0.015$), greater in the palm swamp (80.17 ± 6.44) than in the cerrado *sensu stricto* (66 ± 18.46). These results are possibly related to palm swamps characteristics, since they are humid ecosystems with hydromorphic soils, which can favor the colonization and decomposers action in these places, in comparison to more xeric environment observed in cerrado.

P39 Microbiological activity and plant colonization patterns in a so long abandoned sulfide mine precinct

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Large stacks of gangue, slagheaps of material from the milling process and subsequent extraction by density, wide surfaces affected by acid drainage and dunes of fine material accumulated by wind with steep slopes are the distinctive elements of the current landscape in the so long abandoned area known as San Quintín mines. All the area is affected by sulfide minerals whose transformations lead to the formation of sulfates, hydroxysulfates and hidrous oxides that finally generate acidic solutions. A thorough study of the plant communities composition and colonization patterns related with the soil microbiological activity from the most contaminated core to the less disturbed outer zones may yield clues about the eco-physiological behavior of these species and the basis of their resilience to extreme environmental conditions. For this purpose, 5 zones were delimited: (1) a fine sludge raft (silts); (2) a coarse sludge raft (sands); (3) gangue stacks; (4) an area affected by acid drainage and (5) a transition area with materials coming from the surrounding hillsides. The standard physicochemical soil parameters (pH, electric conductivity, texture and soil organic matter) and the microbiological activity (dehydrogenase, acid and basic phosphomonoesterase, urease and β-galactosidase) were determined in each of the previously defined areas in relation with the mineral composition of the substrate. A correlation was made between the plant cover species, their biomass density and the soil biogeochemistry parameters.

P40 Culturing techniques in the age of omics: Strategies for obtaining uncultured soil microorganisms and genomes from environmental samples

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Rapid advancement in sequencing capabilities and reduction in cost has increased the use of omics based research approaches. However, with these advancements there is presently an information gap forming between omic based and community fingerprinting approaches and traditional culturing studies. Here we anaerobically enriched peat soil with growth substrates, supplements, and antibiotics to identify novel methanogen taxa and potential growth conditions. Over the course of three years we identified 28 taxa (via *mcrA* sequences) that have remained previously uncultured and undescribed beyond distantly-related sequences detected in environmental samples. Evidence suggests that novel methanogens, representing 5 of the 7 known orders, were capable of growing on H_2 as well as acetate and at temperatures ranging from 6 °C to ca. 22 °C. Methods involving the use of ampicillin proved useful and obtaining high methane production in the absence of H_2 was difficult. Our results also indicate that many methanogens may rely on bacterial symbionts (commonly *Clostridium spp.*) and that enrichments are a useful intermediary between maker-gene detection and isolation, allowing us to broaden our understanding of methanogen physiological ecology, while bolstering our reference sequence library to support the plethora of *mcrA* and rRNA gene based community-fingerprinting studies. Due to the relative difficulty in isolating anaerobic microorganisms, and methanogens in particular, we propose that combining enrichments and modern sequencing methods are a way forward in developing an understanding of methanogen diversity and functioning in a variety of ecosystems, effectively bridging the gap between environmental omic based approaches and traditional culturing techniques.

P41 Microbial biomass C and C mineralisation of a seaweed-gorse substrate

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Seaweed that is deposited on beaches in large amounts as a result of tidal or wind action has been used for centuries as a fertilizer in coastal areas. This is because it is particularly rich in potassium and micronutrients as well as growth activators such as auxins, cytokines and alginates, which improve soil structure. Recent studies showed that co-composting of seaweed with other organic residues (fish waste, pine bark, gorse, etc.) could be a promising method to obtain an optimal compost of natural origin for use as an amendment, fertilizer or as a substrate in ecological agriculture. In this study we determined the microbial biomass C and the C mineralisation capacity of different mixtures of a brown alga to which different treatments were applied (untreated, washed, washed and air-dried) with a commercial substrate based on gorse compost (suitable for organic agriculture). The aims of the study were i) to investigate if the brown alga could improve the quality of the commercial substrate, and ii) which of different mixtures gorse-substrate-alga would provide the best results. The mixture of gorse compost with the alga generally caused an increase of C mineralisation, but only the untreated fresh alga caused an increase of microbial biomass C while the washed and the air-dried alga caused a decrease of microbial biomass. Whatever the treatment applied to the alga, the organic C mineralised was proportional to the amount of alga added. However, the microbial biomass C was only related to the alga amount when this was air-dried.

P42 Impact of the ionic liquid [C_1C_1Im] [DMP] on soil microbial activity in a forest soil

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Ionic liquids (ILs) are organic salts formed by one organic cation and one organic or inorganic anion, with melting point below 100 ºC. In recent years, these compounds have attracted a great attention because of both the infinity of cation-anion combinations and their properties (polarity, miscibility, hydrophobicity, etc.) making them promising candidates for multiple applications. In addition, the negligible volatility of ILs has led to consider them as innocuous in some contexts. However, due to accidental spills the ILs could reach surface and subsurface waters and soils, and therefore it is necessary to prove that ILs are also harmless for aquatic and terrestrial environments. The 1,3-dimethylimidazolium dimethylphosphate [C_1C_1Im][DMP] (Nº CAS: 654058-04-5) is an IL with wide potentiality because, among other multiple applications, it can be used as lubricant-hydraulic fluid, as absorbent in heat pumps, as a heat transfer fluid for heaters or freezers, etc. Soil biochemical and microbiological properties are considered as the most sensitive indicators of the modifications to soil functioning caused by anthropogenic activities. The aim of this study was to investigate the soil toxicity of [C1C1Im][DMP]. To do this, several properties reflecting soil microbial activity (C mineralization and dehydrogenase and fluorescein diacetate hydrolysis (FDA) activities) were analysed in an acid, rich in organic matter soil spiked with increasing amounts of [C_1C_1Im][DMP]. FDA activity was almost unaffected by the presence of [C_1C_1Im][DMP], while dehydrogenase activity decreased proportionally to the amount of [C1C1Im][DMP] applied. [C1C1Im][DMP] strongly increased the amount of C mineralised and modified the mineralisation kinetics.

P43 Effect of plant growth promoting endophytic bacteria on Riceberry Rice

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Black rice (*Oryza sativa*) variety Riceberry is increasing popularity as healthy food in Thailand. It contains high vitamins and anthocyanin. Endophytic bacteria are able to colonize plant root systems. Some of the endophytic bacteria can promote plant growth and crop yield through many mechanisms. Objectives of this study were to isolate endophytic bacteria associated with rice plants and to evaluate the plant growth-promoting endophytic bacteria (PGEB) for the growth of Riceberry rice. A total 151 endophytic bacterial strains were isolated from roots, stems, and leaves of rice grown in submerged conditions at different areas of Chiang Mai, Thailand. The isolated endophytic bacteria were evaluated for their ability to produce indolic compounds. Fifteen isolates of the endophytic bacteria could produce indole-3-acetic acid (IAA). Among 15 isolates, 5 strains had high IAA producing activities. The five effective bacteria were able to colonize roots of the Riceberry rice and stimulate the growth of the rice plants under gnotobiotic conditions. The pot experiments of growing Riceberry rice were done in greenhouse condition associated with the selected effective bacterial strains. Rice seeds treated with the IAA producing bacteria increased height and dry weight of the Riceberry plants. The results indicated that the PGEB in this study could be used for growth of Riceberry rice.

P44 Comparison of buried and surface soils microbiomes by qPCR and NGS

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The study was conducted to find out how the structure and diversity of microbiomes in buried soils differ from those in surface soils, and can analysis of microbial DNA from buried soils be used as a tool for paleoecological reconstructions. Samples were taken from buried soils under earthworks (burial mounds or earth fortifications) of different age, and from surface soils of the same area. Total DNA was extracted, and bacterial, archaeal and fungal abundance (by ribosomal genes qPCR) and prokaryotic biome structure (by 16S rRNA gene amplicon sequencing) were investigated. Microorganisms abundance and diversity are decreasing in buried soils. Taxonomic structure of prokaryotes in buried soils differs significantly from that in surface soils. Very low relative abundance of *Verrucomicrobia* is the main difference of the buried soils microbiome structure. Obtained results show that microbiome structure is altered strongly by soil burial and hardly can be marker of ecological conditions in soil before earthworks. Nevertheless, some features of vertical distribution of microbiomes in soil profile (e.g. decrease of abundance from A to B horizon) remains unchanged in buried soils and can carry some information about native soil microbiome.

P45 Bacterial typing of rhizospheric communities of the *Thysanolæna latifolia* (Roxb. ex Hornem.) Honda., fam. Poaceae., associated with iron ore mines

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Rhizospheric diversity of microbes in T. latifolia growing at degraded sites undergoing ecological restoration at Barsua iron ore mines (N21°52.008’, E85°08.893’) in Sundargarh, Odisha was investigated using culture-dependent and culture-independent techniques. T. latifolia also known as “Ravine broom grass” is a pioneer species characterized by high biomass production, ability to conserve moisture and slope stabilization due to an effusive fibrous root system. For typing of rhizospheric microbial communities at spatial and temporal scales, PCR amplifications of 16S rRNA gene fragments, clonal library preparations, restriction-digestion based binning by ARDRA and Sanger sequencing for representative clones was done. Clonal library-based results were validated by Illumina HiSeq-based next generation sequencing (NGS) of metagenomic soil DNAs. The V3-V4 region was characterized. Highly diverse communities of bacteria with members belonging to 113 bacterial classes were detected in varying abundances. More than 6523 bacterial OTUs were observed which included members of PVC super phylum, Proteobacteria, Acidobacteria, Actinobacteria, Gemmatimonadetes, Chloroflexi, and unassigned Genera incertae sedis. A bootstrapped RAxML III tree was generated using unique 16S rRNA gene sequences along with closely-related reference sequences at >97% sequence similarity. Results indicated that rhizospheric bacterial community structure of a metal-tolerant and phyto-stabilizing grass species like T. latifolia from restoration sites sampled in the summer were distinct from those sampled in the monsoon season.

P46 Increasing bacterial contribution in the nitrification following turf disturbances of the translocated wet meadows

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To compensate for the airport build-up on highly valuable wet meadows, 1.3 hectare of turf were transferred to the botanic garden located 15 km apart in 2013 (Southern Poland). Three meadows were monitored for three seasons: before the transfer and two years afterwards (2014, 2015). The domination of ammonia over nitrate, characteristic for wetlands, strongly decreased after the transfer. The content of soil ammonia dropped for a half a year after the transfer. At the same time nitrate content increased two-times and three-times two years later. This suggests increased nitrification resulting from physical disturbances at the time of translocation, oxygenation and also presumed habitat drying and humus decomposition at the receptor place. To evaluate possible changes in the nitrifying community size q-PCR of *amoA* gene of Bacteria (AOB) and Archaea (AOA) was performed. The *Thaumarchaeota amoA* gene copies number strongly dominated over bacteria before the meadows translocation. Following the turf transfer the AOB abundance was increasing each year so that it finally reached the AOA abundance two years after the transfer. The results points on increasing contribution of bacterial nitrifiers at increased soil oxygenation and nutrient enriched conditions, while waterlogged conditions are limiting bacterial nitrification for the sake of *Thaumarcheota*.

P47 The effect of plants with different mycorrhizal preferences on soil fungal community composition

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Evolution and ecology of all plant species is into some extent associated with fungal symbionts. Therefore plants developed number of mechanisms to influence fungal communities in their close neighbourhood. Plant-fungal symbiosis is particularly important for mycorrhizal plants, which largely dependent on their mycobionts. We therefore hypothesized that obligatory rather than facultatively mycorrhizal or non-mycorrhizal plants will have stronger effect on composition of soil fungal communities. We created field experiment where we planted 6 obligatory mycorrhizal, 3 facultative mycorrhizal and 6 non-mycorrhizal plant species into monodominant plots. Soil fungal communities were subsequently repeatedly determine using Illumina sequencing of ITS2 region of rDNA. The results indicate gradual significant shift in soil fungal communities under obligatory and facultatively mycorrhizal plants. These changes were more profound in case of facultatively mycorrhizal plants.

P48 Stimulating saprotrophic fungi in agricultural soils

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Saprotrophic fungi play a crucial role in soil functioning in (semi-)natural ecosystems. On the contrary, their biomass is often low in farmland soils. This is ascribed to the use of chemicals (mineral fertilizers and pesticides) and tillage practices. The restoration of a higher saprotrophic fungal biomass could support the functioning of sustainable agricultural systems, for instance by improving soil aggregation and nutrient retention. Moreover, fungi can contribute to a more resilient microbiome, as they are important for the suppression of plant-pathogens. This study explores the possibilities to enhance the growth of saprotrophic fungi in agricultural soils by the addition of organic materials. Firstly, a range of fourteen organic residues of different composition were mixed with a agricultural sandy soil. Wood sawdust and paper pulp resulted as the best fungus-stimulating materials, as compared to waste materials, composts and plant residues. Moreover, the analysis of the fungal community structure revealed that different groups of saprotrophs, yet not potential pathogens, were activated by sawdust and paper pulp addition. Secondly, a comparison of sawdust obtained from five tree species confirmed the suitability of milled wood for a long-term stimulation of fungi in soil. The consistency of sawdust's fungus-stimulating effect was confirmed in agricultural soils differing in pH, texture and organic matter content. This study serves as a basis for the use of wood sawdust as soil improver via the stimulation of saprotrophic fungi.

P49 Strong legacy effects of intense and frequent droughts on soil microbial community structure and function

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Extreme droughts have profound effects on soil microbial communities, affecting their structure and function. It is forecasted that climate change will increase the frequency of extreme events, but how repeated droughts will impact soil microbial communities has not been tested. We designed a microcosm experiment to test the effects of drought intensity and frequency on soil microbial communities. We evaluated effects on the resistance and resilience of microbial functions, community structure and nutrient availability over a 6 month period following rewetting. We also tested the resistance of bacterial and fungal growth to low moisture and their ability to recover following a drying-rewetting cycle. High intensity drought had a strong negative effect on microbial biomass and function, measured as enzyme activities related with decomposition, and caused a large pulse in inorganic nutrients availability. High drought frequency and intensity combined to exacerbate these negative effects, which mostly persisted 6 months after rewetting. Drought also restructured the functional characteristics of the microbial communities: fungal growth was more resistant than bacterial, and increased immediately on rewetting following mild or moderate drought, but not after severe and frequent drought. By contrast, bacterial growth had a lag period of zero growth, which was shorter in extreme drought soils, and cumulative growth increased with drought intensity and frequency. This suggests that severe drought selects for a more resilient bacterial community, and a shift to more bacterial-dominated decomposition. Our findings suggest that frequent intense droughts have strong legacy effects on the structure and function of soil microbial communities.

P50 Optimization of growth and EPS production of two strains of *Acidobacteria*

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The phylum *Acidobacteria* is a highly abundant group in most soils and can represent up to 52% of the total bacterial community. However, the ecological roles and physiology of bacteria belonging to this phylum remain largely unknown due to difficulties in cultivation under laboratory conditions. Trace elements (TE) are metal ions needed in small quantity for microbial metabolism that play an important role in biological processes. Thus, one strategy that might improve the cultivation and growth rate of acidobacterial strains in laboratory would be the addition of TE to the medium. In this study we assessed the effect of individual TEs and the effect of different concentrations (0, 1X and 10X) of TE solution (SL10) on cell growth of acidobacterial *Granulicella* strains 5B5 and WH15 in PYSL 5 medium. Furthermore, we evaluated the effect of individual TE and nitrogen (N) sources in the extracellular polymeric substance (EPS) production of both strains. At 1X concentration of SL10, OD_{600nm} of both strains increased significantly compared to control. However, at 10X concentration of SL10, there was only significant increase in the growth of 5B5 strain. The addition of individual TEs demonstrated that manganese (Mn), copper (Cu) and iron (Fe) significantly increased the bacterial growth of 5B5 while only Mn significantly increased the growth of WH15. No trace element improved EPS production of both strains. Lastly, organic N sources induced a higher EPS yield compared to inorganic sources, showing that organic N sources are the best for EPS production by both the strains evaluated.

P51 Following the impact of metals on river sediments in microcosms: metals as a community manager

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Metal contamination of soil and sediments causes serious environmental and health issues as metals cannot be degraded. Despite elevated metal concentrations, river sedimentary microbial communities near the MetalEurop foundry (Northern France) display an unexpected high diversity in comparison with an upstream control site (Férin). Recent methodological improvements of 16S rRNA taxonomy profiling has enhanced analytical accuracy and revealed that metals act as drivers of the microbial community structure. In the present study, a follow-up of the evolution of sediment microbial communities sampled in Férin sediments was performed in microcosms with a periodic renewal of the supernatant water. Experimental microcosms were progressively exposed to a mixture of metals to finally reach concentrations observed in MetalEurop: Cd (38.1 mg/kg), Cu (100.0 mg/kg), Pb (913.8 mg/kg) and Zn (3218.5 mg/kg). Microcosms were followed using 16S rRNA gene Illumina sequencing. Functional insights on metal resistance were obtained by quantitative PCR targeting *czc*A and *pbr*A genes coding for metal efflux pumps. The broad host range incP plasmid content was also followed by quantitative PCR. Interestingly, taxonomical analyses revealed a higher specific richness and equitability in metal-contaminated microcosms. This increase can be explained by metals acting as a community-manager together with community coalescence (i.e., the gathering of two different microbial communities). Quantitative PCR analysis coupled with taxonomic evolution suggest a step by step adaptation through the selection of different metal-resistance mechanisms.

P52 Increases in temperature and atmospheric CO_2 can induce shifts in soil microbial communities

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Intensively managed grasslands play an important role in global agriculture and are affected by multiple climate change factors. Soil microbial communities as drivers of ecosystem processes are supposed to respond in different ways to these factors. The aim of the present study was to evaluate direct and indirect effects of increases in temperature and atmospheric CO_2 in a pre-alpine managed grassland in Austria. Effects of individual and combined changes in air temperature (ambient, +1.5 and +3°C) and atmospheric CO_2 concentrations (ambient, +150 and +300ppm) are examined at a multifactorial climate change experiment. Soil samples were taken two years after start of the treatments. Fungal and bacterial communities were analyzed via high-throughput sequencing on the Illumina MiSeq platform of ITS2 and partial 16S, respectively. We observed only minor effects of the climate change treatments on the soil microbial community. However, a few operational taxonomic units (OTUs) showed significant responses to elevated temperature or elevated CO_2. In addition, selected bacterial (*Bacillus* sp.) and fungal (*Mortierella* sp.) OTUs showed a significant increase in abundance in the extreme CO_2 treatment. Temperature increase had a positive effect on the abundance of white rot fungi in general, and especially on white rot fungi with preference for herbivore dung. No specific combined treatment effects could be identified on microbial communities. Besides, the soil fungal community showed a high autocorrelation with plot distance indicating that spatial gradient across the experimental area had an effect on the fungal community composition. Our results indicate only small shifts in microbial community composition by climate change factors after two years of treatment. The greatest change, the observed temperature induced increase of coprophilous white rot fungi may be an indirect effect of mice gathering on heated plots, which is a common phenomenon in those experiments.

P53 Effects of repeated water-logging periods during the growing season on soil conditions and Scots pine seedlings

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Soil water-logging during the growing season is known to have adverse effects on plant growth and soil conditions, as e.g. on peatlands, where the ground water tables are high and can vary within the growing season. For assessing the effects of repeated water-logging periods on above-and below-ground growth of 4-year-old Scots pine seedlings in peat soil as well as on soil conditions, we conducted a laboratory experiment lasting for three simulated growing seasons with three soil water-logging periods during the second growing season. Each water-logging-period lasted one week with one week interval between them. We measured soil oxygen, carbon dioxide, methane and nitrous oxide concentrations as well as ethylene efflux from the soil. In addition we assessed shoot and root growth and biomass and photosynthesis of the pine seedlings. Water-logging had immediate and distinctive effects on the soil gas conditions. Anoxic conditions were observed during the water-logging periods, but oxygen concentrations returned immediately to pre-water-logging values when water-logging ceased. Respectively, CO_2, CH_4 and N_2O concentrations increased instantaneously with water-logging and decreased thereafter. The seedlings themselves were not affected significantly during the water-logging treatments, although there was a trend for slightly decreased shoot and needle growth of the water-logged seedlings compared to those in the control treatment. Our results indicate that Scots pine seedlings seem to be adapted to short-timed changes in ground water-table and do not show to be impaired by short repeated periods of water-logging, even during the growing season.

P54 Small-scale spatial structure of a major group of soil protists (*Cercozoa*, *Rhizaria*) in a temperate grassland revealed by high-throughput sequencing

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How are soil protists communities structured? Which are the main factors - biotic and abiotic - shaping their distribution? We contributed to these questions by an intensive survey of a 10x10 m unfertilized grassland soil in Germany, unveiling the small-scale temporal and spatial distribution of the Cercozoa, a very common group of amoebae and flagellate protists. We compiled a functional traits database, since Cercozoa contain both amoebal and flagellate forms, various nutrition modes as parasites or free-living bacterivores and omnivores, and locomotion modes like freely swimming or gliding on substrates. This will allowing to infer how each of this functional groups is differentially influenced by biotic and abiotic factors and how they influence ecosystems processes and services. From 177 soil samples, collected at six dates from April to November 2011, we obtained 694 cercozoan Operational Taxonomy Units (OTUs) at 97% similarity threshold, representing > 6 millions sequences. All major cercozoan groups were present in this small grassland plot. Saturation was reached - more sequencing would not have revealed more diversity, allowing full comparison between soil samples. Cercozoan communities were both spatially and seasonally structured. Mantel correlograms revealed that communities shared composition similarity up to a distance of ca. 4 m, giving interesting hints to understand how far usually protists disperse.

P55 Soil microbiological activity in differently cultivated Faba bean (*Vicia faba* L.) fields

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The importance of faba bean (*Vicia faba* L.) in cropping systems is not only via biological N_2 fixation but also due to improvement of soil microbiological activity. Beans are grown with different soil management practice, moreover legume seeds often are inoculated before sowing. Microorganisms, introduced in the soil as an inoculum, affects not only the inoculated plants but it can remain in the soil for the next growing season and can affect the subsequent crops. The aim of present study was to estimate the soil microbiological activity in soils where faba beans were grown. Soil biological activity under different tillage systems, in different crop rotation and inoculation variants was analysed. Rhizobia for seed inoculation were obtained from collection of Latvia University of Agriculture. Soil microbiological activity was assessed by soil respiration intensity and soil enzymatic activity by oxidative enzymes (dehydrogenase) activity and activity of hydrolytic enzymes. Compared microbial biomass and the total number of bacteria, fungi and rhizobia were expressed as CFU g^{-1} dry soil. Obtained results show that including beans in crop rotation increased soil enzymatic activity, but level of significance were different under both tillage systems and depended on seed inoculation.

P56 Cross-biome Metagenomic Assessment of Saline Soil Microbial Communities of Kutch Desert, India

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The microbial biomass is key components in the soil biomes. The variation in terrestrial microbiome and role of hidden microbial species in the biogeochemical processes is less explored across the terrestrial ecosystem. In the present study, we have used the shotgun metagenomic sequencing for structural and functional comparison of the 5 different soil microbial communities in 21 metagenomes of the arid desert of the Kutch, India. Soil was collected from the 5 different location of the desert (i) A saline desert - Little Ran of Kutch, (ii) Sandy desert- Greater ran of Kutch, (iii) Semi-arid soil of Banni area, (iv) rhizosphere soil of Banni region and (v) Coastal saline soil -Arabian seashore soil). The statistical and metagenomics analysis was done using MG-RAST, Megan, STAMP and PAST tools. The Proteobacteria phylum was dominant in the Coastal soil, Saline desert and sandy desert metagenome. Whereas, Firmicutes was abundant in both Banni samples. Most of the sample were also indicated the plentiful of the actinobacteria this is due to the tolerance of the stresses. Euryarchaeota was abundantly in the sandy desert. Substantial presences of the Gemmatimonodates in saline and sandy desert suggest its role in the biogeochemical transformation processes. Bacteroidetes and Cyanobacteria were also significant presents most of the samples indicate the primary producer. Shannon- H Alpha Diversity of all the habitats was ranging from 2.02 (Saline desert) to 3.59 Coastal soil. Whittaker Beta Diversity was also calculated to find the similar microbial profiling among the 5 habitats. The presence of stress response genes and biotechnological valuable enzyme-encoding genes suggest the exploration of such habitats for the biotechnological purpose. More than 50 different bacterial species have been isolated and tested for the enzymes production, plant growth promoting traits, xenobiotics degradation, and antimicrobial substances etc. So rich microbial diversity and interaction were trapped.

P57 Heterotrophic nitrate immobilization – a neglected variable in crop BNI performance?

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Biological Nitrification Inhibition (BNI) has been conceptualized as a plant exerted regulation of soil nitrifier activity as a result of production/release of allelochemicals via the root. *Brachiaria humidicola* (Bh) has gained attention due to its remarkable BNI activity, but inconsistencies between BNI ratings from different experiments suggest that BNI performance varies with the soil environment. In order to elucidate this relationship, a two-factorial pot trial with factors “Soil texture” and “Bh genotype” was conducted at CIAT (Colombia). BNI performance is defined as the ability of the plant to reduce activity and growth of nitrifiers in response to ammonium fertilization. Activity of nitrifiers was assessed via *in situ* monitoring of soil nitrate evolution using micro-suction cups. Growth of both ammonia-oxidizing archaea (AOA) and bacteria (AOB) was estimated by quantifying the respective *amoA* genes prior and 14 days after fertilization. Soil texture revealed a significant influence on nitrifier community abundances ($p<0.0001$) and nitrification rates ($p<0.05$), both increasing with clay content. AOA/AOB abundance confirmed the allelopathic activity of Bh with a strong tendency for reduced growth response of both nitrifying populations under the high BNI genotype in all soils ($p=0.0532$). Observed reduction of nitrifier growth did not translate into lower but coincide with higher topsoil nitrate concentrations though. As nitrifier growth response to N shall theoretically be a robust indicator for their metabolic activity, this discrepancy was mainly attributed to differences in subsequently immobilized nitrate by heterotrophic microbes. Ongoing experiments are currently finalized to further elucidate the proposed importance of heterotrophic nitrate immobilization.

P58 Defining sustainable and economic forestry practices with minimal impact on soil biodiversity and maximum benefits for tree growth

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The majority of temperate and boreal forest trees live in symbioses with ectomycorrhizal fungi (EMF). Considering all benefits of EMF, their conservation is economically and ecologically highly important. How EMF biodiversity is affected by harvesting and forest management strategies is debated. Nevertheless, clear-cutting disturbs the fungal community in soils. This study aims at identifying the effect of different harvesting intensities and reforestation practices on fungal biodiversity in soil samples and naturally regenerated or planted seedlings using DNA-amplicon sequencing over a five-years-time period after harvesting. We also study the effect of different harvesting practices (and hence biodiversity chances) on growth and adaptation of nursery pine seedlings, pre-inoculated or not with EMF. In parallel, we are developing a method to make EMF identification in soil samples cheaper and easier using a hand-held spectroscopic. Results on sensitivity and specificity will be compared to data from DNA-amplicon sequencing. The long-term aim of this project is to give forest companies and agencies guidelines for more sustainable forestry practices with least detrimental impact on EMF biodiversity and to provide a new tool to make EMF biodiversity assessment more accessible to non-scientists.

P59 Interaction of manure, soil and bacteria in spreading of resistance to antibiotics

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The increasing prevalence of antibiotic resistance (AR) among bacteria is a dire clinical problem, with important ecological dimensions. The application of animal wastes into agriculture soils play important role in the AR introduction and its spreading in the environment with links to food chain and human health. Processes of introduction, survival and establishment of manure tetracycline resistant bacteria (TRB), selected genes (TRG) and responsible mobile elements (TRME) in soil were studied on the model of HOT-SPOT experiment. This model ensures to focus on interactions among manure TR invaders and soil residents. Six different types of microhabitat and their bacterial communities (niches) were analyzed in frame of the HOT-SPOT experiment to see the above mentioned processes: 1) Manure, sampled at a conventional dairy farm from dairy cows under tetracycline-prophylactic treatment served as source of fecal invading TRB bacteria harboring TRG and TRME; 2) Soils originated from bio-farms without regular tetracycline treatment; 3) Manure/soil interface; 4) Manure/gamma-irradiated soil interface (for better characterization of fecal TRB); 5) Soil enriched by nutrients that simulated nutrient content in manure (for better characterization of nutrient input on indigenous soil TRB, TRG, TRME); 6) Gamma-irradiated soils. TRB composition based on 16S rRNA amplicons libraries isolated from the described niches via nycodenz gradient and TET-enrichment incubation were analyzed through HTS on the Illumina platform. Selected TRG (including all TR mechanisms: efflux pumps, ribosomal protection and enzymatic degradation) were screened and quantified. The biotic and abiotic impact of manure and soil on tetracycline resistome has been evaluated.

P60 Rhizobacterial community composition and potential PGPR associated to the Flowering Desert phenomenon in the Atacama Desert, Chile.

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Short and infrequent rainfalls produce an increase of soil water in Atacama Desert triggering the phenomenon known as Flowering Desert (FD). During FD, the germination and rapid growth of more than 200 Atacama's native plants is produced. Despite that recent studies have shown the natural occurrence of plant growth-promoting rhizobacteria (PGPR) associated with native plants from diverse Chilean extreme environments, there is not information about PGPR associated with FD phenomenon. Thus, the objective of this work was to describe the composition of total rhizobacterial communities and to isolate putative PGPR associated with FD phenomenon. Total DNA was extracted from bulk and rhizosphere soils from *Cistanthe* sp. (a representative plant of FD) and libraries of 16S rRNA genes were built by high-throughput sequencing and taxonomically assigned by using QIIME software. Samples were collected during two consecutives FD events produced under different rainfall regimes in 2014 and 2015. In both years, the results shown a higher relative abundance in operational taxonomic units for phyla *Proteobacteria* (72~33%) and *Actinobacteria* (38~9%) in all the samples. In addition, diverse isolates showed mechanisms commonly found in PGPR, such as indole acetic acid production, phosphorus solubilization and 1-aminocyclopropane-1-carboxylate deaminase activity. This study shows the composition of rhizobacterial communities during FD phenomenon and the natural occurrence of potential PGPR. However, further studies should address which species and functions are directly involve in growth promotion and fitness of native plants during FD phenomenon.

P61 Assisted phytostabilization of Cu-contaminated mine-soil using combinations of soil amendments and bioinoculants

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(Assisted) phytostabilisation has been proposed as a sustainable remediation technique for decreasing the environmental risks associated with metal(loid)-enriched mine tailings. Such phytomanagement options can be optimised through the selection of metal-tolerant plant species, design of adequate plant cropping patterns (e.g. incorporation of leguminous species to promote soil fertility and biological activity), or the use of soil amendments (to reduce acidity, stimulate biological activity and improve soil fertility and structure) and bio-augmentation with beneficial plant-associated microorganisms (e.g. mycorrhizal fungi or bacteria). A pot trial was established using acidic Cu-rich mine tailings to test the benefits and interactions of plant species, soil amendments and microbial inoculants on plant growth and Cu immobilisation. Amendment treatments included: (i) untreated soil; (ii) soil amended with composted sewage sludge (COM, 10% w/w); (iii) soil amended with COM (10%), biomass ash (ASH, 1%) and green liquor sludge (GLS, 1%); and (iv) soil amended with COM (10%), biochar (B, 2%), ASH (1%) and GLS (1%). Doses were selected in previous incubation assays. *Populus nigra* was planted alone or in combination with the legume *Trifolium repens*. Plants were inoculated with (i) a combination of rhizobacterial strains (previously isolated from contaminated soils and characterised for plant growth-promoting capacity), (ii) a commercial mycorrhizal inoculant (INOQ Forst), or (iii) both the rhizobacterial strains and mycorrhizal inoculum. Non-inoculated plants were also established. Effects on soil physicochemical properties, Cu availability and fertility, as well as plant Cu accumulation and nutrition, and microbial diversity, were evaluated. This study forms part of the PhytoSUDOE Project (SOE1/P5/E0189).

P62 Rhizosphere bacterial communities of Ni-hyperaccumulating plants in ultramafic soils analysed using traditional isolation and culture independent techniques

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Soils derived from ultramafic rocks typically present high concentrations of trace elements such as Ni, Co and Cr, nutrient deficiency and Ca imbalance and low organic matter contents. Metallophyte plants colonising these environments have developed specialised mechanisms to tolerate these conditions, such as the (hyper) accumulation of of trace elements (TEs) such as Ni. Nickel hyperaccumulating plants are of great interest for the development of phytomining techniques in Ni-rich soils or other secondary resources which are not adequate for conventional mining activities. Detailed studies of the rhizosphere bacterial communities associated with Ni hyperaccumulating plants is a valuable tool for the identification of key members of the community involved in plant growth, stress resistance and/or mechanisms of metal hyperaccumulation. Ultramafic areas of the Iberian Peninsula host the endemic Ni hyperaccumulating *Odontarrhena serpyllifolia* (syn. *Alyssum serpyllifolium*). Populations can be found in the NW Iberian Peninsula (NW Spain and NE Portugal) and S Spain (previously classified as the subspecies: *A. serpyllifolium* ssp. *lusitanicum* and ssp. *malacitanum*). The rhizosphere bacterial community in different populations of the hyperaccumulating *Odontarrhena* growing in ultramafic soils was analysed by pyrosequencing of 16S rRNA fragments, as well as, using a culture-dependent approach aimed at the isolation of rhizobacterial strains. Rhizobacterial isolates were also analysed for their plant growth-promoting properties and Ni resistance in an attempt to identify useful bioinoculants for phytomining. Pyrosequencing showed OTUs with high relative abundance were affiliated to the actinobacterial genera *Blastococcus, Arthrobacter* and *Lentzea* and to the *Bacteroidetes* genus Flavisolivacter. The isolates collection was dominated by strains of Arthrobacter and Streptomyces, although other actinobacteria of genera *Rhodococcus, Curtobacterium, Microbacterium, Amycolatopsis, Lentzea* and some *Proteobacteria* and *Firmicutes* were also cultivated. Further comparison and discussion of the results obtained using the two approaches will be presented.

P63 Designing microbial inoculants that improve the ability of compost amendments to restore degraded soils

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Soil degradation represents a pressing worldwide problem that is being accelerated by the processes of erosion, depletion of soil organic matter, soil compaction, acidification, salinization and drought. Applying organic soil amendments has often been used as measure to improve the physical and biological properties of soil, for instance to increase organic matter, improve soil structure and water retention capacity and increase microbial diversity and function. However, the success of such measures is often modest and unpredictable. We propose that the success of compost amendments can be improved by the addition of microbial species with specific traits that allow for successful compost/soil colonization and delivery of desired services such as improving soil aggregate formation, increasing water holding capacity and allowing greater carbon retention. To this end, we first established a bacterial culture collection of 132 strains that were assessed for drought resistance, salinity tolerance, growth rate, Exopolysaccharides (EPS) and biofilm production, as well as enzymatic activity. Based upon these traits, bacterial strains are selected for growth and activity trials in compost materials and soil amended with bacterially inoculated compost. Impacts of amended composts are tracked over time with respect to changes in soil physical-chemical properties, as well microbial community structure and function. Using this approach, we seek to determine the best bacterial consortia, consisting of the optimal combination of bacterial traits, to improve soil quality (aggregate formation, C retention, water holding capacity, etc.) by the application of ecologically engineered bio-organic compost amendments.

P64 Fungal communities in winter wheat – effects of cropping practices

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Reduced tillage regimes are increasingly used in agriculture in many parts of the world. While these practices are often considered an important step towards a sustainable agriculture, one of the major challenges is the control of plant pathogens that can use the increased amounts of crop residues for their survival and growth. One way to limit the problems is a careful planning of the sequence of crops grown. We are investigating the effects of tillage and the preceding crop on fungal communities and plant disease in winter wheat. We found that the cereal crops (winter wheat and oat) preceding the winter wheat resulted in lower winter survival and grain yield compared to the non-cereal crops (oilseed rape and pea), and that the pattern of survival was reflected in fungal communities on wheat roots sampled in early spring. Soil fungal communities in samples from late autumn also differed depending on the preceding crops grown, and the communities were more similar between the two cereal crops than between with the non-cereal crops. Further, effects of the preceding crops were pronounced under non-inversion tillage, for plant growth as well as for fungal communities on plant roots and in the soil.

P66 Foraging association between myxomycetes and fungal communities on coarse woody debris

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Myxomycetes are one of the major microbial predator groups found in detrital food webs within terrestrial ecosystems. They are typical inhabitants of deadwood. However, the association between fungal communities and the foraging habits of myxomycetes has not been explored sufficiently in the field. Our study aimed to find community relationships between myxomycetes and fungi, a potential prey, on deadwood, and the trophic status of saproxylic myxomycetes using stable isotope analysis of their sporocarps. Records of sporocarps present on 184 *Pinus densiflora* logs during a 3-year period listed 37 species of myxomycetes and 45 species of fungi. Ordination analysis using occurrence data of 34 dominant species (17 myxomycetes and 17 fungi) revealed their dynamic succession during log decay. Fungal dominants were clearly divided into two groups—earlier and later— and the majority of myxomycetes occurred during the middle stages of log decay between the first and second groups of fungal dominants. Isotopic nitrogen ($\delta^{15}N$) values of myxomycetes were significantly higher than those of wood-decay fungi, but few myxomycetes showed $\delta^{15}N$ values higher than those of ectomycorrhizal fungi. Isotopic carbon ($\delta^{13}C$) values of myxomycetes were not significantly different from those of fungi. $\delta^{15}N$ values of myxomycetes and fungi and $\delta^{13}C$ of myxomycetes significantly increased with an increase in wood decay. These results suggested that wood-decay fungi could be one of the important diets for saproxylic myxomycetes while they have long been assumed to be bacterivorous, and their trophic status may be affected by prey community succession during wood decay.

P67 Bacterial communities of rehabilitated biological soil crusts in desert phosphate mines

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In the Negev Desert, phosphate mining has been practiced for five decades, destroying local habitats and fragmenting the landscape. Since the biological soil crust (BSC) layer is a pivotal contributor to desert ecosystem function, it is imperative to evaluate its health following a severe disturbance. To that end, we have monitored BSCs in four phosphate mining sites and investigated the bacterial communities over spatial (between rehabilitated and undisturbed plots) and temporal (various restoration years between 2008-2015) scales. We hypothesized that BSC communities will vary in diversity and composition on both scales. To test this hypothesis, 48 composited BSC samples were collected, their physico-chemical properties and bacterial community composition evaluated using deep sequencing of the 16S rDNA. Our results suggest that bacterial diversity in undisturbed plots is significantly higher than rehabilitated plots, for all sampling sites. In addition, the community composition also varies between undisturbed and rehabilitated plots; whereas the dominant phylum in undisturbed BSC is Cyanobacteria, rehabilitated plots are dominated by Actinobacteria and Proteobacteria. Along the temporal gradient, there is an apparent shift in community composition, as the Cyanobacteria relative abundance gradually increases together with the communities' diversity. These results indicate that BSC communities are altered following the mining disturbance, with possible ramifications to the entire ecosystem health.

P68 Ecotoxicological effects of wastewater borne contaminants on microbial communities from soils previously exposed to pesticides.

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Nowadays, agriculture is facing critical challenges resulting from water scarcity especially in countries with uneven rainfall patterns which rely exclusively on natural sources. This problem can be additionally aggravated by climate change effects and poor water management practices compromising watering of crops. One way to mitigate this shortage is by irrigating agricultural fields with treated wastewater. However, this poses the problem of introducing micropollutants such as pharmaceutical and pesticide residues into the terrestrial environment. Within the framework of the Water JPI European program, the AWARE project aims to evaluate the fate of pesticides and wastewater borne contaminants and assess their environmental risks. In this context the ecotoxicological impact of waterborne contaminants on microorganisms from soils previously exposed to pesticides will be evaluated in a two-tier-scenario experiment (from lab-to-field). Soil samples will be collected and monitored for xenobiotics' mineralization. DNA will be extracted from soils to assess by next generation sequencing methodologies microbial diversity and abundance. Microbial functions involved in key ecosystem services (N cycle) will also be assessed by qPCR analysis of specific microbial groups. The information gained from this work will contribute to assess the environmental risk of using wastewater to irrigate crops. Obtained results will help to create strategies to mitigate pesticide and wastewater borne pollutants in soil-crop systems by providing recommendations for stakeholders in the agricultural sector to implement best suitable irrigation practices. Moreover, results will enrich future regulations of reclaimed water irrigation and contribute to the standardization of regulatory frameworks to increase wastewater reuse rate and acceptability.

P69 Ecotoxicological impact of oxamyl on the abundance and diversity of bacterial communities in an agricultural soil adapted to enhanced degradation.

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Pesticides are largely applied to crops and end up on soils where they may affect non-target soil microorganisms involved in important ecosystem functions. Although in the past two decades microbial-ecology and –ecotoxicology were revolutionized by the incredible developments of molecular methods applied to nucleic acids (both DNA and RNA), within the EU regulation the current evaluation of the ecotoxicological effects of pesticides on soil microorganisms relies on single broad test (i.e. carbon mineralization), non-sensitive enough to detect shifts in diversity and function of microorganisms. Within the framework of the Love-to-Hate IAPP EU project, we tested the interest for combining high throughput sequencing and microbial functional measurements to assess the ecotoxicological effect of the carbamate oxamyl on the diversity abundance and activity of microorganisms in soils previously exposed to this nematicide. Oxamyl was rapidly mineralized concomitantly to a significant increase of the abundance of oxamyl-degraders. Bacterial diversity and composition for the overall microbial community were not affected by oxamyl exposure. However, when analyzing the active microbial community by a RNA based approach, α-diversity indices were significantly higher than those of overall microbial community. Additionally, a significant effect on the composition of microbial communities was observed over time. Likewise, the most abundant bacterial groups remained constant for the overall microbial community but significantly shifted for the active Bacteroidetes and Gemmatimonadetes bacterial groups. Further analysis to detect the OTUs responsible for these significant differences led to the identification of seven different species belonging to the Proteobacteria, Acidobacteria and Actinobacteria bacterial groups. To conclude, the effects of oxamyl on the soil bacterial community were exclusively observed when analysing the active microbial communities and abundance of oxamyl degrading microorganisms. It emphasizes the need to focus on functional based analysis to better understand the ecotoxicological effects of pesticides on soil microbial communities.

P70 Rhizoremediation of mixed contaminated soil using *Brassica napus* and a bacterial consortium

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Physical and chemical approaches of soil remediation can be very effective but, frequently, at the expense of an unacceptable alteration of the soil ecosystem. In contrast, biological methods of soil remediation, which rely on the metabolic activity of microorganisms, plants or their combination, usually respect the integrity of the soil ecosystem. Here, we carried out a rhizoremediation experiment, using *Brassica napus* plants and a bacterial consortium (4 endophyte strains with plant growth-promoting traits: 3 *Pseudomonas* strains and 1 *Microbacterium* strain; 3 strains with the ability to degrade organic compounds: *Paraburkholderia xenovorans* strain LB400, *Paenibacillus* sp. and *Lysinibacillus* sp.) in mixed contaminated (hydrocarbons, PAHs, heavy metals) industrial soil treated with organic amendments for microbial biostimulation (composted horse manure *vs.* dried cow slurry). In addition, the mixed contaminated soil was supplemented with a rhamnolipid biosurfactant to enhance the removal of sorbed contaminants from soil, and linear alkyl benzene as inductor of hydrocarbon degradation. Apart from contaminant removal, we assessed the recovery of soil functioning through the determination of a variety of soil microbial indicators that reflect the biomass (microbial biomass carbon, total bacteria and fungi via qPCR), activity (potentially mineralizable nitrogen; enzyme activities: β-glucosidase, chitinase, β-xylosidase, phosphomonoesterase, leucine aminopeptidase, alanine aminopeptidase, arylsulphatase) and diversity (16S rRNA amplicon sequencing through next-generation sequencing) of soil microorganisms. Apart from a significant reduction in contaminant concentration, we detected a stimulation of soil microbial communities and, hence, soil functioning.

P71 Antibiotic resistant genes in agricultural soil amended with sewage sludge

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Sewage sludge is regularly added to agricultural soil due to its fertilizing properties and capacity to increase the content of soil organic matter. Nonetheless, sewage sludge can be a source of antibiotic resistance bacteria and antibiotic resistance genes (ARGs), as well as of mobile genetic elements (MGEs) involved in horizontal gen transfer, thereby potentially facilitating the dissemination of antibiotic resistance. Here, we assessed the effect of the application of sewage sludge on soil physicochemical and microbial properties, as well as on the abundance of ARGs (as emerging environmental contaminants) and MGEs (integrons, transposons). Soil was sampled (0-10 cm) from agricultural fields amended (from *ca.* 20-90 t ha^{-1}) *vs.* non-amended with sewage sludge. The following parameters were used for the soil physicochemical characterization: pH, electrical conductivity, organic matter, cation exchange capacity, total nitrogen, Olsen phosphorus, extractable potassium, texture and heavy metals. In addition, soil enzyme activities (β-glucosidase, β-glucosaminidase, β-xylosidase, phosphatase, leucine aminopeptidase, alanine aminopeptidase), respiration and microbial biomass carbon were determined to assess the impact of sewage sludge application on the biomass and activity of soil microbial communities. Pertaining to ARGs and MGEs, the abundance of 95 genes was quantified using the Fluidigm Biomark HD System – qPCR. Soils amended with sewage sludge presented higher values of leucine aminopeptidase activity. Similarly, the gene abundance of 4 ARGs (1 for aminoglycosides, 1 for β-lactamases and 2 for tetracyclines) and 2 MGEs (2 transposases) was higher in sewage-amended soils. Interestingly, the abundance of these genes appeared positively correlated with total metal concentrations.

P72 Functional diversity of soil microorganisms in natural and managed forest ecosystems: influence of forest stand age and tree species

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The goal of this work was to evaluate the effect of stands with different tree species and age on functional diversity (FD) of soil microorganisms within the forest floor (FF) and to find out, how the FD differs between managed and natural forests. The study was performed in Poľana Mts. (Slovakia). Samples were taken at 28 plots in the natural forests, and at 35 plots in the Norway spruce and 40 plots in the beech managed stands of different age. The plots are located in the altitude 950-1250 m a.s.l. FD of soil microorganisms in samples from the FF was determined using Biolog EcoPlates. The results showed that the management of forest stands had significant effect on FD. Higher average values were found in the natural forests. The FD seems to be very responsive to forest age classes; however, the differences between beech and Norway spruce stands were not so obvious. Within the younger stands of Norway spruce (0-40y old) we found more functional groups of microorganisms than within the younger beech stands. At the age of 20 y, the declination of FD starts to occur until it reaches the level of beech stands. Compared to the whole progress FD is very low in the middle-aged forest stands and starts to increase at the beginning of 5th age class (80-100 y old). FD maximum occurs in the oldest age class.

P74 Linking archaeal diversity to potential functions in Amazonian wetlands' sediments

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The Amazon Rainforest plays an essential role in global ecological processes, controlling temperature, precipitation, and balancing atmospheric gases. Here, the archaeal taxonomic profile of three wetlands and one primary forest in Eastern Amazon, Brazil, was analyzed during wet and dry seasons using high-resolution sequencing of the 16S rRNA gene. The results were correlated with physicochemical properties and used to predict the functional profile of these communities using the software FAPROTAX. The wetlands sediments, regardless of the season, had higher diversity of Archaea compared to the forest soil. Thaumarchaeota, Euryarchaeota, Bathyarchaeota and Woesearchaeota were the major phyla of these Amazonian wetlands, and their relative abundance varied according to the season and the physicochemical properties. The Euryarchaeota phylum, related to the anoxic production of methane, was abundant in the wetlands and confirmed the methane emission potential of these wetlands. Similarly, these areas presented a high abundance of the Bathyarchaeota phylum, in which the presence of genes related to the production and consumption of methane has been reported. Furthermore, the Woesearchaeota phylum, which ecological functions are still unclear, presented a strong correlation with sulfur concentrations, indicating the participation in this element cycle. The functional prediction indicated that hydrogenotrophic methanogenesis was the head potential function in the wetlands. In contrast, 95% of the Archaea community in the forest soil was composed by the nitrogen-related Thaumarchaeota phylum, which showed a positive correlation with nitrogen and organic matter. These data encourage further investigation for better understanding the functional activities of the Archaea communities in Amazonian wetlands.

P75 Influence of soil temperature and water content on microbial extracellular enzyme activities

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Upper soils layers are highly heterogeneous and variable environments holding microbial communities that play critical roles for soil function and services. Those microbial communities present huge diversity both from the taxonomic and functional perspectives. Soil upper layers are highly variable and two of the decisive environmental factors affecting the behavior of microbial communities in soils are temperature and water content. Temperature has been reported to influence the activity of these communities and specifically of their extracellular enzymes which represent the limiting step towards the processing of soil organic matter by microorganisms. Besides, water content in soil upper layers is highly variable and can reach very low content at arid zones or during drought periods. This study evaluates the influence of temperature and water content on microbial extracellular enzyme activities as a decisive aspect to understand the actual role of microbial communities on soil functioning, nutrient cycling, and their consequences on global estimates of soil-atmosphere carbon balance in a changing climate scenario. The results suggest different responses of enzyme activities from mesophiles and thermophiles. The effect of water content (estimated by water activity of the studied soils) allowed to detect specific adaptation of certain microorganisms and their extracellular enzymes to dried or wet conditions. From this study, we can confirm the existence of microbial enzymes preferentially adapted to dry environments such as the case of soil upper layers. This scenario is a typical example, for instance, in the Mediterranean area where high temperatures and drought-like conditions are frequently and seasonally observed.

P76 Distribution of soil extracellular phosphatase activity across soil macro – and micro-environments

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Microbial nutrient cycling in soil takes place in a complex matrix that includes organic aggregates and inorganic particles ranging in size over multiple orders of magnitude. We asked whether the surface microenvironments of particles, with sizes corresponding approximately to clay, silt, sand and coarse-sand, have similar or different extracellular phosphatase activities for a given specific surface area. To investigate this in different environmental settings, we used two heavily contaminated and one uncontaminated soil. We separated soils into four microenvironments based on particle-size: coarse sand (425 – 2000 µm), sand (75 – 425 µm), silt (2 – 75 µm), and clay (< 2 µm) and measured extracellular phosphatase activity and specific surface area of each particle size fraction. When normalized to specific surface areas, alkaline phosphatase activities varied significantly between collection sites. On the other hand, alkaline phosphatase activities did not vary between particle size fractions obtained from the same site. This indicates that within a study site, a given area of any of the surfaces studied (clay, silt or sand) supports similar amounts of phosphatase activity. The findings suggest that in our soils alkaline phosphatase activity depends on soil macro-environment but not on soil micro-environments found on different particle surfaces.

P77 Bacterial plasmids and their ecological role in Arctic permafrost environment

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Horizontal gene transfer (HGT) serves as a major force shaping bacterial diversity and adaptation. Permafrost soil, with its low biomass, spatial heterogeneity and strong environmental fluctuations, makes it an interesting microbial environment when studying the response of the microbial community to changing environmental conditions. The thawing of high Arctic permafrost, releases nutrients and leads to higher microbial activity, thus, creating a potential “hot spot” for plasmid exchange. Sequencing of plasmids and genomes has provided insight into plasmid-mediated plasticity of soil bacteria. This has so far been investigated by isolation and analysis of plasmids from pure bacterial cultures and through detection of plasmids in metagenomic analysis. However knowledge on the total environmental plasmid abundance and diversity in Arctic is scarce. Structural and functional annotation was applied for sequenced metaplasmidome from two sites of Samoylov Island, Siberia. This was combined with 16SrRNA gene sequencing and bacterial quantification by qPCR, supported by PCR replicon typing for identification of plasmid incompatibility groups. Analysis of plasmid sequences revealed the highest similarity with genomic sequences of bacteria of the genus *Acinetobacter*, *Pseudomonas*, *Serratia* and *Janthinobacterium*. The plasmid from the cultivable fraction of bacteria showed high potential for mobilization (the presence of tra genes) and involvement in microbial stress tolerance (multidrug efflux systems [SMR, RND], heavy metal resistance genes [e.g.*Czc*D, *Ter*C], and UV resistance systems. This may suggest an important role of plasmids in adaptation of bacteria to harsh changing environmental conditions in the Arctic.

P78 Nutrient availability and vegetation cover as drivers of fungal diversity in reconstructed oil-sands soils and natural boreal forest soils

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The Athabasca oil sands is one of the largest single oil deposits world-wide. Following surface mining, companies have to restore soil-like profiles to support previous land capabilities. This study assessed if soil fungal diversity and structure (α- and β- diversity) in oil-sands soils reconstructed 20-30 years previously and planted to coniferous or deciduous trees or grassland were similar to those found in natural boreal forest soils subject to wildfire. Fungal α- and β- diversity were assessed by amplifying and sequencing the ITS2 region using Miseq. Fungal OTUs and α-diversity was higher in reconstructed soils planted with trees than in reconstructed soils planted with grass or natural forest soils. Vegetation cover was the best predictor of α-diversity in soils. β-diversity differed among all treatments except reconstructed soils planted with trees. Ectomycorrhizal- and saptrotrophic- Agaricomycetes species, and oligotrophic-archaeorhizomycetes and leotiomycetes species, were less abundant in reconstructed soils than in natural forest soils. Putative denitrifying fungal species of classes eurotimocytes and sordiomycetes were more abundant in reconstructed soils planted to trees than in natural forest soils. Constructed soils planted with grass had more arbuscular mycorrhizal Glomeromycota phyla than any other soils. Soil NO_3^- content and CEC were the main drivers explaining differences between fungal communities in reconstructed and natural soils, whereas plant species and canopy cover influenced differences among reconstructed soils planted with trees versus grass. These results indicate key soil and site characteristics such as NO_3^- content, CEC and vegetation cover resulted in contrasting fungal communities in reconstructed and natural forest soils.

P79 Fine-root decomposer fungi are largely decoupled from dominant vegetation and edaphic gradients through secondary succession

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Fine roots are the dominant plant litter inputs in forest soils, yet the fungal communities decomposing this substrate, the factors that structure these communities, and how this affects fine-root decomposition rates, is poorly understood. Succession following disturbance is a key determinant of fungal community composition in forests soils, likely resulting from shifts in vegetation and soil properties as succession proceeds. Here, we identified vegetation and soil properties that best explained variation in fungal community composition in decomposing *Pseudotsuga menziesii* fine-root litter buried in three forest stand-ages (6, 13 and 70 years post-harvest). We recovered fine-root litter at two stages of decay (43-days or 1-year after burial). We also determined if fine-root decomposition rates over a 2-year period differed among stand-ages. Vegetation composition and soil physicochemical properties were different among stand-ages; nitrogen availability was high and ruderal plants abundant in young stands; soil C and N increased in older stands. Despite clear differences in environmental factors among treatments, fine-root decomposer fungi were only weakly structured by these factors. Species, but not guild, composition differed among stand-ages, but fine-root carbon mass loss did not differ among treatments at the 43-day or 1-year sampling time, indicating some degree of functional redundancy in decomposer capacity at these decay stages. However, after two years decomposition, fine-root carbon loss was higher in younger vs older stands, suggesting the observed differences in fungal species composition, and/or in environmental factors, may only affect decomposition rates in later decomposition stages.

P80 Assessment of the natural microbial community in a cattle manure-amended soil in presence/absence of the antibiotic sulfamethoxazole

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Livestock and aquaculture activities involve the use of antibiotics. The use of manure and digestate in agricultural practices can introduce antibiotics and promote resistant bacteria into terrestrial and aquatic environments. Sulfamethoxazole (SMX) is one of the most commonly prescribed and consumed sulfonamide antibiotic for its ability to inhibit both Gram-positive and Gram-negative bacteria. However, current knowledge about its persistence and effects on natural microbial communities are quite scarce. We investigated in microcosm laboratory experiments the effects on the structure and functioning of a soil natural microbial community treated with cattle manure in presence/absence of the antibiotic SMX (20 mg/kg). At fixed times (0, 7, 13, 20, 60 days) microbiological abundance, viability, activity and SMX residual concentrations (ASE extraction and HPLC-UV detection) were analysed. Moreover, the microbial community diversity was investigated with NGS analyses. The results showed that although SMX had an initial acute negative effect on the cell abundance and viability, the antibiotic was then degraded in just a few days. The microbial community composition was influenced by the different treatments and the effect on different bacterial groups will be shown

P81 Next-generation soil quality monitoring

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Routine soil quality monitoring relies mainly on physico-chemical analyses, despite the known functional importance of microorganisms for soil ecosystems. To assess the potential of physico-chemical and microbiological data for revealing differences in soil quality, we compared their performance in discriminating samples according to their exposure history. Our experimental system allowed discrimination of three categories, i.e., waterlogging, agricultural management, and field site. We sampled seven arable fields where either winter wheat or sugar beets were grown, and all were partially affected by intermittent waterlogging. We took composite soil samples in waterlogged and drained areas and recorded organic carbon (C_{org}), nitrogen (N), C/N-ratio, phosphorus, potassium, pH, water content, and soil texture. Soil microbial community structures (SMCS) were determined using a metabarcoding approach. Permutational analysis of variance showed that SMCS were significantly ($p<0.001$) explained by clay, phosphorous, and C_{org} content. Discriminatory power of physico-chemical and microbiological data for the three categories was assessed by canonical analysis of principal coordinates (CAP). CAP showed that physico-chemical data correctly classified 73.8% of the samples to the correct waterlogging status and similar values were obtained for agricultural management (76.2%) and field site (63.1%). In comparison, all samples were correctly classified to the categories using either soil prokaryotic or fungal community structures. Furthermore, we identified a prokaryotic indicator group for waterlogging stress, showing that metabarcoding can be used for general soil monitoring purposes as well as the development of bioindicators for a targeted monitoring. Therefore, next-generation DNA sequencing paves the way for next-generation soil quality monitoring.

P82 *Funnelisformis mosseae* alters soil fungal community dynamics and composition during litter decomposition

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Although arbuscular mycorrhizal fungi (AMF) are not thought to have saprotrophic capabilities, recent studies have indicated that AMF are able to influence litter decomposition through interacting with the soil fungal community. However, it remains unclear exactly which constituent groups of the soil fungal community respond to AMF during litter decomposition, and in what ways. In order to fill this knowledge gap, we investigated the effect of AMF on soil fungal communities in a subtropical forest in southwestern China. Our experimental set–up included a dual microcosm unit with two treatments: inoculated with AMF (AM) and uninoculated (NM). Destructive soil sampling was carried out at different times (T_0, T_{90}, T_{120}, T_{150} and T_{180}) and Illumina sequencing was used to detect changes in soil fungal community composition. We found that the composition and operational taxonomic unit richness of the fungal community, at higher taxonomical levels (e.g. phyla, order), remained stable across treatments. However, the relative abundance of some key genera including *Mycena, Glomerella, Pholiotina,* and *Sistotrema* were significantly affected by AMF inoculation. Soil fungal community structure was also significantly altered by AMF inoculation during the later stages of litter decomposition, but the diversity of the soil fungal community was unaffected. Our study provides new insight into understanding the interaction between AMF and soil fungal communities during litter decomposition.

P83 With or without tree: What impact of a Mediterranean agroforestry system on microbial biomass CNP in drought stress conditions?

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Soil microbial communities in Mediterranean agroecosystems have to deal with severe drought, followed by heavy rains. Agroforestry systems associating crops and trees may present higher resilience to climate change than conventional cropping systems. The aim of our study was thus to assess i) the impact of a Mediterranean agroforestry system on the resistance and resilience of soil microbial communities to drought associated or not with heat stress, and ii) the stoichiometric response of the soil microbial biomass to these stresses. Our hypotheses were that resistance and resilience of microorganisms are greater on the tree row than in the cropped inter-row or in conventional crop, and that drought stress induces microbial biomass C:N:P imbalance. Soils were sampled at several distances from the tree row in a 20-year-old walnut agroforestry system and in contiguous conventional crop in Southern France. We simulated two cycles of drying-rewetting disturbance in lab conditions, for two treatments (drought combined or not with heat/drought stresses). We monitored microbial respiration along the incubation. Microbial biomass C, N and P were assessed during resistance and resilience periods. Our results showed similar resistance to drought stress whatever the position whereas we found lowest resistance to combined heat/drought stresses for those microorganisms located on the tree row. The C:N and C:P ratios of the soil microbial biomass strongly increased as a response to both stresses while N:P ratio was only decreased by the combined heat/drought stress. One month after the end of combined heat/drought stress, microorganisms did not recover their initial stoichiometric ratios

P84 Decomposers' activity along a spatial gradient in a Mediterranean agroforestry system

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Litter decomposition is an important process involved in nutrient cycling and soil fertility in ecosystems. In alley-cropping agroforestry systems, contrasted litters from the intercropped annual and perennial plants are more or less mixed and decomposed depending on the distance from the tree lines. Our aim was to unravel the determinants of C, N and P mineralization in such a heterogeneous agroecosystem. We hypothesized that there is a spatial gradient of functional capacity of decomposers perpendicular to the tree line. Decomposers would rather be K-strategists close to the tree line and r-strategists in the middle of crop alley. We also aimed at testing the Home Field Advantage hypothesis in our system. We thus conducted an *in situ* experiment for 7 months at Restinclières (France) with walnut trees intercropped with peas/cereals. We placed litterbags made of a mixture of pea and walnut leaves, or each of the two separately, on the tree line, at 1.5 and 5.25 meters from it. After 2, 4 and 7 months, we measured soil microbial activity, nematode abundance, litter quality and mass loss. Our results highlighted significant effect of litter quality on both decomposition rates and microbial biomass C, N, P. Moreover, greater microbial biomass on the tree line was not correlated with greater decomposition. Similarly, nematode abundance showed higher values on the tree line, and also for the pea litter. These first results validate our first hypothesis, showing a difference in decomposers' functioning within our agroforestry system according to the distance from the tree line.

P85 Composition of soil and root-associated bacterial communities along plant diversity gradient

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Plant diversity is a key determinant of ecosystem functioning, enhancing its productivity, and is tightly interlinked with the composition and functioning of soil microbiota, which mediate multiple ecosystem processes, such as decomposition of organic matter, carbon sequestration and nutrient cycling. The mechanisms of plant diversity effects on soil microorganisms are not fully understood; increased litter input, and altered root exudation and/or soil chemistry are believed to be possible drivers. Although it has been clearly demonstrated that plant species differ in their root-associated microbiomes, it is unclear how these are affected in natural environments where soil microbes are under influence of multiple plant species. Here we studied the effects of three different plant species on their root bacterial communities and bacterial communities in soil along a natural plant diversity gradient using 16S rRNA Illumina sequencing. For each plant species, we established 30 plots covering three adjacent sites with plant diversity increasing from very low to very high, where we determined plant community composition, soil pH and nutrient content, shoot and root biomass of the studied plant, and the composition of its bulk soil and root-associated bacterial community. Our results showed that bacterial communities in the bulk soil were shaped mainly by soil chemistry, namely pH and nitrogen, only weakly by plant diversity and plant species identity had no effect. Conversely, the diversity of surrounding vegetation followed by plant species identity were the best predictors of root-associated bacterial communities, suggesting the influence of root exudates not observed in the bulk soil.

P86 Inclusion of mycorrhizal symbiosis could reform the phosphorus fertilization of strawberry

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Arbuscular mycorrhizal fungi (AMF) contributed significantly to the strawberry yield and growth in three year field experiment and in two separate pot experiments with low level of soluble phosphorus in soil (<5mg/l). In these experiments that were conducted with micropropagated plants of ever bearing strawberry cultivar Ria, added phosphorus (P) fertilization had no positive impact to yield in field. Also dry weight accumulations and yields of the pot experiments showed that AMF can provide the needed P. The field experiment was established in Sotkamo on a field with poor levels of soluble P (3.1 mg/l). Four P levels were created with solid and maintained with liquid fertilizers. Two separate pot experiments were conducted in Laukaa. First pot experiments studied the impact of AMF inoculation on the growth of strawberry on an artificial growing medium including peat, sand and perlite. The experiment had an uninoculated control and five P levels. The second pot experiment studied the impact of natural AMF colonies and it had four different P levels. Mycorrhiza free control was created by steaming the soil three times. In all experiments the needs of other nutrients except P was fulfilled with fertilizers. According to our results the current P fertilization recommendations of strawberry should be evaluated critically and the impact of AMF symbiosis further studied in other crops as well. If AMF is not considered, it can decrease yields and affect economic losses to growers.

P87 Effects of vegetation and chemistry on diversity and composition of bacterial community across temperate montane forests

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Bacteria fulfill important roles in forest soil ecosystems including the cycling of C and N. They can act as decomposers, comensalists, plant root symbionts or pathogens and contribute to biomass recycling, N fixation, weathering and other processes. Their community composition may be influenced by soil chemistry but also by vegetation and the relative importance of these factors is unclear. The aim of this work was to describe the effects of vegetation and chemistry on the diversity and community composition of bacteria in litter, soil and plant roots in a montane forest. The study area was the Bohemian Forest National Park, Czech Republic with 60 selected sampling sites located within 2000 km^2 that represented wide gradients of vegetation and chemical diversity. The composition of bacterial community was characterized by 16S rRNA sequencing on the Illumina MiSeq. The composition of vegetation was determined by phytocenological relevées. Litter, plant roots and soil were inhabited by different bacterial communities ($p < 0.001$). The effect of plant diversity on root bacterial community was marginally significant and less clear in soil and litter. Bacterial community composition was shaped mainly by chemistry followed by vegetation. Tree layer composition was more important than the composition of all vegetation including the ground layer.

P88 Diverse crop rotations impact the root microbiome and soil microbial processes

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Inter-year crop rotation diversity is an important component of healthy agroecosystems. In addition to diversifying economic risk and breaking disease cycles, crop rotation affords a variety of host plants that differ in quantity and quality of plant inputs. Over time, this aboveground diversity may affect nutrient cycling and other edaphic factors, improving crop performance. Here we evaluate two long-term field experiments (>25y) which compare continuous cereals with diverse crop rotations in a humid corn based system and a semi-arid wheat-based system. Amplicon based 16S rRNA and ITS gene profiling of root, rhizosphere and bulk soils sampled at three times in the growing season showed significant differences between crop types and, more specifically, between continuous vs. rotation corn and wheat. Microbial extracellular enzyme activities and nutrient concentrations in soil varied between crop types and between continuous and rotation cereals. Soil organic matter characterization showed an accumulation of lignin and increased syringyl:vanillin ratio in continuous wheat and corn indicating that there was greater turnover of recent plant C inputs in diverse rotations. Conversely, microbially-derived amino sugars varied more with crop type than rotation history. Over the long term, differences in plant residue inputs and crop nutrient uptake influenced soil organic matter composition, nutrient cycling and ultimately the soil microbial community. Our results indicate that different crop types have strong selective influence on root and rhizosphere associations in these soils and further, that interactions with edaphic factors resulting from crop diversity also affect the development of the plant root microbiome.

P89 Enrichment of plant growth promoting bacteria and fungi by means of crop rotation and organic matter amendments in field soil

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Extensive monoculture cropping and the use of mineral fertilizers have resulted in the decline of organic matter content in arable land at many places in Finland. Phosphorus (P) quantity in Finnish field soils may be high, but a great proportion of the P is bond on soil particles and therefore not readily available as essential nutrient for crops. Organic matter improves field soil resistance to erosion, its moisture holding capacity, aeration, and function in nutrient retention and release. These factors in turn increase soil biodiversity and maintain fertility of arable land. Symbiotic fungi and P-solubilizing bacteria may be utilized to increase the bioavailability of precipitated P in soil and to enhance crop growth. Therefore, the aim of our study is to investigate, if natural P-solubilizing bacteria and fungi can be stimulated and enriched in field soil through crop rotation, and organic matter amendment such as paper mill residues. Special crops (e.g. *Vicia faba* and *Fagopyrum esculentum*) release different root exudates, and leave different quality of residues in the field which may cause selective enrichment of microbes in the rhizosphere. Microbial community structures and interesting functional genes will be analyzed by molecular biological methods. Plant nutrient use efficiency will be analyzed comparing P in the soil and in the crop yield. Final aim is to develop diverse crop rotation which produces yield every year, and sustains beneficial microbes in the field soil.

P90 Impact of top canopy Scots pine harvesting on soil fungal communities and litter decomposition in a primary successional site.

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Soil fungal communities in a sandy seashore habitat might experience shortage of carbon source due to extremely nutrient poor soil.Saprophytic fungi are affected by the availability of litter, while ectomycorrhizal (ECM) fungi acquire carbon as tree derived photosynthates but may also decompose litter. We studied responses of saprophytic and ECM fungi to top canopy tree harvesting. We expected that tree harvesting and lodging residual addition will enhance saprophytic fungal community, generally reduce ECM fungi, and affect sporocarp production. Consequently, we expected an altered litter decomposition in the soil. A three-year Scots pine tree harvesting experiment was conducted in a primary successional site on Hailuoto island in the Bothnian Bay. After cutting of the trees, needle litter, twigs, stumps and the root system were left in the site. Litter mass loss and ergosterol concentration were measured in Scots pine litter bags buried in study plots for two years. Fungal communities in litter bags were studied using Ion Torrent sequencing of amplifying ITS2 region of fungal rDNA. Tree harvesting did not affect ECM fungal (operational taxonomic unit, OTU) richness and abundance in the litter bags. Wood saprotroph richness and abundance were higher near harvested trees. Mycorrhizal sporocarps did not change. Saprophytic sporocarp number was higher near harvested trees. Litter mass loss did not affected. Ergosterol consentration was high near control trees. Results indicate that tree harvesting has significant impacts on soil saprophytic fungal community composition via lodging residue addition to the soil. In contrast, ECM fungal community encountered no significant negative impact.

P91 Exploring soil biological complexity across different urban agroecosystems on the Wasatch Front

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Increased soil biological complexity in urban agricultural systems may enable global food production to cope with global food security challenges brought upon by exponential population growth and loss of arable lands. More specifically, arbuscular mycorrhizal fungi have been shown to greatly influence plant productivity and drought tolerance of plants. The Wasatch Front (Utah, United States) is currently experiencing rapid urbanization. We investigated how to effectively introduce soil biological complexity found in natural systems into the highly artificial soils of community gardens and green roof gardens across the Wasatch Front. Green peppers (Capsicum annuum L.) and parsley (*Petroselinum crispum*) are grown in rooftop garden units and community gardens in a factorial design of three soil and two water treatments. The three soil treatments are commercial arbuscular mycorrhizal fungi that consists of a single species *Rhizophagus irregularis*, locally sources arbuscular mycorrhizal fungi from the rhizosphere of Artemisia tridentata, and sterile soils. The two water treatments are continual or pulsed watering. Preliminary results suggest suggests that plant biomass was greatest when grown in commercial inoculum in both water treatments. Photosynthetic rates of plants in all treatment combinations are measured throughout the experiment, and are are highest in peppers grown in continual watering with commercial inoculum (4.23+0.46 µmol CO2 m-2 s-1). Plants will be grown until maturity in early July, at which point they will be harvested and measured total biomass, percent AMF root infection, and nutrient concentrations of N, Ca, P, Mg, K, Na, Fe, Mn, Cu, Zn, and B.

P92 Effect of differently changed biochar on cornerstones of Soil Food Web

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The Soil Food Web is the basis for a number of key processes in ecosystems. The Soil Food Web is at the beginning of mineralization and it is a very complex network consisting of many intertwining levels where the size of an organism does not often play crucial role. Disruption and shortening of these links pose a major environmental risk. At present, one of the risks is retreat of organic fertilizers supplemented by mineral fertilizers with the basic feature of the crop yields promotion but to the detriment of soil organisms. Biochar is a carbonaceous organic substance that is currently thought to be soil support used for carbon sequestration, or as a bioremediation sorbent. Each science field using biochar tends to change its properties in order to improve its usability in practice. Thus, there are emerging a lot of works which do not use fresh biochar but change it by physical, chemical or biological modification. A great source of information is the Terra Preta soil which is hundreds to thousands years old, and where these changes have already occurred. The aim of the work was to evaluate how biochar can be modified and what is the resulting effect on the cornerstones of the Soil Food Web. At the same time, the results from our team's work, which evaluated the effect of artificially aged biochar on biological activity of the soil, are presented.

P93 Effect of salt stress on aerobic methane oxidation and associated methanotrophs; a microcosm study

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Salinization by intrusion of seawater is a threat to rice cultivation and rice yields in coastal areas. The impact of salinization extends to belowground microbially-mediated processes, including methane cycling. Rice paddies are an important source of methane, a potent greenhouse gas, where methane emission is regulated by methane production and oxidation rates. While recent studies showed that salinization adversely affects methanogenesis, less is known on the response of methane oxidation and the associated methanotrophs. We determined the response of aerobic methane oxidation and the associated methanotrophs to salt stress in a NaCl gradient ranging from 0 M (un-amended reference) to 0.6 M NaCl (seawater salinity) in a laboratory microcosm study with paddy soil. Methanotrophs were quantified using group-specific quantitative PCR (qPCR) assays, whereas the community composition was monitored using MiSeq sequencing targeting the *pmoA* gene. Methane oxidation potential was not affected at 0.005 M NaCl, but activity was inhibited at > 0.3 M NaCl amendment. Ammonium concentration increased proportionally with NaCl concentration, indicating a release of soil adsorbed ammonium and possibly, an associated competitive inhibition of certain methanotrophs. Within gammaproteobacterial methanotrophs, the type Ia subgroup was selectively stimulated by increasing salinity (< 0.3 M NaCl), while the type Ib subgroup was negatively affected. Although some methanotrophs were compromised by salt stress, methanotrophic activity was remarkably resistant and showed a rather high salinity threshold at more than half seawater strength before activity fully ceased.

P94 Effect of different soil types of organic matter application on biological parameters of soil

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The biological properties of soil are an important indicator of its health and quality. Biologically active soil provides better conditions for plant growth and generally improves physical and chemical parameters of soil. One way to promote soil biological activity is to apply organic matter into the soil, possibly soil amendments or combinations of both. In our work, we focused on the biological activity of soil, namely on its condition after a three-year experiment (application of organic matter and soil amendments). The experiment was carried out in 2014 - 2017 in the Czech Republic on soil type luvisols (Rapotín locality) and cambisols (Postoupky locality) on arable land. The first experimental area is located at an altitude of about 345 m a. s. l. and the second at 220 m a. s. l. The individual variants (in soil) were various variants of manure, biochar, bentonite, soil amendment, activator of biological transformation of organic matter of manure or their combination. The aim was to find changes in microbial carbon, respiration, dehydrogenase activity, C/N and the microbial community in various variants of application of organic matter and soil amendments. In Rapotín and Postoupky locations, statistical analysis confirmed that the addition of various organic matter and soil amendments has a statistically significant effect on soil biological activity and the overall state of the microbial community. The best option for the improvement of soil biological activity was the variant Manure + Z'fix + NPK.

P95 *Bacillus subtilis* F29-3 produces a novel polyketide compound to promote plant growth and its interplay with fengycin and surfactin

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The genome of *Bacillus subtilis* F29-3 has the operons responsible for biosynthesis of fengycin and surfactin, but only fengycin production has been detected and involved in antagonism against several plant pathogenic fungi. *B. subtilis* F29-3 also produces a novel yellowish polyketide compound with unclarified structure and unknown function. To investigate the role played by this polyketide compound, several mutants deficient in fengycin and the polyketide were constructed and tested for induction of systemic resistance, promotion of plant growth, antagonism of fungal growth, and swarming motility. Since *B. subtilis* F29-3 did not produce surfactin, the wildtype did not show swarming motility. Either fengycin or polyketide had no effect on surface motility of *B. subtilis* F29-3. Interestingly, while the mutant cannot produce fengycin and polyketide, the double mutant re-gained strong swarming motility, reflecting that surfactin was synthesized. The polyketide was able to enhance plant growth but fengycin and surfactin not. In contrast, surfactin could trigger systemic resistance in maize against southern leaf blight but the polyketide had no effect on induction of plant resistance. No effect of the polyketide on inhibition of fungal growth was observed. Based on our data, three classes of secondary metabolites play different biological roles in *B. subtilis* F29-3 during the interactions with plants and the environments. The interplay among fengycin, polyketide and surfactin fine tunes their production in *B. subtilis* F29-3.

P96 Implementing metabarcoding of soil microbial communities into a long-term soil monitoring network

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The Swiss soil monitoring network (NABO) is based on more than 100 sites, which have been assessed every five year since 1985 using physico-chemical analyses. In order to expand soil quality assessment, analysis of soil microbial diversity was launched in 2012 on 30 of these sites. Standardization, reproducibility and cost-benefit-ratio of applied methods are crucial for long-term monitoring programs. Therefore, metabarcoding was evaluated from 2012 to 2016 by analysing yearly, triplicate samples from the 30 sites. Barcodes of the ribosomal operon were sequenced to determine soil microbial (bacterial and fungal) community structures (SMCS). Alpha-diversity revealed low correlations to environmental factors, with the highest value for pH ($r = 0.51$). Interactions between environmental and community structure data were more pronounced. Permutational analysis of variance showed significant differences between SMCS of different land-use types (arable land, grassland, forest), and between sites. Variability of SMCS was much lower over time than among sites. Time (sampling year) explained only 1% of data variance compared to more than 70% by the sites. These results showed that community data was better suited for monitoring purposes then sum-parameters like DNA-biomass or alpha-diversity. Furthermore, the stability of SMCS over several years allowed for the definition of site-specific baselines in the network of NABO sstem. Based on the numerous metadata collected at the sites, we intend to relate possible future changes of SMCS to environmental factors and to assign sensitive taxa to specific environmental stresses. The definition of such indicator taxa for soil quality is a long-term objective of our research.

P97 Urban green space, human microbiome and immune-mediated diseases – comparisons between urban and rural elderly in the Lahti region

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In urbanized societies allergies and numerous immune-mediated diseases e.g. type 1 diabetes and asthma have increased rapidly recently. High hygiene level is the main reason for this increase. Urban people do not expose to environmental microbial communities needed for the natural development of human immunity. Reduced contacts with natural environment and biodiversity – including environmental microbiota – lead to altered human microbiota, immune dysfunction and finally to chronic inflammatory diseases. This study examined the connection between doormat microbiota and stool microbiota among elderly people in rural and urban settings. Bacterial communities were analyzed using Illumina Miseq sequencing. Our results show that both doormat and stool bacterial communities tended to respond to urbanization. We also showed that sampling season affected bacterial community composition in doormats, but not in stools. The gender effect is significant on bacterial community composition in stools, however when we only studied persons who lived alone, there is no significant difference between men and women regarding bacterial community composition in doormats. We also detected a number of environmental vectors influencing community composition and diversity in both doormats and stools, e.g. plant inventory and land-use data. It is interesting to note that the effect of berry shrub diversity on doormat and stool bacterial communities tended to become more pronounced in rural environment where berry shrubs were more abundant comparing with urban environment. Our results advanced the knowledge on the bacterial communities of Lahti residents, which can be utilized by environmental health industry to develop new products improving immunities of urban residents.

P98 epicPCR to study host range of antibiotic resistance genes

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Wastewater treatment plants (WWTPs) collect wastewater from various sources for a multi-step treatment process. By mixing a large variety of bacteria and promoting their proximity, WWTPs constitute potential hotspots for the emergence of antibiotic resistant bacteria. Concerns have been expressed regarding the potential of WWTPs to spread antibiotic resistance genes from environmental reservoirs to human pathogens. We utilized epicPCR (Emulsion, Paired Isolation and Concatenation PCR) to detect the bacterial hosts of antibiotic resistance genes in two WWTPs. We identified the host distribution of four resistance-associated genes (*tetM*, *int1*, *qacEΔ1*, $bla_{\text{OXA-58}}$) in influent and effluent. The bacterial hosts of these resistance genes varied between the WWTP influent and effluent, with a generally decreasing host range in the effluent. Through 16S rRNA gene sequencing it was determined that the resistance gene carrying bacteria include both abundant and rare taxa. Our results suggest that the studied WWTPs mostly succeed in decreasing the host range of the resistance genes during the treatment process. Still, there were instances where effluent contained resistance genes in bacterial groups not carrying these genes in the influent. By permitting exhaustive profiling of resistance-associated gene hosts in WWTP bacterial communities, the application of epicPCR provides a new level of precision to our resistance gene risk estimates. The method has also been tested with soils samples to analyze the hosts microbes of functional genes of interest.

P99 Seasonal changes of bacterial and fungal communities in *Picea abies* forests

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The microorganisms in forests provide essential functions in forest ecosystems. In litter and bulk soil, bacteria and fungi are responsible for the remineralization of nitrogen and phosphorus while also recycling some of the recalcitrant carbon in dead plant material. In the roots and rhizospheres of forest trees, bacteria and fungi provide many benefits, such as acquiring nitrogen for their plant hosts. Root-associated fungi, but likely also other soil microbes, depend on the seasonal supply of photosynthetic carbon from their hosts. Therefore, we expect that whole microbial communities will change according to season. In this study, we determined the composition of bacterial and fungal communities in four seasons in *Picea abies* roots, rhizosphere, litter, and bulk soil in the Bohemian Forest National Park in the Czech Republic. The bacterial and fungal communities were characterized by sequencing the 16S rRNA and internal transcribed spacer 2 (ITS2) regions respectively on DNA and cDNA produced from RNA templates. There was no clear distinction in the microbial communities from different seasons at higher taxonomic levels. However, at genus level, the dominant bacteria and fungi differed between warmer and colder seasons with greater magnitude, although the taxa that were dominant were mostly present in all samples. The absence of photosynthetic carbon in colder months was clear in root and rhizosphere samples, while lower temperatures in colder months are expected to have had smaller effects on community composition. Finally, the seasonal changes observed in community profiles were more evident in samples from RNA templates than those from DNA templates.

P100 Carbon to agricultural fields: Impacts of organic soil amendments on soil microbes and transformation of soil organic matter

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Soil organic matter (SOM) is central to biological productivity of agricultural land and environmental impacts and sustainability of agriculture. Recently, SOM has drawn particular attention because of its potential to sequester atmospheric carbon dioxide (CO_2) and thus mitigate climate change. In conjunction with the Paris climate conference in December 2015, the French government proposed to increase the carbon stock of SOM on agricultural land globally by 0.4% per year (http://4p1000.org/). This initiative is included also in Finland's mid-term climate plan. Soil microbes are crucial to SOM formation and stability. Their roles in decomposition of SOM and production of CO_2 have been well-acknowledged, and now their role in converting SOM into more stable forms in soil has got more attention. Microbes may have priming and entombing effects in soil system, depending on their abilities to use and store plant- or elsewhere derived carbon compounds and their interactions with other organisms and abiotic environment. In this project, impacts of organic soil amendments on characteristics of soil microbial communities that are relevant for SOM transformation and decomposition are studied. Microbial communities will be detected using Illumina sequencing. Active metabolic pathways taking place in soil will be identified using metatranscriptomics. Also, root fungal colonization of crop plants will be studied. These results will be linked to the results on carbon use efficiency and the transformations of microbial residues in soil. The new knowledge will be added to Yasso model to improve soil C decomposition estimates in climate models. A detailed plan will be presented.

P101 Impact of Polycyclic Aromatic Hydrocarbons (PAHs) on Active Naphthalene-Degrading Bacteria in Urban Soils

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Naphthalene degradation by microbes has been investigated in different environment, yet the impact of hydrocarbons remains largely unknown. Our research utilises DNA Stable-Isotope Probing (DNA-SIP) enabled metagenomics to study the influence of Polycyclic Aromatic Hydrocarbons (PAHs) mixture on the microbial community diversity and active naphthalene degraders in an urban Tellus soil in Northern Ireland, United Kingdom. A Time-course DNA-SIP incubation was setup with fresh soil from a mild PAH-contaminated Tellus site using ^{13}C-naphthalene with the addition of Acenaphthene, Phenanthrene, Fluorene and Biphenyl hydrocarbons, and a control microcosm for SIP incubation with ^{12}C substrates. The nucleic acid (DNA) isolated from these incubations was subjected to isopycnic ultracentrifugation to separate both ''heavy'' and ''light '' DNA for downstream applications that includes naphthalene functional gene probing. The naphthalene-degrading microbes assimilated the ^{13}C-naphthalene substrates in the naphthalene-only microcosm at 21 days incubation contrary to 42 days for microcosm with added PAHs, this implies earlier naphthalene breakdown in the naphthalene-only microcosms. PCR amplification of the genes (*nahAc* genes) encoding for naphthalene dioxygenase from the labelled DNA confirmed the presence of functionally active naphthalene degraders. The heavy and light DNA were further subjected to shotgun metagenome sequencing to identify active naphthalene-degrading community and differentiate the microbial community structure in the naphthalene-only enrichment and naphthalene plus mixed PAHs. This study reveals an active naphthalene degradation in the Tellus soil by the indigenous soil microbes that assimilated the ^{13}C-naphthalene substrates are affected by the presence of other PAHs mixtures.

P102 Reclamation of acid soils with biomass ashes from pyrolytic wood liquefaction

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Fast Pyrolysis Bio-Oil (FPBO) is a 2nd generation bio-fuel employing a fast pyrolysis process in which organic material is heated in the absence of oxygen to 500 °C within a few sec. Arising vapours are condensed into a highly viscous liquid, FPBO. Additionally, the by-products, 10-15% biochar and 15-20% calorific gases, are combusted to thermally drive the process, resulting in the production of ashes that contain Ca, Mg, K, P, and micronutrients. Acid soils are globally abundant and a proper management is necessary to reduce Al toxicity or Mo deficiencies.The main objective of this study was to investigate if FPBO ashes can be used as a lime replacement without endangering soil microbial processes and plant development. For this purpose, acidic grassland soil was placed in 11cm Perspex columns and amended with 2% FPBO fly ashes derived from pine wood chips, and planted with wheat. Unamended soil was used as control. Amending with ashes increased soil pH by almost 2 units. Moreover, ash addition also increased soil plant available P and soil nitrate. Soil organic matter (SOM) was found to be lower in the ash-amended soils compared to the control, indicating priming effects associated with microbial activities.

P103 Old foes and novel suspects lead to an extended model of apple replant disease

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Apple replant disease (ARD) is a complex syndrome that causes reduced growth and diminished production in apple trees that are replanted in the same orchard. The etiology of the disease is unclear, several hypotheses are proposed, (i) the 'specific ARD hypothesis' states that only a small part of the microbiota is involved, (ii) the 'non-specific hypothesis' states that many different microorganisms are responsible, (iii) the "ecological hypothesis" proposes an equilibrium shift within key habitat factors, and (iv) the 'keystone-pathogen-hypothesis' proposes that interaction of one key microbial player can trigger a specific host response making it more susceptible to pathogens. The aim was to identify the presumed microbiological drivers in soils affected by ARD based on reanalysis of published molecular data. Sequencing datasets from ARD-affected soil microbiomes anddata on environmental variables were selected from literature. The sequencing datasets of bacteria and fungi were analyzed using a taxonomic approach in mothur, SILVA and UNITE databases. Variation partitioning and network analysis were used to identify the extent of variability related to environmental, spatial, environmental or methodological sources. The structure of microbiota in ARD-affected and healthy soils differed significantly, exhibiting a pool of co-occurring microbial OTUs in ARD-affected soils. The variables that affected most both bacterial and fungal microbial communities were the presence of ARD, types of soil treatments and the plant rootstock. The lack of congruency in reported soil characteristics precluded the inclusion of numerous measured soil parameters recorded in published literature, hampering the depth of reanalysis. The data suggest that ARD can be better defined as an opportunistic microbial infectious disease, created by certain prevailing environmental conditions affecting microbial metabolism and their interaction with the plant host. Since the different methods employed in the studies that were the basis for this research, we are calling for a universal standard for soil parameters.

P104 Arbuscular mycorrhiza facilitated phosphorus acquisition by *Medicago truncatula* even under severe drought

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It is well established nowadays that arbuscular mycorrhizal fungi facilitate phosphorus (P) uptake of their host plants from soils. It remains poorly documented, however, whether this holds under different soil water availabilities. Here we challenged the hypothesis that P uptake benefits were less important in well-moistened soils, but become much more important if water resources in the soil become depleted. To test this, we established a greenhouse experiment in which model plants *Medicago truncatula* were either inoculated or not with *Rhizophagus irregularis* 'PH5' and grown in sand-zeolite-soil substrate in rhizoboxes featuring two equally sized (1 L) compartments, separated or not by a nylon (root-exclusion) mesh. After the establishment stage, we created a 15-step gradient of soil moisture, ranging from luxurious water supply (ca 66% of water holding capacity - WHC) down to the point of severe plant wilting (ca 31% WHC). Shortly before harvest the planting (primary) compartments were labeled with ^{33}P and the secondary compartments with ^{32}P (both isotopes in orthophosphate form) to trace uptake of P via roots and/or mycorrhizal hyphae. Both roots and hyphae took up P at water moisture levels down to 40% WHC, under which level the differences between the inoculation treatments converged, although the mycorrhizal plants under all situations contained more P than their nonmycorrhizal counterparts. Although our original hypothesis was not confirmed, our data provide a rare insight into mycorrhizal functioning under different water supplies – and it remains to be uncovered what important threshold the 40% WHC in our case actually mean.

P105 Response to environmental stresses of decomposition respiration and microbial biomass of dead wood inoculated with *Lentinula edodes*

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Dead wood is an important component of forest ecosystems. Extreme climate conditions including high temperatures and drought caused by climate change seem to influence wood decomposers and decomposition processes. We incubated wood disks inoculated with *Lentinula edodes* (LE) in a laboratory and subjected the disks to environmental stresses such as high temperature, flooding, and drought, then examined the response of the decomposition respiration rate and microbial biomass of LE to these stresses. We obtained disks (diameter: 6 cm; thickness: 3 cm) from living tree branches of *Quercus serrata* to inoculate them with LE. We prepared wood disks without inoculation as a control. Each disk was inserted in a glass bottle and incubated at 23 ˚C in a laboratory. Two months after inoculation, we separated the disks into 4 groups: without stress, high temperature stress, flooding stress, and drought stress. We measured the respiration rate by infrared gas analyzer and microbial biomass of LE by qPCR a month before the stress treatment and once a week after the stress treatment. Compared to the inoculated samples without stress, for each stress condition, the respiration rate decreased between 60 to 70% and the microbial biomass of LE decreased between 20 to 50%. This shows that environmental stresses have severe effects on the physiology of wood-decomposing microbes.

P106 Microbial communities are not linked to vegetation changes induced by long-term warming across the Arctic

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Large scale studies of soil microbial communities across the Arctic, similar to analyses regarding vegetation, are lacking which hampers general conclusions concerning the effects of warming and vegetation shift on soil nitrogen (N) and carbon balance. Here, we analyzed the microbial communities in the soil from 19 ITEX experiments across 13 subarctic-alpine and arctic sites to link directional changes in aboveground plant communities with belowground microbial communities. We test the hypothesis that warming-induced changes in vegetation towards increased shrub abundance results in a more closed N cycle, with N cycled mainly through organic forms, as a consequence of increased ectomycorrhizal fungal abundance. High-throughput sequencing was used to determine community composition of soil bacterial and fungal communities and several functional genes representing major inorganic N cycling pathways were quantified. The sites were heterogeneous with regards to soil properties as well as vegetation composition. As shown in previous studies, warming had a negative effect on the abundance of mosses and lichens, and a positive effect on shrubs in some sites, indicating that warming effects are site specific. However, these warming-induced changes in vegetation were not reflected in the belowground microbial communities. Similarly, the genetic potential for microbial nitrogen cycling varied more among sites than between treatments. Our results suggest that vegetation and soil microbial communities are tightly linked in the Arctic, but that overall response of microbial communities to warming may be slower than responses of the vegetation. However, belowground community responses may occur at a finer scale, e.g. specific taxonomic or functional groups might be responding and this is something we are currently looking into.

P107 Plant species and elevation shape composition and phylogenetic diversity of root-associated bacterial communities

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Understanding the mechanisms shaping spatial patterns of biodiversity is a key challenge in ecology. Little is known about the patterns and drivers of the root-associated bacterial communities in natural systems in relation to elevational gradients. Contrasting results have been reported for soil communities, but most commonly alpha-diversity shows a linear decrease, with increasing altitude. If this is a general pattern, the diversity of root-associated bacterial communities would also decline with elevation since the pool of taxa from where the community recruits its members is smaller. We characterized the bacterial communities (based on the amplicon pyrosequencing of 16S rRNA gene fragments) associated with the roots of plant species along an altitudinal gradient (33 to 479 m) on the Aucella Mountain in Greenland. We sampled roots from six focal plant species: *Bistorta vivipara*, *Cassiope tetragona*, *Dryas octopetala x integrifolia*, *Salix arctica*, *Saxifraga oppositifolia*, and *Silene acaulis*. The plant species differed in the phylogenetic composition and diversity of the root-associated bacterial communities. To a lesser extent, the bacterial communities were also influenced by elevation, with the composition varying linearly with altitude, whereas the diversity showed a hump-shaped relationship with elevation. The phylogenetic diversity was largest at mid-altitudes, a pattern that was consistent across plant species. Overall, we demonstrate that the different plant species are linked to different bacterial communities, but that the environmental context may affect these root-associated bacterial communities in a non-linear fashion. Such insights are important for our ability to predict environmentally-induced changes in the belowground plant community.

P108 Elevated Temperature Changes the Ratio between Auto- and Heterotrophic Soil Respiration in an Agroecosystem

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The importance of agro-ecosystems for feedback mechanisms to climate change and climate change mitigation through carbon sequestration is largely unconsidered in current research. Separation of soil respiration in its root-dependent (autotrophic) and basal (heterotrophic) component enables more accurate estimation of soil organic matter stabilization, as heterotrophic respiration is representative for the decomposition of organic carbon stored in soil. We expect that warming changes the intensity of soil respiration and its ratio between autotrophic and heterotrophic respiration. We used the “Hohenheim Climate Change experiment” (HoCC) which was established in 2008 to pulse-label barley with 20-atom% $^{13}CO_2$ for 4h on warmed and control plots in an agricultural field. Labeling was done during three stages (advanced tillering, booting and grain-filling) of the vegetation period, at which C-sink strength of shoot and root differs according to plant development. First results of field measurements of $^{13}CO_2$ fluxes illustrate that total CO_2 production rates increased throughout the vegetation period (2.5-fold for ambient and 4.6-fold for warmed plots). The ratio between auto- and heterotrophic respiration varied during the vegetation period. The heterotrophic CO_2 production rate was higher (5% - 82%) than autotrophic respiration, and even further increased under elevated temperature. Nevertheless, we found one exception of this general trend at grain-filling time. In conclusion, warming contributed to greater CO_2 emissions, mainly due to decomposition of soil-derived carbon. Our results allow better estimations of direction and strength of feedback mechanisms of terrestrial C cycling under a warming climate.

P109 Unravelling the role of protists in microbial networks in agricultural soil

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Soil protists is a highly diverse but often overlooked group of microbes. Most free-living protists are consumers of other microbes, exerting a considerable selection pressure on microbial populations. Protist predation on bacteria contribute to nutrient release and increased plant growth. However, their effect on other functions performed by the soil microbiome and their interactions with other organisms than bacteria is less well known. The overall aim of this project is to investigate how agricultural management affects protists, bacteria and fungi in soil and their co-occurrence networks. A first substudy addresses protists as potential predictors of soil disease suppressiveness. We hypothesize that protists stimulate antagonistic bacteria important for disease suppressiveness. We are using a long-term field trial where different organic and inorganic fertilizers are applied in cereals. The structure of the microbial communities will be related to disease suppression in a greenhouse trial and the occurrence of antibiotics genes. We aim to identify networks of taxa important for disease suppression with special focus on protists. In a second study, we are assessing the effect of soil tillage on the vertical distribution of bacteria, protists and fungi in soil. Sampling was carried out at three depths in a long-term field experiment including a tillage gradient. We expect a gradual enrichment of taxa sensitive to disturbance from ploughing to direct drill. Our aim is to understand how tillage affect the complex networks within the microbiome. This knowledge can be used to design cropping systems promoting microbial interactions beneficial for plant health and productivity.

P110 Production of levan by newly isolated *Bacillus* strains from *Eisenia fetida* microflora.

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For the last twenty years, *Bacillus sp. strains* have attracted interest as potential probiotics. There is growing evidence that they play an important role in the intestinal tract. Microbiome analysis has shown that *Bacillus subtilis* is the most abundant species in the intestines; therefore, natural isolates might be more valuable for research and probiotic applications. Potential probiotic and Generally Recognized as Safe (GRAS) microorganism, *Bacillus subtilis*, produces levan (fructan), a biopolymer that consists of D-fructofuranose units joined by β-(2,6) linkages and is produced by both plants and bacteria. Microbial levan has a very wide range of potential applications in the food industry, cosmetics, pharmaceuticals, and medicine. The strains that overproduce levan are sought for industrial-scale use. Microflora from *Eisenia fetida,* a soil worm, were isolated and pre-classified: 96 isolated strains were tested for protease, lipase, and hemolytic activities and 19 were tested for biosurfactant biosynthesis. Biosurfactant producers were also screened for exopolysaccharide production. The presence of the levansucrase encoding gene (*sacB*) was identified in the genomic DNA of all the isolated bacteria; however, from the 19 selected strains, only 10 of them were identified as levan-producing strains since the colonies had a slimy mucoid appearance on agar plates with sucrose. Levan production was confirmed using ^{1}H NMR (Proton nuclear magnetic resonance). Four out of 10 strains were identified as *Bacillus subtilis* strains by 16S rRNA sequencing.

P111 Cu application disrupts the bacterial community structure and the soil N cycle

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Long-term use of copper (Cu)-based fungicides in agriculture has increased soil Cu concentrations. This results in soil Cu concentrations that can have irreversible effects on soil microbial community and functions. The present study aims to evaluate the ecotoxicological impact of Cu on the bacterial community and N cycling parameters. A greenhouse pot experiment was established, with two contrasting low-Cu-containing Austrian agricultural soils, an acidic sandy soil from Lasberg (L), and a weakly alkaline loamy sand from Deutsch Jahrndorf (D). Both soils were spiked with a Cu-based fungicide in 7 concentrations (0 to 5000 mg Cu kg^{-1}soil) in 5 replicates. Lucerne was grown in pots and soil was sampled in the beginning of the growth period two weeks after Cu application and at harvesting time, i.e. 100 days later. Bacterial abundance declined with high application rates of Cu. A strong reduction of the phylum of proteobacteria was observed for both soils, especially the class of γ-proteobacteria. At the same time, there was a shift towards higher relative abundance in α- and β-proteobacteria with increasing Cu-concentrations. The order of Pseudomonadales and some others (e.g. Enterobacteriacae, Aeromonadacae, Xanthomonadales) decreased sharply with increasing Cu, while a positive correlation was found between Cu and the abundance of some bacteria which play a major role in the nitrogen cycle. Nitrate concentrations declined and ammonium concentrations increased with increasing Cu in the soil of site L. These results together with the abundance of archaeal amoA gene abundance support the hypothesis that nitrification, or more specifically ammonia oxidation is inhibited by Cu. In summary, our results showed distinct Cu toxicity effects on bacterial community composition and on N cycling processes with higher sensitivity in the acidic sandy soil and a stronger buffering capacity of the calcareous loamy soil.

P112 Bacterial rRNA operon profiling of Arctic tundra soils by Oxford Nanopore MinION sequencing

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The windswept tundra heaths on Malla Fell, Finland are characterized by low and fluctuating winter soil temperatures, freeze-thaw cycles and reduced availability of labile C and N compared to snow-accumulating tundra, which impacts the ratio and composition of *Acidobacteria*, *Proteobacteria* and *Actinobacteria.* Top soils were collected from windswept and snow-accumulating sites on Malla Fell in February. The soil microbiomes were assessed using an rRNA operon profiling approach with the Oxford Nanopore (ONT) MinION system. Operon amplicons contained both 16S and 23S ribosomal subunits for phylogenetic assignment (4.200 bp of sequence), plus the ITS region for additional species/strain-specific information. Over 700,000 raw reads were collected from a single barcoded library over a 12 h run. Albacore quality scoring, basecalling, and barcoding yielded over 400,000 reads. The number of raw reads per sample varied between 22,000-50,000 and were trimmed to 3,700-5,700 bp. This raw sequence data was analyzed using Last, BlastN, and Discontinuous Megablast on 16S rRNA gene and ribosomal RNA operon databases. Initial screening detected less than 2,300 operational taxonomic units (best hit against the database) for all samples using the various algorithms. Bacteria affiliated with *Acidobacterium*, *Granulicella*, *Conexibacter*, *Acidothermus*, *Ktedonobacter*, *Bradyrhizobium*, *Burkholderia* and *Legionella* were detected as dominant members of the microbial community. From the reads assigned to a specific OTU consensus sequences of the full operon were generated. The rRNA operon profiling will enable strain-specific identification of community members and help delineate guilds active in the utilization of carbon and nitrogen and their responses to fluctuating environmental conditions.

P113 Microbial community structure of biochar enhanced sandy soil in response to altered physiochemical properties

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Biochar is a charcoal produced by gasification or pyrolysis of agricultural mass. Biochar can be stored in the soil for carbon sequestration as it is rich in highly stable carbon that can persist in the ground for thousands of years. Moreover, this produced charcoal can enhance soil properties for agricultural use by improving its physical and chemical properties to retain more water and nutrients, the availability of water and nutrients between the pores of soil encourages the growth of microbes that transfer nutrient to plants. The objective of this study was to study bacterial community structure in response to physiochemical changes in the soil mixed with biochar. Samples were collected from a plot of quinoa designated for a field experiment at the International Center for Biosaline Agriculture. The samples used were: a control NPK, two biochar treatments of different rates; 20 and 30 tonnes/ha + NPK and an untreated soil with no plants. The water holding capacity, pH, electrical conductivity, calcium, magnesium, chloride, potassium, sodium, phosphorus, and total nitrogen of biochar treatments were analyzed and compared to the control. A molecular technique fluorescent *in situ* hybridization was used in studying the bacterial community population. Analysis of chemical and physical properties showed that biochar addition improved the physical and chemical properties of soil and thus enhanced the growth of bacterial communities. The major bacterial genera observed in samples were Bacteroidetes, *Acinetobacter,* and *Nitrobacter* out of ten targeted bacterial groups. In conclusion, addition of biochar improved soil properties and microbial growth probably due increase in water and nutrient holding capacity of soil amended with biochar.

P114 Bacterial community structure of sandy soil treated with green compost, composted sludge and compost with bio-fertilizer

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In an arid environment, sandy soil contains less than 2% of organic matter which is not suitable for agriculture productivity. Organic matter is considered as a major component of soil due to its effects on physical, chemical, and biological properties. Organic amendments such as green compost, composted sludge, and compost with bio-fertilizer can be added to sandy soil to improve soil fertility. It will also help in managing organic waste produced daily in millions of tons ending up in landfills. This study aimed to analyze the effect of treatments on the physio-chemical properties of sandy soil and to understand bacterial community structure of the modified sandy soil. Experiments were conducted to evaluate the physical, chemical, and microbial community structure of sandy soil with and without treatments. The results obtained varied due to the nature of organic treatments on sandy soil chemical characteristics and microflora content. The bacterial community was investigated by using fluorescence in situ hybridization (FISH) with targeted rRNA oligonucleotide probes and provided visualization of targeted bacterial community members via fluorescence microscopy. The results indicated that application of all types of treatments (in comparison with untreated soil) had an improvement in moisture content, the soil water holding capacity, whereas a decrease in pH and EC values were observed except for EC of composted sludge. A high concentration of main chemical elements such as Ca, Mg, Cl, P, and N was found in both green compost and composted sludge treatments in contrast with the control sample. The obtained results showed an increase in abundance of Alphaproteobacteria, Betaproteobacteria, and Gammaproteobacteria subclasses of the bacterial community in all treated samples that contained a higher moisture content and organic content compared to the soil without treatment. The overall findings of this study indicate that there is a significant improvement in sandy soil health after amendments with green compost and composted sludge and these modifications can be attempted under controlled conditions. If properly managed, these practices could also contribute to the reduction of organic waste dumped in the landfills.

P115 Effects of 15 Years of Nutrient Addition on Ericoid Mycorrhizal Colonization at Whim Bog

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We studied the effects of nitrogen (N) deposition on peatlands at the long-term fertilization experiment at Whim bog, Scotland. The predominant groundcover plants are ericoid species, which rely on ericoid mycorrhizal fungi (ERM) for access to organic sources of nutrients such as N and phosphorous (P). Hence we hypothesize that the relationship between hosts and their fungal symbionts will change under nutrient load. We examined peatland plant-mycorrhizal relationships by analyzing diversity and abundance of vegetation, mycorrhizal colonization and root enzymatic activity. Sampled plots comprised triplicate controls and treatments of either NH_4Cl or $NaNO_3$ at 6.4 g N m^{-2} y^{-1} with and without K_2HPO_4. Aboveground vegetation diversity and abundance were estimated by point-intercept method. Roots from ericoid plants, (*Calluna vulgaris*, *Erica tetralix*), were microscopically quantified for fungal colonization. The decomposition potential of these roots and associated fungi was tested using a multi-enzyme assay with ITS sequencing to directly link ERM species and enzymatic activities. Most nutrient addition treatments shifted vegetation abundance from ericoids to the sedge *Eriophorum vaginatum*. Unexpectedly, ERM colonization rates were unchanged while the frequencies of endophytic morphotypes shifted, indicating an altered root-associated fungal community structure. $NaNO_3$ produced a slight suppressive effect in *C. vulgaris* root enzymatic activity. In treatments including phosphorous both ericoid species presented depressed acid phosphatase activity while generally increasing other enzyme activities. Tentative sequencing results indicate increased enzymatic activity of *E. tetralix* root inhabiting fungi belonging to the *Hyaloscyphaceae* while under $NaNO_3$+P treatment, though interestingly, acid phosphatase activity was not suppressed.

P116 *In situ* phytoremediation of soil polluted with both oil and heavy metals; the function of the rhizosphere microbes of *Populus* sp.

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Oil and heavy metal polluted sites have largely been remediated by excavating the contaminated soil to landfills and possibly introducing clean soil instead. More sustainable, in situ remediation methods could offer more opportunities remediation of larger areas. A four-year EU Interreg, Central Baltic project, INSURE (Innovative Sustainable Remediation, www.insureproject.se) aims to develop remediation techniques for practical use. Pilot sites for remediation have in INSURE been established, three in Finland, one in Sweden and Latvia. One pilot site is situating in Pirkanmaa lake-district, Finland, where we are doing in situ phytoremediation of oil hydrocarbon and heavy metal (Pb and Hg) contaminated soil. Remediation efforts using phytoremediation with trees and their associated microbes have been started. Clonal seedlings of hybrid aspen and European aspen (Populus tremula) have been planted in October 2017. The total area for phytoremediation is 1 500 m2. We will follow the seedling growth by photographing the site via an airborne drone and use the data to produce GIS maps to be able to assess the plant success and variation in above ground growth. By measuring nutrients, the pollutant concentrations and studying the bacterial community we get useful information of the proceeding phytoremediation. DNA Illumina sequencing of soil DNA amplified with 16SrDNA targeting primers enables assessment of the changes in the abundance and diversity of bacteria as well as approximating the roles for different bacterial taxa in the phytoremediation. This study will increase the understanding about the function of the rhizosphere microbes during the remediation process in the field.

P117 How does tree species change affect forest soil C stocks, C mineralization rates, organic matter stability and microbial diversity?

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Tree species change has been suggested as one of the government policies to mitigate climate change in Norway with the aim to increase the annual uptake of CO_2 and the long-term storage of carbon (C) in forests. The strategy includes replacing native, deciduous species with fast-growing species, mainly Norway spruce. A shift in tree species is expected to affect the pools and fluxes of C in the stand as well as the microbial community. As part of the BalanC project, we assess C storage related to shift in tree species cover in western Norway and whether a corresponding shift in soil microbial communities are happening. The study aim at integrating results on soil respiration, C mineralization, soil stability, diversity of bacteria, fungi and micro-eukaryotes, soil nutrient pools, litter inputs and edaphic factors at the stand level in order to identify key drivers for changes in the soil C stocks. Fifteen paired plots of native birch and planted Norway spruce at five locations were sampled. Preliminary results suggests a redistribution of C from the mineral soil to the forest floor in the spruce stands, with minor changes in the total soil C pools over the 45-60 years since the tree species change. The in situ soil respiration and heterothropic respiration, as well as C mineralization rates, were higher in birch than in spruce stands. Differences in C mineralization rates attenuate with depth between forest types. The microbial communities of the three organismal groups were all strongly structured along the vertical depth.

P118 Interaction of nickel with bacteria isolated from a nutrient-poor boreal bog

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Nuclear energy production, Ni mining and industrial use result in environmental Ni pollution. Many environmental microbes have an ability to bind nickel, and various Ni uptake mechanisms, including biosorption on cell wall structures and active bioaccumulation, have been presented. In the boreal regions, nutrient-poor bogs provide unique growth environments for distinct microbial populations, but only limited knowledge about their metabolism is available. In this study, Ni uptake by *Peanibacillus*, *Burkholderia*, *Methylobacterium* and *Pseudomonas* strains isolated from a boreal bog was studied using batch experiments (in 1% Yeast extract and 1% Tryptone; at +4°C and +20°C; incubation time 7 or 14 days; at pH 5-8) and sorption isotherms (Ni 10^{-13}-10^{-6} mol/L; at pH 6 and 8.5). All studied isolates, unaccompanied by other bacteria, removed Ni from the broth and the uptake efficiency was affected by nutrient source, incubation temperature and time. The highest Ni uptake ability was shown by *Pseudomonas* PS-0-L in 1% Tryptone (20°C, 7 d), with a maximum K_d value of 1890 L/kg DW. Compared to other *Pseudomonas* V4-5-SB (K_d 640 L/kg DW) and T5-6-I (K_d 420 L/kg DW), Ni uptake was three times higher in *Pseudomonas* PS-0-L. The isolated *Pseudomonas* strains was found to differ in substrate utilization patterns in the RapID test, which may affect their ability to remove Ni under variable nutritional conditions. Based on sorption isotherms of *Pseudomonas* PS-0-L and V4-5-SB, a slight deflection in the isotherms may indicate saturation of the exchange sites, multiple sorption sites for Ni or competition between different ions of the solution. However, variation in the solution pH did not affect interaction for Ni. As energy-independent interaction mechanisms (e.g. biosorption) would be affected by pH, the results may indicate Ni bioaccumulation by these bacterial isolates.

P119 The microbial community of cambisol at plots with different land use

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In this thesis I focused on the evaluation of physico-chemical and microbial soil properties at plots with different land use. The plots differ mainly due to the environmental conditions as a consequence of different usage patterns, which can affect soil properties, and especially micro-organisms living there. My thesis focused on the comparison and evaluation of soil properties in forest land, grassland and arable land. In addition, I also focused on the comparison of individual properties of soil during the growing season (in the spring, summer and autumn). We collected soil samples in 2016; the study plots were situated near the village of Tŕnie. Samples were analysed after sampling in the laboratory for the determination of physico-chemical properties: soil moisture, soil reaction in the water, and potassium salt, the contents of nitrogen and carbon, and the C/N ratio. Among the microbial properties we determined: basal respiration, activity of catalase, N-mineralization, microbial biomass carbon, abundance and diversity of functional groups of soil microorganisms. Based on the results of the physico-chemical analyzes, we found the highest value of all physico-chemical attributes in the forest land, lower values were observed in the grassland, while the lowest values were recorded in the arable land. Microbial properties did not exhibit such a uniform pattern; however, most of the characteristics reached the highest values also in forest soil and conversely, the lowest in the arable soil. Generally, physico-chemical properties did not differed significantly between the seasons unlike of soil microbial properties. In conclusion we can say that the highest value of soil attributes was observed in areas least affected by man, that is in forest land, and conversely, the lowest in arable land, which is strongly influenced by man.

P120 Role of exotic woody plant species in introductions of non-native symbiontic fungi

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Many plant species have been introduced to new habitats throughout the world, and some also spread and grow in abundance and extend beyond original points of introduction. Studies show that plant–fungal associations are frequently key drivers of plant invasion success and impact, but solid evidence and integration across studies are needed to understand frequency of fungal co-introductions into novel habitats. In our study we aim to identify potential non-native fungal taxa associated with exotic woody plants in old castle parks. Besides that we also study invasive potential of the non-native fungi to spread into a surrounding native vegetation.

P121 Decomposition of beech litter: early fungi colonization and late bacterial communities structure

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The decomposition of litter represents a major process of nutrient release to the forest floor. A litter bag experiment was selected as a suitable approach to describe early colonization of litter by fungi and their influence on element outflow from the litter at a microscale, and also microbial communities inhabiting litter in later stage of decomposition. The experiment was carried out in Jizera Mountains forest (Czech Republic), a region affected by acidification. Litter bags were sampled in triplicate every month from May to November, and then after 15, 19 and 29 months. Scanning electron microscopy and elemental mapping were used for microscale image of fungi succession. Raman spectroscopy was used to describe main fungi minerals. Structure of bacterial communities was assessed by Illumina sequencing of V3-V4 region of 16S rRNA gene. Rapid increase of litter bag mass was observed during first sampling period due to colonization by fungi. This process caused calcium redistribution between litter and fungi hyphae. Weddellite, a calcium oxalate dihydrate was determined as a major Ca form in fungi hyphae. However, mass of litter decreased to around 32% of initial mass after 29 months, possibly because of the switch of dominant decomposers from fungi to bacteria. The structures of bacterial communities were similar after 15 and 19 months but differed in the latest sampling. Relative proportion of *Proteobacteria* increased approximately by half (families *Bradyrhizobiaceae* and *Burkholderiaceae*), while *Firmicutes* decreased fivefold. *Actinobacteria* remained in a similar proportion over the studied period but changed in representation of families.

P122 Effect of rangeland management on soil microbial communities in a sandy savanna and clayey grassland ecosystem, South Africa

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The supply of soil nutrients in rangelands depends on the maintenance and performance of soil microbiological communities. The focus of this study was to explore how different rangeland management systems can affect the structure and functioning of soil microbial communities by comparing a clayey grassland and sandy savanna ecosystem in South Africa. The sandy savanna ecosystem had a drier climate and were encroached by *Acacia* bush. Soils in continuous and rotational grazing systems were sampled along a gradient with increasing grazing pressure. Soil enzyme activities and phospholipid fatty acids (PLFA) were analysed. Results showed elevated enzyme activities and PLFA contents in the clayey grassland ecosystem compared to the drier, sandy savanna ecosystem, irrespective of the rangeland management practice applied. Soil texture most likely played a significant role in maintaining microbial communities. Yet, after microbial activity was normalized to carbon, nitrogen and microbial biomass, the sandy savanna ecosystem showed significantly higher specific enzyme activities, indicating that microbe functioning was more efficient here. Additionally, these microbial parameters reacted more sensitively than other chemical or physical soil properties to grazing pressure in the clayey grassland ecosystem, while in the sandy savanna ecosystem this was not the case. Reducing the grazing pressure on rangelands, by practicing rotational grazing, seemed to encourage microbial functioning and thus microbial mediated nutrient mineralization with positive effects on plant growth.

P123 Influence of different types of fertilization, crop rotation and geochemical composition on soil microbial structures

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Crop rotation and fertilization are typical agricultural practices used to keep sustainable crop production. Both of them enhance nutrient content or avoid of its loose. But little is known about the influence of fertilizers (organic or mineral) and crop rotation on soil microbial community structures. In this study, effects of sewage sludge, manure and mineral (N-P-K) fertilizers application were compared together with influence of crop rotation on microbial diversity on four different geological locations. From these soils, DNA was isolated followed by 16S rRNA gene amplification (V4 and V5 region) and sequencing with Illumina Miseq. Further evaluation of influence of fertilizers, crop rotation or geochemical composition was conducted using multivariate statistical analyses and ordination plots. It was found that the main factors shaping the microbial community structures are soil composition and geographic location together with crop rotation. The influence of application of organic or mineral fertilizers was also confirmed and the highest changes in soil microbial diversity were detected after manure application. Simultaneously, species that were typical for use of each type of fertilizer were identified and species that come directly from organic fertilizers to soil were found using Venn diagrams and calculation of their overlapping.

P124 Methylotrophy as metabolic adaptation and survival strategy of *Azospirillum* in wetlands

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Azospirillum is one of the most important genus of plant growth-promoting rhizobacteria found worldwide under a variety of environmental and soil conditions associated with different crops. In spite of the progress made in ecological studies, such as the identification of preferential habitat, plant-bacteria interactions, nitrogen fixation and plant hormone production, little information is available concerning the survival of *Azospirillum* species in the absence of the host plant. In this study, we hypothesized that versatile metabolism e.g. ability to use unusual carbon sources, are essential for their adaptation in water saturated environments without vascular plants. *Azospirillum* sp. B2 was isolated from a methane-enrichment culture originated from a oligotrophic *Sphagnum* peatland. It was experimentally demonstrated their ability to use methanol for growth and nitrogen fixation, but genome sequencing failed to identify the key genes for methanol oxidation. Species -specific primers for the PCR-amplification and sequencing of moxF1 encoded methanol dehydrogenase large (Alpha) subunit were designed based on total genome announcement of *A. brasilense* Sp245 and tested on 12 strains isolated in this study from Peruvian selva with intensive methane cycling. The results indicate that the sequencing of moxF1 is a suitable method for a confident molecular identification of *A.brasilense*. The major impact of this work will be to guide subsequent studies for a better understanding of the new ecological aspect in Azospirillum growth in waterlogged environments as an association with methane-oxidizing bacteria.

P125 Natural reforestation impact on the microbial communities in gray forest soils

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Reforestation is an important tool for reducing or reversing biodiversity loss and mitigating climate change, but the recovery of ecosystems after their withdrawal from agricultural use is poorly understood. Currently, in Russia, the former arable lands occupy about 20% of the territory and more than half of them are not used in agriculture since the early 90-s. In this study, we examined bacterial community structure in gray forest soils from eight sites, which represent different stages (5-, 7-, 10-, 15-, and 25-years) under postagrogenic forest regenerating from a wheat field to the secondary wood in Moscow region, Russia. Arable and native forested sites were also studied as references. The diversity of bacterial taxa was analyzed by high throughput sequencing of 16S rRNA genes amplified from DNA extracted directly from the soil samples. The dominant bacterial phyla (more than 10% in the community) were *Proteobacteria, Acidobacteria Verrucomicrobia* and *Bacteroidetes* at all stages, but their abundance ratio varied at different successional stages. We have found that changes in soil microbial communities were correlated with the soil age and prevailing environmental conditions. The clear patterns of microbial secondary succession related to soil age were found. *Proteobacteria* and *Acidobacteria* were overrepresented at the late stage of succession. *Alphaproteobacteria* showed the same pattern as the phylum level, but *Gammaproteobacteria* had demonstrated the inverse relation. *Firmicutes* and *Parcubacteria* were found only in the early successional stages.

P126 Ecophysiology of arsenic- and antimony-metabolizing microorganisms in peatlands treating mining-affected waters

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Large amounts of wastewater are produced in mining operations. Contaminants such as arsenic (As) and antimony (Sb) occur in mining-affected waters and have to be removed before the water can be discharged into downstream waters. At our study site in Finnish Lapland, process and drainage wastewaters containing elevated concentrations of As and Sb have been treated in two originally pristine peatlands (treatment peatlands) for up to 10 years. As retention has been good in both peatlands, while Sb retention has decreased in the TP receiving drainage wastewaters with over the course of the years. Microorganisms adapted to high As and Sb concentrations are likely play an important role in As and Sb turnover and removal. Thus, this study assessed (i) potential of the peat microbial community to oxidize/reduce As and Sb under oxidizing/reducing conditions, and (ii) the effect of As/Sb concentration, temperature and carbon substrates on As and Sb turnover. Arsenite/antimonite oxidation and arsenate/antimonate reduction potentials were assessed in oxic and anoxic microcosms, respectively. Supplemental arsenite/antimonite was oxidized to arsenate/antimonate and supplemental arsenate/antimonate was reduced to arsenite/antimonite within 9 days of incubation. Antimonite was removed from the anoxic solution almost completely after 19 days of incubation, indicating that the produced antimonite was removed by precipitation or binding to the peat matrix. Oxidation/reduction rates increased with increasing initial concentrations of supplied As/Sb. Arsenite oxidation and antimonate reduction rates increased with increasing incubation temperature (5 to 30°C), while arsenate reduction rates were highest at 20°C. The collective data indicate that (i) peat soil microorganisms possess a high potential for oxidation/reduction of As and Sb species, and (ii) oxidation/reduction processes occur at a range of *in situ* relevant temperatures.

P127 Remediation of oil-polluted soils *in situ* through stimulation of the indigenous microbes with physical and chemical treatments

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INSURE (Innovative Sustainable Remediation) is an Interreg Central Baltic project running from September 2015 until August 2019. The project aims to decrease the spreading of contaminants into the Baltic Sea and to develop sustainable remediation techniques. INSURE consists of seven partners from Finland, Latvia and Sweden, and in each country pilot sites have been investigated. We study the remediation of oil-polluted soils using biostimulation, where different chemical and physical treatments provide better growing conditions to indigenous microbes and thus, enhance the microbial degradation of the pollutants. One site is located in Lahti, Finland. The site was contaminated due to a heating tank filling accident in 2001. The site was treated by introducing nutrient amended water to enhance microbial growth. Electro-osmosis was used to secure horizontal dispersal of the nutrient solution. In 2017, the site was considered clean. The second pilot site is located on a residential area in Janakkala, Finland. The site was contaminated due to a leaking from the private heating oil tank dug into the ground. The soil was treated with chemical oxidation based on Fenton's reagent. The results after treatment showed a clear decrease in oil hydrocarbon levels, but some hot spots remained. Calcium peroxide and nitrate-ammonium fertilizer were thereafter added to provide oxygen and nitrogen for microbes. The total reduction after 10 months of biostimulation was 94% from the original concentration. The third site is located close to Lake Vättern, Sweden where the biostimulation treatments are ongoing. Our study provides useful knowledge to management decisions.

P128 Do foliar ^{15}N patterns indicate shifts in mycorrhizal abundance and function under nutrient load?

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Will carbon allocation to mycorrhizal fungi, in exchange for organic nitrogen (N), decrease in peatlands under increased atmospheric inorganic N deposition? The decrease in mycorrhizal organic N uptake would translate into increased foliar ^{15}N values in ericoid mycorrhizal shrubs. The rationale is based on fungal discrimination of ^{15}N during synthesis of transfer compounds that depletes plant N in ^{15}N relative to the source, and enriches fungal N in ^{15}N. We tested whether foliar ^{15}N patterns indicate the degree of mycorrhizal colonization under experimental nutrient additions where other factors influencing ^{15}N values are constrained. The study was carried out at two of the longest-running nutrient addition experiments on peatlands, Whim Bog, United Kingdom, and Mer Bleue Bog, Canada. We analyzed foliar ^{15}N patterns in dominant ericoid mycorrhizal shrubs as well as a nonmycorrhizal sedge under different nutrient addition treatments. We microscopically quantified abundance and morphology of fungal colonization in roots of ericoid shrubs. Overall, long-term fertilization increased foliar ^{15}N values, though this was less in the nonmycorrhizal sedge than in ericoid shrubs, presumably owing to a shift in the N source and diminished role of mycorrhizal fungi in ericoid shrub N uptake. Unexpectedly, mycorrhizal colonization rates did not change significantly, but the presence of other root associated fungi in ericoid roots increased under nutrient load. Ongoing analyses on functional changes in fungal symbionts will further clarify the utility of the ^{15}N natural abundance approach to predict the role of mycorrhizal fungi in plant N uptake in peatlands under changing nutrient availability.

P129 Responses of microbial degradation patterns of soil organic matter to a gradient of anthropogenic pressure on agrosystems

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Soil microbial functions involved in nitrogen (N) recycling and carbon (C) storage are shaped by human operations such as soil and crop managements and N fertilization. Here, we aimed at characterizing the effects of the intensity of anthropogenic pressure on the microbial patterns of soil organic matter decomposition. We selected 16 experimental situations within a Long Term Ecological Research (LTER) network in France, constituting a gradient of anthropogenic-disturbed agrosystems with permanent grassland, temporary meadows in crop rotations, and rotation of annual crops. Under laboratory conditions, we determined the dynamics of mineralization of C and N of the soils taken from the 0-10 cm top layer in each situation, and after their amendment with ^{13}C-labelled wheat straw. Microbial biomass C (MBC) and the initial bacterial and fungal community sizes through pyrosequencing were also determined. Marked gradient in soil C, N and C:N (10 to 123 g C, 1.1 to 12.5 g N kg^{-1} soil, C:N 8.8 to 10.5) was observed between situations. In permanent grassland, microorganisms had the lowest rate of soil C mineralization and of priming effect per unit of soil C, and the highest production of litter-derived microbial C, i.e. a pattern of strong potential to stabilize C. In meadow-crop rotation, microorganisms had the soil highest N mineralization and the ratio N immobilized-to-litter-derived MBC the lowest, suggesting higher potential for mineral N recycling. The bacteria-to-fungi ratio did not correlate with the anthropogenic gradient but, but for a given agricultural situation, higher N input caused this ratio to increase.

P130 Temperature affected the formation of arbuscular mycorrhizas and ectomycorrhizas in *Populus angustifolia* more than a mild drought

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Arbuscular mycorrhizal (AM) and ectomycorrhizal (EM) species dominate in different vegetation zones. AM associate with lower soil organic matter, higher soil pH, lower phosphorus and higher nitrogen availability than EM. However, these soil conditions correlate strongly with climatic factors, and we suggest that temperature and humidity regimes have also direct roles in the success of mycorrhiza types with their host plants. The hypothesis here is that AM tolerate drought better and EM tolerate low temperatures better than the other type. *Populus angustifolia*, narrowleaf cottonwood is able to form both AM and EM. We tested the mycorrhiza formation and plant performance at 14, 20 and 26 °C in factorial combinations with two water regimes: adequate watering and a cyclic mild drought for 4 and 7 weeks. Plant growth was reduced more by the low temperature than mild drought. As expected, the percent of EM root tips of total root tips was largest after growth at 14 °C, while the proportional root length with AM was largest at the two higher temperatures. However, unlike expectations, drought did not affect EM formation while the AM formation was slightly lower in the dry treatment. In nature, temperature and humidity regimes are tightly correlated, and temperature as such may be a stronger determinant for the success of mycorrhiza types than has been previously considered.

P131 Selectivity of Peltigera frigida for bacterial groups of their microbiome

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Diversity of the classical symbiotic members of lichens (mycobiont and photobiont/s) has been extensively studied. Recently, many research articles are focused in the functioning and origin of the lichen-associated bacterial communities. It has been proposed that these bacteria could come from two principal sources: (i) the lichen reproductive propagules, which would transport bacteria highly-dependent of the thallus composition, and (ii) the lichen-subjacent substrate, whose contribution would mainly depend on environmental conditions. We propose that lichen bacterial members would be differentially structured according to their expected function and phylogenetic identity. We studied two alphaproteobacterial orders: Sphingomonadales and Rhizobiales. Sphingomonadales would degrade old thallus parts, so lichens should be highly selective towards them and carry them throw propagules. Rhizobiales, instead, are involved in nitrogen fixation, and considering that their function depends on the environmental conditions, lichens should be less selective towards them. Twelve terricolous Peltigera frigida lichen thalli and their substrates were sampled from a Nothofagus pumilio forest in Coyhaique National Reserve, Chile. The fungal species identity was confirmed using ITS; while, using 16S rDNA, it was determined that they were associated with the same cyanobacterium. Then, from both lichens and substrates, Illumina 16S sequencing was performed and analyses were made in the qiime2 pipeline to identify Sphingomonadales and Rhizobiales. In lichens, Sphingomonadales were more abundant; while in substrates, Rhizobiales were larger in number. Finally, previously designed indices were adapted to quantify the lichen selectivity for those bacterial groups. As predicted, the selectivity of lichens for Sphingomonadales was higher than for Rhizobiales.

P132 A novel unculturable Parcubacteria presents a versatile metabolism adapted to long-term effects of anoxic conditions in deforested Amazon soil

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Land-use change followed by deforestation has changed the microbial diversity in Amazonian soils. Only a small fraction of microorganisms is prone to be cultivated at laboratory conditions, impairing taxonomical and functional studies, due to the lack of reference genomes. Here, we applied a computational approach to reconstruct microbial genomes from metagenomes, besides inferring microbial ecophysiology of unculturable microorganisms. Microcosms were assembled with Amazonian soil samples from forest and pasture areas under a moisture-controlled experiment. After a 30-days incubation period, soil DNA was extracted and sequenced on an Illumina HiSeq. The computational framework applied was divided into five main steps: quality control, assembly, binning, annotation and microbial ecophysiology predictions. 240,000,000 paired-end reads were assembled generating a total of 847,310 contigs. From the pasture metagenomes, we reconstructed eight high-quality and non-contaminated microbial genomes, including the first Amazonian Parcubacteria genome. This Parcubacteria has a genome of ~ 1 Mbp, and was identified only in the pasture samples. This phylum host genes involved in the breakdown of complex polysaccharide (e.g., cellulases) and homolactic fermentation (glycolysis, Embden-Meyerhof-Parnas pathway). Furthermore, it encodes genes for Type II secretion proteins. Interestingly, we identified only three genes related to amino acid biosynthesis. Our model suggests the Amazonian Parcubacteria as an ectosymbiont since it host a small genome, lacking genes for biosynthesis of essential amino acids. The reduction of Parcubacteria genome is likely an adaptive response to its symbiotic lifestyle and its ecological success seems to be benefited by the anoxic conditions of deforested Amazonian soils.

P133 Zinc and arsenic over-accumulation trait in *Russula* spp.

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The propensity of fungi to accumulate large amounts of heavy metals and metalloids in their sporocarps has been known for decades; however, the mechanisms of the accumulation and the evolutionary emergence of the possibly responsible genetic traits are being uncovered only recently. In our work, we have followed the Zn and As over-accumulation trait in Russula species and explored the mechanisms that might be responsible for the sequestration of Zn and As in their sporocarps. We identified a clade of Zn over-accumulating *Russula* spp., comprising of *R. bresadolae*, *R. pumila*, *R. viscida*, *R. ochroleuca*, *R. alnetorum*, and *R. vinacea*. We have established a possible link between the large amounts of Zn found in the sporocarps from both European and American *Russula* spp. - a novel, highly conserved peptide, named Zinc Binding Peptide (ZBP), whose genomic, transcriptomic, and protein information has been traced across this Zn-rich clade. The genomic and transcriptomic sequences of this peptide have been successfully isolated and expressed in mutant *Saccharomyces cerevisiae* strains to test the ability of ZBPs to increase the yeast Zn and As tolerance. It appears that only the Zn-accumulating clade contains ZBPs and the corresponding genes, suggesting a possible emergence of the *ZBP* gene together with the Zn accumulation phenotype. Interestingly, a different, yet unidentified peptide has been discovered in *R. pumila*, which besides Zn over-accumulates As.

P134 Responses of biological N_2 fixation to multiple environmental changes

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It is more realistic that global change involves multiple environmental changes simultaneously, including temperature increase, precipitation pattern change, CO_2 increase, N deposition increase, and others. Nevertheless, how biological N_2 fixation responds to multiple environmental changes remains poorly understood. Here, seedlings of three N_2 fixing tree species, i.e., *Alnus cremastogyne* (AC), *Erythrophleum fordii* (EF) and *Cajanus cajan* (CC), were planted in plastic pots filled with calcareous lithosols (limestone soil) and ferralsols (red soil), respectively. The seedlings were grown under urban and suburban conditions, respectively. Significant responses of symbiotic N_2 fixation (SNF) on a nodule basis to multiple environmental changes were only found for the species AC, but the response pattern was modulated by soil type. When grown in limestone soil, SNF on a nodule basis was higher in urban site than in suburban site, but the pattern was inverse when grown in red soil. Nodule biomass was significantly lower in the urban site for AC and EF regardless of soil type, but the pattern was modulated by soil type for CC. The responses of SNF rates on a plant basis to multiple environmental changes were both species and soil type specific. When grown in limestone soil, the rate was significantly greater in urban site than in the suburban site for AC, but the pattern was inverse for the other two species. When grown in red soil, significant effect of environmental changes were only found for AC, with the rate lower under the urban conditions. The patterns of nodule density were similar to those of nodule biomass. N_2 fixation in the rhizosphere soil was consistently lower in the urban site for the three species irrespective of soil type. Our findings suggest that the responses of SNF to multiple environmental changes may be species specific and modulated by soil type.

P135 Soil bacterial response to different fertilizer-crop managements in a boreal climate

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To assess the soil bacterial response to different fertilizer-crop treatments in a boreal climate, we established a three-year (2013-2015) field experiment in Finland. In our split-plot design, nitrogen fertilizer treatments (control, organic, synthetic) was the main plot factor and crop treatments (fallow, red clover, timothy, and a mixture of red clover and timothy) was the subplot factor. The nitrogen fertilizer was applied in early summer and late summer each year with level at 40, 20 kg N ha-1 in 2014, and 75, 75 kg N ha-1 in 2015, and the crop was harvested twice each year during growing season. We harvested the crops twice per year in 2014-2015. The crop growth and soil properties were measured. After extracting soil DNA, we investigated the soil bacterial community by amplicon sequencing targeting the V3-V4 region of 16S rRNA gene. The soil bacterial response will be analyzed during April and May of 2018, then our results will be presented in our poster during the conference.

P136 Guild patterns of basidiomycetes community associated with *Quercus mongolica*

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Depending on the mode of nutrition exploitation, major fungal guilds are distinguished as ectomycorrhizal and saprotrophic fungi. It is generally known that diverse environmental factors influence fungal communities; however, it is unclear how fungal communities respond differently to environment factors depend on fungal guilds. In this study, we investigated basidiomycetes communities associated with *Quercus mongolica* using 454 pyrosequencing. We attempted to detect guild pattern (ectomycorrhizal or saprotrophic fungal communities) by comparing the influence of geography and source (root and surrounding soil). A total of 515 mOTUs were detected from root (321) and soil (394) of *Q. mongolica* at three sites of Mt. Jeombong in Inje County. We found that patterns of diversity and community structure were different depending on the guilds. In terms of alpha diversity, only ectomycorrhizal fungi showed significant differences between sources. In terms of community structure, however, geography significantly influenced the ectomycorrhizal community, while source appeared to have a greater influence on the saprotrophic community. Therefore, a guild-based view will help to elucidates novel features of the relationship between environmental factors and fungal communities.

P137 Microbial phylogenetic structure and interactions along primary succession

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The succession of microbial community has been comprehensively surveyed, but ecological and evolutionary mechanisms underlying this process are still lacking. Here, the phylogenetic structures, interactions and functions of bacterial and fungal communities were investigated along primary succession on post-mining spoil heaps across chronosequence spanning 54 years. Microbial phylogenetic and function turnover were greater during the first 21 years (early successional stages) than that in the later successional stages (21st-54th years). Bacterial assembly was dominated by deterministic process, and phylogenetic clustering increased until 21st year and then kept relatively stable, which corresponded well to the variations of organic carbon and total nitrogen in soil. Conversely, stochastic process mainly influenced fungal community assembly. Bacterial interactions decreased along succession while fungal interactions showed the opposite pattern, and the former crucially affected bacterial phylogenetic structure. Although the phylogenetic relatedness among participants in both fungal and bacterial interactions influenced microbial interactions especially the cooperation, the interdependence between phylogenetic structure and interactions along primary succession was tighter in bacterial community. Consequently, this study revealed differently ecological and evolutionary responses of bacterial and fungal communities to soil primary succession.

P138 Microbial communities at two coal tar waste contaminated sites

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Coal tar waste exhibits hazardous characteristics, as it contains toxic, mutagenic and carcinogenic substances like polycyclic aromatic hydrocarbons (PAHs). PAHs are persistent in the environment due to strong adsorption to soil organic matter and low solubility, especially of high molecular PAHs. Some microbes have the potential to utilize them as an energy and carbon source, but conditions for effective aerobic PAH-degradation are usually limited by oxygen depletion. Knowledge on the microbial community composition in contaminated soil and groundwater is essential to estimate the potential for natural attenuation and bioremediation approaches. At two former gas plant sites in Thuringia, Germany, leakage of coal tar waste pits led to widespread contamination plumes. Sequencing of the 16S rDNA with Illumina MiSeq was applied to investigate the bacterial communities in soil and aquifers. The two sites showed a similar community composition, with varying proportions accounding to location and level of contamination. In all soil and sediment samples anaerobic filamentous bacteria and nitrite oxidizers were present. Soil close to the surface was dominated by *Acidobacteria*. The groundwater community is characterized by strictly or facultatively anaerobic genera, among them sulfate reducers, syntrophic bacteria, sulfur oxidizers and anaerobic respirators. In an effort to promote the growth of aerobic PAH degraders, we tested the combined supply with oxygen with a bacterial inoculum via a drilling, which led to a short-term community shift. The occurrence of well-known PAH degraders as well as chemolithoautotrophs show that the bacterial community is well adapted to the nutrient-limited environment. There is a general potential for natural attenuation, with oxygen supply being the limiting factor and posing a technical challenge.

P139 Uptake and reduction mechanisms of selenium (IV) in two heterotrophic aerobic *Pseudomonads* strains – effects on plant uptake by *Arabidopsis thaliana*

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Considerable amounts of Se enter the environment via anthropogenic activities including coal combustion and mining. In addition, ^{79}Se is one of the high priority radionuclides in the long-term-biosphere-safety-assessment of spent nuclear fuel. While bacterial Se reduction has been shown an environmentally important process, only a few $Se(IV)O_3^{2-}$ respiring bacteria have been isolated and specific Se(IV) uptake mechanisms and transporters have not yet been identified. In this study, the uptake and reduction of Se(IV) by two previously isolated boreal bog *Pseudomonas* sp. strains (T5-6-I & PS-0-L) and their effects on Se plant uptake by *Arabidopsis thaliana* was examined. A formation of brick-red reduced elemental Se^0 after incubation of these *Pseudomonas* strains in Se(IV)-cultures under aerobic conditions was observed. Intracellular Se^0 granules were verified using TEM and EDX in both strains. Nitrate, nitrite and sulfate additions enhanced Se(IV) uptake, but uptake sustained also under sulphur and nitrogen starvation. This indicates two distinct Se(IV) transport mechanisms; a low affinity transport system regulated by nitrate, nitrite or sulfate and a distinct Se(IV) regulated transport system. The proteome analysis of Se(IV) supplement and temperature responses by SDS-PAGE and MALDI-TOF showed variations in the protein expression on the 10 – 60 kDa regions following these stress factors, probably through enzymes associated to oxidative stress, uptake or temperature adaptation. The effect of these bacteria on plant uptake of Se(IV) by *Arabidopsis thaliana* was examined using ^{75}Se-labeled Se(IV) on plants grown on MS-salt agar with and without *Pseudomonas* sp. additions. The transfer of ^{75}Se to plant roots, leaves and stems was verified using autoradiography. On these tests especially *Pseudomonas* T5-6-I enhanced Se(IV) plant-uptake. Experiments using Xanes to verify the chemical form of Se taken up to the plant are on-going in our lab.

P140 Soil chemistry and environmental conditions but not land-use history affect soil microbial community composition in temperate forests in Europe

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The soil microbial community is essential in regulating soil nutrient pools and maintaining ecosystem functioning. The composition of the soil microbial community is highly divergent at the global scale, which may cause by multiple factors. Yet, knowledge about these causal relationships is largely lacking. We collected soil samples around four understorey species (*Geum urbanum*, *Milium effusum*, *Poa nemoralis* and *Stachys sylvatcia*) in ancient and recent forests in eight regions in Europe and evaluated the microbial community composition through phospholipid fatty acids (PLFAs).We assessed the compositional differences of the soil microbial community among species and the relation of soil microbial community composition to soil chemistry, climate and nitrogen deposition (environmental conditions) and land-use history (i.e. ancient or recent forest). Out of the 32 PLFA biomarkers, 24 showed significant differences between the four species. Soil chemistry significantly explained the variation in the microbial community composition for each understory species, but which chemical variables were related to which functional group PLFA of the soil microbial community differed among species. Environmental conditions were not important for explaining the variation of the microbial community composition in *Geum* and *Stachys,* while soil chemistry and the environmental conditions jointly explained the microbial community composition in *Millium* and *Poa*. Land-use history did not explain a significant amount of the variation for any of the four understorey species. The significance of the soil chemistry in our data elucidates the critical role of soil abiotic factors in controlling the composition and dynamics of the soil biota.

P141 Biodiversity and community composition of arbuscular mycorrhizal fungi in selected biodiversity hot spots of the Balkan Peninsula

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Arbuscular mycorrhizal (AM) fungi are functionally-important plant root endosymbionts that are ubiquitous in soils. Despite the fact that their diversity has been well characterised across most of Europe, some regions still contain major blank spots of missing distributional data, including the majority of the Balkan Peninsula. Yet, alongside Iberia this area harbours the richest flora in Europe, possessing not only the largest number of plant species, but also hosting significant numbers of endemics and Quaternary relicts. We have investigated the community ecology of AM fungi in selected regions in Slovenia and Serbia, based on concomitant morphological and phylogenetic analyses and supported by additional vegetation, climatic and soil studies. Simultaneously, high resolution amplicon sequencing of AM fungal DNA from plant roots and morphologically based surveys of AM fungal spores from soil was used in order to study the changes in AM fungal community composition across a range of different ecosystems (e.g. different types of pristine forests, extensive grasslands and secondary succession gradients). The seasonality of the patterns and spatiotemporal shifts in AM fungal community composition was studied. We found high diversity of AM fungi not only in grassland, but also in *Pinus* and *Tilia* forests that are dominated by typically ectomycorrhizal trees, but have a rich understory vegetation. Research into this valuable genetic pool is not only important from a biodiversity view point, but also represents a resource for site-directed sustainable forestry and agriculture, reclamation of disturbed soils and ecosystems, and nature conservation.

P142 Influence of oats cover crop vs no cover crop preceding dryland lucerne establishment on some aspects of soil microbial ecology

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Soil samples were collected at 5 depths (0-5, 5-10, 10-15, 15-20 and 20-30 cm) from plots in newly established dryland lucerne pastures in the Western Cape in South Africa. The year preceding this establishment, the plots were either under oats cover crop or no cover crop (managed with herbicides). Aspects measured were soil aggregate stability, active carbon (KMnO4 oxidation) Solvita(R) N and C, protozoa (MPN) as well as carbon utilisation (Biolog Ecoplates(R). Principal component analysis (PCA) clearly showed associations between variables tested and the cover crop treatments (with or without cover crop) and the 5 depth treatments. PCA explained 72.9% with the first three components (F1, F2 F3). Protozoa seperated clearly from the other variables. Discriminant analysis (DA) showed three distinct groups namely: 0-5 cm in both cover crop and no cover crop, 5-10 cm in cover crop while all the others were in group 3. From these preliminary results, it is clear that there are definitely differences in the effect of either a cover crop or no cover crop on soil ecology.

P143 The structure of microbial communities is related to seed predation by carabid beetles

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Plants are colonized by microorganisms, which support their growth, productivity, utilization of nutrients, production of secondary metabolites and also suppress pathogens or protect plants from herbivores. In our work we focused on interactions between bacteria associated with seeds in a soil seed bank and consumption of those seeds by carabid beetles. Specifically, we tested how the structure of bacterial community and its changing over two year’s burial in soil influences seed consumption. Seeds of seven plant species differing in size and shape but with known palatability to carabid beetles were used in the experiment conducted at one ruderal site. Bacterial diversity increased significantly after burial of all seed species but remained similar in the second year. It was possible to distinguish three types of seeds with respect to changes of bacterial community composition: 1) Remained unchanged over the two years burial, 2) Changed in the first year after burial and then remained the same. 3) Changed gradually over the two years. In most species the diversity of microbial communities did not or only very loosely correlated with change in viability or seed mass. The only exception was *P. lanceolata*, for which both the viability and relative mass strongly negatively correlated with microbial diversity. In a simple model the overall mass consumption but not the total consumption was reduced by increased bacterial diversity, but in the more complex model, which included also seed species and interactions this effect was overpowered by the effect of differences between the individual seed species.

P144 Exploring the potential of *Micrococcus luteus* culture supernatant for enhancing the culturability of soil bacteria

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According to estimations, only around 1% of Earth’s microorganisms are culturable. Isolation in pure culture still remains the best way to thoroughly characterize a bacterium. In their natural environment, microorganisms can be found dormant, so it is possible that microorganisms remain dormant when they are cultured on laboratory media. *Micrococcus luteus* secretes a growth-promoting factor called Resuscitation Promoting Factor (Rpf). Rpf’s enzymatic activity is able to resuscitate *M. luteus* from dormancy and to increase its culturability on solid medium. A method for enhancing the culturing of soil bacteria using Rpf from *M. luteus* cultures is proposed herein. *M. luteus* NCTC2665 (Fleming strain) culture supernatant which contains Rpf (SRpf) was added to the soil extraction step for soil bacteria. An extraction with PBS only and inactivated supernatant were used as controls. After 24 hours of extraction, the soil slurry was diluted and plated on solid media. Similarly, SRpf-enhanced extraction was used for the retrieval of bacteria which were used to bioaugment sterile soil. The method’s potential to isolate poorly culturable representatives was assessed by differences in numbers of colony-forming units on solid medium and diversity assessments via direct screening of the colonies formed using MALDI-TOF mass spectrometry, or by 16S rRNA gene amplicon sequencing in the case of the treated slurries. Both the number of colonies in all experiments and the diversity of colonies isolated increases during the extraction amended with SRpf, as compared with the control extractions.

P145 Elevated blue light alters ectomycorrhizal fungal communities in roots of Scots pine seedlings and soil enzyme activities

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Light quality, i.e. spectrum and intensity of light, affects directly and undirectly many living organisms. Light spectrum varies between northern and southern areas and northernmost latitudes obtain higher proportion of diffuse blue wavelengths. Light quality affect the growth of forest trees, and northern origins of trees may be more sensitive to quality changes than southern ones. As root-associated fungi largely depend on carbon gained from their autotrophic hosts, changes in light quality may also have an impact on ectomycorrhizal fungi associating forest trees. We studied the impacts of elevated blue light on root-associated fungal communities on Scots pine seedling roots and on soil enzyme activities in a short-term pot experiment in a climate chamber. Scots pine seedlings (n=48) of three different latitudinal origins were planted in pots with natural fungal inocula in peat-sand mixture. Pots were divided randomly in two groups, the other one receiving full light spectrum and the other elevated blue light. After 4 months, seedlings were harvested, roots and rhizosphere soil were collected. Fungal ITS2 rDNA from roots was sequenced by Ion Torrent, and enzyme activities from soil measured. Our preliminary analysis shows that dominant fungal associate in roots was different in control and elevated blue light treatments. Blue light also reduced enzyme activities in soil. We conclude that light quality may shape belowground communities and their functions.

P146 Microbial utilization of carbon in the soil of a temperate forest

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A lot of attention has been recently drawn to the importance of forests in the global carbon cycle. Microorganisms represent a critical part of carbon cycling in forests as they are decomposing various carbon compounds ranging from simple to highly recalcitrant ones. The aim of this experiment was to track the microbial utilization of carbon using Stable Isotope Probing with ^{13}C labelled substrates by measuring respiration and carbon incorporation by individual microbial taxa. Six ^{13}C labelled substrates of various complexity (glucose, citric acid, cellulose, hemicellulose, chitin, whole plant biomass) were added to the microcosms containing homogenized soil from a temperate forest in the Czech Republic and incubated for 1 or 3 weeks. Fungal and bacterial taxa that incorporated ^{13}C were identified by amplicon sequencing of ITS2 and 16S. While the mineralization of ^{13}C chitin was low after one week of incubation, considerable increase was observed after 3 weeks, showing the importance of fungal biomass as a C source in the soil. Furthermore, our results have shown that numerous fungi and bacteria can utilize different sources of C, both plant – derived and fungal biomass. The substrates largely differed in carbon use efficiency, i.e. the ratio of C incorporated and C mineralised, the lowest values being observed for citric acid. This indicates that certain substrates serve preferentially for respiration and energy generation while others are incorporated into biomass. This distinction between energy- and biomass-generating substrates may help to explain the phenomenon of priming decomposition by simple C compounds.

P147 The black truffle *Tuber melanosporum*, ectomycorrhizal with trees and endophyte with herbs

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The black truffle *Tuber melanosporum* is an ectomycorrhizal ascomycete which produces edible ascocarps after mating between two individuals. Ascocarps contain the ascospores issuing from meiosis. The maternal partner establishes ectomycorrhizas with trees and nourishes the ascocarp (spores and fleshy tissues); on the contrary, the ecological niche of the paternal partner, whose alleles are only found in the ascospores, remains unknown. At the bottom of trees colonized by *T. melanosporum*, vegetation is scarce, and the determinism for this zone, called 'brûlé', remains mysterious. Unlike host trees, herbaceous plants of the brûlé are not ectomycorrhizal. We tested the presence of *T. melanosporum* on herbaceous plant roots from brûlés by molecular and microscopic approaches, and hypothesized that it could be the paternal partner's niche. Specific PCR and NGS sequencing revealed the presence of *T. melanosporum* in 51% of the >1000 tested roots and 93% of the 106 species. In situ hybridization visualized alive *T. melanosporum* hyphae within the non-ectomycorrhizal healthy roots of brûlés herbs. Microsatellite genotyping confirmed the presence of maternal individuals, but never of paternal individual, whose ecological niche is still under investigation. These results suggest that *T. melanosporum* can be endophytic in herbaceous plants in addition to being ectomycorrhizal with trees. Our results support the same for other ectomycorrhizal species, from which DNA sequences were also found in our samples (totalling ~15% of all reads). This supports the growing evidence that some fungi occupy several ecological niches, perhaps recapitulating evolutionary trajectories between trophic strategies (e.g. from endophytism to mycorrhizal symbiosis).

P148 Monitoring of soil bacterial communities across the diverse landscape of Switzerland

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Nation-wide soil monitoring programs are implemented to determine current and long-term soil quality in order to ensure sustainable land-use. They also provide an excellent frame to study soil microbial communities across spatial and environmental gradients that shape these communities. From a Swiss-wide grid-based soil monitoring, 256 sites were sampled in 2014 and 2015 covering the entire country and harboring diverse ecosystems. Sites were characterized based on plant richness, land-use types as well as climatic, geologic, and geographic factors; soils according to pH, carbon-, and nitrogen-content. Bacterial community structures were assessed using metabarcoding of ribosomal marker regions V3-V4 of the 16S rRNA gene in four independent field replicates from the top 20 cm of soil to capture the within site variation. Bacterial OTU-richness strongly correlated only to soil pH ($r=0.7$; $p<0.001$). Sites harbored distinct bacterial community structures, as shown by a mean reclassification success for communities to their sites of origin of 85%. Therefore, potential contributions of environmental factors on the structure of soil bacterial communities were assessed using averages per site (centroids). Permutational analysis of variance (PERMANOVA) of centroids revealed that, in descending order of contribution, the variables pH, index of indicator plants for nutrients, elevation and carbon-to-nitrogen ratio followed by the geographic region and the land-use type explained in total 45% of the variation. Pairwise linear geographic distance were significantly non-correlated with bacterial community dissimilarities ($r=0.08$; $p=0.001$). Our results revealed that site-specific combinations of environmental factors explained much of the variation in bacterial communities across Switzerland.

P149 Legacy of drying-rewetting affects soil microbial response to freeze-thawing

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Terrestrial ecosystems will experience altered frequency and intensity of drying-rewetting and freeze-thaw events due to climate change. These fluctuations will affect soil moisture availability, which is an important driver of soil microbial activity and carbon dioxide release. However, the question remains if the legacy of one type of fluctuation influences the microbial response to the other. We hypothesized that freezing-thawing and drying-rewetting cycles have similar effects on the soil microbial community and soil respiration. Three microcosm experiments were performed using grassland soil from the Netherlands, where we had knowledge of prior climate. In the first experiment, we exposed soil microbes to a freeze-thaw or a drying-rewetting cycle and control treatments. The second and third experiment consisted of two phases. In the first phase, soil microcosms were exposed to a similar treatment as in experiment one. In the second phase, soil microcosms were exposed to the other cycle than in phase one. We measured soil respiration and extracted RNA to investigate the potentially active fraction of the microbial community using amplicon-sequencing. We observed a larger CO_2 pulse upon rewetting than upon thawing. Importantly, the legacy of the drying-rewetting treatment affected the response of the microbial community and CO_2 emissions upon the second freezing-thawing event. In contrast, the legacy of the freezing-thawing event did not affect the response of the microbial community to a drying-rewetting event. Our results suggest that drying-rewetting has a bigger influence on soil microbial communities than freezing-thawing and leaves a legacy in the soil microbial community.

P150 Breeding for resistance to soil-borne pathogen impacts rhizosphere microbiome in common bean

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The rhizosphere microbiome plays a key role in plant growth and health, providing a first line of defense against root infections by soil-borne pathogens. Here, we investigated the composition and metabolic potential of the rhizobacterial community of common bean (*Phaseolus vulgaris*) cultivars with variable levels of resistance to the root pathogen *Fusarium oxysporum* (*Fox*). For the different bean cultivars grown in two soils with contrasting physicochemical properties and microbial diversity, rhizobacterial abundance was positively correlated with *Fox*-resistance. Pseudomonadaceae, Bacillaceae, Solibacteraceae and Cytophagaceae were more abundant in the rhizosphere of the *Fox*-resistant cultivar. Network analyses showed a more complex and highly connected bacterial community in the *Fox*-resistant cultivar. Also, specific functional traits such as protein secretion systems and biosynthesis genes of antifungal phenazines and rhamnolipids were more abundant in the rhizobacterial community of the *Fox*-resistant cultivar. Metatranscriptome data revealed that community assembly in the rhizosphere follows niche-based mechanisms, presenting lower diversity and distinct community structure comparing to the bulk soil. In comparison with the susceptible plant, the microbiome of the *Fox*-resistant cultivar presented high expression of genes affiliated to the family Paenibacillaceae, a group known by its antifungal activity. The *Fox*-resistant cultivar also presented high expression of genes related to metabolism of nutrients and specific functional traits related to pathogen suppression, such as motility and chemotaxis, and phenazine and colicin V. Our findings suggest that breeding for *Fox*-resistance in common bean have co-selected for other unknown plant traits that support a higher abundance of specific beneficial bacterial families in the rhizosphere with functional traits that support a more complex rhizosphere microbiome and reinforce the first line of defense against the pathogen.

P151 Iron reducing bacteria in humid temperate rain forest soils maintain lignocellulose decomposition under anoxic conditions

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Until recently, fungi were thought to dominate the decomposition of ligninocellulose and soil organic matter. However, increasing evidence shows that iron (Fe) reducing bacteria (IRB) are also able to degrade lignocellulosic materials, especially under anoxic conditions. Humid temperate rain forest soils of southern Chile are subjected to high mean annual precipitation >5000 mm and are frequently oversaturated. These soils have large quantity of Fe(III), and IRB may play an important role for soil organic C (SOC) oxidation. We hypothesized that in soil rich in Fe and organic C, IRB contribute importantly to decomposition of lignocellulosic SOC under anoxic conditions. The objective of this study was to isolate and inoculate IRB from Ah mineral soils in three sterilized (gamma radiation) and non-sterilized soils incubated at 20ºC for 15 days. Decomposition of lignocellulose was assessed by fluorescence intensity in a confocal microscope and enzyme activities (lignin and manganese peroxidase) during the incubation. CO_2 released from soils inoculated with IRB, was 240% more than in non-sterilized. This amount represented 60% of total CO_2 from control soil without IRB. Fe(II) increased 362% over control and its was maximal in soil with highest C content, reflecting high microbial activity and large microbial biomass content. Peroxidase activity increased with Fe(II) and it was greater in soil with highest content of Fe-oxides. Fluorescence intensity decreased in presence of IRB, indicating that lignocellulose degradation explain the rapid SOC turnover. Concluding, under anoxic conditions IRB use Fe(III) as an electron acceptor to decompose lignocellulose through peroxidases release.

P152 Microbial community changes in a short-term fertilization experiment on temperate forest soils

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In forests, trees and mycorrhizal fungi take up most of their phosphorus (P) as phosphate from the soil solution. The soil solution is then replenished by the release of phosphate from absorbed phases, by the dissolution of P containing minerals or by biological mineralization and/or enzymatic hydrolysis of organic P compounds. Within the framework of German priority program on ‘Ecosystem Nutrition’ we investigated the importance of soil organic matter turnover on P cycling under environmental changes. Soil microorganisms excrete extracellular phosphatases that convert organic P into phosphate. So far, three alkaline phosphatase genes have been identified: *phoA*, *phoD* and *phoX*, which encode the alkaline phosphatase enzymes PhoA, PhoD and PhoX. In contrast, only a few acid phosphatase gene families have been characterised, such as *acpA* and *appA*, encoding the acid phosphatase enzymes AcpA and AppA. A two-year long field experiment was set up. From the soil samples taken at different time points we conducted molecular fingerprinting analyses to explore the community structure of total and *phoD*, *appA* and *acpA* phosphatase gene harboring microorganisms after N, P and N+P addition in soils. Changes in the diversity of total and in particular of potentially active acid and alkaline phosphatase harboring microbial community were expected to occur as an impact of the nutrient addition. In particular an increase in the abundance of the phosphorus mineralising microbial community might be more significant under low P availability conditions.

P153 Impact of treated wastewater irrigation on proliferation of antibiotic resistant genes and Class 1 integrons in soil and crops

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The use of treated wastewater (TWW) for irrigation is becoming more prevalent and could help mitigate water scarcity, especially in arid and semiarid regions. Wastewater tretament plants does not completely remove antibiotics, antibiotic resistance bacteria (ARB) or antibiotic reistance genes (ARGs). Thus, effluents released from these facilities may contribute to ARGs accumulation in TWW irrigated soil and crop. We hypothesized that TWW irrigation would increase the level of ARGs in the irrigated soil and crops due to selective pressure generated by residual antibiotic compounds, and to the introduction of ARGs and ARB. To test our hypothesis, we assessed the abundance of seven ARGs, class 1 integron and 16S rRNA encoding genes in 114 samples of TWW and freshwater irrigated soils and crops. The samples were collected during two consecutive seasons cultivating vegetable crops (cucumber and melon), testing water quality (TWW and freshwater), soil types (sand, loamy sand and clay) and soil treatments (surface and subsurface drip irrigation and soil plastic cover). The results revealed that TWW contains a diverse and abundant array of ARGs, lacking in freshwater. Yet, ARG levels in the irrigated soils and crops were low regardless of the irrigation water quality or soil treatment, while the levels differed among soil types. The results indicate that ARB and ARGs harbored in TWW may not persist in the irrigated soil and thus do not transfer to the crops, suggesting that the impact of TWW on the irrigated soil resistome might be negligible.

P154 Bacterial communities affected by organic amendments down to one meter in a long-term field experiment

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Agricultural studies seldom assess soil characteristics and microbial activity below the tillage depth, and biogeochemical cycles deeper in the soil are not well-understood. We investigated the effect of different organic amendments in the first meter of the soil profiles in the long-term maize cropping system experiment Tetto Frati in northern Italy. The treatments applied since 1992 were: 1) crop residue removal (CRR), 2) crop residue incorporation (CRI), 3) crop residue removal with bovine slurry fertilisation (SLU), 4) crop residue removal with farmyard manure fertilisation (FYM). An equal total amount of nitrogen was applied annually as mineral fertiliser in the first two and as organic fertilizer in the latter two treatments. Soil organic carbon was significantly higher in the treatments with organic amendments (CRI, SLU and FYM) compared to CRR in 0-25 cm, but not deeper. Potential N mineralisation was higher under organic than mineral N fertilization in all sampling layers except for 25-50 cm. Bacterial diversity decreased down the soil profile much less than microbial biomass. Incorporation of crop residues alone showed no positive effects on either biomass or diversity, but organic N fertilization increased both compared to mineral N fertilization, even below 50 cm soil depth. Although the main factor determining soil bacterial community composition in the entire dataset was soil depth, indicator taxa separating mineral from organic N fertilization treatments were identified especially in the deepest sampling depths. Many of these are poorly known candidate taxa with potential effects on nutrient cycling and leaching, and greenhouse gas dynamics.

P155 Simulated winter incubation of soil and swine manure differentially affects multiple antimicrobial resistance elements

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A major concern for animal production is that antibiotic use may enrich antibiotic resistant (AR) bacteria and genes in the gastrointestinal tract and with the subsequent application of manure nutrients for row crop production, AR bacteria and genes may become enriched in the environment. In the United States, manure applications to crop fields typically occur during the fall with slow decomposition and mineralization until spring planting season. A laboratory soil incubation study was conducted mimicking swine manure application to soils, and selected AR genes were monitored during simulated 120-day winter incubation with multiple freeze-thaw events. Additionally, the effects of two antecedent soil moistures and two manure treatments, control versus hydrated lime alkaline stabilization (HLAS) were assessed using four replicates per treatment-moisture. Fourteen tetracycline resistance genes were initially evaluated; *tet*D, *tet*G, and *tet*L were detected in soil while manure contained *tet*A, *tet*B, *tet*C, *tet*G, *tet*M, *tet*O, *tet*Q, and *tet*X. By day 120, the manure-borne *tet*M and *tet*O were detected in all samples. *tet*C, *tet*D, *tet*L, and *tet*X were detected less frequently. Other *tet* resistance genes were detected rarely, if at all. Four resistance elements [*int*I1, *bla*$_{\text{ctx-m-32}}$, *sul*(I), *erm*(B)] and 16s rRNA were measured using quantitative PCR. AR gene relative abundances were initially 100x to 1000x greater in the manure compared to soil, but in the manure/soil incubations abundance decreased 10x to 100x. The HLAS treatment significantly decreased the relative abundance of *int*(I1), *sul*(I), and *erm*(B) during incubation while antecedent soil moisture had little effect.

P156 Effects of freeze-thaw and dry-wet events in an arable soil

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Freeze-thaw and dry-wet events are predicted to negatively impact upon many aspects of plant and soil microbial functioning. The change in environmental conditions associated with these events may induce stress within the plants, roots and associated soil microbial communities. Although many studies have described stress tolerance mechanisms in plants, the impact of climate extremes on root-soil interactions are poorly understood. Previous studies have frequently observed a pulse of CO_2 from soils after freeze-thaw and dry-wet events. The enhanced release of CO_2 to the atmosphere may be linked to greater root exudation and may thus influence soil carbon storage and net greenhouse gas emissions. However, the origin of this carbon and the mechanisms responsible for its release have not been well characterised. To better understand the response of plant roots to these two stressors (freezing and drying), we investigated the effect of freeze-thaw and dry-wet events on intact plant-soil systems. We measured CO_2 and dissolved organic C (DOC) from planted and unplanted soil before and after applying freeze-thaw and dry-wet events. These events induced strong physiological response in soil-plant carbon cycling. The results will be discussed at the conference.

P157 Effect of agronomic practices on arbuscular mycorrhizal root colonisation and inoculum density in two cultivars of spelt wheat (*Triticum spelta*)

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Arbuscular mycorrhizae fungi (AMF) are mutualistic symbiotic association fungi living in soil, and can translocate nutrients, especially immobile nutrients such as phosphorus (P). In agroecosystems, the existence and function of AMF is affected by agricultural practices and varies between genotypes. Two years (2016- 2017) of field plot experiments were conducted to find out the effect of crop protection management (conventional, and organic), fertility input type (composted FYM and mineral N), tillage system (minimum, and conventional), and spelt variety (Oberkulmer Rotkorn, and Filderstolz) on AMF colonisation in spelt roots, inoculum density in the soil, biomass and grain yield, P (concentration, uptake and total) in straw and grain, under field conditions at Nafferton farm in northeast England. Roots and soil were sampled in July 2016 and July 2017, root staining was conducted, and spores were counted. The (2016 & 2017) results showed that crop protection had a significant effect on inoculum density of AMF and was higher where organic approaches were used compared to conventional. Minimum tillage increased inoculum density, while conventional tillage increased arbuscule colonisation. Fertility management also had a significant effect on both inoculum density and AMF root colonisation which were greater when compost was used. Highest inoculum densities were measured where the spelt variety was Oberkulmer, while AMF colonisation was highest for Filderstolz. Preliminary results indicate that adoption of organic management practices with minimum tillage could be a strategy to increase AMF populations and colonisation. Selective breeding could also enhance the ability of spelt to form associations with these beneficial organisms.

P158 Cloning of *Saccharomyces cerevisiae* halo-tolerance *Hal*1 gene into *Escherichia coli* XL10

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The role of agriculture has increased in importance and is a key factor in the economic growth rate. Saline water covers 71% of the earth's surface restricting agricultural and other industrial activities to the remaining space and resources, thereby warranting the need to find an immediate and practical solution to overcome this issue. The *HalI* gene plays an important role in maintaining cellular Na^+/K^+ ion homeostasis and confers salt tolerance when over expressed in yeast cells. Cloning of halo tolerance trait hitherto the deficient microbes may help to overcome this restriction with significant economic impact. In this study, we have demonstrated the successful cloning and transfer of a eukaryotic halo-tolerance gene *Hal*1 from *S. cerevisiae* into a prokaryote, *E. coli*. PCR amplified *Hal*1 product from *S. cerevisiae* was cloned into the pTZ57R/T vector transformed into competent *E. coli* XL10 cells and selected using blue/white colony discretion. The gel electrophoretic analysis performed, confirmed the transfer of the cloning vector with *Hal*1 payload. Nucleotide BLAST (NCBI) analysis of the amplified product from transformed *E. coli* XL10 clones indicated 99% sequence similarity with the *S. Cerevisiae Hal*1 gene reiterates the successful transfer of the target eukaryotic gene into prokaryotic cells. *Hal*1 gene expression experiments in the *E. Coli* XL10*Hal*1$^+$ clones are in progress. Our research work aimed at developing the cultivars to give maximum yield under salt stress condition, therefore demonstrating the increased salt tolerance of transgenic lines to alterations in Na^+ and K^+ homeostasis.

P159 Bioactive potential of *Halomonas pacifica* MML1909 isolated from Saltpan

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Salt pans a potential source of bioactive metabolites. The Larger population of halophilic bacteria in saline habitats may be considered for the possibility of discovering novel bioactive agents. This study aimed to evaluate the bioactive potential of a halophilic bacterial isolate. Totally 18 sediment samples were collected from various saltpan of Kelambakkam, TamilNadu, Chennai. The Antioxidant potential of the halophilic crude extracts was measured by DPPH scavenging activity and cytotoxicity by MTT assay method. Totally 41 crude extracts exhibited antioxidant activity and 42 crude extracts showed cytotoxicity and 30 crude exhibited both antioxidant and cytotoxicity. Based on aforementioned activity 12 halophilic bacterial crude extracts were shortlisted. The Polyphasic taxonomical study revealed the most effective strain, MML1909 as *Halomonas Pacifia* and further subjected to column chromatography resulted in 18 fractions. The selected fraction was further purified by column chromatography followed by preparative TLC. The pure compound was characterized by various spectral analyses such as IR, UV, ^{1}HNMR, and ^{13}CNMR, revealed as $C_{20}H_{30}N_4O_6$ and molecular weight as 422.48 by ESI-MS. The IC_{50} value of pure compound of *H. pacifica* MML1909 was determined as 45 µg and 25 µg on A549 and MCF-7 cell lines, respectively. Apoptosis was confirmed by flow cytometry and DNA fragmentation analysis. Not much work has been done globally on the bioactivities of halophilic bacteria in the genus and *Halomonas* spp. in particular. These results highlighted the importance of *H. Pacifica* MML1909 as a bioactive potential compound. Therefore, further elaborate research is warranted and it's worth investigating.

P160 Bacterial profiles in the submerged soil around direct-seeded rice and involvement of several organic acids in poor seedling emergence

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Among the systems for cultivating rice (*Oryza sativa* L.), the direct seeding method is becoming more popular than the seedling transplant method in the world because the former requires less labor and time. However, this cultivation technique has experienced limited use in Japan due to poor seed germination and seedling emergence. The poor seed germination and seedling emergence of rice plants is typically considered to be caused by several stresses produced with a drastic decrease in the soil oxidation-reduction potential (ORP) around the direct-seeded rice under submerged conditions. Additionally, several studies indicated that poor seed germination and seedling emergence was frequently occurred under submerged condition with organic matters such as straw. However, data on the environmental changes of the soil around the direct-seeded rice under submerged conditions with organic matters are lacking. In this study, environmental changes including bacterial profiles and substrates produced under submerged soil conditions with straw were examined. The seedling emergence of wet-direct seeded rice was severely inhibited by coexistence with straw. The relative abundances of Clostridium, Coprococcus and Bacillus significantly increased under submerged condition with straw. Additionally, several organic acids including plant hormone-like substances were detected in this submerged soil condition. Several aroma carboxylic acids such as 3-phenylpropionic acid and benzoic acid tend to delay seed germination. On the other hand, seed germination was apparently suppressed by several plant hormone-like substances detected in the submerged soil. In this presentation, presumed inhibition mechanisms of seed gemination and seedling emergence in wet-direct rice seeding system are discussed.

P161 Bacterial profiles in the submerged soil around direct-seeded rice with different seed-coating materials

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The direct seeding method of rice (*Oryza sativa* L.) is becoming more popular globally than the seedling transplant method due to lower labor and time requirements. However, this cultivation technique has experienced limited use in Japan due to poor seedling emergence and establishment. In Japan, to accomplish stable seedling emergence and seedling establishment, rice seeds coated with several coating materials such as iron and calcium peroxided are frequently used in this cultivation system. However, data on the environmental changes of the soil around the direct-seeded rice with different coating materials under submerged conditions are lacking. Thus, the objectives of this study were to (1) reexamine seedling emergence of direct seeded rice with different coating materials (no coating, iron-coating and calcium peroxide coating), (2) visualize changes of ORP (soil oxidation-reduction potential) around these differently coated seeds using methylene blue dye and (3) examine bacterial profiles in the soil around these differently coated seeds using the next generation sequencing technique. Seedling emergence rate of no coating, iron-coated and calcium peroxide coated seeds were 47, 33 and 83 %, respectively. The ORP around rice seeds of calcium peroxide coating tend to decrease slowly, compared with those of no-coating and iron-coated seeds. Bacterial profiles in the soil around these coated seeds were remarkably changed at 4d after submerging treatment. Especially, the relative abundances of Geobacter, Symbiobacterium, Oxalobacteteraceae and Clostridium significantly increased. Additionally, the relative abundances of Clostridium and Coprococcus was higher in no-coating seeds and iron-coated seeds than in calcium peroxide coated seeds.

P162 Submerged soil collection method for studies on soil microbial changes around directly seeded rice seeds

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In Japan, poor seed germination and seedling emergence can be problems sometimes in the wet-direct seeding method of rice (*Oryza sativa* L.) due to a drastic decrease of oxidation-reduction potentials (ORP) around direct seeded rice seeds under submerged soil conditions. Although it is well known that a drastic decrease of ORP around direct-seeded rice are mainly ascribed to consequences of bacterial activities around direct seeded rice seeds, data on environmental changes of bacterial profile of the soil around the direct-seeded rice under submerged conditions are limited due to the methodological difficulty of collecting the submerged soil surrounding direct-seeded rice seeds. We have developed an effective soil collection method that makes the visualization of the changes of soil ORP possible by using an acrylic box and methylene blue (MB) dye. For the collection of the soil surrounding direct-seeded rice, we designed and produced a colorless and transparent acrylic box (7cm ×2cm ×5 cm). One side of the box has a hole with 1.3 mm of diameter attached with an acrylic cup with O rubber ring to prevent any leakage of soil solution. Consequently, we could simply collect the submerged soil around direct-seeded rice seeds visualizing changes of soil ORP with MB. Our results indicated that MB had no effects on DNA extraction, PCR amplification and bacterial profiles. Therefore, this technique can be employed to observe specific changes in the activity of microbial communities in soils containing rice seeds under submerged conditions. In the presentation, we show the collection procedure of soil.

P163 Bacterial profiles in the soil around direct-seeded rice coated with calcium peroxide under submerged soil conditions

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In Japan, poor seed germination and seedling emergence can be problems sometimes in the wet-direct seeding method of rice (*Oryza sativa* L.) due to a drastic decrease in the soil oxidation-reduction potential (ORP) around the direct-seeded rice under submerged conditions. Consequently, calcium peroxide (O_2 supply material) coated rice seeds are sometimes used in this cultivation system for stable seedling emergence and establishment. Although it is well known that the drastic decrease of ORP around direct-seeded rice are mainly ascribed to be the consequences of bacterial activities around direct seeded rice, data on environmental changes of bacterial profile of the soil around the direct-seeded rice under submerged conditions are limited. In this study, effect of calcium peroxide- coating on bacterial profiles in the soil around direct seeded rice were examined under submerged soil condition with or without rice straw application. Under submerged soil condition without straw application, seedling emergence rates of non-coating and calcium peroxide-coated seeds were approximately 47 and 87 %, respectively. Under submerged soil condition with straw application, seedling emergence rates of no coating and calcium peroxide-coated seeds were approximately 10 and 43 %, respectively. After the submersion treatment, bacterial profiles were remarkably changed from anaerobic bacteria to aerobic bacteria such as *Bacillus, Symbiobacterium Clostridium* and so on. Especially with straw application conditions, the relative abundances of *Clostridium* apparently increased with time. Additionally, the relative abundances of *Clostridium* were significantly higher in non-coating seeds than in calcium peroxide-coated seeds. Calcium peroxide-coating on rice seeds tends to suppress the increase of relative abundances of *Clostridium* in the soil around direct seeded rice and help seed germination and seedling emergence thorough suppression of a specific microbial activity and microbial metabolites.

P164 Soil depth matters: Bacteria, fungi and micro-eukaryotes are all strongly structured by soil depth

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The boreal forest is a key ecosystem for global C sequestration and storage. Microorganisms in soil have crucial functions in regulating these processes. Fungi are typically sharply structured with soil depth, but we largely lack such information for other microorganism, including bacteria and other micro-eukaryotes. To improve our knowledge of how different microorganisms are structured vertically and how they might interact, we investigated the communities of bacteria, fungi and micro-eukaryotes in four different soil horizons in natural birch forests in Western Norway. The communities of all three organismal groups were strongly structured along the vertical depth. Our results support the hypothesis that natural decrease in nutrient availability and pH differences between organic and mineral horizons affect the distribution of soil microorganisms. Proteobacteria, Actinobacteria and Planctomycetes dominated in the uppermost organic layer while Acidobacteria and Firmicutes in mineral layers. Proportionally, fungi dominated in mineral layers whereas other micro-eukaryotes (Metazoa, Apicomplexa, Conosa, Ochrophyta and Chlorophyta) in organic layers. Ascomycota were relatively more abundant in mineral layers compared to Basidiomycota and Cryptomycota. Nematoda, Annelida and Arthropoda showed decreasing trends with depth. Furthermore, different optima in the depth distribution of ectomycorrhizal and saprotrophic genera was observed, supporting the view that different genera are adapted to different niches along the soil depth gradient. Network analyses will be used to infer tentative biotic interactions between the microbial groups and how this varies with soil depth.

P165 Intra-annual variation of soil microbial communities

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There have been many studies of the biogeography of soil microorganisms, which have provided meaningful insights into the determinants of soil microbial community structure. Relatively little research has been done on the temporal dynamics, or stability, of microbial communities. We sampled five soils representing three climatic regions in Oregon, USA, on a monthly basis. Bacterial (16S rRNA gene) and fungal (ribosomal ITS region) community composition was assessed by amplicon sequencing. For three of the five soils we found that within site variability of microbial communities was greater than within year variability. At two of the sites, however, we observed seasonal dynamics of microbial community structure despite the spatial variability of microbial communities. These results have potential implications for sampling soil microbial communities.

P166 Living *Sphagnum* layer hosts essential microbes with potential for biotechnological applications

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The peat is mainly formed from decomposed *Sphagnum* species (sp.). However, the peat gathers exceedingly slowly and harvesting cause environmental problems. Therefore, the living, renewable *Sphagnum* top layer is a sustainable alternative to peat in the horticulture and growing medium industry. Peatlands are characterized with high water table level and are nutrient poor, cold and acid habitats. Partly, due to the extreme growth conditions *Sphagnum* sp. are colonized by symbiotic bacteria that promote the growth of mosses. Similarly, the endophytic microbes of mosses would be beneficial for crop plants. Some symbiotic microbes are antagonistic to pathogens and the others help in releasing or fixing nutrients or induce excretion of essential hormones or enzymes. We assume that *Sphagnum* sp. associated bacteria are a reservoir for the biological control of plant pathogens or for the isolation of bioactive compounds. Our aim was to study microbial composition of three general *Sphagnum* species that live on the same mires but prefer different microhabitats. *Sphagnum fallax* grows on wet patches, whereas *Sphagnum fuscum* is found from drier hummocks. *Sphagnum magellanicum* is less sensitive to water level changes. Preliminary results indicate that the microbial composition of mosses is species specific. i.e. *S. fallax* had less microbial species than *S. fuscum* and *S. magellanicum*. Moreover, microbial biosensors were used to evaluate the bioactivity of the moss extracts. The chemistry of mosses, microhabitat and time of harvesting may have an influence on hosted microbes.

P167 Eastern Amazonian soils' methane emission varies due to changes in moisture and temperature

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Climate changes projections for Amazon by 2040-2100 indicate drought in the eastern, while wetness in the western. This study aims to understand the effects of climate change to methane emissions by soil microbiota. Microcosms were set in triplicates with intact core soil samples from Oxisols under Pristine Forest and Pasture from the Tapajós National Forest, PA, Brazil. Treatments were as follows: 17%, 35% or 70% moisture field capacity, and temperatures of 25°C or 30°C. Samples were incubated in closed headspace in the dark for 15 days, followed by measurements of the gases CH_4, CO_2 and N_2O. The CH_4 cycle marker genes were used for quantification of methanotrophs (*pmoA*) , methanogens *mcrA*), and the 16S rRNA gene. FOREST**.** Under 35% moisture, the increase in 5°C was responsible for a significant enrichment of all studied populations with increases in CH_4 emission. Drought under 25°C resulted in the highest CH_4 emissions. The increase in moisture enriched the soil for all populations, however there was a decrease of CH_4 emissions at 35% moisture, increasing again in a more humid state. PASTURE**.** Under 35% moisture and 25°C there was an increase in total number of Bacteria and Archaea with a slightly increase in emissions for all gases. Both drought and wetness with increase in temperature lead to significant increase in CH_4 emission. Increase in moisture enriches the microbiota abundance in Forest and Pasture, increasing the potential for CH_4 emissions. However, CH_4 emission itself increases significantly in dry and wet Forest soils under 25°C, or Pasture soils under 30°C. We conclude that once the predicted climate changes take place, there might be a significant increase in biological CH_4 emissions in Eastern Amazonian Forest and Pasture soils.

P168 Development of PLFA profile of soil microbial communities during pot growth of *Miscanthus* x *giganteus* in contaminated soils

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Phytotechnology using second generation biofuel crops as *Miscanthus x giganteus* is promising way how to produce energetic biomass at marginal lands and simultaneously improve soil parametres. To evaluate influence of *Miscanthus x giganteus* growth to soil microbial communities pot experiment with four different soils was established. Control agricultural soil and post-military soil from former military airport were collected at locality Ralsko (Liberecký region, Czech Republic) and to simulate historic contamination by hydrocarbons also mixed variants with soil from airport and oil refinery in ratios 3:1 and 1:1 were prepared. Beside hydrocarbon contamination also significant concentrations of several heavy metals (Zn, Pb, Cd, Cu) were detected. Phospholipid fatty acids (PLFA) determination was used to describe living microbial biomass and rough structure of soil microbial community during two years experiment. Total PLFA content revealed significantly higher abundance of microorganisms in oil contaminated soils compared to control and post-military soil. However microbial community structure and *cy/pre* stress indicator suggest that in contaminated variants microbial community is exposed to higher stress. Comparison of year-on-year results indicates positive influence of *Miscanthus* growth on the amount of living microbial biomass. This effect was more pronounced in control and post-military soil while in mixed soils plant growth was highly limited by contamination.

P169 Biodegradation of synthetic aliphatic polyesters: using stable carbon isotope labeling to track polyester fate in soils

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Conventional plastics accumulate not only in aquatic but also terrestrial systems, including soils. One strategy to overcome this accumulation is to replace non-degradable with biodegradable polymer materials, including aliphatic polyesters. Yet, the rates and extents at which these polyesters degrade in soils remain poorly studied, mainly due to a lack of analytical approaches to track polyester carbon during biodegradation in soils. This work introduces an analytical workflow that involves incubating ^{13}C-labeled polyesters with soils in flow-through chambers, allowing for continuous monitoring of polyester biomineralization by quantifying formed $^{13}CO_2$. Additionally, after terminating the incubations, mass balance on polyester carbon can be closed by quantifying $^{13}CO_2$ formed from combusting soil aliquots. We validated this approach by tracking carbon of three position-specifically ^{13}C-labeled poly(butylene succinate) (PBS) variants incubated in soils. Over 425 days of incubation, 65±1 % of the ^{13}C added in PBS was mineralized to $^{13}CO_2$. Soil combustion showed that 34±2 % of the added ^{13}C-PBS had remained in the soil, thereby demonstrating closed ^{13}C-PBS mass balances over the incubation. Using Soxhlet extraction, we showed that most of the ^{13}C that remained in the soil was still present as bulk PBS. Fitting of the data with a biodegradation model showed that hydrolysis of ester bonds in PBS was the rate-determining step in overall biodegradation. Furthermore, the modeling results were consistent with PBS bio-degradation slowing down when nutrient availability decreased in the soils. The PBS results are discussed in the broader context of polyester biodegradation in soils.

P170 An increasing trend in soil solution nitrate concentrations during a twenty-year-monitoring period in a Norway spruce forest

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Time series of soil solution nutrient concentrations during the rotation period of a forest stand are rare. Soil solution water chemistry have been studied over a twenty year period as a part of the long-term ecological monitoring (ICP ForestsLevel II Programme) in Finland. The aim on this study is detect trends in pH, nitrogen and dissolved organic carbon concentrations in soil solution of a spruce stand during the 20-year-monitoring period, as well as to depict their seasonal patterns. The sampling has occurred at 2–4-week intervals during the snow-free period. Five zero-tension lysimeters are located at three depths: 5, 20, 40cm and six suction cup lysimeters at 20 and 40cm depths. The samples have been analyzed monthly, e.g. for pH, ammonium (NH_4) and (NO_3) and DOC. Methods are described in the ICP –forests manual (www.icp-forests.net). A clearly increasing trend was observed for nitrate concentrations, apparently related to thinning followed by rot damage observations and a bark beetle outbreak (*Ips typographus*).

P171 Impact of treated wastewater irrigation on soil and crop microbial communities

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Global water scarcity drives the use of treated wastewater (TWW) for agricultural irrigation, especially in arid and semiarid regions. However, the effect of TWW irrigation on soil health is still debated, because this water contains dissolved organic matter, salts and microorganisms, including pathogens. We hypothesized that TWW irrigation would alter the composition of the soil microbial communities. To test our predictions, we investigated the diversity of bacteria, fungi and protist communities in water-soil-crop continuum during two-year field experiments. We compared water qualities (TWW and freshwater), soil types (clay, loam and loamy sand), soil treatments (drip irrigation, subsurface drip irrigation and plastic cover) and crops (cucumbers and melons). More than 400 samples of water, soil and crop (surface and tissue) were tested for their physico-chemical and microbial characteristics as well as the presence, abundance and source of pathogens, using 16S and 18S rDNA amplicon sequencing. The microbial and pathogen communities significantly differed between water types, yet these differences were not carried to the irrigated soils and crops. Moreover, the source of pathogens in the soil and crop could not be linked to TWW irrigation. Soil treatments and crop types did not significantly alter the soil microbial or pathogen communities but, the communities in the various soil types were significantly different, particularly from clay soil. Our results suggest that TWW irrigation does not strongly affect the soil microbial community composition regardless of soil treatments, crops or soil types and thus does not present a health hazard to the irrigated soil and crop.

P172 Presence and abundance of nitrogen metabolism genes explain fungal community shifts and ecosystem-carbon dynamics in nitrogen enrichment field experiments

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Fungi are key drivers of ecosystem carbon (C) cycling and are highly susceptible to soil N (nitrogen) depositions. In field experiments, simulated N deposition results in an accumulation of soil carbon, an increase in recalcitrant compounds, and a decrease in soil respiration. What adaptation strategies are fungi undergoing that may be driving these ecosystem C dynamics? To answer this question, we analyzed genomes and taxonomical traits of fungi reported in N amended soil to gain a comprehensive understanding of the ecosystem-level observations under elevated N deposition. We found that 90% of the fungi found exclusively in N plots have less ammonium and nitrate transporter gene copies than fungi from control plots. Moreover, a higher percentage of fungi in N amended plots had less genes for C decomposition. We also detected a shift in the taxonomical distribution of fungi. The order Agaricales, Polyporales, and Russulales decreased in response to N; whereas, Hypocreales, Pleosporales, and Pezizales increased. Concomitantly, we detected an increase in functional guilds associated to fungal and lichen parasites, an overall increase of saprotrophs, and a decrease of endophytes and ectomycorrhizal fungi in response to N. Finally, we found that white and soft rot are present in both, control and nitrogen plots, but some species are slightly more abundant in N plots. We provide genome- and functional-level evidence of the response of fungi to simulated N deposition and suggest that N may serve as a selective force on fungal communities, driving changes in C dynamics at the ecosystem-level.

P173 Biosorption of nickel by the fungus *Trichoderma* isolated from soil, leaf litter and marine substrata

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Among our serious environmental issues that require immediate attention is nickel contamination in terrestrial and aquatic habitats. The use of microorganisms has been employed in the bioremediation of these contaminated sites. In this study, six strains of *Trichoderma* were isolated from soil, leaf litter and marine substrata collected in coastal areas in the Philippines. The isolated fungi were initially characterized morphoculturally. The identities of the fungal strains were then confirmed based on gene sequence analysis of the ITS gene. The *Trichoderma* strains were also tested for their tolerance and later, for their biosorption of nickel. Our results showed the growth of *Trichoderma* strains on Trichoderma Selective Medium (TSM) with 50 to 1,200 ppm of nickel ($NiSO_4$), indicating their ability to tolerate higher concentration of nickel. Highest radial growth was also observed on TSM with 50 ppm nickel. Interestingly, more terrestrial strains (13) grew on this medium as compared to marine strains (8). Among the fungal isolates, *T. asperellum* S03 isolated from soil exhibited the best growth after 2 days of incubation. For the biosorption of nickel, the accumulation or uptake efficiency by selected six *Trichoderma* was determined in Potato Dextrose Broth supplemented with 50 ppm of nickel using Flame Atomic Absorption Spectrophotometer. The percent uptake efficiency of three strains of *Trichoderma asperellum* (S03, S08 and LL14) was computed to be 20-66% while *Trichoderma virens* (SG18 and SF22) achieved 29-68% and *Trichoderma inhamatum* (MW25) achieved 68% uptake efficiency. The six *Trichoderma* strains were also observed under the scanning electron microscopy to check the surface morphology of the fungal mycelia before and after exposure to nickel. Scanning electron microscopy revealed no damage on the surface morphology of the *Trichoderma* biomass. Our study showed the potential of terrestrial and marine strains of *Trichoderma* for the bioremediation of nickel.

P174 Soil microbial and structural properties as sensitive soil quality indicators affected by long-term crop sequence and manure use

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In sustainable crop production, good soil quality is a key issue when targeting to production of high yields with low environmental impact. We investigated the chemical, structural and microbiological properties of mineral soils on ten pairs of organic and conventional fields on farms. Our aim was to examine the effects of long-term crop sequence and manure use on the structural and biological properties of soil quality. The fields within the pairs were situated directly next to each other and have similar soil texture. The clay (particle size < 0.002 mm) content of the topsoil (0−20 cm) of the fields was 14 to 72%. Organic farming had been continued more than 10 years before the study and contained regularly grass in crop sequence and manure as fertilizer. In conventional farming system, cereals were cultivated either as monoculture (mineral fertilizing) or in crop sequence with grass (manure and mineral fertilizing used). From soil samples, microbial biomass, phospholipid fatty acids, net nitrogen mineralization, total organic carbon, POM (Particulate Organic Carbon), pH_{H2O}, soluble nutrients, dry bulk density, saturated hydraulic conductivity and volume of macropores (> 0.03 and 0.3 mm) were determined. The statistical analyses of the data were based on generalized linear mixed models. Long-term grass cultivation in crop sequence and manure use improved soil microbiological properties and macroporosity. The difference in soil C content was not significant. Changes in soil properties and quality occur slowly. Microbiological properties were found to be sensitive soil quality indicators.

P175 Exopolysaccharide production and biofilm formation in soil- dwelling *Acinetobacter oleivorans* DR1 under oxidative stress

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Many bacteria secrete exopolysaccharides (EPS) that contribute to their nutrient trapping, surface attachment, and protection against abiotic or biotic stresses. Like other *Acinetobacter* species the genome of soil-dwelling *Acinetobacter oleivorans* DR1 contains three distinct EPS operons [two PNAG (poly-N-acetyl glucosamine) operons and the K locus]. Our transcriptomes and quantitative RT-PCR analysis showed that the levels of their expression vary under different EPS-producing conditions: H_2O_2, hexadecane, NaCl, and cold temperature. Morphologically distinct biofilms by those abiotic stresses were observed using confocal laser scanning microscopy, indicating involvement of different components in each biofilm formation. The results of RNA sequencing and Northern blot analyses showed that the expression of PNAG1 and K-locus operon genes were highly upregulated under H_2O_2 treatment although genes in the K-locus has constitutively high level of expression. Interestingly, the Δ*oxyR* and Δ*pgaC1* mutants displayed increased production of EPS and higher biofilm formation, but not Δ*pgaC2* and Δ*wzc-wza* mutants which are defective in EPS production from PNAG1 region and the K-locus. Due to the possible replacing role of the K-locus genes products in the PNAG1-knockout background, the Δ*pgaC1* mutant was capable of producing more EPS and biofilm formation. Electrophoretic mobility shift assays using purified OxyR revealed that the H_2O_2-sensing OxyR might be involved in the regulation of those three EPS operons through different degrees of promoter's bindings. Further experimental data will be discussed to explain the regulation of OxyR-dependent EPS productions and their contribution to biofilm formation.

P176 Fungal biomass and species composition in boreal peatland forests estimated by in-growth mesh bag method

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The role of fungi in peatlands drained for forestry is not comprehensively understood. These fungi may significantly affect the soil C balance after drainage, however. We used fungal in-growth mesh bag method to estimate fungal biomass production and identify fungal species in drained peatland forests. External mycelia of symbiotic mycorrhizal fungi were analyzed using mesh bags filled with quartz sand and placed in two depths (0-15 cm, 15-30 cm) in four peatland forest sites representing different levels of fertility. Bags were recovered after 2, 5, and 12 months. To detect decomposing fungi, mesh bags filled with either corn or wheat litters were placed into root-trenched plots in one nutrient-rich and one nutrient-poor peatland forest sites. Fungal biomass estimations were based on ergosterol and chitin extracted from harvested mycelia. Fungal identification was based on fungal ITS region. There were significant differences in mycorrhizal fungal biomasses among sites and incubation times. The most nutrient-rich mesotrophic and the one nutrient-poor ombrotrophic site had significantly higher mycorrhizal biomass production and amount of living biomass after 1 year compared to other sites, possibly due to fertilization of these sites with phosphorus and potassium soon after drainage. Biomass of decomposing fungi was biggest in the nutrient-rich site, 0-15 cm depth, and corn litter. Most likely decomposing fungi in the nutrient-rich site are able to utilize more efficiently increased resources due to decreased competition with mycorrhizal fungi because of the trenching. Fungal identifications from ITS sequences are still going on.

P177 Bacterial communities in mushrooms: what determines their structure and function?

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Bacteria and other microbes are widespread organisms, occupying different environments from soil and water to eucaryotic tissues. Bacteria may interact with each other and also with eukaryotic organisms in varying degrees, participating in the formation of immunity, organism development or in several metabolic processes. While interactions between bacteria and fungi have extensively been studied, the community composition, function, and origin of bacterial communities in fungal fruiting-bodies, are largely unknown. Fruiting-bodies of mushrooms are ephemeral and mostly formed above the ground, though fungi spend most of their lifetime in soil. By applying high-throughput sequencing, specifically 16S rDNA metabarcoding and metagenomics, we found considerable overlap between bacterial communities in soil and fruiting-bodies, but also several bacterial groups more abundant in one of these habitats. In addition, several soil properties, especially soil pH, were shown to strongly affect bacterial community composition in various fungal taxa. The fungal microbiome is also significantly affected by taxonomic identity of the host fungus and even the individual host genotype within one species. The detection of factors shaping the microbial communities in fruiting-bodies will help to better understand the microbiome formation processes, its functions and bacterial interactions with the host fungus.

P178 Metagenomic analysis of microbial communities in soils along a natural climate gradient in the Scandinavian sub-Arctic

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Arctic soils comprise as much as half of the Earth’s below ground carbon stock. Soil thawing due to pronounced warming in high northern latitudes might lead to a positive warming feedback loop, as previously frozen organic matter is metabolized by microorganisms releasing carbon dioxide and methane to the atmosphere. Nevertheless, microorganisms involved in the production of greenhouse gases are not well known and a more thorough knowledge on the functional potential of microbial communities in Arctic soils is needed. Here we analyzed metagenomes from 50 soil plots within a natural climate gradient in the Scandinavian sub-Arctic. The climate gradient encompasses local abiotic and vegetation heterogeneity but the spatial variability of microbial communities is not known. Analysis of reads mapped to 16S rRNA genes revealed microbial communities dominated by Proteo-, Actino- and Acidobacteria, and analysis of functional genes evidenced a high proportion of genes involved in the breakdown of amino acids, carbohydrates and lipids. A first assembly of reads from 16 samples yielded five metagenome-assembled genomes (MAGs) with >70% completeness and <5% contamination, which were assigned to the three main microbial phyla in the studied communities. Further phylogenetic and functional analyses of the obtained MAGs are being currently carried out, and assembly of the remaining samples will potentially result in the recovery of additional MAGs. These analyses will allow us to investigate the metabolic potential of the soil metagenome in more detail, for example, regarding the importance of methanogenesis and methane oxidation in the studied soil ecosystem.

P179 Jasmonic acid signalling pathway alters the structuring of the root microbiome in Grey Poplar

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Tree roots are colonized by rhizospheric/endophytic bacteria and fungi, incl. ectomycorrhizal (EcM) fungi - the microbiota. EcM fungi play a key role in the host nutrition, whereas endophytic associates modulate the plant resilience to biotic and abiotic stresses. The molecular mechanisms shaping the tree microbiota are not well known. We aim to determine how the tree defense signalling pathways regulate the root microbiome in Grey poplar (*Populus tremula x alba*). We surveyed the root microbiota from wild-type (WT) and poplar lines constitutively expressing MiSSP7 (Mycorrhizal-induced Small Secreted Protein 7 kDa) grown in natural soil for 6.5 weeks. MiSSP7 is naturally secreted by the EcM fungi *Laccaria bicolor* and is required for symbiosis establishment by repressing jasmonic acid (JA)-related defence signalling pathways. We show that the fungal colonisation of MiSSP7-expressing roots was up to 30-fold higher than WT lines, suggesting that the alteration of JA signalling by MiSSP7 facilitated fungal colonization. Metabarcoding analyses revealed that MiSSP7-expressing roots were more colonized by EcM fungi than WT whereas roots of WT lines were more colonized by potential fungal endophytes. This observation was confirmed by our metabolomic analyses as MiSSP7-expressing roots accumulated more markers of EcM associations than WT poplars. The expression of MiSSP7 in poplar roots also impacted bacterial communities although in a lower extent than fungal communities. Altogether, our results suggest that MiSSP7 may not only play a role in the formation of mycorrhizal symbiosis but that it could also influence the structuring of root-associated microbial communities.

P180 Response of soil microbial communities and soil functions to long-term soil perturbation and nitrogen fertilization in a perennial cropping system

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Soil bacteria and fungi contribute essentially to soil functions such as mobilization of nutrients, litter decomposition and build-up of organic matter. In vineyards, tillage of inter-row vegetation cover as well as fertilization is applied to optimize grape yield and quality. However, the combined effects of these practices on microbial communities and ecosystem functions has hardly been addressed, particularly not on a decade long time scale. Therefore, we investigated the effects of soil treatment and fertilization in a long-term vineyard experiment, where these practices are constantly applied since 1985. Plots in this vineyard (Hesse, Germany) are treated with different yearly amounts of nitrogen fertilizer (0, 30, 60, 90, 120, 150 kg N/ha) in four replicates in combination with two types of inter-row cover treatment (tillage vs. permanent cover). We analyzed the microbial community (bacteria and fungi) of the top soil (0-10 cm) by Next Generation Sequencing techniques, measured soil chemical parameters related to fertility (soil organic matter content, total nitrogen, pH, P, K, Mg), and assessed decomposition using the teabag approach. While tillage practice had a strong impact on soil bacterial and fungal communities, soil chemical and decomposition parameters, the long-term nitrogen fertilization only slightly shifted microbial community composition and had no significant effect on decomposition and most of the soil chemical parameters.

P181 The enzymatic landscape of undisturbed soils – Evaluation and improvement of enzyme zymography

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The visualisation of the distribution of soil enzymes is an important challenge in microbial ecology. Recently, soil enzyme zymography using fluorescent substrates was developed to investigate the spatial distribution of enzyme activities and successfully applied to specific hot spots like the rhizosphere. The spatial distribution of soil enzymes is driven by complex interactions of production, turnover and sorption of enzymes and disentangling these processes requires further methodological developments and thorough testing. Our aim was to test and optimize important steps and conditions of the zymography assay. More specifically, we were interested in the following research questions: i) What is diffusing through the agarose gel, which separates the substrate saturated filter from the soil surface: the enzymes or the substrate? ii) What is the thickness of the surface layer, which contributes to the observed enzyme patterns? iii) How can we optimize the incubation procedure to avoid long-lasting contamination of the surface layer with fluorescence, which will hamper the consecutive measurements of several enzymes? Consequently, we disentangled substrate application from detection of the fluorescent product to determine the legacy/memory effect of initial substrate addition. First results showed that the substrate is diffusing through the agarose gel and that back diffusion of the reaction product is lasting for several hours. Further testing will clarify whether extracellular enzymes originally bound to the organo-mineral surfaces might be released from the organo-mineral surfaces and migrate through the agarose gel towards the membrane. This mechanism was originally described as the basic assumption of the zymography assay.

P182 Impact of long-term *in situ* warming on bacterial rhizobiome from Antarctic vascular plants

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Antarctic Peninsula temperature has increased 3.7 °C in the last 100 years. A biological evidence of warming is the increased flora coverage due to ice and permafrost melting. To understand, whether vascular plants successful colonization is related with the effect of warming on rhizobacterial communities, we investigated potential changes induced by warming on rhizobiome and their possible metabolic changes with positive consequences on vascular plants colonization. Characterization of rhizobacteria communities in response to *in situ* long-term experimental warming was performed using Open Top Chamber (OTC) and Open Space (OS) soil as control condition. Soil samples were obtained from Admiralty Bay, King George Island, Antarctica. The rhizobacteria structure analysis was performed using 16s rRNA gene (v3-v4 region). Bioinformatic prediction of functional metabolic pathways changes on rhizobacteria communities was developed with Phylogenetic Investigation of Communities by Reconstruction of Unobserved States (PICRUSt) alghoritm. The taxonomic analysis revealed a predominance of *Proteobacteria* (31.2%-45.7%), *Actinobacteria* (14.2%-13%) and *Acidobacteria* (13.4%-9%) Phyla in OS and OTC, respectively. Likewise, *Proteobacteria* Phylum, *Methylotenera* and *Burkholderia* genera are highest in OS and OTC. However, these bacterial genera increased under OTC conditions (17.4%). Functional pathway prediction, carbon and nitrogen energetic metabolism should be higher in OTC than OS. These metabolic processes have a critical role in bacterial soil community in warming conditions. In conclusion, this study suggests that response of rhizobiome structure to warming benefits Antarctic vascular plants coverage. Thus, this information could contribute understand biological mechanisms behind the increase vegetation coverage in the Antarctic Peninsula.

P183 Highly sensitive quantification of methanogenic and methanotrophic microorganisms via droplet digital PCR (ddPCR)

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Droplet digital polymerase chain reaction (ddPCR) is a new method to quantify DNA without the need of an external standard. The principle of ddCPR is based on traditional PCR amplification and fluorescent-based or probe-based detection. Compared to quantitative real-time PCR (qPCR), ddPCR differs in the way the sample target is measured. In ddPCR the sample mix is partitioned into thousands of individual reaction droplets and data acquisition is performed at end point. DNA quantification is based upon the pattern of positive and negative droplets, according to Poisson distribution, and there is no need of standard curves. In environmental and especially soil microbiological studies DNA extraction from soil results in coextraction of other soil components, mainly humic acids or other humic substances that negatively interfere with DNA in downstream analyses. Due to the partitioning of the PCR reaction during ddPCR analysis, the influence of inhibitors is minimized and the discriminatory capacity of assays is improved. Furthermore, end-point measurement enables nucleic acid quantification independently of the reaction efficiency by evaluating the positive-negative signal for every single droplet. In our investigation, we quantified the abundance of methanogenic and methanotrophic microorganisms in samples of a forest soil in Austria, Tyrol and compared results to real-time PCR. Our results showed that the strength of ddPCR lies especially in the quantification of low-target DNA where until now sample dilution requirements had to be fulfilled to assure acceptable reaction efficiency and primer annealing of qPCR, a fact that often lead to undetectable or overestimation of target levels.

P184 Dispersed variable-retention harvesting mitigates N losses on harvested sites despite changes in soil microbial community structure

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As an alternative to clear-cutting, variable-retention harvesting is consistently being employed due to benefits associated with maintaining mature forest species and forest structural diversity. Although there is some evidence that variable-retention harvesting, particularly single-tree retention will mitigate the impacts of clear-cutting on soil microbial communities and nutrient cycling, findings have been inconsistent. We examined microbial community structure (PLFA), $\delta^{13}C_{PDB}$ PLFA to deduce C sources used for microbial growth. and nutrient availability (PRS^{TM} probes) in a retention patch and over three harvesting treatments: dispersed retention, clear-cut and clear-cut edge two years after harvest. Unlike previous studies, we did not observe elevated nitrate in the harvested areas, instead ammonium was elevated. Availability of N and other nutrients were surprisingly similar between the dispersed-retention treatment and the retention patch and labile C from plants was the major C source for microbes. The microbial community, however, was different in the clear-cut and dispersed-retention treatments, due to significantly lower abundance of fungi combined with an increase in, specifically, Gram-negative bacteria. This shift in microbial community composition in the dispersed-retention treatment did not appear to have a major impact on microbial functioning and nutrient availability, indicating this harvesting practice has potential to maintain generic microbial functions/processes. However, Mn levels were twice as high in the retention patch compared to the harvested treatments, indicating the other ‘narrow’ processes (performed by a small number of specialized microorganisms), such as lignin degradation, catalyzed by Mn peroxidase, which concomitantly removes Mn from solution, may be altered by harvesting regimes.

P185 Reactions of ectomycorrhizal communities of spruce and beech to repeated extreme droughts

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Increasing frequency and severity of drought periods during the vegetation period threaten forest tree species such as Norway spruce and European beech. At the Kranzberg roof (KROOF) experimental site, four years with rain exclusion during March and November changed ectomycorrhizal community composition and functions exemplified by soil exploration and potential enzyme activities. During evaluation of data from KROOF experiment, an interactive platform was established in the R computing environment (R-Core-Team 2016). This platform displays a spearman's rank correlation matrix containing qualitative enzyme activities and ECM fungal species abundances. The user can specify year of experiment, treatment, soil depth and tree species. This enables inspection of interrelationships between qualitative EAs and ECM fungal species abundance as well as within these sets on the sample type scale. However, clear trends were only detectable after aggregating data at ecosystem level. Yet, data analysis at this fine scale showed how transient and variable the examined system reacted to throughfall exclusion.

P186 Greening of daycare yards modifies skin and gut microbiota and enhances well-being of urban children in Finland

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Exposure to greenness in early childhood has been associated with benefits to immune system and health. While comprehensive health benefits might be both physical and mental, benefits for immune system arise from contact with natural microbial diversity. According to the biodiversity hypothesis, contact with diverse environmental microbiota affects human commensal microbiota and drives effective immunoregulation that persists into adulthood. Unfortunately, high hygiene level and modern urban life-style decrease exposure to diverse microbiota and may result in imbalanced human microbiota and prevalence of immune mediated diseases. We examined biodiversity hypothesis in real urban environment by greening daycare yards in Lahti and Tampere in 2016. For transforming the yards, we used forest floor vegetation, sod, peat blocks, and planters for vegetable and flower growing. We hypothesized that this intervention changes both soil microbiota in the yards and children's commensal microbiota and increases the abundance of health-associated environmental microbiota that are beneficial to immunoregulation. We also hypothesized that greening of the yards have positive impacts on children's physical exercise and play, and their perceived well-being. In this presentation, we will show how greening of the daycare yards affected the skin and gut microbiota of children, and how these changes were associated with beneficial microbes to immune system and health. Based on survey and interview data, we found that green yards diversified children's play and physical exercise and increased their well-being. The results can be used in designing health-enhancing yards to daycare centres, schools, retirement homes, and other public and private green spaces.

P187 Links between soil CH_4 cycling and tree-derived CH_4 emissions on a forestry-drained peatland

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Recent studies have revealed the contribution of trees to the global methane (CH_4) emissions and thus questioned the nature of boreal forests solely as CH_4 sinks. However, the related mechanisms are still uncertain. We examined the potential role of soil CH_4 production and subsequent transport through the trees as a source of these emissions. Methane consumption in the soil profile and in the field layer mosses was also assessed. Measurements were conducted on two adjacent forested peatland subsites located in southern Finland (60°38' N, 23°57' E). Subsites differed in their water table level due to a partial tree removal, which decreased the evapotranspiration of the harvested subsite (HRV). In accordance with the higher water level, potential CH_4 production was higher in the HRV soil than at the control subsite. Similarly, the tree-derived CH_4 flux was significantly higher at the HRV subsite. Preliminary microbial analyses showed higher methanogen (*mcrA* gene) abundance in the HRV soil but no signs of methanogens in the trees. These results, and the decreasing CH_4 flux upward the tree trunk, were a strong indication of the transport of soil-derived CH_4 through the trees. Based on the fluxes, soils of both subsites were generally small CH_4 sinks, but there were differences in their potential for high- vs. low-affinity CH_4 oxidation. Mosses showed low CH_4 oxidation activity. Methanotrophic community structures are expected to reflect the above mentioned oxidation patterns. Combined, this study will give a detailed view on the role of different ecosystem components in the forest CH_4 cycling.

P188 Selection of high performance strains of edible mycorrhizal fungi for improved abiotic stress resistance

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Ectomycorrhizal Fungi (EcM) may play an important role in improving tree vigor and enhancing ecosystem services delivered by trees. It is important to develop resilient EcM-inocula to improve tree health, including urban trees. The use of native strains with strong adaptive skills to different abiotic and biotic challenges could be determinant for the success of tree establishment. The present work focus on screening high performance strains of edible ectomycorrhizal specie *Lactarius deliciosus* and assess its performance and ability to grow and adapt to stresses scenarios to ensure a more sustainable choice of isolates. The ability of *L. del* to grow and acclimate to abiotic stresses was studied by analyzing the effects of exposure on growth and biochemical traits. Fungal plugs were placed in fresh medium, on top of a cellophane sheet and grown for four weeks at 3 levels of temperature, (15°C, 22°C, 29°C), water stress (0%, 15% and 30% of PEG 6000) and pH (5, 6, 7). They were also subjected to temperature shifts. Box-PCR technique was used as a molecular tool for fingerprinting to differentiate *L. del* strains. Among the different treatments the highest growth was obtained at 25°C, and 35°C was lethal to the mycelium after 15 days of exposure. Temperatures of 15°C and 30°C were clearly stress temperatures to be considered in subsequent studies. These points will represent innovative contributions to the understanding of what triggers mycelium development for sustaining healthy ecosystems.

P189 Integrated Biodiversity Conservation and Carbon Sequestration in the Changing Environment (IBC-CARBON)

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Climate change represents a major threat to biodiversity (BD) as well as to the sustainable management of the ecosystem services (ES). Successful integration of BD conservation with sustainable forest use under global climate change is a major challenge for the Finnish society. The consequences of the planned large shift towards bio-based economy are poorly known, and the sustainability of these policies needs to be evaluated. Land use changes and increased biomass withdrawal can have far-reaching consequences on BD conservation, carbon (C) sequestration and soil quality, as well as downstream waters. Climate change directly influences many ecosystem processes and indirectly affects the development of mitigation and adaptation strategies that are likely to have substantial environmental impacts. The key aims of the IBC-CARBON project (2018-2023) include development of integrated model-based tools to determine spatially optimized land-use in forest ecosystems for the joint BD conservation and C-sequestration targets. Integrated impacts of climate change, forest bioenergy policies and other drivers on BD indicators and C-sequestration/balances (also accounting for biophysical effects) are also studied. Earth Observation (EO) based variables are developed and tested to provide cost effective tools to detect and quantify changes in forest BD and ES. The project is carried out by a multidisciplinary team from the Finnish Environment Institute SYKE, and Universities of Helsinki and Eastern Finland.

P190 Consequences of brownification for ecological indicators in Lake Pääjärvi-past and future

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Browning of surface waters due to increased terrestrial loading of organic carbon is observed in boreal regions. It is explained by large scale changes in ecosystems, including decrease in sulphur deposition that affects soil organic matter solubility, increase in temperature that stimulates export of dissolved organic carbon (DOC) from peatlands, and increase in precipitation and thus runoff. Land use changes and forestry measures are also observed to increase transport of DOC to surface waters. Browning affects freshwater productivity through limiting light penetration and creating more stable thermal stratification. Productivity has an effect on several services that ecosystems provide, like drinking water and recreation. The research question of the river Mustajoki-lake Pääjärvi combination is brownification of the lake, and influence of water colour on submerged macrophyte depth distribution. We studied both past trends based on observations, and made simulations for future by the physical Persist and INCA models. DOC concentration in the lake was calculated by the MyLake model. Simulated DOC concentration was transformed to water colour and light climate of the lake by empirical equations. Growing depths of macrophyte decrease from 2 m to 1.2 m. This change corresponds to observed shift from reference lakes to impacted lakes. In worst scenario almost half of large isoetids population is disappearing causing dramatic change in whole ecosystem. Change in land use did not seem to have any effect on growing depth, but it was driven only by the change in climate, rather in temperature than in precipitation.

P191 Hot experience for cold-adapted microorganisms: temperature sensitivity of soil microbial enzymes

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High latitude and cold ecosystems, which constitute major environment on Earth, are particularly threatened by global warming. Consequently, huge amounts of SOC stored in these ecosystems may be released to atmosphere by accelerated microbial decomposition. Effects of intensive warming on temperature sensitivity and catalytic properties of soil microbial enzymes were tested in cold-adapted alpine grassland of the Tibetan Plateau. We hypothesized that 1) maximal reaction rate will be insensitive to intensive warming at high temperature range (V_{max}-Q_{10}=1); 2) substrate affinity (K_m) remains constant at elevated temperatures due to expression of enzymes with less flexibility. These hypotheses were tested with kinetics of six enzymes involved in cycles of carbon, nitrogen and phosphorus after soil incubation at temperatures from 0 to 40°C. Q_{10} and E_a decreased at high temperature. However, enzymes that degrade low quality polymers remained temperature-sensitive even above 25°C, which explains faster decomposition of recalcitrant C compounds under warming. Above 25°C, K_m of C and N cycles remained nearly constant, while V_{max} gradually increased from 0–40°C. These results reveal two important implications of warming: i) enzymes that degrade low quality polymers are temperature-sensitive within the whole range of temperatures (0 – 40 °C); ii) soil microorganisms are able to maintain stable or flexible enzyme systems with low or high substrate affinity within wide temperature ranges to ensure efficient enzymatic functioning under diurnally and annually varying temperatures. This ensures easier adaptation of microbially driven decomposition to changing climate. Thus, acclimation may involve expression of enzyme at warmer temperature, potentially with same K_m but not necessarily. We conclude that considering temperature thresholds of strong changes in enzyme-based processes is crucial to modeling the consequences of warming for C, N and P cycles and predicting fate of soil carbon stocks in a warmer world.

P192 Combined effects of land use intensification and climate change on microbial decomposition processes in soils

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Soil microbes drive important soil processes such as degradation of organic matter and nutrient cycling. However, facing land use intensification and climate change, soil microbial communities are subjected to increasing environmental pressure. We studied the combined effects of two major global change drivers, land use and climate, on decomposition processes using the “Global Change Experimental Facility”. The land use types included a conventional and an organic cropping system, an intensively- and an extensively-farmed meadow, and an extensively grazed sheep pasture. Climate change was simulated by an altered precipitation pattern (reduction in summer, addition in spring and fall) and warming. Activity potentials of soil hydrolytic enzymes, which are involved in C, N, and P cycling, were assessed every three weeks over a period of two years. Involved bacterial genera were isolated on functional media and identified by partial 16S rDNA sequencing. Litter decomposition rates were determined by tea bag indices. The results revealed highly dynamic enzyme activities along the course of a growing season. These intra-annual variations were higher than the differences caused by land use and climate treatments. Nevertheless, we found significant differences between the land use types, whereby enzyme activities were increased by land use intensification. This land use impact was even more pronounced in the rhizosphere soil compared to that in the bulk soil. The climate change scenario showed only minor effects, but rain reduction by 20% during summer significantly decreased enzymes activities. Interestingly, this reduction and the land use-specific pattern were also mirrored by tea decomposition rates. In contrast to these differences, we found that the cultivable fraction of the soil bacteria, that is involved in the degradation of cellulose, chitin and P-containing complexes, was consistently dominated by *Streptomyces, Phyllobacterium*, and *Pseudomonas*, which suggests a high resilience of these bacterial genera to land use and climate change.

P193 Shifts in the structure of rhizosphere microbial communities of avocado (*Persea americana* Mill.) after Fusarium dieback

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Rhizobacteria are critical for plant growth and protection against pathogens. The infection by fungal pathogens may modify microbial interactions at the rhizosphere level, as pathogens may compete with the existing microbial community or alter the composition of root exudates, thereby restructuring the rhizosphere microbial community. Our objective was to determine the shifts in rhizosphere microbial communities of Fusarium dieback (FD)-infected avocados (*Persea americana* Mill.), a disease triggered by the symbiotic fungus of an invasive ambrosia beetle (*Euwallacea* nr. *fornicatus* sp.). FD has become a serious threat to the avocado industry in California and is now threatening the Mexican avocado production. In 2015, we collected rhizosphere soil samples of five healthy and five FD-infested avocados in an orchard in Escondido, California. After extracting soil DNA, we used high-throughput sequencing of the 16S rDNA gene to analyze the structure of bacterial communities, and ecological network analysis to model the stability of microbial interactions at the rhizosphere level. The diversity of the rhizosphere bacterial community associated with healthy avocado trees was larger than that of infected trees, and both communities were significantly distinct. The observed differences were caused by OTUs of low relative abundance and exclusively associated with healthy or infected trees. Bacterial genera such as *Myxococcus* or *Lysobacter*, which have been described as effective biocontrol agents, were exclusively found in samples from infected trees. Our results show a restructuring of the microbial community associated with avocado rhizosphere after infection by Fusarium dieback, which could potentially affect microbially-mediated processes in the soil.

P194 Mycorrhizas of white poplar (*Populus alba* L.) in riparian forests with diverse hydrological conditions

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White Poplar is a deciduous tree species directly related to the valleys of large and medium rivers in central and southern Europe, where on moist and fertile humus it builds riparian forests seasonally flooded by river. Hydraulic structures (flood embankments, dams) used to regulate rivers flow reduce the extent of flooding in the areas below the dam, contributing to the loss of hydrological conditions appropriate for riparian habitats. This study was conducted in the valley of the River Vistula, the largest river of Poland and the one of 10 largest rivers of Europe, in three riparian forest stands differing in hydrological conditions. Construction of an embankment there in 1935 resulted in the suppression of periodic flooding of the river at one of the study sites. The two other sites received exceptionally long-term flood (in excess of the size and length of duration) in 2010. The purpose of the study was to determine how the cut off a riparian forest for 80 years from the seasonal flood and the long-term flooding of the forest sites located in close vicinity influenced mycorrhizal associations of mature White Poplars with ectomycorrhizal (ECM) and arbuscular mycorrhizal (AM) fungi. The tree riparian forest sites had similar ECM/AM colonization but differed with the composition, frequency and abundance of ECM fungi. The inhibition of periodic flooding did not affect the biodiversity of ECM symbionts compared to the flooded sites. Prolonged flooding reduced the number of ECM species, but only in the year of the excessive flood.

P195 TANIA: Treating contamination through nanoremediation

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Interreg Eu project TANIA aims to improve the design and implementation of policy and technical measures supporting the uptake and diffusion of nanoremediation of contaminated soil and groundwater. Remediation technique coupling nanomaterials with bioremediation has been introduced as one of the technical solutions for supporting the uptake and diffusion of nanoremediation in TANIA partner countries. Nanomaterials are known to degrade contaminants through reduction and catalytic reactions. Some nanomaterials can also stimulate microbiological degradation and hence be used as biostimulators. The most commonly used nanomaterial in environmental remediation is zero-valent nano-iron (nZVI). When used as a biostimulator, anaerobic corrosion of nZVI produces H_2, which can work as an electron donor for dechlorinating bacteria. This enhances the bacteria's dechlorination capability of chlorinated volatile organic compounds (CVOCs). The addition of nutrients or direct current (DC) can accelerate the degradation even further. Groundwater area contaminated with CVOCs can be remediated by of a mixture of nutrients and nZVI. Compounds are introduced to the plume by injecting them several times through boreholes. Since nZVI spreads poorly in environmental matrixes DC can be used to spread nZVI in the plume. Even an 80 percent decrease in the concentration of total CVOCs, without the accumulation of recalcitrant catabolites can be reached with this technique. TANIA partners in Finland are currently searching for pilot groundwater sites contaminated with CVOCs where nZVI remediation coupled with DC and biostimulation could be tested.

P196 Do forest management and environmental variables drive diversity patterns of ectomycorrhizal fungi in mixed coniferous forests?

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This study focuses on understanding the diversity of ectomycorrhizal (ECM) fungal community in continental mixed coniferous forests (*Querco roboris–Pinetum*) with *Pinus sylvestris* as a dominating tree. By our studies we would like to join a heated debate if managed or unmanaged forest are more species rich and fill in an important research gap in this subject in terms of ECM fungi. The studies were performed at three pairs of 80 years old forest stands, located within the forest reserves and mature managed forest in Poland. To determine ECM community structure, traditional fruiting bodies inventories were used along with molecular identification (Sanger sequencing) of ECM morphotypes. We advance the following hypotheses: 1. Quantitative community structure of ECM fungi (species richness) will not differ among protected forests and managed forests; 2. Qualitative community structure of ECM fungi (species composition and abundance) is influenced by forest management. After four seasons (spring and autumn 2015-2016) we found that ECM fungal species richness did not differ significantly between managed and not managed forests. However, a tendency to higher fungal diversity in managed stands was observed. Individual pairs of stands were differentiated in terms of species composition and abundance. In order to find the main drivers of ECM biodiversity we discuss our results in relation to several environmental factors (tree species composition, plant cover, dead wood volume, soil temperature and humidity, soil chemistry, etc.).

P197 Soil fungi isolated from DDT-polluted soils: assessment of tolerance, interspecific metabolic diversity and efficacy of rhizo-bioremediation

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DDT (dichloro-diphenyl-trichloroethane) was widely used worldwide to control agricultural pests and vectors of several insect-borne human diseases, but its use was banned in most industrialized countries since 1972 due to toxicological concerns. However, due to its persistence in the environment, residues still remain in environmental compartments becoming long-term sources of exposure affecting organisms. The metabolic and enzymatic versatility of fungi can be exploited for DDT biodegradation purposes. We have selected two fungal strains (*Trichoderma harzianum* and *Rhizopus stolonifer)* from DDT-contaminated agricultural soils, to study their tolerance to high concentration of DDT and to evaluate fungal interspecific functional diversity and catabolic versatility at the presence of DDT, by using Phenotype MicroArray™ system. Both strains showed clear tolerance to high DDT concentration. Fungi were able to use the most of available microplate substrates, resulting in both high metabolic versatility and relevant ecological functionality in the colonisation of new substrates/habitats. The phenotype profile highlighted both inibithion and stimulation of co-metabolic activities in the presence of this xenobiotic, suggesting the activation of specific metabolic responses to cope with chemical stress. Rhizo-bioremediation trials were also performed using *Cucurbita pepo* cv. Soraya plants. Both fungi increased the capacity of the plant to uptake DDT isomers and metabolites in roots. The increased uptake was reflected also in higher translocation to green-tissues of the plant which would ease removal of residues from polluted sites. The results showed that the fungal species studied might provide powerful insight into the potentiality of rhizo-bioremediation.

P198 Functional analysis of Zn transporters of the ectomycorrhizal Zn-accumulating fungus *Russula atropurpurea*

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Ectomycorrhizal fungus *Russula atropurpurea* can accumulate in its sporocarps remarkably high concentrations of zinc (Zn). Accumulation of heavy metals largely relies on uptake and metal tolerance of the cells in which metal binding with ligands (e.g. metallothioneins) and subcellular compartmentation (e.g. vacuoles). We have previously shown that almost 40 % of the intracellular Zn in R. atropurpurea is sequestered by MT-like RaZBP peptides. To gain an insight into other mechanisms, the transcriptome of *R. atropurpurea* was analyzed and screened in silico for potential Zn transporters. The homology-based search allowed us identify several cDNAs of CDF family (Cation diffusion facilitator) and ZIP family (Zrt-, Irt-like Protein) membrane transporters. We characterized two predicted transporters of the CDF family (RaCDF1 and RaCDF2) and one predicted transporter of the ZIP family (ZIP1) in mutant *Saccharomyces cerevisiae* strains. The results of these analyses indicated that RaCDF1 is the functional protein responsible for the transport of Zn into vacuoles and that the role of RaCDF2 is in the export of Zn ouside of the cell. Accordingly, RaCDF1 and RaCDF2 tagged with green fluorescent protein (GFP) localized to tonoplast and plasma membrane, respectively. Immunofluorescence microscopy detected functional hemagglutinin-tagged HA::RaZIP1 on the yeast cell protoplast periphery and RaZIP1 substantially increased cellular Zn uptake. Altogether, these results improve our understanding of the genetic determinants involved in the accumulation and handling of intracellular Zn in *R. atropurpurea*.

P199 How do changes in either plant or soil microbial diversity affect agro-ecosystem functioning?

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Biodiversity loss has become a global concern as evidence accumulates that it affects the functioning of ecosystems. While most studies have targeted plant communities, a large part of biodiversity remains hidden below ground. We designed a pot experiment to investigate whether and how changes in either plant or soil microbial communities affect plant performance and overall soil functioning. Our two main hypotheses were that (i) higher soil microbial diversity would favor plant performance by enhancing the functioning of the ecosystem and (ii) higher plant diversity would promote soil microbial diversity, thus also resulting in an increase of beneficial ecosystem functions. We tested the first hypothesis by growing barley in pots that contained experimentally manipulated communities, which were obtained by inoculating sterilized soils with three different dilution levels of suspensions originating from the same soil. For the second hypothesis, we grew combinations of barley and two commonly associated weeds (*Alopecurus myosuroides* and *Avena fatua*) in pots in which the soils where inoculated with suspensions of the same dilution level. Both plant and soil samples were collected 21 days after sowing and we are currently conducting a comparative analysis of microbial diversity (16S and 18S rRNA genes), metabolic potential (qPCR of N-cycling genes, shotgun metagenomics) and plant traits across the different treatments.

P200 Exclosures and eucalyptus plantations on degraded land improve soil properties and shift the soil fungal community composition in Ethiopian highlands

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In the last few decades, the conversion rate of the Ethiopia highland native forests to agriculture has been accelerating. Degraded agricultural land is often planted with eucalyptus or left for natural regeneration (exclosure). In this study we link the land use to changes in soil properties and the soil microbial community. Soil samples were collected from five land use types: natural forest, grassland, cropland and eucalyptus plantation and exclosure on formerly degraded land. Land use change from natural forest to cropland and grassland significantly decreased major soil quality indicators such as soil organic C, total soil N, molybdate-reactive bicarbonate-extractable P, and arbuscular mycorrhizal fungal spore density, but exclosure and eucalyptus plantation restored soil C and N as well as soil aggregate stability. The bacterial community was not significantly different between afforested sites and agricultural land whereas the fungal community was significantly different. The difference in the fungal community was mainly driven by soil nutrients (C, N and P). The study highlights the positive effects of reforestation on soil properties, and the higher sensitivity of fungal communities in contrast to bacterial communities to land use changes in the Ethiopian highlands.

P201 The long term effect of reindeer grazing on soil fungal communities and enzyme activities in boreal coniferous forests in Finland

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Semi-domesticated reindeer (*Rangifer tarandus* L.) are the most numerous and significant large mammalian herbivore grazers in northern boreal forest of Fennoscandia. Reindeer alter forest floor vegetation by selective grazing and trampling. The impacts of grazing on soil fungal communities are still not thoroughly known. With 454-pyrosequencing and extracellular enzyme activity measurements, we investigated the fungal community differences in four study sites in northern Finland, each divided by a fence into grazed and non-grazed sites. We also conducted a litterbag experiment where needle litter was buried into the organic horizon, and litter decomposition rate and plant cell wall degrading enzyme activities were measured after one year from the litterbags. In total, pyrosequencing of 38 samples yielded over 200 000 high-quality sequences that were classified into 1186 OTUs with 97% similarity. Basidiomycota and ECM fungi dominated fungal communities in all sites. Reindeer grazing affected the fungal community structure but not diversity or species richness. Ground vegetation biomass, number of small trees per hectare, ground vegetation root biomass, tree root biomass and number of big trees per hectare were statistically significant environmental variables explaining the variation in the fungal community structure. Grazing also affected the enzyme activities measured from the needle litter. Lignin modifying laccase activity was significantly decreased and cellulose chain hydrolyzing CBH I activity was increased by the grazing. Our results indicate that with longer time scales, grazing may affect SOM decomposition through changes in fungal community structures and enzyme activities in the northern boreal forests.

P202 Changing soil environments and the role of microorganisms at high temperatures

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Climate changes are leading to an increase of high temperature events. Together with misuse of soil capabilities and poor management of vegetation, this will lead towards desertification and formation of semi-arid and arid soils. Soils with poor plant cover are exposed to intense solar radiation which leads to increasing temperatures at the upper soil layers, well above the optimum for commonly studied mesophilic soil bacteria. For instance, at South European countries, values above 40ºC are frequently observed in top-soils. Microbial activity at upper soil layers has been suggested to be highly reduced during such extreme temperature events. However, recent reports have highlighted the occurrence of peaks of enzymatic activity in soils at high temperature (55ºC -75ºC) and the ubiquitous presence in soils of thermophilic bacteria (STB). These STB are mostly present in temperate soils as vegetative viable cells which strongly suggest that they can be potential participants of soil biogeochemical reactions. Our work demonstrated that thermophilic gram-positive bacteria of the Firmicutes phylum, mainly represented by Geobacillus-related species were able to release significant quantities of sulfate and ammonium under high temperature conditions as metabolic products. This represents a process involving a dissimilatory organic-sulfur mineralization pathway which suggests that soil thermophilic bacteria can be actively involved in C, N and S cycling in soil upper layers and refutes the prevailing view of bacteria as poor S-mineralizers. Usual phytosanitary treatments in agricultural lands influence STB communities and sulfate release in soils with consequences to natural soil fertilization.

P203 Metagenomic analysis of long-term land-use effects on soil microbial communities in 600-year Alpine pasture system

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This study aims to obtain a comprehensive profile of microbial communities, antimicrobial resistance (AMR) and metal and biocide resistance determinants in two proximal soil systems with a different treatment history, located at the alpine Glaspass (Switzerland). One of the sampling fields has been amended with manure for the past centuries (termed intensive), whereas the other corresponds to a free-range grazing area free of manure applications (extensive). DNA was extracted from one pooled sample [10 equidistant pooled (5 replicates) samples] per soil system. Two metagenomic approaches were undertaken to estimate microbial diversity: (i) DNA was directly sequenced using a single run Illumina MiSeq per soil sample, yielding 12 (extensive) and 17 (intensive) million reads. Reads and assembled contigs are being investigated. The five most abundant classes detected were Betaproteobacteria, Actinobacteria, Alphaproteobacteria (all predominant in the dataset termed intensive), Acidobacteria Gp1 and Gammaproteobacteria (both predominant in extensive). Chitinophagaceae and Xanthomonadaceae were the predominant families detected in the intensive and extensive dataset, respectively. Gp5 and Gp6 were the most abundant genera in intensive, while Gp1 and Gp2 were prominent in extensive. The MEGAres database was used to search for AMR determinants. Entries retrieved from both soil systems included numerous (multi)drug efflux pumps (for tetracyclines, macrolides, phenicols); antibiotic target protection proteins (macrolides-lincosamides-streptogramins, tetracyclines, fluoroquinolones); antibiotic modifying (aminoglycosides, lincosamides, phenicols, tetracycline) or degradation enzymes (betalactams); and antimicrobial target replacement proteins (diaminopyrimidines, sulfonamides, glycopeptides, beta-lactams). Further characterization using BacMet (metal and biocide resistance genes), PlasFlow (plasmids) and antiSMASH (biosynthetic gene clusters) databases is being undertaken.

P204 Microbial composition and antimicrobial resistance determinants in one of the oldest experimental agricultural field soils in Europe

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This study examines (i) bacterial profiling, (ii) antimicrobial, metal resistance, (iii) plasmid profiles and (iv) biosynthetic-gene clusters in the oldest Swiss experimental farming trial, which consists of several management systems: organically fertilized (OF) (manure, sludge, compost), chemically fertilized (CF) (PK, NPK), mixed fertilization and no-fertilization (control). Entire metagenomics from the bacterial fraction revealed the following taxonomic differential patterns: (1) Acidobacteria increased in OF, specially in compost+PK; (2) Actinobacteria revealed more abundant in control and CF soils (but also in manure+PK) while lower in Bacteroidetes; (3) Candidatus saccharibacteria were more abundant in control and NPK treated soils; (4) Chloroflexi were more abundant in control while Alphaproteobacteria were reduced, (5) Betaproteobacteria were increased in manured soils. Remarkable low percentage of sequence ID (mean 75%) was observed between our samples and those from NCBI database. New bacterial genomes are being reconstructed and quantified. Using MEGAres database at cut-off of 90% ID, in total, 0.07% of reads retrieved hits against the DB, with Sludge+PK and PK showing the highest number of reads, and Control and NPK the lowest, respectively. Considering all hits (>60% ID), multidrug-resistant efflux pumps (MDRep) were predominant. Resistance to cationic-antimicrobial-peptides (CAP), rifampin, Bacitracin, macrolides-lincosamides-streptogramins (MLS), aminoglycosides, and b-lactams were prominent. Based on proteins from assembled contigs, after MDRep, resistance to MLS, b-lactams, CAP, bacitracin, and tetracyclines were dominant (≥40% ID). General synteny was observed between ratios (for both reads and proteins) of AMR genes per treatment, with differential values for specific agents at specific ID percentages. 2.4% of contigs carried ≥3 AMR determinants. In-depth analysis of candidate contigs is being performed. Similar procedures are being followed using BacMet, PlasFlow, and antiSMASH databases.

P205 The plant microbiome is shaped by an interplay between top-down and bottom-up processes

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It is well recognised that plant-microbe interactions are pivotal for plant health. Recent research revealed a strong differentiation between phyllo- and rhizosphere and the importance of host genotype and plant immune system to shape a plant's microbiome. Also the relevance of bacterial interactions was shown to be substantial. However, plants and their associated microbiomes do not exist in isolation. Micro-eukaryotes can affect the microbiome-plant interaction as shown for grazers like amoeba. In a previous study we could show that endophytic heterotrophic micro-eukaryotes identified using 18S rRNA gene metabarcoding are an integral part of *Arabidopsis thaliana*'s microbiome and that their community patterns are strongly shaped by plant organ. To better understand trophic interactions in and on plant organs we linked the bacterial microbiome assessed by 16S rRNA gene metabarcoding with the cercozoan community. When studying plant associated bacteria we observed highly similar patterns to those detected for cercozoa. Betadiversity metrics of both groups were strongly linked indicated by Mantel test ($p=0.001$). This interaction differed depending on plant organ. Especially in the phyllosphere plant associated cercozoa were linked tightly to the bacterial microbiome as shown by a co-occurrence network. We identified keystone taxa for the different plant organ networks. Our results highlight the importance of a multi-trophic perspective on the phytobiome to gain a more holistic understanding of plant-microbe interactions

P206 Grassland microbial communities respond to soil drainage and phosphorus availability

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Soil microbes play a central role in the biological phosphorus (P) cycling where they act as sink and source of P. However, microbial responses to changes in grassland P status remain largely elusive. We hypothesised that intensive management of grasslands with a high P index will sustain distinctive belowground microbial communities when compared to low P index grasslands. In addition, we compared the effect of available P alongside soil drainage as a microbial community determining factor. Twenty grassland soils were selected, based on drainage class (well or poorly drained) and available P content (high and low P, determined via Morgan's), resulting in four soil groups ($n=5$). Bacterial communities were clearly affected by both, soil drainage and available P. This was evident from the denaturing gradient gel electrophoresis DGGE fingerprints as well as from the sequence based alpha- and beta-diversity (next generation sequencing, NGS). Relatively higher proportions of Acidobacteria were detected in poorly drained soils and Firmicutes were more abundant in well drained and low P soils ($p<0.05$). Distinct DGGE profiles from fungi and AM fungi were found in poorly drained soils with low P status. Sequencing revealed that Ascomycota and Zygomycota were less abundant in low P soils while Basidiomycota were more abundant (NGS). Fungal alpha-diversity was less affected by drainage and P than the bacterial. Beta-diversities from this study suggest that bacterial and fungal communities were affected by P and drainage status with environmental factor soil pH being more influential on the bacterial diversity.

P207 The effect of sulfate fertilization of grassland columns on soil microbiota and nematodes

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Sulfur (S) is an essential macronutrient for plants. The plant-available form of S is sulfate and constitutes only about 5% of the total soil S content. Currently, the common effect of S limitation in agriculture is the result of reduced atmospheric pollution. However, the widespread use of sulfate fertilizers to compensate for plant S limitation may affect soil microbes and micro-fauna involved in natural S mobilization from otherwise plant unavailable organo-S. In this study, soil columns were setup in a greenhouse, planted with *Lolium perenne* and fertilized with 0, 5, 10 and 20 kg/ha inorganic sulfate S alongside a full complement of other nutrients. Weekly measurement of sulfate in soil solution revealed significantly higher amounts in the medium and high S treatments. Destructive sampling revealed a significant decrease ($P<0.05$) in sulfatase activity, bacterial-feeding nematodes, mycorrhizal colonization rates in the high and medium S treatments but no significant effect on cultivable bacterial abundances, including sulfonate-utilizing bacteria. High and medium S treatments significantly shifted the bacterial, fungal and AM community structures compared to the control. Medium and high S treatments had significantly higher grass dry matter yield compared to the control. Overall, our results suggest that plant growth benefits at 10-20 kg/ha S outweighed the negative effects of the fertilizer application on the soil microbiota and nematodes. Therefore, S should not be overlooked in grassland nutrition including utilizing more sustainable strategies of S supply.

P208 Soil ionoMICS – Linking elemental composition of microorganisms to soil fertility and their C and N storage capacity

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Plant residues are the primary source of soil organic matter (SOM) and are decomposed by soil microorganisms. However, the amounts of plant carbon stored at first in microbial biomass or released as CO_2 during respiration depend on the carbon use efficiency (CUE) of the microorganisms. As SOM consists of up to 50 % of microbial necromass, their CUE and biomass substantially contribute to soil fertility by SOM built-up. To allow microbial communities to fulfil this soils’ ecosystem service, substrate and nutrients have to be available and habitat conditions have to be optimal. Some scientists hypothesised that CUE of soil microorganisms is related to their elemental stoichiometry. Therefore, the aim of our project is to understand the influence of (micro)nutrient availability for microbial C and N use efficiency and their contribution to C and N sequestration in soils. Based on the chloroform fumigation extraction method the extractability of a larger set of elements beyond C, N, P and S was analysed. Two extraction solutions ($CaCl_2$ and NH_4NO_3) were tested on four soils differing in texture (loamy sand and silty loam) and farming system (conventional and organic). Overall, $CaCl_2$ yielded higher amounts of microbial elements, but for phosphorus and silicon there were also interactions with soil. The method will be further evaluated and developed to eventually allow for comparison of soil microbial communities as affected by different land use (field, pasture, forest), land management (e.g. conventional and organic farming) and environmental stresses (drought, salinisation) and to link microbial elemental composition to CUE.

P209 Towards to physiological status of soil microorganisms determined by RNA:DNA ratio

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Despite many soil organisms have very low rates of metabolic activity and frequently spend most of their lifetime in dormant or resting phases, the input of readily assimilated substrates shifts microbial population from dormancy to activity and may induce microbial growth. Under steady-state, the double stranded DNA (dsDNA) content is considered as a measure of total soil microbial biomass while the RNA content mainly indicates the active microbial fraction in soil. In growing population, however, an increase in DNA is solely related to replication of microbial cells, while the RNA, besides growth, is also involved in non-growth processes. Therefore, the dsDNA and RNA content increase differently during microbial growth, applying the RNA:dsDNA ratio as promising indicator of growth-related and non-growth microbial activity. To what extend the ratio can be used to comparatively infer investment in microbial biomass production versus maintenance related synthesis following substrate induction remains to be studied. We measured the RNA:dsDNA ratios of representative soil types of four different ecozones before and after glucose addition to prove the prediction capacity of physiological status of soil microorganisms. The RNA:dsDNA ratio remained stable after activation of microorganisms in Retisol and Luvisol indicating balanced growth. In contrast, very moderate increase in DNA in sandy Calcisol was accompanied by disproportionally high increase in RNA. As a result, the RNA:dsDNA ratio in Calcisol with low nutrient status increased by 36-fold after glucose amendment, indicating strong non-growth related processes. The RNA recovery decreased exponentially with increasing clay content, indicating the strong association to the textures of the soil types. This suggests, that the underestimation of RNA yields in clayey soils biased the RNA:dsDNA ratio, and subsequently the physiological state of the microbial community is not adequately represented in soils clay contents exceeding 30.

P210 Food for microbes - C:N:P stoichiometry of microbial biomass and incorporation of nutrients into cellular pools respond to altered nutrient levels

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Microbial element turnover plays an important role for soil fertility, as microorganisms are one of the main drivers to mobilize and immobilize nutrients. We studied the response of microbial biomass (MB) carbon (C_{mic}), nitrogen (N_{mic}) and phosphorus (P_{mic}), CO_2 efflux and DNA content to element additions in two temperate forest soils with contrasting P availability. Each soil was treated with a low (5 % MB) or high (200 % MB) concentration of P, C and N, respectively. The microbial incorporation of the labeled nutrients into MB, DNA and PLFA was followed during the 17-days incubation. Results show microbial function to be affected differently in the low and high nutrient addition treatments, and also between the two soils with either low or high P availability. P addition influences microbial activity and growth; as the easily available P was preferentially used for microbial biomass increase (growth) in the P-rich soil, but was utilized for non-growth related processes in microbial cells (maintenance) in the P-poor soil. C:N:P stoichiometric ratio in MB changes according to different soils and nutrient addition levels; as well as incorporation patterns of labeled P into MB, DNA and PLFA. The dynamics of nutrients in microorganisms changes with nutrient level and is strongly dependent upon the interlinked relationship between C, N and P availability in soil. Possible reasons for the influence of nutrient dynamics on microbial growth and activity will be discussed.

P211 Microfungi, algae and cyanobacteria in soils polluted with fluoride (Kola Peninsula, Russia)

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The aim of this study is to give the algological and mycological characteristics of soils along the gradient of pollution with aerotechnogenic emission from the Kandalaksha aluminum smelter (KAS). The KAS is the only aluminum smelter in the world beyond the Arctic Circle. The aerial emissions from the smelter contain significant amounts of pollutants including hydrogen fluoride, difficultly soluble fluorides, resinous substances, polycyclic aromatic hydro carbons, and inorganic dust. These elements migrated to greater distances from the source of the contamination (up to 15– 20 km). In the soils, 47 species of microscopic algae from the Chlorophyta (33 species), Charophyta (2), Ochrophyta (9), Cyanobacteria (3) were found. The largest species diversity is characterized by the families Trebouxiaceae (6) and Chlorococcaceae (6). Cyanobacteria, diatoms and xanthophytes were noted by their considerable diversity on highly polluted areas in conditions of degradation of vegetation cover. Emissions from the aluminium plant have reduced the number and the diversity of fungi and have caused an increase of fungal communities in the part of potential pathogenic fungi. Only in the polluted soil rare or just atypical species for zonal soils are selected: *Aspergillus niger var. niger*, *Paecilomyces variotii*, *P. chermesinum*, *P. variabile, Phoma medicaginis, Thielaviopsis basicola, Torula allii, Myxotrichum cancellatum*, and *Trichocladium asperum*. Among these there are activators of opportunistic mycoses.

P212 Have bioinoculants won the race against chemical fertilizers: Case study with pigeonpea!

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With increasing concern over the negative effects of chemical fertilizers, biofertilizers have been increasingly applied as an eco-friendly alternative in agriculture. Despite establishment of their efficacy in plant growth promotion, limited information is available on the ‘non-target’ impact they exert on rhizospheric microbial communities. Present study aimed to get a deeper understanding of the (target and non-target) effects of bioinoculants (*Azotobacter chroococcum, Bacillus megaterium* and *Pseudomonas fluorescens*) on growth parameters of pigeonpea (*Cajanus cajan*), and resident rhizospheric microbial community. With respect to plant growth parameters, the mixed consortium was comparable to chemical fertilizers in pot and field trials. Compared to control, the mixed consortium showed 1.08-, 1.22- and 4.2- fold enhancement in the abundance of culturable nitrogen fixers, *Pseudomonas* and *Actinomycetes*, respectively. Functional differences between the microbial communities of control and treated plants was evident by community level physiological profiling. Denaturing gradient gel electrophoresis was employed to quantitatively assess the similarity levels between bacterial community structure by using 16S rRNA gene as marker. It revealed significant differences in the profiles generated for control samples and treatments, emphasizing on the contribution of non-target effects on plant growth promotion. The study thereby goes a step further in understanding the mechanism of action of bioinoculants together with propagating the application of these sustainable amendments.

P213 Forest disturbance causes loss of functionally dominant fungi in a tropical rain forest in SW China

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Forest disturbance is a significant threat to biodiversity, but the response of soil fungal communities remains poorly understood. We used plots established along a forest degradation gradient in a tropical rainforest to examine the effects of disturbance on soil fungal communities. Using metabarcoding approach, we measured fungal richness, functional composition and identified factors associated with shifts in community composition temporally and across land use types from mature forests, regenerate forests to open-lands. Fungal richness was similar among forest sites, but 40% higher in open-lands. The species richness of saprotrophic fungi were negatively correlated with the degree of disturbance, while the opposite was true for mycorrhizal fungal richness. Penicillium (P solubilizing saprotrophic fungi) dominated in mature forest, but was less abundant in regenerating forest and showed the lowest abundance in open-land sites. Correlation and path analysis demonstrated that soil saprophytic and mycorrhizal fungi responded directly to forest disturbance or indirectly via the effects of disturbance on soil pH and P concentration, but tree diversity had a minor influence. The effects of wet-dry seasonal changes on fungal community were more significant in open-land as compared to forest sites. These results demonstrated that forest disturbance causes loss of functionally dominant fungi, especially in highly disturbed open-lands. The changes of fungal community potentially indicated a change from soil P limitation in mature tropical forest to soil C limitation in disturbed sites. The loss of fungal decomposer and increased mycorrhizal fungi in disturbed habitats might contribute to reduced soil health and intensified plant competition.

P214 Re-evaluation for indirect-inhibition effect of *Fusicolla acetilerea* on establishment of seedlings from iron-coated seeds of rice, comparing with *F. merismoides*

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A fungus, *Fusicolla acetilerea* (Tubaki, C. Booth & T. Harada) Gräfenhan & Seifert was reported to be indirectly able to inhibit establishment of seedlings from iron-coated seeds of rice without pathogenicity to the plant, using an isolate (MAFF150069) of the fungus (Mori et al., 2017). In this study, the indirect-inhibition effect of MAFF150069 was re-evaluated comparing with an isolate (MAFF236504) of *Fusicolla merismoides* (Corda) Gräfenhan, Seifert & Schroers. Iron- and non-coated seeds of rice with or without treatment immersing in conidial suspension (3×10^5 conidia/mL) of each isolate at 24-26ºC for 2 days were grown under submerged conditions in soil at 30ºC under 12 h light (12 h darkness) for 14d in cell trays. In results, seedling growth from the seeds with the treatment tended to be poorer than that without the treatment. The inhibition of seedling growth appeared more strongly on iron-coated seeds than non-coated seeds, as well as for MAFF150069 than MAFF236504. No lesions were recognized on all seedlings. The indirect-inhibition effect of *F. acetilerea* seemed to be stronger than that of *F. merismoides*. MAFF150069 vigorously developed colonies on iron-coated seeds compared with those on non-coated seeds, whereas colony development little appeared for MAFF236504. Decrease of oxidation-reduction potential (ORP) in soils around direct-seeded rice under submerged conditions causes poor establishment of the seedlings (Mori et al., 2015). *Fusicolla acetilerea* may well-propagate on the iron-coated seeds under low ORP.

P215 On the new genomospecies "*Candidatus* Pectobacterium maceratum", a necrotrophic bacterium with own insect vector

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The *Pectobacterium carotovorum* is one of the most dangerous plant pathogens. Taxonomy of this bacteria is a challenging task. Recently, comprehensive whole-genome comparative analysis was shown that subspecies of *P. carotovorum* have a genomospecies status. It is difficult to find any phenotypical differences between the subspecies, however, on the basis of whole-genome comparisons the genetical differences are very clear. Today for “*P. carotovorum*” group about 60 whole-genome sequences in NCBI GenBank is available. The aim of this study is to determine systematic position of the five novel strains of *Pectobacterium* spp., isolated from plant hosts. Our current sequencing project allows us to deposite five sequenced strains (F018, F131, F135, PB69, PB70) to the database. To reveal taxonomy of the strains, we have used two highly recommended computational methods: average nucleotide identity and digital DNA-DNA hybridization. Our genome set for calculation contains 50 genomes, including not only *Pectobacterium* spp., but also representative strains from *Dickeya* genus and *Erwinia amylovora* strain as the outgroup. It was shown that the five strains form unique clade of the new genomospecies “*Candidatus* Pectobacterium maceratum”. We found that recently published *Pectobacterium* strain SCC1 is also belongs to the genomospecies. Considering that SCC1 strain with complete genome was investigated in details, we propose that is a type strain of “*Ca.* Pectobacterium maceratum”. Interesting feature of all these strains is presence of *evf* gene, which encodes a virulence factor for persistence in the *Drosophila* gut. We propose that the associative symbiosis with fly insect vector is important ecological aspect of the plant pathogen dissemination. Role of horizontal gene transfer is discussed.

P216 The impact of plant-derived carbon flow on root litter decomposition

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Large fraction of boreal forest´s carbon (C) stocks are stored in the soil. When the climate warms and the atmospheric CO_2 levels rise, also the plant photosynthesis rate and the flow of recently assimilated C to the soil may increase. The increase in photosynthetic-C flow belowground accelerates the microbial activity and microbial degradation of soil organic matter including recalcitrant pools. We studied in a four-year root and fungal hyphal exclusion (trenching) experiment, the effects of artificially altered plant C flow to litter-inhabiting fungal and bacterial communities’ activities. The trenching plots were set up at the Hyytiälä forestry field station and consisted of a combination of three above ground vegetation treatments and three below ground soil trenching treatments (total of nine different treatments). In the vegetation treatments, the vegetation of the plot was kept normal, cut to leave only shrubs, or cut away completely. In the soil trenching treatments, entrance of plant roots and fungal mycelia to the plot was allowed (control), entrance of only fungal mycelia was allowed (50 µm mesh), or entrance of both plant roots and mycelia was restricted (1 µm mesh). The effect of these treatments to root litter degradation and microbial community’s activities was followed by burying litter bags into the trenching plots and harvesting one set of bags after each growing season. The preliminary results indicate that the trenching treatments caused no statistically significant difference in the root litter degradation rate but did induce differences in the bacterial C usage profiles.

P217 Soil nitrogen cycling in relation to terpenes and tannins: Examples from forest bioenergy harvest

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In short-term laboratory experiments, exposure of forest soil to different terpenes or condensed tannins often inhibit those N cycling activities that increase the risk for N mobilization and losses. We studied how soil concentrations of these plant secondary compounds and N cycling activities are related in field conditions. Organic layer samples were from conifer logging residue experiments in thinning stands and final fellings, established to study the effects of forest bioenergy harvest, and included logging residue and control treatments. We compared short- and long-term effects of logging residues, consisting of fresh branches and stem tops, on soil N cycling and plant secondary compound composition. In thinning stands, logging residues increased the rate of net N mineralization but the rate of net nitrification was always negligible. On a recently clear-cut site, logging residues strongly stimulated net nitrification during the first years. In both short and long term, net N mineralization and nitrification were generally stimulated with increased concentrations of condensed tannins and various terpenes. For instance, volatile monoterpenes, that in laboratory exposure experiments strongly inhibit net nitrification, were emitted on the clear-cut in large amounts from the residues to the soil. Still net nitrification was intensive. Correlations - if any - between the concentrations of terpenes and tannins and N mobilization activities were positive. Input of these compounds to soil occurs together with a large variety of other compounds that unsettle the situation, and extrapolating results from simplified laboratory addition experiments is not straightforward.

P218 Genetic and functional diversity of soil bacterial communities in an olive grove managed with sustainable or conventional approaches

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The aim of the present work was to evaluate the medium-term effect (18 years) of two soil management systems, so called 'sustainable treatment' (ST) and 'conventional treatment' (CT) on bacterial genetic and functional diversity in soils of an olive (*Olea europaea* L.) orchard located in Southern Italy (Basilicata Region). ST system included no-tillage and endogenous and polygenic organic matter inputs deriving from spontaneous cover crops and pruning material left on the field. CT soil was tilled, without cover crops, and pruning residues were removed. Microbial analyses were carried out by culture-based (plating, spectrophotometry, Biolog®) and molecular-based approaches (DGGE, 16S DNA cloning/sequencing and metagenomic analysis). Significant differences were observed between the treatments regarding the number of many classes of culturable bacteria, the activities of microbial soil enzymes, Biolog® carbon source utilization patterns and related indices, and DNA abundance and presence of the bacteria involved in soil dynamics, such as C and N biogeochemical cycles, lignin degradation, humification and organic matter mineralization. Generally, the data revealed a significantly higher bacterial abundance, activity, diversity and complexity in ST soils. This higher biodiversity could lead to greater soil stability and multifunctionality, positively affecting also plant status and product quality. The results obtained highlight that in Mediterranean orchards, under semi-arid climatic conditions, the application of endogenous organic matter can be a key factor to enhance soil quality/fertility and produce in a sustainable way, preserving natural resources and avoiding detrimental effects on the environment.

P219 Screening of soil bacteria with antimicrobial activity against several microbial residents on human skin

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This study focuses to screen bacteria that can produce antimicrobial substances to replace harmful chemical antiseptics used for prevention of contamination of cosmetics such as parabens. Thounds of bacterial strains were isolated from various soils and their antimicrobial activity against human skin microbes, *Staphylococcus aureus*, *Bacillus subtilis, Escherichia coli, Pseudomonas aeruginosa, Candida albicans* and *Aspergillus niger* was examined. *Burkholderia gladioli* DS518, *Pseudomonas fluorescens* DS1386 and *Paenibacillus elgii* DS1515 showed 14 to 26 mm diameter of growth inhibition zone against all target organisms on agar plates. Antimicrobial substances in the culture supernatants of DS518 and DS1515 were extracted using ammonium sulfate precipitation method and freeze drying, and that of DS1386 was extracted with ethyl acetate. Purified compounds from each strains showed low minimum inhibitory concentration (MIC) against all target organisms (0.156-10 mg/ml). Time-kill assay with 1 MIC purified compounds indicated a significant antimicrobial effect on target organisms. Colonies of all target organisms were undetectable after 4-24 h incubation in the presence of purified compounds (1 MIC). Antimicrobial compounds from DS518 and DS1515 may be antimicrobial peptide and biosurfactant such as lipopeptide, respectively. Culture supernatant of DS1515 showed clear zone in oil spreading test and reduced surface tension of culture from 60 to 42 mN/m. DS1386 produced 0.087 mmol/ml of siderophore. These results suggest that isolates DS518, DS1515 and DS1386 may be utilized to produce environment-friendly biocontrol agents against some human skin microbes in cosmetics.

P220 Degradation of aflatoxin B_1 and inhibition of aflatoxigenic fungi by some soil bacteria

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Aflatoxin B_1 (AFB_1), a common contaminant on grains produced mainly by *Aspergillus flavus* is one of the most hazardous mycotoxin for human and livestock. The aim of this study is screening of bacteria that can degrade AFB_1 and inhibit aflatoxigenic *A. flavus*. Over 350 strains were isolated, and their AFB_1 degrading capability was measured by HPLC and inhibition of growth, spore formation and germination of aflatoxigenic *A. flavus* were examined. Isolates identified as *Bacillus subtilis* AF11, *Streptomyces panaciradicis* AF34, *S. thermoviolaceus* AF125 and *Rummeliibacillus pycnus* AF129 indicated antifungal and AFB_1 degradation activity. Some strains decreased up to 80% fungal colony radius and inhibited sporulation up to 99%. Reduction of spore germination was also observed (20 to 70%). Production of siderophore which selectively absorbs iron from environments, and chitinase and β-1,3-glucanase which break down fungal cell wall was part of the antifungal activity of these isolates. When the isolate and aflatoxigenic fungi were inoculated simultaneously in yeast extract sucrose medium, mycelial growth and AFB_1 concentration decreased in all experimental groups. Especially, AF11 strain decreased 97.1% of fungal growth and completely reduce AFB_1 at 30°C, 200 rpm and pH 5.5~7. Strains AF34, AF125 and AF129 degraded 100 µg/L of AFB_1 to 0, 9.9 and 14.9 µg/L, respectively, and more than 83% of degradation occurred by cell-free supernatant. These results suggest that these isolates can be used to protect crops against toxigenic fungi and treat mycotoxin contaminated grains, and therefore decrease economic damage in agriculture.

P221 Soil pH modulation impacts microbial activity and 16S rDNA operon copies number in Amazon soils

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The Amazon region now accounts for more than 450.000 km² of degraded lands. To recover these areas to agriculture use, manage the soil pH is a first action. We investigated in a greenhouse experiment the effect of pH amendment to agronomic levels on microbial activity, bacteria and archaea community composition and traits. To this, soils were collected from Ariquemes/RO (09°54'58"S 63°02'27"W), of Primary Forest (FP), Degraded Pasture (DP) and Conserved Pasture (CP). The initial pH_{CaCl2} (FP – 4,0; DP – 4,7; CP - 4,6) of all soils were amended to 5.8_{CaCl2}. The CO_2 fluxes were measured during 120 days in static chambers using infrared gas analyzer (UGGA, Los Gatos Research). After 40 days, DNA was extracted (PowerLyzer, QIAGEN) and 16S rDNA gene sequenced (Illumina Miseq). Archaea relative abundances does not change with pH amendment, but the global microbial activity increased in all soils, as well the bacterial mean weighted 16S rDNA operon copy number. This is a trait of r-specialist microorganisms related to cell growth rate, sporulation, motility, and competence. Besides, the only microbial group that significantly increases (ANCOM, $q<0.05$) with pH amendment in all soils is a BALO (Bdellovibrio-and-like organisms), from *Peredibacter ssp*. genus. These microorganisms are typical gram-negative bacteria predators, and potentially relevant to bacterial population control in the soil. In conclusion, pH modulation of acidic soils to agronomic levels increases microbial activity and bacterial diversity, but not of archaea. This investigation opens new insights into studies of agriculture practices and microbial ecology.

P222 How does long-term different tillage management affect soil microbiota?

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Soil microorganisms fulfill important functions in biogeochemical cycling and support ecosystem services. Nevertheless, agricultural soil management may affect soil microbial communities over time. Microbial properties like phospholipid fatty acids (PLFA) and neutral lipid fatty acids (NLFA) as well as soil enzyme activities are well known indicators for changes of ecosystem function in agricultural fields. At the AGES research station Fuchsenbigl in Lower Austria a field experiment established in 1988 examines the effects of tillage treatments - conventional ploughing (CT), reduced (RT) and minimum tillage (MT) - on soil and crops. Alkaline phosphomonoesterase activity was analyzed between 1989 and 2002 and, again, in 2016 in three soil depths (0-10cm, 10-20cm, 20-30 cm). In addition, the microbial community structure using PLFA and NLFA contents were determined in 2016. In 2016, alkaline phosphatase showed similar values compared to the previous data of 1989-2002. Phosphatase activities were significantly higher after long-term MT compared to RT and CT in 0-10cm in 2016. A tendency for higher activities in CT was found in 20-30cm. We found similar patterns for different PLFA biomarkers and NLFA 16:1ω5 (indicating endomycorrhiza) in 0-10 cm, however, the sum of PLFA – referring to the total microbial biomass - could significantly distinguish between the three tillage treatments MT>RT>CT with 74, 52, 30 mol%, respectively. In conclusion, minimum tillage did not only change microbial community composition and P mineralization in the upper soil layer, but also modified the spatial distribution and function of soil microorganisms within the ploughing layer.

P223 Comparison of whole-cell MALDI-TOF MS and 16S rRNA gene analysis for dereplication of soil bacterial isolates

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Matrix Assisted Laser Desorption/Ionization Mass Spectrometry with Time-of-Flight detector (MALDI-TOF MS) has been proposed as a promising tool for the dereplication of recurrent bacterial isolates. In this study, we aimed to establish thresholds that would group MALDI-TOF mass spectra of soil isolates analogically as 16S rRNA gene sequence analysis. Whole-cell MALDI-TOF mass spectra as well as 16S rRNA gene sequences were obtained from 49 environmental cultures and evaluated comparatively. In order to use MALDI-TOF MS without reliance on reference mass spectra databases for dereplication of recurrent bacterial isolates, we recommend a similarity-based approach to analyze a mass range of 4 to 10 kDa, which contains the majority of culture-determining peaks. We demonstrate that a cosine similarity (CS) threshold of 0.79 separates mass spectra analogously to species delineation by a 98.65% sequence similarity threshold of the 16S rRNA gene proposed previously, with corresponding precision and recall values of 0.70 and 0.73, respectively. A further increase in CS threshold to 0.92, with associated precision and recall values of 0.83 and 0.64, respectively, leads to MS spectra separation, which matches species delineation by assigning the closest type strain based on 16S rRNA gene sequence similarity. Such values could potentially be improved if higher reproducibility was achieved between biological replicate measurements. Overall, our research indicates that a similarity-based MALDI-TOF MS approach can rival 16S rRNA gene technique in the efficient dereplication of isolates for downstream analyses with minimal loss of unique organisms.

P224 Long-term litter decomposition in the montane forest of Central Europe

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Aboveground litter input of both trees and the ground vegetation is an important source of C and other nutrients in forest soils. While short-term litter decomposition was frequently addressed, there is less information on the long-term fate of litter. Here we have investigated the fate of the needle litter of *Picea abies* and the litter of the dominant grass *Calamagrostis villosa* in the mountain spruce forest during five years either in a closed stand immediately following bark beetle attack or in a grassy stand that established four years after the tree dieback. The initial decomposition rates were higher for the grass litter that was more nutrient-rich and contained less lignin than the needle litter. There were no differences in decomposition rates among the site types except the increased rate of needle litter decomposition at the end of the experiment in the more recently affected sites.

The initial fungal community was dominated by Ascomycota, which slowly gave away to Basidiomycota and Mucoromycotina/Mortierellomycotina towards the end of the experiment in both litter types. Similarly, saprotrophic species increased in abundance over the course of the study replacing pathogenic fungi that were abundant in the initial stage of decomposition. The two litter types shared very few fungal taxa in the initial stages and although this specificity lasted during the whole observed period, it decreased over time and fungal communities became gradually more similar. Community composition of fungi was affected by the forest stand type only in needle litter in the initial phases of decomposition.

P225 Potential for growth enhancement by arbuscular mycorrhizal fungi in potato

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Arbuscular mycorrhizal fungi (AMF) are obligate root symbionts capable of colonising the roots of most terrestrial plants species. The most important advantage that AMF provide to a host plant is enhancing P uptake, and plant P status is usually the major controlling parameter in the plant-fungal association. Potato is a phosphorus-demanding plant which grows in symbiosis with AMF. Therefore, the significance of this association and its management is of considerable agricultural interest. This research aims to investigate the influence of genotype and crop management practices on root colonisation, species diversity and function of AMF in potatoes and also study how potato genotype and management practices interact to influence AMF colonisation. Archived potato root samples from a fertiliser trial with different genotypes conducted in 2011 were analysed. AMF community diversity was assessed using terminal restriction fragment length polymorphism (T-RFLP) by targeting larger subunit AMF rDNA using a nested PCR approach with first-step primers LR1/FLR2 and FLR3/FLR4 for the second step. This was complemented by a traditional root staining method to visualise and quantify the level of AMF root colonisation. The results from root staining show that crop management practices significantly affect AMF colonisation with the highest colonisation in the unfertilised treatment (72.5 %). T-RFLP results indicated that 3 main OTUs dominated the samples, although diversity indices (Shannon's, richness, evenness) were not significantly affected by crop management practices or potato genotype. Further studies will assess the species composition of the AMF community using next-generation sequencing.

P226 Responses of bacterial and protist communities to organic and conventional fertilization in distinct soil types

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Microbe relationships are essential for functionality of soil system. However, most studies focus on single taxa, while their interactions remain poorly understood. Here, we investigated how different organic and inorganic fertilizations affect the resident and active bacterial and protist communities in different soil types. We observed that the composition of both bacteria and protozoa communities are influenced more by soil types than fertilization type. Overall, organic amendments did not change microbial richness and diversity when compared with conventionally managed soils in the two different soil types. The resident bacterial community in system with organic amendments harbored a dispersed community, characterized by copiotrophic organisms adapted to nutrient-rich environments. For protozoa, the resident and active protozoan community in organic fertilizer regimes was characterized by specific guilds related to grazer traits. Moreover, bacterial and protozoa communities were not affected by each other's composition and structure in soils with both organic and inorganic fertilizations. Our results provide a new perspective of how soil management changes might affect resident and active taxa differently without a synergetic effect on the interaction between the bacterial and the protozoan soil community.

P227 Impact of microalgae-fertilizer on soil microbiome, greenhouse gases emissions and plant growth

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The use of microalgae for sustainable wastewater treatment is effective in recovering nutrients at low-costs. Furthermore, the simultaneous production of a residual biomass is considered a valuable waste with potential of biofertilization. However, the efficiency and the impact of algal biofertilizers on the environment is not known. This study is one of the first to comprehend the total environment linking interdisciplinarity factors related to the sustainability of microalgae as i) plant productivity, ii) greenhouse gas emissions and iii) the underlying nitrogen cycling pathways, as compared to a mineral fertilizer (NPK) or no fertilization (control). Barley was grown in a greenhouse pot experiment over 120 days with emissions of CO_2 and N_2O measured and soil sampled on days 8, 14, and 30 for quantitative PCR analyses. We found no significant differences in root-, shoot-, or grain-biomass from the fertilized treatments. However, the cumulative N_2O emissions from the microalgae treatment were 4.6-fold higher than from the NPK, and 15-fold higher than the control. Quantitative PCR analyses showed nitrification through ammonia-oxidizing bacteria (AOB) and archaea (AOA) to be the primary N_2O-producing pathways. Significantly higher CO_2 fluxes from the microalgae correlating with the peak N_2O emissions suggests that the addition of the extra carbon from the microalgae produced a priming effect by mineralizing soil organic N to produce higher N2O emissions. Microalgae from wastewater show potential as a biofertilizer, however follow up research investigating its sustainable use is needed.

P228 *Pseudomonas alcaliphila* JAB1 – a versatile degrader of aromatics of both natural and anthropogenic origin

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Gram-negative soil strain *Pseudomonas alcaliphila* JAB1 (DSM 26533) was isolated from aged polychlorinated biphenyl (PCB)-contaminated soil based on its ability to grow on biphenyl as a sole carbon source. In its complete genome sequence (GenBank accession no. CP016162), several putative (super)operonic regions were revealed supposedly enabling degradation of aromatic substances through initial reactions mediated by aromatic dioxygenases/monoxygenases. Namely, clusters of genes *bph* (enabling utilization of biphenyl and related compounds), *ben*/*tol* (utilization of benzoate and its derivatives), *phe* (degradation of phenolic compounds) were found, as well as both catechol and protocatechuate branches of the β-ketoadipate pathway, which is used to funnel intermediates of degradation of aromatics to the central metabolism. Degradation/utilization of many of aromatic substrates was also confirmed experimentally, e.g. JAB1 strain was able to degrade certain PCB congeners, (di)chlorobenzoates, toluate, phenol, etc. Moreover, JAB1 was found to degrade flavonoids, both non-hydroxylated flavon and its hydroxylated derivatives, supposedly through the cleavage of both B and C rings mediated by *bphA* gene product, a putative KF707-type biphenyl-dioxygenase. In the presented poster, a survey on the hypothesized induction of transcription of the *bphA* gene by a range of aromatic secondary plant metabolites (SPMs) will be discussed. This work contributes to the understanding of bacterial metabolism of aromatic compounds in soil ecosystem, as well as a role of aromatic dioxygenases in plant-microbe interactions mediated by SPMs.

P229 Xyluloitic and cellulolitic activity of *Bacillus subtilis* strains isolated from microflora of the soil worm *Eisenia foetida*

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Rapeseed middlings contain a high fraction of cell wall polysaccharides and are a major source of proteins, amino acids, polysaccharides, and carbohydrates in animal feed. Most rapeseed middlings are not digested by monogastric animals. To increase the bioavailability of animal feed contents, supplementary feedstock mixes (SFM) are produced that have various enzymatic, prebiotic, and probiotic properties. Enzymes that deconstruct the cell wall of plants, such as xylanases and cellulases, are among the SFM components that increase the assimilation of key minerals of the feedstock. In our studies, the microflora of a soil worm, *Eisenia foetida,* was isolated as a source of bacterial strains with special metabolic properties. The isolated bacteria were tested in terms of secreted lipases, esterases, and proteases and hemolytic activity. From the 96 isolated strains, 19 were identified as biosurfactant producers as well. Further analysis revealed that four strains belonged to the *Bacillus subtilis* genus (16S rRNA homology sequencing) and had high enzymatic (xylanase, cellulase) activity. The most significant cellulotic activity, approximately 30 µmole of glucose/min/mg, was shown in the exponential growth phase, whereas the highest xyluloitic activity was shown in the stationary growth phase, where best strain produced approximately 45 µmole of xylose/min/mg from rapeseed middlings.

P231 Canola rhizosphere microbiome: potential source of genetic variability for future canola breeding

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The plant microbiome is a potential source of genetic variability for breeding efforts, however, the rhizosphere microbiome is not very well understood for its rational optimization and benefit to the plant. In this study, we determined the core- and genotype-associated rhizosphere bacteria in sixteen *Brasica napus* (canola) lines sampled weekly for ten weeks. The most abundant bacterial phyla across weeks and canola lines were Proteobacteria, Actinobacteria and Acidobacteria. Abundance of these phyla increased up to fourth week (start of flowering) followed by stability up to seventh week (end of flowering) then a decline. However, this pattern is not observed at lower taxonomic levels where their abundance showed modality. The two most common members of the canola core microbiome were Pseudarthrobacter and Bradyrhizobium present in 95% and 90% of the samples respectively. Compared with the reference canola line, the number of differentially abundant taxa in the fifteen canola lines ranged from 193 to 476. For example, in Line 2, Aetherobacter is significantly more abundant whereas Stenotrophomonas is significantly less abundant. These bacterial taxa are thought to have roles in alleviating salt stress and fungal disease resistance respectively. Measurement of differentially abundant taxa and their functional attributes in each line provide a direct way to link cultivar performance and bacterial association. This work could augment efforts to improve canola growth and development either through adjusting soil bacterial community structure artificially or using the rhizosphere microbiome as a source of genetic variability in next generation canola breeding.

P232 Fine Root Dynamics and Its Possible Implications in Structuring the Rhizosphere Microbial Community in Sixteen *Brassica napus* (Canola) Lines

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In canola, root length was indicated as best indicator of seed yield. However, little is known about its root growth dynamics and possible implication in shaping rhizosphere microbial community. In this study, we examined weekly fine (FRL) (0.5 – 2mm), extra fine (< 0.5mm) and coarse root length (CRL) and root biomass in sixteen *Brasica napus* lines grown under field condition. We hypothesize that lines with distinct root dynamics would exhibit variability in their rhizosphere microbial community. Among the fifteen canola lines only Line 10 showed significant difference in all the measured root parameters with the reference Line. Line 10 followed by Line 9 exhibited the highest number of bacterial phyla, classes and orders that contributed to variability of canola lines with the reference line. This might indicate that their significant difference in root parameters with the reference line might have contributed to this difference. For all measured root parameters, mixed effect models indicated significant effect of sampling week. Hence, to further investigate the root growth dynamics along week we run generalized additive models. For FRL, reference line exhibited sharp increase up to the beginning of flowering followed by gradual decrease and stability till the end of flowering followed by increase and decline. Whereas Line 10 showed a gradual increase in FRL up to end of flowering followed by period of stability. Indicating differences in dynamics pattern. We will be further exploring the results to identify correlation between fine root responses and bacteria. This work contributes to the less explored area of linking root growth and development dynamics in crops with possible influence on rhizosphere microbial community.

P233 Distribution and diversity of anammox bacteria in NW Portuguese coastal environments

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The discovery of anaerobic ammonium oxidation (anammox) revealed the existence of a shortcut in the classic nitrogen cycle where ammonium is converted directly to dinitrogen gas, and removed from the system. Anammox bacteria have been reported in a variety of habitats, from marine anoxic basins to freshwater lakes. Despite the widespread occurrence, low diversity of anammox bacteria has been reported with only five genera reported so far. In this study, we aimed to examine the diversity and distribution of anammox bacteria in natural habitats along the NW Portuguese coast. Sediment and soil samples were collected in different estuaries, coastal lagoons and saltmarshes. Total community DNA was extracted and anammox bacterial 16S rRNA gene and *hzs*A gene sequences were amplified. The amplicons were cloned and sequenced. Sequences were compared to reference sequences, aligned and submitted to phylogenetic analysis. Anammox-like sequences were recovered from samples from different locations including Cávado, Ave, and Douro estuaries, and agricultural soils. Phylogenetic analysis of the 16S rRNA genes has revealed the presence of *Candidatus* Scalindua, Kuenenia, and Brocadia. Obtained results will enable the selection of samples for further characterization using next generation sequencing to characterize community composition, and identify anammox lineages. The broad anammox bacterial distribution indicates that anammox might play an important role in removing fixed nitrogen from the sampled systems.

P234 Biocontrol Potential of Forest Tree Endophytes

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In the natural forest environment, the spread of pathogens may have dramatic effects on ecosystem functioning. To successfully control devastating forest pathogens, application of endophytes as biocontrol agents is an emerging area of research. There are several ways by which endophytic microorganisms can protect their tree hosts against pathogens. Endophytes promote plant growth by producing beneficial secondary metabolites (e.g. phytohormones) or providing nutrients (e.g. phosphorus). Endophytes can compete with pathogens and herbivores by successfully utilizing available substrates (colonization of shared niche can restrict pathogen invasion), or endophytes can produce antagonistic metabolites. Endophytes can enhance plant resistance by triggering and priming host defensive reactions. Endophytes could provide several opportunities for application in integrated pest management (IPM) to gain sustainable forestry practices. To utilize endophytes as biocontrol agents, the mechanisms behind the possible mode of action should be determined. Novel advances in cultivation-independent techniques including next generation sequencing technology (NGS), association analyses and network inference modelling will greatly facilitate identification of endophytes and unravel potential beneficial functions of endophytic communities. A further understanding of the mechanisms of fungal root endophytes could help to minimize the use of environmental harming chemicals in plant and forest tree protection. Here we propose simple guidelines that could facilitate the use of root fungal endophytes as biocontrol agents and simultaneously study their ecological functions.

P235 Multifacted bioformulations enhancing nodulation and growth attributes of pigeon pea under multi-stress conditions

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Pigeon pea (*Cajanus cajan*) is an important pulse crop grown in the Northern regions of India. The production of this crop has been severely affected due to elevated temperature (± 45°C) and high soil pH (± 8.8) prevalent in the Northern belt. These abiotic factors have proven detrimental to nodulation of pigeon pea crop, turning more than 2.5 million hectares of cultivable land in the Indo-Gangetic plains unfit for agronomic purposes. Hence, the aim of the present study was to strategically design multifaceted bioformulation that could mitigate the effect of these multiple stresses, and augment nodulation and yield of pigeonpea. High pH and temperature tolerant strains of rhizobia were screened, and assayed for various plant growth promoting activities as well as production of different metabolites. Talc based formulation was developed from *Rhizobium* cells, individually and in combination with other metabolites. Efficacy of these formulations was tested with pigeon pea seeds (*Pusa 991*) under *in planta* assay. Further validation was performed in alkaline field in Uttar Pradesh, (pH 8.8) during the month of April- September (temperature ± 45°C). Seeds receiving amalgamated formulation enhanced plant parameters like nodule number and seed yield by one fold and two fold respectively in comparison to control under stress conditions. Results suggest potency and efficacy of utilizing such multifaceted bioformulations for ameliorating multiple stresses and enhancing growth of this important crop in India. Enhancement resulting upon application of combination of bioinoculant with its metabolite proves to be an interesting concept for future applications.

P236 The ubiquitous mycenas – purely saprotrophs or potential plant root symbionts?

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The transition from saprotrophic to mycorrhizal lifestyles has occurred several times independently during evolution in the fungal kingdom. Recent studies indicate that the border between a saprotrophic and mycorrhizal lifestyle is more blurry than earlier appreciated and that numerous saprotrophic fungi can associate with plant roots as facultative biotrophs *in vitro*. *Mycena*, a speciose genus in Agaricales, has commonly been described as saprotrophic, and have profound ecological importance as litter decomposers. However, several recent studies have suggested that some *Mycena* spp. may have a biotrophic lifestyle. In this study, we investigate the putative interaction between *Mycena* spp. and plant roots using *in vitro* growth experiments. Seedlings of *Betula pendula* and 17 *Mycena* species were grown in microcosms. We used cryomicrotome sectioning, differential staining and fluorescent microscope imaging to visualize fungal growth in the fine roots. All *Mycena* spp. associated closely with plant roots and we observed hyphal penetration into fine roots in all microcosms, in some cases intracellularly. Our preliminarily data suggest that with most species of *Mycena*, seedling growth was impaired, and there was no evidence of growth benefits for the seedlings, but several *Mycena* spp. seem to be facultative biotrophic *in vitro*. We are also investigating potential nutrient transfer between *B. pendula* and *Mycena* spp. using ^{14}C and ^{32}P radioactive isotopes. Our preliminary results show the need to reconsider the previous view on the genus *Mycena* as purely saprotrophic. The ecology and nutritional modes of *Mycena* is likely far more complex, plastic and flexible than earlier believed.

P237 Metagenomic assessment of dominant bacterial communities in metal contaminated rice paddy soils

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We conducted metagenomic assessment of bacterial communities in rice paddy soils along the Janghang smelter in South Korea that had elevated levels of arsenic, cadmium, copper and lead, and identified populations whose dominance in highly contaminated soils may have applications for bioremediation. Overall abundance and diversity indices of bacterial populations did not significantly vary between differentially contaminated soils based on pyrosequencing data. However, non-metric multidimensional scaling (NMDS) using Yue and Clayton theta measure of dissimilarity showed significant differences ($P < 0.001$) in bacterial composition according to sites, based on homogeneity of variance (HOMOVA) analysis. High percentages of the bacterial sequences from pyrosequencing data were found to be exclusive to each site: 7839 OTUs (28.6%) were found only in highly contaminated soil; 9337 OTUs (34.1%) were unique only to highly contaminated soils that had undergone short term phytoremediation trial; and 9023 (32.9%) in less contaminated soils. Metastatistical analysis carried out to identify specific OTUs responsible for the clustering of bacterial populations showed that 89% of the top 100 OTUs significantly differed in abundance between sites. Highly contaminated site 1 soils were significantly predominated with unclassified members of Acidobacteria subdivisions 2 and 13, sulfur-reducing (OTUs 20383, 26767) as well as sulphur-oxidizing (OTUs 3, 16505, 16485, 16491, 22426, 22485) bacterial populations and dissimilatory iron-reducing bacteria (DIRB) (16483, 16484, 17673), most of which have been previously isolated from metal and toxic impacted environments, activated sludge, and nitrite-reducing environments. Our results shows that changes in the structure of bacterial communities under conditions of metal stress are more likely attributed variations in abundance pattern of specific lower taxa populations rather than shifts in abundance of higher taxa levels.

P238 Pink seeds of barley attributed to infection with *Erwinia rhapontici*

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Pink seeds of barley (*Hordeum vulgare* L.) have been occasionally harvested in Japan in recent years. The coloration was revealed to be due to a pigment of proferrorosamine, and a bacterium like *Erwinia rhapontici* (Millard 1924) Burkholder 1948 emend. Hauben et al. 1998, which characteristically produced the pigment, was frequently isolated from the pink seeds. The bacterium could be sometimes isolated even from apparently-normal barley seeds. For 16S rDNA, the isolates had 99-100% sequence similarities with previous data in the DDBJ/EMBL/GenBank databases for strains identified as *E. rhapontici*. Physiological properties of the present isolates evaluated using a diagnostic kit, API 20 NE (bioMérieux Japan Ltd.), also well agreed with the description for *E. rhapontici* by Huang et al. (2003). Therefore, the isolates were confirmed to be *E. rhapontici*. This bacterium has been already known to be with a wide distribution in Japan (Nishiyama et al., 1985), but its isolation from barley will be the first time in the world. Pink seeds of bread wheat (*Triticum aestivum* L.) and durum wheat (*Triticum turgidum* L. ssp. *durum*) have been recognized in Europe, North America and Russia, and found to be due to infection with *E. rhapontici* (Bockus et al., eds., 2010). The present symptom on barley is also attributed to the infection. *Erwinia rhapontici* has been isolated from not only plants but also soil (Feistner et al., 1983). We will investigate its emergent ecology as well as try reproduction of the present symptom by inoculation of barley with the isolates.

P239 Generation of nitrate non-utilizing mutants of *Phomopsis longicolla* Hobbs isolated from soybean

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Stem blight of soybean by *Phomopsis longicolla* Hobbs has been reported from China (Chen et al., 2013; Cui et al., 2009). We have also isolated the fungus from wilted soybean with stem blight in our trial fields located in Hiroshima Prefecture in western Japan since 2012. Clear-cut reproduction of the natural symptom in Japan by inoculation with the isolates has not been successful so far. But, we confirmed that the isolates could cause poor seedling establishment of soybean. Nitrate non-utilizing mutants (nit mutants) are known to be useful as markers for analyzing fungal ecology, vegetative compatibility, pathogenic specialization and so on. In order to get to know more about emergent ecology of *P. longicolla*, we tried to generate nit mutants from the isolates (MAFF150072-150075 preserved in Genetic Resources Center of National Agriculture and Food Research Organization, Japan). Single-hyphal strains tolerant to chlorate (potassium chlorate) were obtained from each isolate, and their phenotypes based on utilization of five nitrogen sources (sodium nitrate, sodium nitrite, ammonium tartrate, hypoxanthine and uric acid) were determined through the method by Brooker et al. (1991). In results, the phenotypes of nit1 (non-utilizing nitrogen from sodium nitrate) and Nit3 (non-utilizing nitrogen from sodium nitrate and sodium nitrite) were obtained from MAFF150073-150074 and MAFF150075, respectively. The nit mutants were judged to be comparable with respective wild types for mycelial growth and sporulation. We will confirm compatibility of the present nit mutants with soybean to evaluate their applicability to the studies for emergent ecology of *P. longicolla*.

P240 Changes in the soil fungal community across the mountain birch tree line ecotone

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Ecosystems all over the world are affected by climate change and in particular high latitude and altitude ecosystems. One observed consequence of global warming is an upward shift in the tree line. In Norway we predict that the tree line, mostly formed by mountain birch (*Betula pubescens*), will migrate upwards due to climate change as well as changes in domestic grazing pressure. There is normally a marked vegetation turnover in this ecotone, ranging from the subalpine mountain birch forest to the treeless alpine vegetation, but the corresponding belowground microbiome is in comparison poorly characterized. Our aim is to analyze changes in the soil fungal community in this ecotone, especially considering the major functional groups, which are ectomycorrhizal, ericoid mycorrhizal and saprotrophic fungi. We sampled soil from nine different sites along 200 m transects stretching from mountain birch forest to alpine vegetation above the tree line. Fungal community composition will be determined using DNA metabarcoding, compositional changes will be analyzed using ordination methods and ergosterol measurements will be used to quantify changes in fungal biomass. Based on the results from our findings we aim to infer potential consequences of changes in the tree line with regards to the soil fungal communities.

P241 Relationship of soil microbial community with plant roots and greenhouse gas emission in full-drained peatland forests

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Soil microbial community structure and abundance was studied in full-drained peatland forests which are common in Northern Europe. Soil samples were obtained from three forest types - a Scots pine forest of *Vaccinium*-site type, a Norway spruce forest and a Downy birch forest of both *Oxalis*-site type. In addition to soil microbial characteristics following parameters were recorded - belowground biomass, fine roots parameters, as well as gaseous C and N fluxes between the ecosystem and the atmosphere. In both birch and spruce forests, high N_2O emission was measured, while CH_4 flux was low in all forests studied. Fine root turnover was lower in pine forests compared to spruce and birch forest. The relationships between soil microbial community characteristics, soil and plant root parameters, and GHG fluxes were dependent on the forest type. There was a strong positive relationship between the N_2O emission and *nosZ*II gene abundance in soils of birch and pine forest. In birch forest, high values of both N_2 and N_2O emission indicated that consumption of N_2O by microbes possessing nitrous oxide reductase genes (*nosZ*I&II) did not compensate N_2O production. In pine and spruce forests the N_2O flux was positively related to the abundance of soil archaea. The abundance of denitrifying microbes correlated positively with CO_2 emission in soils of birch and spruce forests.

P242 Sugarcane harvest managements alter the structure, composition and potential functions of the soil microbial community

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Here, microbial soil community structure, composition (high-throughput sequencing/ Illumina MiSeq) and functions (GeoChip 5.0) were analyzed in two Brazilian sugarcane fields - mechanical harvest and pre-harvest burning. Taxonomic analysis of the bacterial community revealed Proteobacteria (37%), Actinobacteria (30%) and Firmicutes (7%) as the most abundant phyla present in soil samples. A total 75,8% microbial functional genes targeted by GeoChip 5.0 were detected across all soil samples. Approximately 14% of the detected microbial functional genes were associated with carbon cycling. The microbial functional gene families '*mcr*A' (production of methane) and '*mmo*X' (oxidation of methane), were more abundant in soil samples from sugarcane field with mechanical harvest. In turn, '*pmo*A' gene family was more abundant in soil samples from pre-harvest burning. Statistical differences were found between mechanical harvest and pre-harvest burning regarding to the number of microbial functional genes associated with carbon cycling. As anthropogenic actions soil attributes were affected, mostly related to CO_2 production such as carbon content, porosity, moisture and soil oxygen content. The use of harvesting machinery can alter a spatial organization of soil compaction, affecting aeration and consequently a microbial activity of the soil, which could at least in part explain the increase of the genes involved in the degradation and carbon sequestration and the production and consumption of methane in sugarcane soils mechanical harvest. These results showed a clear effect of sugarcane harvest systems on the structure, composition and potential functions of the soil bacterial community in bulk soil from sugarcane fields.

P243 The H2020 Diverfarming project: assessing the impact of crop diversification on soil biodiversity across Europe

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A new European project whereby soil biodiversity will be investigated and compared in conventional and diversified cropping systems under low input practices has just started. The project Diverfarming is a Research and Innovation action (EC H2020, Rural Renaissance, Fostering innovation and business opportunities). The Diverfarming consortium wants to develop innovative farming strategies. Main aims are to increase the long-term resilience, sustainability and economic revenues of agriculture across the EU by assessing the real benefits and minimizing the drawbacks of diversified cropping systems under low-input agronomic practices. The project is testing the effects of rotations, multiple cropping and intercrops systems, in conventional and organic management on soil biodiversity. Among eleven work packages, Work Package 4 is assessing: i) the capability of diversified cropping systems to modify soil biodiversity, ii) how this is controlled by the climate and soil type, iii) the functional correlations between soil biodiversity and activity within different crop associations and nutrient inputs, iv) the development of soil-borne diseases, and v) the abundance of concomitantly occurring faunal key species. To assess soil biodiversity, earthworms will be identified and NGS will be used for bacteria and fungi. To clarify microbial activities in relation to microbial diversity, we will measure key enzymatic activities regulating main biochemical cycles and the expression of selected target genes by using qPCR. Visibility at esm2018 aims to advertise the Diverfarming project among colleagues for new connections and possible collaboration with regional projects as well as widening the participation in future Diverfarming meetings.

P244 Effects of grassland and forest land use intensity on the abundance and activity of methane-oxidizing microorganisms

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Methane (CH_4) is next to CO_2 the second most important greenhouse gas, with rising atmospheric concentrations. Aerated upland soils act as a sink for CH_4 by oxidation of atmospheric CH_4 through methane-oxidizing bacteria (MOB). Intensified agricultural activity, such as livestock farming and fertilization, may reduce the CH_4 sink capacity of soils. We investigated the influence of land use intensity on CH_4 oxidation potentials and abundance and diversity of MOB in 300 forest and grassland soils of three climatically different regions, within the German research platform Biodiversity Exploratories (http://www.biodiversity-exploratories.de). Land use of the grasslands ranged from unmanaged to highly grazed or fertilized plots, in the forest a wide range of management practices were applied. Potential CH_4 uptake rates at atmospheric concentrations (~1.8 ppm) were measured at defined soil moistures at 20 °C. Potential methane oxidation rates ranged from 0.006 to 1.695 ng CH_4 g^{-1} DW h^{-1} and were generally more pronounced in forest than in grassland soils. The fine textured grassland soils of one region exhibited the lowest CH_4 oxidation potential. Sandy soils had a lower methane oxidation rate than the organic-rich Histosols and Gleysols. Ongoing work relates potential CH_4 oxidation rates to the abundance of different taxa of aerobic and anaerobic methane-oxidizing bacteria and archaea (as determined by group-specific qPCR assays) as well as to soil properties (like texture, mineral N, pH) and land use intensity to yield information on driving environmental factors on CH_4 oxidation potentials and taxonomic identity of the associated functional guilds.

P245 Relation between silver fir (*Abies alba* Mill.) phenology and belowground fungal composition in Slovenia

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As higher plants are sessile organisms, they have to compete with other plants for resources, which require very efficient communication and co-ordination of resource allocation and signaling between above-and below-ground plant parts. We collected 24 soil samples with fine root from naturally regenerated silver fir plot at Lehen na Pohorju (Slovenia). Four different groups were selected based on phenological data of silver fir trees (project LIFEGENMON). For identification of root associated fungi, ITS2 region of fungal rRNA gene was amplified and sequenced on Illumina MiSeq platform. For diversity estimation, Shannon-Wiener and Simpson indexes were used. Differences in fungal community were tested using PERMANOVA on Bray-Curtis distances. Analyzed data showed statistically significant differences in fungal communities of silver fir between groups of early and late flushing saplings. Also, alpha diversity indexes differed between mentioned groups, as there was an indication on higher OTUs diversity in fungal community of silver fir of phenologically early young trees. Other groups have showed no statistically significant differences in fungal communities, although there were some differences in alpha diversity as well as in fungal composition between early flushing adult trees compared to late flushing adult trees. There is an increasing body of literature, showing that fungal communities impact on plant growth and vigor, as they influence the quality, direction and flow of energy and nutrients between plants and fungi. Moreover, many of the observed plant growth responses may be also regulated in part by alterations in fungi endogenous phytohormone levels.

P246 Seasonality drives arbuscular mycorrhizal community composition and diversity in tropical dry forests

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Within the next decade, tropical dry forests are predicted to experience substantial reductions in rainfall and longer, more intense dry seasons, both of which could push these forests beyond their climatic threshold. Our knowledge of how soil microbes respond to such changes is limited. In addition, the seasonal aspects of microbial communities are generally neglected even though seasonality shapes the fluxes of belowground carbon (C) and nutrients such as nitrogen (N) and phosphorus (P). Here, we present results from the study of arbuscular mycorrhizal fungal (AMF) communities in a tropical dry forest in the Yucatán, Mexico. We asked: could AMF be sensitive to changes in rainfall or potentially resilient and adapted to increasing soil moisture deficits? We examined seasonal variations (wet versus dry) in AMF communities over three consecutive years using adapted AMF barcoding primers NS31 and AML2 for custom dual-indexed Illumina sequencing. Reads were processed using a QIIME bioinformatics pipeline. More than 200 distinct AMF OTUs covering eight AMF families were identified, with *Glomus* species dominating the community. Twenty OTUs (18 *Glomus*, 2 *Diversispora*) accounted for 96% of the community with the remainder shared amongst the other taxa (i.e. most AMF were rare). Abiotic niche and spatial factors were drivers of AMF community diversity but not host plant identity. AMF taxa were more abundant, and root and soil AMF communities more diverse in dry versus wet seasons. Shifts in AMF community composition and diversity were significantly correlated with levels of soil NO_3 and N: P supply ratio as well as soil moisture. A higher AMF diversity in the dry versus wet season suggests that AMF communities are resilient to soil moisture deficits. Nevertheless, increases in tree mortality or length of dry seasons could alter AMF resilience in ways that are distinct from AMF responses to predictable (seasonal) water deficits.

P247 Functional potential of microbial communities in cryoturbated organic matter from Herschel Island

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The significant source of C (ca. 400 Gt) is buried in deep soil pedons in the arctic soil, because of the cryogenic processes. Warming of tundra will leads to the deepening of the seasonally freezing-thawing active layer, making these buried soil C vulnerable to microbial transformation. To identify the structure of microbial communities and their functional potential in the buried soil we investigated four sites from Herschel Island (HI), western Canadian Arctic. We assessed total community structure by Illumina sequencing of bacterial 16S rRNA gene and fungal ITS1 region and abundance by quantifying 16S rDNA-bacterial, 16S rDNA-archaeal, 18S rDNA-fungal, mcrA-methanogenesis and nifH-nitrogen-fixing genes marker by qPCR, respectively. Illumina tag sequencing revealed that cryoturbated organic matter (CryoOM) comprised a high proportion of Actinobacteria (28%) and Proteobacteria (27%) among the prokaryotic community and Ascomycota (55%) among the fungal community. The bacterial gene abundance in CryoOM (1.3E+11) was as higher as topsoil (1.6E+11) but fungi were significantly lower in CryoOM (1.5E+9) vs topsoil (6.1E+9). This also led to much lower fungi to bacteria ratio in CryoOM, although the carbon and nitrogen contents were almost similar as in topsoil. The abundances of nitrogen-fixing bacteria (nifH gene) and methanogens (mcrA gene) were similar in topsoil and CryoOM which suggests a similar degree of N fixing as well as similar CH4 emission potential in topsoil and CryoOM. It shows the potentially high source of methanogens in CryoOM of HI with future warming condition. Our results support the previous finding of lower fungal to bacterial abundance in CryoOM and also supplement the current knowledge on microbial communities' structure from the Arctic.

P248 Cultivated endophytic bacteria from garden pea (*Pisum Sativum* L.)

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The possibility of using endophytic bacteria in agriculture is one of the factors making this research field of great interest. These microorganisms may have a positive impact on plant growth and development, which can be used in the environment-friendly crop production. To study the diversity of endophytic bacteria of pea, three genotypes were selected: K-8274 which is highly responsive to inoculation with beneficial soil microorganisms (‘effective macrosymbiont’), K-3358 – low-responsive genotype (‘non-effective’), and commercial cultivar “Triumph”, the ‘effective’ descendant of K-8274. Endophytic bacteria were isolated from surface-sterilized leaves and stems of plants at the flowering stage using the set of different growth media. Taxonomic status of isolated strains was determined using sequencing of the diagnostic (V3-V9) fragment of 16S rRNA. In total, 230 morphotypes of endophytes and epiphytes were isolated; for 80 of them the taxonomic status was determined. Eight strains identified as *Bacillus sp., Rahnella sp., Enterobacter sp., Serratia sp.*, and *Acinetobacter sp*. have shown the significant growth promoting effect on lettuce roots. The highest number of growth-promoting bacteria was found in the ‘non-effective’ pea genotype K-3358 having the longest stems among tested genotypes. The genomes of these endophytic strains were sequenced in order to find the common genetic determinants associated with endophytic lifestyle. The results of analysis will be discussed. In general, this work has created the necessary basis for further analysis of the microbial community of aerial parts of pea plants.

P249 Investigation on the interaction between enhanced nutrient availability and soil biota on plant community in grasslands – a mesocosm experiment

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The area of species-rich grasslands in Western Europe declined dramatically during the twentieth century in response to agricultural intensification. Several European countries seek to restore semi-natural grasslands through conversion of agricultural land. Yet, development of grassland communities on abandoned agricultural land faces several major bottlenecks. Besides the potential unavailability of seeds of target plant species, the high nutrient levels and disturbed soil organism communities may further hamper restoration. Until recently, the microbial community has been largely disregarded as possible driver of plant community dynamics, and information on how soil resources affect the microbial influences on plant communities is scarce. In order to fill the gap, we set up an experiment using 110 mesocosms in unheated greenhouse where we test the interactive effect between N, P and soil biota (microbiota and nematodes) on plant community development. For soil inoculation treatments, in addition to the sterilized control, we collected soils from three different soil types (i.e. eutrophic, mesotrophic and oligotrophic) that are associated with different soil biota ranging from bacterial-dominated to fungi-dominated foodwebs. Mesocosms were then planted with mixtures of fast, mid and slow-growing grasses and forbs, each growth-rate form typical of a given soil type. Then we subjected them to additional full factorial treatments of three levels of N and three levels of P. Since March 2016, the start of the experiment, we have been able to quantify interesting but contrasting results across the years. While during 2016, P had a significant positive effect on harvested biomass, soil biota was the main factor affecting the biomass collected in 2017 with a large reduction in biomass in the control treatment (no soil fauna added) compared to bacterial-dominated soils. This lecture aims to find out if and how N and P bioavailability interact with soil biota in influencing plant communities in grassland ecosystems.

P250 Community adaptation to temperature explains abrupt soil bacterial community shift along a geothermal gradient

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Understanding how and why soil microbial communities respond to temperature changes is important for fundamental understanding of the drivers of microbial distribution and abundance. Moreover, in the context of climate change research, including microbial (community) dynamics and associated temperature sensitivities in ecosystem models may improve our ability to predict responses of biogeochemical cycles to changing conditions A unique geothermal system in Iceland ,where soil temperatures span a gradient of ambient to +40 °C, allowed us to investigate the shape of the response to temperature of soil microbial communities, and their associated community temperature adaptation. We used 16S rRNA sequencing to profile bacterial communities, and bacterial growth based assays (Leu-incorporation) to characterize community level temperature adaption in samples taken from 9 different levels of warming, under both grassland (*Agrostis capillaris*) and forest (*Picea sitchensis*) vegetation. Both community composition and temperature adaptation indices showed threshold dynamics along the soil temperature gradient. There were no significant changes up to soil warming of approx. 5-8 °C), beyond which both indices shifted abruptly. The consistency of these responses and lack of corresponding changes in soil and vegetation related drivers gives strong support for a central role of direct temperature effects in driving bacterial community shifts along temperature gradients at this site.

P252 Optimizing crop rotation cycles that support natural mycorrhization

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Arbuscular mycorrhizal (AM) fungi can be used as a tool to re-establish natural sustainable agriculture, as natural biofertilizers they enhance the whole ecosystem functioning. The promotion of AM fungi will enable to reduce the use of easy soluble fertilization and agrochemicals without compromising the yields. Although the host specificity of AM fungi is low, it seems that the best gain is achieved when the rotating plants share their fungal communities. By identifying the shared AM fungal species of the best preceding crops in rotation of our most valuable vegetables on farmlands we aim to further optimize our cropping recommendations. We will a present a research frame studying how to promote the natural AM fungal permanence in agricultural fields.

P253 Global distribution of dominant fungi in the environment

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It is clear that distribution of fungi is not governed by dispersal limitations only, but also by the availability of suitable ecological niches reflecting the abiotic and biotic conditions of the environment. In this study we have focused on the identification of climatic drivers on the distribution of individual fungal taxa based on the records of their occurrences and abundances across the globe. For the study, we have selected top 200 globally distributed species from environmental samples taking the 98.5% species hypothesis (SH) as a proxy of fungal species. To explore the influence of climatic drivers on the distribution of fungi, CHELSA climatic dataset was combined with GPS coordinates of samples and Gradient Forest algorithm was used. Based on this analysis we proved that for more than 75% of dominant fungal species, their distribution is significantly affected by climate. Mean Diurnal Range, Mean Temperature of the Wettest Quarter, Precipitation of the Coldest Quarter and Precipitation Seasonality were most often among the important bioclimatic variables that shape fungal distribution. In average, temperature-related variables explained 18% of the total variation, followed by precipitation variables (9%) and combined variables (7%), but the share of explained total variation ranged up to more than 70%. No difference in the share of the total variation in distribution explained by climatic variables was observed between fungi belonging to different ecophysiological groups, e.g. saprotrophs, ectomycorrhizal fungi, plant pathogens, etc. This study shows that climate belongs among the important factors that shape fungal distribution at a global scale.

P254 Effects of element inputs on P-solubilizing bacteria and on phosphatase activity in two grassland soils in South Africa

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Phosphorus (P) limits plant growth in many soils. P availability is strongly affected by microorganisms that mineralize organic P and solubilize bound inorganic P. Stoichiometric controls over bacterial P solubilization and communities are unknown. Therefore, we studied how processes of microbial P mobilization are affected by N and P availability in two highly weathered grassland soils in South Africa fertilized with nitrogen (N) and P in a full factorial design (Ctrl, +N, +P, +NP). We screened for P-solubilizing bacteria (PSB), determined their proportion, and identified PSB based on 16S rRNA. In addition, we analyzed phosphatase activity, microbial biomass carbon (Cmic), community composition (using ARISA) and soil chemical variables. We found that the proportion of PSB in the non-fertilized treatment was 8.5 % and 46 % at the first and second site, respectively. It was 10 % lower in 0 - 15 than 15 - 30 cm depth, whereas total P, available P and available N were higher in 0 -15 cm depth. The proportion of PSB decreased by up to 30 % at the N+P fertilized plots, whereas phosphatase activity increased with N fertilization. Cmic and total community composition did not differ significantly between treatments. However, the community composition of PSB was highly treatment- and site-specific. Most PSB belonged to *Pseudomonas* sp., *Acinetobacter* sp. and Enterobacterales. In conclusion, we found that increased N and P availability decreased the proportion of PSB, N fertilization increased phosphatase activity, and fertilization affected the P solubilizing community, which provides novel insights into the plant-soil-microbial P cycle.

P255 The plant root microbiome diversity and resilience in a changing climate

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All living plants are closely associated with a high diversity of microorganisms essential for their functioning. Belowground, plant roots live in symbiosis with root associated fungi (RAF) and also host a rich diversity of prokaryotes, together known as the plant root microbiome. RAF have been shown to have a surprisingly important role in carbon storage and sequestration. It is nonetheless largely unknown how the plant root microbiome responds to climatic changes, such as shifts in temperature and precipitation regimes. The DRIVE project aims to study the response of ectomycorrhizal and arbuscular mycorrhizal plant root microbiomes to a changing climate. The project utilizes already established climate sites on the West coast of Norway consisting of 12 sites covering three temperature- and four precipitation regimes. The climate effects will be investigated using high throughput sequencing (HTS) of *Bistorta vivipara* and *Potentilla erecta* plant root communities in three subprojects. The first sub-project will investigate current status of the plant microbiome of the different climatic regimes. The second sub-project will look at effects on the plant root microbiomes of plants transplanted in direction of predicted climate change scenarios of western Norway (wetter and warmer). The third sub-project will examine effects of the plant root microbiome on plant growth and performance under different temperature and precipitation regimes in a common garden experiment.

P256 Bacterial community alternation under tillage intensity and their contribution to soil functions

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Soil microbial ecological function has a close relation with soil function, and the changes in the structure and composition of soil microbial populations can directly affect soil functions. Because of methodological difficulties of microbial researched, there is still lack of information about compositional and functional responses of bacterial communities to different tillage. The aim of the present study was to identify bacterial community composition and diversity under different soil tillage. *Dystric Glossic Retisol* was analysed, geographical coordinates 55°43'38″N, 21°27'43″E. We assessed soil bacterial communities in two different management regimes - deep ploughed and more environmentally friendly - shallow ploughless tillage. Composition and diversity of soil bacterial communities were assessed by sequencing of 16S rRNA genes. All sequences were classified below phylum level. Results show that two types of bacteria are dominant: *Actinobacteria* and *Proteobacteria*. Their relative abundance ranges about 33% and 28% respectively. The most widespread family was *Micrococcaceae*, and *Hyphomicrobiaceae*, which accounts for 6% and 3% respectively. The number of taxonomic units in different agroecosystems shows the abundance of organisms but does not allow for the estimation of biodiversity; therefore, five different biodiversity indices were calculated. Shannon and Simpson biodiversity indices found that 10 most abundant species were the same in tested soils, just relative abundance various. The ACE, Chao1, and JackKnife biodiversity indices varied in the analysed soils – the highest indices calculated for shallow ploughless soil. This leads us to the assumption that mentioned the type of soil management contributes to the protection of soil functions.

P257 Linking soil nitrogen cycling to microbial community composition and function to differentiate nitrogen uptake among diverse *Brassica napus* (canola) lines

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Brassica napus L. (canola) is a dominant oilseed crop in western Canada; however, crop production is nitrogen (N) intensive and N fertilizer is the highest input cost to canola growers. Thus, improving N use efficiency has become an important goal in canola production. The objectives of this study were to characterize microbial community composition, extracellular enzyme activities, and soil N processes, and to test relationships between these factors to N uptake among diverse *B. napus* lines over time. Sixteen diverse lines of *B. napus* were grown on a Kastanozem soil in Saskatchewan, Canada. Root-associated soils were collected from each line weekly from the rosette stage to maturity, and aboveground plant material was harvested and analyzed for N content. Both nitrate-N and ammonium-N decreased over the growing season, with significant differences between lines for nitrate, but not for ammonium. Interestingly, both nitrate-N and ammonium-N peaked around the flowering-early pod filling stages, but decreased again towards plant maturity. Aboveground plant N and seed N were significantly different across canola lines. Additionally, urease and B-1,4-N-actylglucosaminidase activities were measured to assess N cycling activity, while rhizosphere microbial community composition was determined through amplicon sequencing of bacterial 16S rRNA genes. Redundancy analyses will be used to analyze N transformation from the soil to the *B. napus* lines in relation to microbial diversity and function. By characterizing N uptake and soil N processes, this research will advance efforts to develop *B. napus* lines capable of efficiently utilizing N resources.

P258 Soil microflora and -fauna response to biochar amendment

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Biochar is the by-product of thermal gasification of biomass and can be used as soil amendment to sequester carbon, increase pH and supply nutrients to crops. The effect of biochar on soil microflora and –fauna abundance and diversity was tested in a sandy loam field soil with reduced-tillage management after three annual amendments. Earthworms had a priming effect on protist abundance, basal soil respiration, and oligotrophic culturable bacteria. Earthworms did not affect eutrophic culturable bacteria and extracellular enzymatic activities. Biochar increased soil pH while no significant harmful effects of biochar were detected on earthworms. In earthworm drilosphere biochar decreased the abundance of protists while biochar increased the protist abundance increased. Structural microbial diversity measured by PLFA analysis was not significantly affected by either earthworms or biochar. Metagenomic analysis based on amplicon Illumina sequencing was more sensitive than activity based functional assays and revealed effects of pH, glucosidase and proteinase activity on bacterial communities (16S rDNA) and effects of pH, abundance of active protists and culturable bacteria, and phosphatase activity on fungi/protist communities (18S rDNA). Most striking was significant effect of earthworms on the protist metagenomics diversity, clearly distinguishing bulk soil and drilosphere soil. Generally, the addition of biochar as soil amendment and alternative fertilizer had limited effect on soil microorganisms and fauna in this field study performed at farm level agricultural conditions under normal agricultural practises. Therefore, biochar show potential as a climate smart agriculture mitigating climate change by sequestering carbon, supplying fertilizers for plant growth and supporting soil biodiversity.

P259 Lignin-enhanced polycyclic aromatic hydrocarbons remediation and involved soil microbes

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Bioremediation of polycyclic aromatic hydrocarbon (PAH)-contaminated soil can be enhanced by stimulating microbial degradation and increasing pollutant bioavailability. To explore the remediation potential of lignin, which is a class of plant-derived aromatic polymers, both ^{14}C- and ^{13}C-PAH spiked microcosm experiments were performed. The ^{14}C experiment showed that lignin amendment led to enhanced PAH mineralization and nonextractable residue (NER) formation, and the increased adsorption was mostly with humic acid. The ^{13}C-DNA-SIP suggested *Mycobacterium* was enriched in heavy fractions, thus suggesting their involvement in pollutant degradation. A subsequent pot experiment was carried out with a long-term contaminated arable soil. A 41.7% reduction in 15 priority PAHs was achieved in the combined ryegrass, lignin and rhamnolipid treatment after 90 days. In contrast, there was no PAH reduction with any treatment used alone. The rhamnolipid was indispensable for successful remediation, as shown by the lack of PAH transformation in all non-rhamnolipid treatments. High-throughput sequencing analysis demonstrated that lignin addition substantially changed the fungal and bacterial communities; however, there was no indication of lignin selection for known bacterial PAH degraders. Taken together, these findings demonstrate the potential of lignin in PAH-contaminated soil remediation, and highlight the importance of simultaneous improvement of pollutant bioavailability and microbial activity for *in situ* clean-up.

P260 Organic farming practices in a desert habitat increased the abundance, richness and diversity of arbuscular mycorrhizal fungi

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Desert ecosystems are known for their fragility due to the limitation of their natural resources. Therefore, agricultural practices in these ecosystems need to rely more on sustainable inputs and players. One of the naturally occurring supporters for plant health and fitness is the symbiosis between plants and arbuscular mycorrhizal fungi (AMF). Agricultural practices are known to affect the diversity and efficiency of AMF. While agricultural practices in general have been evaluated for their effects on AMF communities in some desert ecosystems, organic farming practices received little attention. In the light of this lack of knowledge, we aimed to evaluate the abundance, richness and diversity of AMF community under organic farming of a desert ecosystem in the Arabian Peninsula and to compare it with an adjacent conventional farming system and native vegetation. In total, twelve sites, including six plant species, were sampled from both farming systems and the native site. Spore morphotyping revealed 24 AMF species, with 21 species in the organic farming system compared to 14 species in the conventional one and none from rhizosphere soil of the native plant (*Tetraena qatarensis*). Dominikia emiratia, a new AMF species was discovered in both farming systems. AMF spore abundance, species richness and Shanon-Weaver diversity index were higher under organic farming. In both systems, the AMF community composition and abundance associated with different crops followed almost the same trend, with pomegranate having highest values followed by lime, grape, mango and lemon. Our study demonstrates that organic farming in such a desert ecosystem is an advocate for AMF diversity. This might imply that AMF play an important role in the sustainable production of food in such a resource-limited desert habitat.

P261 Microbial diversity and activity in top and deep soil horizons of podzolic soil under spruce trees

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Global climatie change affects C and nutrients cycling in terrestrial ecosystems through the intensification of soil organic matter (SOM) decomposition. The latter depends on spatial distributuon of so-called „hot spots“, first of all, rhizosophere as a key component of soil-microbe-plant systems, down the soil profile. Rhizodeposits are known to stimulate microbial activity and SOM decomposition in topsoil, while their role in deep horizons has not been sufficiently estimated. We hypothesized that the increased microbial activity in rhizosphere was linked with higher diversity of rhizosphere microbial communities, with more pronounced rhizosphere effect in the top than in deep soil. We determined C turnover rates, nutrients stoichiometry in SOM pools, and microbial community structure in podzolic soil under spruce trees. The rhizosphere factors (Rf) expressed as a ratio of soil characteristics in rhizosphere to those in bulk soil were determined in the top AEL and deep EL horizons. The maximal rhizosphere effect (Rf > 1.5) was revealed for microbial biomass and basal respiration. C:N ratio in rhizosphere microbial biomass was higher than that in bulk soil, while C:P had the opposite tendency. Rf values for SOM turnover were 1.5 and 6 in the top and deep soils, respectively. 16S rRNA amplicon sequencing showed dramatic differences between bulk soil and rhizosphere in microbial community structure. Rhizosphere had higher microbial diversity, with significant contribution of both Gram-positives and Gram-negatives, including *Acidobacteria*, *Alphaproteobacteria*, *Betaproteobacteria, Gammaproteobacteria, Solibacteres*, and *Spartobacteria*. Bulk soil showed dominance of Gram-positives representing *Bacillales* and *Clostridiales* with the total relative contribution of more than 80% and 50% for top and deep horizons, respectively. Thus, we confirmed our first working hypothesis on the relationship between high microbial diversity and microbial activity in rhizosphere, and rejected the second one on higher Rf values in topsoil.

P262 Soil faunal contribution to litter mass loss as affected by global climate and land use changes

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Litter decomposition is a key ecosystem process determining the cycling of different nutrients. Soil fauna play an essential part in this process by fragmenting and burrowing litter material, paving the way for microbial decay. However, decomposition may be influenced by interacting agents of environmental changes. Here we used a large-scale global change experimental field to test the potential interactive effects of land use type (croplands and grasslands differing in land use intensity) and predicted climate change on surface litter mass loss of standardized crop residues over a period of two years. To evaluate the effects of soil fauna on litter mass loss in different land use types and climate scenarios, litter bags with two mesh sizes (5 mm and 0.02 mm) were differentiated. Our results indicated that soil faunal contribution was more than 65% of surface litter mass loss. Notably, the effect of soil fauna on litter mass loss was decreased in summer season under future climate treatment in grasslands, but less so in croplands. These results indicated that climate change-induced alterations in litter decomposition pattern as well as changing contributions of soil fauna to litter mass loss depend on the land use type and the specific period of the year. Moreover, land use type (not land use intensity within each type) profoundly affected litter mass loss rates, which was significantly higher in croplands than in grasslands. This counterintuitive result may indicate a “home field advantage” with cropland-dwelling soil fauna efficiently decomposing crop residues. Additionally, although mesofauna (Collembola and Oribatida) are the most abundant detritivores in the soil, their abundances was not significantly correlated to surface litter mass loss, and so did macrofauna abundances.

P263 Tropical peat decomposition under land-use change: adaption to resources and conditions (TROPDEC)

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There is a need to better understand how established cropping systems effect the GHG emissions of degrading peat and the underlying microbial communities. A central issue is the diversity and abundance of microbes and how it effects CO2, CH4 and N2O formed in peat carbon and nitrogen cycling. We have chosen an extreme environment for study, the tropical ombrotrophic peatland, where the annual fluctuations in the water regime are large, the temperature for biochemical processes is high. The experimental sites are: deep drained and strongly fertilized plantations with moderate vegetation biomass, less fertilized agricultural areas with low biomass and pristine ombrotrophic tropical peatland forest. In TROPDEC-project we do both in situ and in vitro experiments to elucidate the forming of GHGs to figure out functions of both microbial communities and individual microbes. Through this experimental set up we can learn how established change in land use effect GHG emissions and the underlying microbial communities. We aim at elucidating the plasticity and resilience of bacteria, archaea and fungi at different depths of the peat profiles during different seasons with typical management and water table conditions. Through preliminary field measurements and analysis results, in vitro experiments are planned for the soil samples. In these, the CO2 formed in heterotrophic processes is elucidated, methanogenesis and CH4 oxidation as well as N2O dynamics are determined in oxic and anoxic environments in peat. The hypothesis is that the increase in labile carbon and nitrogen availability will increase the decomposition where the availability and degradation of litter has been small, and this can be seen in rising abundance of certain archaea and bacteria and in increasing emissions of GHGs.

P264 Torreya grandis root disease is strongly linked to change in microbial catabolic activity rather than community diversity in root-zone soils

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Aims Root-rot disease is one of the main catastrophic diseases of Torreya grandis cv. Merrillii, which causes yield reduction and economic losses. The aim was to investigate the how soil properties and composition and activity of microbial community in the root-zone are influencing Torreya grandis root-rot disease. Plant physiological characteristics were compared between the healthy and diseased Torreya grandis trees. The root zone soils were sampled in the field, and abundance, composition and diversity of both bacterial and fungal communities were determined by qPCR and pyrosequencing. Soil extracellular enzymes involved in C, N, P and S cycling and microbial carbon-source utilization profiling were concomitantly assessed. The diseased trees showed lower mean height, fine root biomass, total chlorophyll and N contents in leaf, and higher peroxidase activity compared with the healthy ones, indicating a physiological stress from the root-rot disease. The soil physicochemical properties and microbial community structure were also altered. The soils of diseased plants were characterized by significantly lower bacterial and fungal gene abundance, but higher enzyme activities involved in C, P and S cycling and enhanced carbohydrate and phenolic compound utilization rates. The taxa Gibberella, Cryptococcus, Mortierella and Lectera were more prevalent in the diseased soil. RDA indicated that the plant physiological characteristics rather than soil properties were closely correlated with changes in microbial community composition and enzyme activities. This work suggests that soil enzyme activity and microbial metabolic potential rather than microbial diversity could serve as best indicators of disease conducive soil.

P265 Fate of polycyclic aromatic hydrocarbon in soil affected by laccase amendment and the resulting soil bacterial responses

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Laccases produced by white-rot fungi are capable of oxidizing polycyclic aromatic hydrocarbon (PAHs) rapidly. It was thought that the metabolites with an increase in water solubility caused by the oxidation may stimulate the subsequent mineralization. However, to data there has been no experimental evidence to support this. In this work, the mineralization of three typical PAHs, anthracene, benzo[*a*]anthracene and benzo[*a*]pyrene, after oxidation by fungal laccase was first investigated. The results showed that laccase amendment promoted the mineralization of benzo[*a*]anthracene (increased from 3.4% to 7.4%) and benzo[*a*]pyrene (increased from 0.8% to 1.4%), but inhibited that of anthracene (reduced from 12.9% to 9.1%), indicating the different effects on low-molecular-weight (LMW) PAHs and high-molecular-weight (HMW) ones. Then, the fate of benzo[*a*]pyrene affected by laccase amendment was investigated due to its high carcinogenicity, revealing large amounts of benzo[*a*]pyrene was dissipated as formation of bound residues (> 70%). Compared with the parent compound benzo[*a*]pyrene, over 15% of the increase in bound-residue fraction was formed after benzo[*a*]pyrene was transformed by laccase, mainly owing to enhanced chemical binding to humin fraction of soil organic matter (> 10% of increase). Finally, a pyrosequencing analysis showed that the metabolites of benzo[*a*]pyrene oxidized by laccase resulted in a less shift in bacterial community composition, revealing an effect of alleviated disturbance to soil microbial ecology. These results suggested that HMW PAHs can be detoxified by laccase amendment mainly due to enhanced chemical binding to soil organic matter.

P266 AsChip: a high-throughput qPCR chip for comprehensively profiling of microbial arsenic biogeochemical cycling genes in the environments

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Arsenic (As) is a ubiquitous toxic element adversely affecting human health worldwide. Microbe-medicated As biotransformation is associated with detoxification and metabolic pathways, and vital for biogeochemical cycling of environmental As. Quantitative polymerase chain reaction (qPCR) is currently considered as the gold standard for precise monitoring of As genes, but routinely limited by the relatively low number of primer sets handled by conventional microliter scaled qPCR approaches. Hence, we first developed a high-throughput qPCR (HT-qPCR) based AsChip for comprehensive monitoring of As genes in environmental samples. The novel nanoliter qPCR based AsChip contained 81 primer sets targeting 19 As genes and a 16S rRNA gene as a reference gene. Sequencing result showed high identity (> 96%) of newly designed primer corresponding to their targets. Serial dilution test showed the good-fitting linear regression of standard curves resulting from C_T values and target copies (Pearson's r = -0.99), with the high-efficiency average at 1.0 ($R^2 = 0.98$). A high correlation was observed between C_T values of AsChip assay obtained from AsChip HT-qPCR and conventional qPCR (Pearson's r = 0.962, $P < 0.001$). These validations revealed the high specificity, sensitivity, and efficiency of AsChip. To show its capacity, we successfully applied AsChip on soil samples from a copper-chromium-arsenic contaminated site located in Fredensborg, Denmark. Taken together, these results suggested that the AsChip is robust for rapid quantitative profiling of genes involving in As biogeochemical cycles and has the potential for tracking As biotransformation in environments.

P267 Changes in microbiome in chronosequence of soil formation in tundra zone

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Chronosequence approach was used for the investigation of microbiome changes during soil-forming process. Sand fixation chronosequences on the shores of Pechora River were studied. Sampling sites were near Nelmin Nos (67°58'34.3"N, 52°55'19.9"E) and Naryan-Mar (67°36'23.2"N, 53°08'12.2"E). Three types of surface were sampled: 1 - unfixed sand, 2 - semi-fixed surface with mosses and lichens, 3 - mature soil with typical tundra vegetation. The comparison of microbial communities from different samples was performed using isolated DNA. Bacterial, archaeal and fungal ribosomal genes were quantified by real-time PCR. Same analysis was performed for functional genes associated with processes of nitrogen cycle. For studying of structures of microbial communities, 16s rRNA libraries were obtained using Illumina sequencing and analysed in QIIME environment. An two-order increase in the number of bacterial, archaeal and fungal ribosomal genes among the chronosequences from unfixed sands to mature soils was observed. A similar pattern was discovered for functional genes. The diversity of microbial community increased in one chronosequence, while in another the changes between all diversity indices were inconsistent. PCoA quantitative analysis showed similarity in microbial community compositions of two mature soils and semi-fixed surfaces, while microbiomes of two sand samples formed separate clusters. Phyla *Proteobacteria* and *Acidobacteria* were predominating in all studied samples (up to 35 % of relative abundance). The abundances of phyla *Thaumarchaeota*, *Chloroflexi*, *Cyanobacteria* and *Gemmatimonadetes* were higher in the unfixed sands, while *Planctomycetes* and *Proteobacteria* were more abundant in the mature soil.

P268 Wildfire impact on permafrost bacterial communities and functional genes in Canada boreal forests

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Wildfire release pre-frozen liable carbon from permafrost has accelerated because of climate change. It contributes to greenhouse gases (GHG) emission and indirectly increased microbial activity by heating up the active layer. In this study, we ask whether fire impact on bacterial communities and potential metabolisms (indicated by functional genes) in permafrost soils collected across a fire chronosequence from 3 to >100 years. We determined geochemistry, bacterial community structure via 16S RNA gene sequencing and functional gene structure using GeoChip 5.0. We found that wildfire slightly impacted on bacterial community composition and potential metabolism. Dominance bacterial community members in near-surface permafrost were shifted markedly, including a higher abundance of phototrophic and nitrogen (N) fixation bacteria after a fire. We observed these changes consistent with ground vegetation biomass, soil temperature, and soil pH. The functional gene data reveal that fire affected genes, not only in the near-surface but the deep layers, involved in carbon (C), N and phosphorus (P) cycle. Because of the huge amount of C stock in the permafrost, these results are crucial for estimating whether wildfire results in an increase or decrease of GHG emission in the long term.

P269 Effects of softwood biochars on soil biota in medium-term field experiments in Finland

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Biochar soil amendment could be used to sequester carbon, enhance soil fertility and potentially increase crop yields. It can have significant impacts on soil organic carbon levels and physicochemical conditions, which consequently affect soil micro- and macro-biota. It is therefore important to understand how key biological components in the soil such as microbial and earthworm communities response to biochar application in the long-term. This study was conducted in Southern Finland in a fertile Stagnosol and a nutrient deficient Umbrisol, four and five years after biochar amendment, respectively. Biochars were produced from spruce (*Picea abies* (L.) H.Karst.) and pine (*Pinus sylvestris* L.), and applied at the rates of 10 and 30 t ha^{-1}, respectively. Earthworms and soil samples for microbial analyses were collected in September 2015. Soil microbial communities were studied by using phospholipid fatty acid profiling and 16S rRNA gene amplicon sequencing. Casts from the sampled earthworms were collected to investigate the consumption of biochar and the potential of earthworm bioturbation to affect biochar distribution. Additionally, greenhouse gas emissions from soil were measured. Biochar and fertilizer treatments or their interaction had no statistically significant effects on the earthworm abundance, community composition or greenhouse gas emissions in either field. Earthworms had ingested biochar as earthworm casts from biochar treated-plots contained significantly more black carbon than those in the control plots, demonstrating that earthworm bioturbation is a potentially important factor in the translocation of applied biochar in the soil profile. Microbial community structure data will be presented in the final presentation.

P270 Microbes respond to unfavorable environmental conditions by extra- and intracellular metabolic adaptations

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Soil biogeochemists' view on microbial C transformations has rarely exceed a simplified concept assuming that C gets either oxidized to CO_2 via catabolism or incorporated into biomass via anabolism. Consequently, response of microorganisms to changing environmental conditions was frequently solely quantified as changes in net CO_2 efflux without consideration of entire metabolism and its controlling factor. However, the technique of metabolic tracing, i.e. metabolic flux modelling following application of position-specific labelled key metabolites, covers this gap

We identified that temperature reduction from +5 °C to – 5 °C induced a sequence of metabolic adaptations from classical pentose phosphate pathway (PPP) towards glycolysis to feed the demand for intracellular cryoprotection compounds. With further decrease of temperature to -20 °C, PPP got more pronounced due to C demand for extracellular adapations. Similarly, strongly enhanced C export from microbial cells was observed by exposing microorganisms to respiration-inhibiting toxicants such as sodium azide (NaN3). Initial respiration reduction by factor 2 was rapidly overcome by extracellular electron disposal. Moreover, microbial biomass recovered rapidly from its 3-fold decrease following inhibition without any de-novo synthesis of microbial fatty acids from the added ^{13}C glucsoe, demonstrating the overwhelming role of microbial necromass recycling in population recovery.

Consequently, metabolic tracing provides a huge potential for unraveling microbial adaptations to the challenges of the soil environment. Shifts from intra- to extracellular adaptation strategies with increasing stress level were unraveled as well as the frequently underestimated role of necromass recycling for rapid microbial recovery in soils.

P271 Settlements of sea animals increase nitrous oxide emissions in Antarctic soils

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Soil ammonium comes not only from the fixation of atmospheric nitrogen but also from the mineralization of organic compounds, part of which are represented by animals' depositions. As a consequence of microbial activities of the nitrogen cycle, emissions of nitrous oxide (N_2O) are produced. The aim of this work was to determine the abundance of key bacterial functional groups in the nitrogen cycle and their relationship with N_2O emissions in soils influenced by animal settlements located in Cape Shirreff (Livingston Island, Antarctica), including marine birds (*Larus dominicanus, Pygoscelis antarctica* and *P. papua*) and mammals (*Arctocephalus gazella* and *Mirounga leonina*). In the soil samples, edaphic parameters (pH, water content, organic matter, ammonium, nitrate and phosphorus), the abundance of key nitrogen cycle genes (*nifH, amoA, narG and nosZ*) and the production of N_2O (in aerobic and anaerobic conditions) were measured. Soils o animals' settlements were slightly acid and, specifically penguins' soils, had the highest values of organic matter. Ammonium, nitrate and phosphorus contents were higher in the soil of animals' settlements, but only significant differences between the penguins' soils and the controls' soils were observed. The soils with animal influence had less copies of *nifH* and more copies of *amoA* and *narG* than the control soils. These results suggest that both nitrification and denitrification would potentially be involved in the emission of N_2O from soils of animals' settlements. However, the abundance of *nosZ* was not only greater in the soils of the animal settlements, but it was the only one that presented significant differences with respect to the control soils, specifically in the soils of penguins, which could mitigate N_2O emissions from these soils. N_2O emissions were higher from soils with animal influence than from the controls' soils, being they higher in anaerobic than in aerobic conditions, therefore denitrification would be the process responsible for the emissions of this gas in Antarctic soils influenced by animals. This could be explained because in acid soils the synthesis and assembly of the enzyme N_2O reductase are inhibited. Finally, significant positive correlations were found between the abundance of *amoA* and the ammonium content, between the abundance of narG and the ammonium and phosphorus contents, and between the abundance of *nosZ* and the ammonium, nitrate and phosphorus contents. In addition, positive correlations were found between the amount of ammonium and nitrate and the emissions of N_2O in both aerobic and anaerobic contexts.In conclusion, Antarctic marine animals, through changes in edaphic parameters, favor the emission of N_2O. Although the emission due to the nitrification process cannot be ruled out, this greenhouse gas would come mainly from anaerobic processes, such as denitrification. Financial source: Projects INACH RG_14-14 and DT_10-15

P272 Efficiency of phosphate solubilizing microorganisms and Vesicular - Arbuscular Mycorrhiza for increasing baby corn yield on acid sulfate soils

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The study of using microorganisms enhancing phosphorus benefits in the soil to grow baby corn was carried out in the areas in southern Thailand, having acid sulfate soils. The objective of this research was to study the method of using Phosphate Solublizing Microorganisms (PSM) together with Vesicular-Arbuscular Mycorrhiza (VAM) for the purpose of enhancing phosphorus benefits in the areas with acid sulfate soils. It was found that: the pH, %OM and P increased, K extracted decreased and the amount of aluminum decreased. The control plots yielded the lowest productivity (6,563.93 kg ha-1 while the application of rock phosphate as a fertilizer at the rate of 150 kilograms of P2O5 per rai + PSM + VAM yielded the highest productivity, accounting for 7,923.63.78 kg ha-1. For the number of spores of VAM it was found that the number of spores was found to be at the most (760 spores per 100 grams of soil) of using rock phosphate at the ratio of 150 kg of P2O5 ha-1 +VAM+PSM. The number of PSM was found to be at the most (7.6x105 cells per 100 grams of soil) for the treatment of using rock phosphate at the rate of 150 kg of P2O5 ha-1 together with VAM and PSM; and for the control experimental treatment, the number of PSM was found to be at the least (6.4x103 cells per 100 grams of soil). When the productivity from two years was take into consideration in terms of the analysis of the mean of economical returns it was found that the application of rock phosphate as a fertilizer at the rate of 150 kg of P2O5 ha-1 together with PSM and the application of VAM resulted in the highest net income of Baht 58.9 kg ha-1.

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