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Simulation and prediction of biomass turnover and soil organic matter formation

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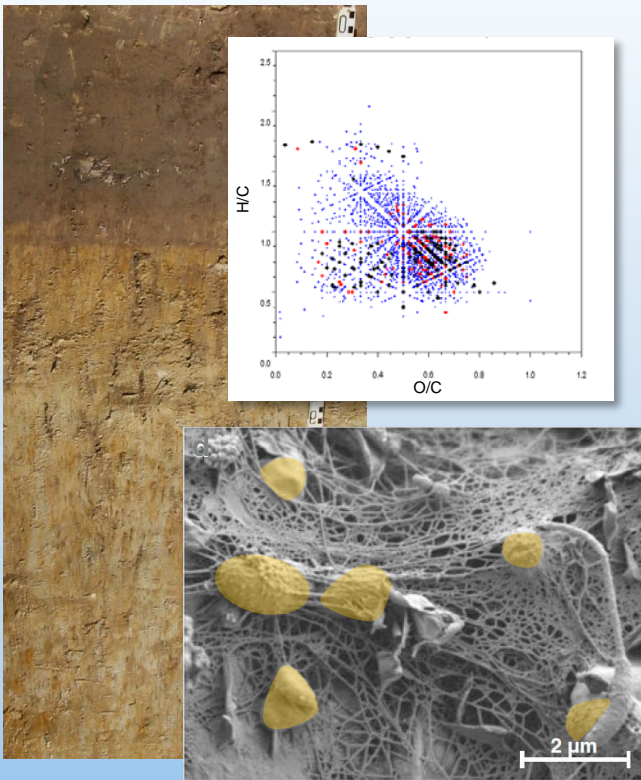
Microbial Contribution and Impact on Soil Organic Matter, Structure and Genesis

Helmholtz Centre for Environmental Research – UFZ, Leipzig

Trier University

at Leipziger KUBUS and IOM

9–11 November 2016

Program and Abstracts

HELMHOLTZ
CENTRE FOR
ENVIRONMENTAL
RESEARCH – UFZ

Universität Trier

DBG
Deutsche Bodenkundliche Gesellschaft

DFG
Deutsche Forschungsgemeinschaft

Workshop Program and Abstracts

International Workshop on

Microbial Contribution and Impact on Soil Organic Matter, Structure and Genesis

SOM_mic_

9–11 November 2016

Leipziger KUBUS and IOM

Leipzig, Germany

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Editorial

Within the last decades considerable progress by previous joint research programs (SPP1091) was made in understanding soil organic matter (SOM) as a continuum of plant, animal, and microbial residues and also the links of biogenic SOM to the mineral matrix (SPP 1315). In particular the shift of focus from `humic´ matter towards the microbial contribution led to growing understanding of the related processes of SOM formation and genesis.

There is increasing evidence showing that microorganisms do not only determine the biochemical processes of degradation and modification of organic compounds in soil but also microbial biomass or necromass itself is the most underestimated part of SOM. Microbes and microbial communities are thus drivers and substantial contributors of SOM dynamics in soil. This new understanding offers various options to assign properties and effects in soils to processes of living organisms, which was previously not possible. The microbial impairment interacts also with the mineral components of the soil system that are similarly prone to be modified by microbes but also triggering abiotic processes.

Life science explored new options for investigations in terms of science of the system by making use of the so-called meta-omics methods (Metagenomics, Metaproteomics, Metametabolomics). Hence it seems to be timely and highly productive to apply these methods also to the integral system soil. Of course, the complexity of soils may serve problems in applying these methods but once solved they will provide important steps forward in understanding of the soil system. In marine science elevated concepts for a new understanding of the microbial and biogeochemical compound turnover were already developed (`microbial pump´ concept, `marine snow´) and their validity is worth to be proven for the soil system. These concepts are gaining additional aid from the new options of low invasive high-resolution methods of visualization and to analyze microscale spatial heterogeneity with high density data (e.g. simultaneous determination of thousands of organic compounds). The related analytical processes such as confocal laser microscopy, optical coherence tomography, high resolution soil tomography, NanoSIMS, FT-ICR-MS, isotope tracer technologies and many others are providing a new quality of characterization of compound turnover in soil together with the identification of the turnover driving microorganisms and their metabolism, which was not available during the previous joint research programs on soil organic matter. The relation of microbial activity to the present biodiversity is thus an upcoming field of research that was barely noticed previously. Also latest modelling approaches, e.g. in systems ecology and environmental thermodynamics, will open up new vistas to study the outlined topic.

Such integrated systems-related approaches will enable developing new basic understanding of biotic processes dominating soil properties, functions, and energetics as well as the biodiversity and functional redundancy in soil and their importance of for SOM formation and the material contribution of soil biota. Currently, the knowledge on these processes is still fragmentary giving only mosaic-like pictures, since often only single causal relationships have been studied in disciplinary research. Based on these results the details of the processes are understood but the understanding of the interactions is far away to enable integrated prospective modelling of e.g. carbon and nitrogen turnover and the resulting alterations by global changes e.g. of CO_2 concentrations, temperature and water regimes.

Keynote Speakers

Dr. **Teri Balser**, Curtin University, Perth, Professor

In her work, Dr. Balser focuses on the role of soil and soil community response to anthropogenic disturbances in either exacerbating or mitigating current global-scale ecological changes. She works collaboratively around the world in urban, forested, grassland and boreal ecosystems. Projects in the Balser lab have included quantifying the impact of invasive plant species and elevated CO_2 on natural methane fluxes from soil, patterns of microbial community development in restored prairie soils and rain gardens, as well as understanding patterns and consequences of community shifts following long-term chronic multiple global change manipulations.

Source: https://balserlab

Dr. **David J. Burdige**, Old Dominion Univ., Norfolk, Professor

The expertise of Dr. Burdige is in the fields of biogeochemistry, organic geochemistry and mathematical modeling of geochemical processes paying specific attention to the marine environment with his competences in aquatic chemistry, geochemistry of marine sediments, chemical oceanography. Recent research activities are focused on topics such as organic carbon oxidation and iron remobilization in shelf sediments; dissolved organic carbon (DOC) transformations in deep sub-surface sediments and its role as a source of "old" DOC to the water column; the investigation of groundwater-carbon coupling in large peat basins and its relation to climate change.

Source: https://www.odu.edu

Dr. **Claire Chenu**, Centre AgroParisTech, Paris/Grignon, Professor

Dr. Chenu's research interests include interactions between soil organic matter, microorganisms and soil mineral matrix. Understanding these interactions is crucial for managing soil structure and enhancing carbon sequestration in soil using appropriate cropping systems. Current research topics are the dynamics of soil organic matter, its processes of stabilization and role within the soil. She works on interactions of organic matter and the soil structure and the spatial distribution of microorganisms within the soil.

Source: http://siafee.agroparistech.fr

Dr. **Mary Firestone**, Univ. of California, Berkeley, Professor

Dr. Firestone is a soil microbial ecologist. She works on the microbial processing of carbon and nitrogen with emphasis on root-microbial interactions in soil. Over the past decade her lab has been exploring microbial mediation of root C transformation and stabilization. Her research group is mapping the flow and fate of C from root exudates and decomposing materials into and through bacterial, fungal, faunal, and phage communities. The importance of bacterial, fungal, and AMF interactions with soil minerals is being assessed as these interactions result in mineral-associated C.

Source: https://ourenvironment.berkeley.edu

Dr. **Markus Kleber**, Oregon State University, Associate Professor

In his research work, Dr. Kleber deals with the processes at the interface between organic matter and mineral surfaces, including mineral surface properties, organic matter properties, bonding mechanisms, adsorption processes, mineral-microbial interactions, and organic matter turnover dynamics. His recent projects are focused on biochar for stormwater treatment and as a cover for dairy manure lagoons; the role of protein-mineral interactions for protein oxidation and hydrolysis and the spatial variation in microbial processes controlling carbon mineralization within soils and sediments.

Source: http://cropandsoil.oregonstate.edu

Dr. **Joshua P. Schimel**, Univ. of Santa Barbara, Professor

Dr. Schimel's research is situated at the interface of ecosystem and microbial ecology. He is interested in the role of soil microbes in controlling ecosystem scale processes. His particular interests are in the linkages between plant and soil processes, and how changes in microbial community structure affect ecosystem-scale dynamics. Latest research is focused on understanding the dynamics of soil organic matter, the controls on microbial activity in freezing and frozen soils, and plant soil interactions and how changing plant communities interact with changing soil processes, particular nitrogen cycling.

Source: https://www.eemb.ucsb.edu

Workshop Dinner

The World's Oldest Head Rail Station One of Leipzig's landmarks is the Bayerischer Bahnhof. It was built in 1842 and is the oldest preserved head rail station in the world. Today, the Bayerischer Bahnhof is a tavern, brewery, beer garden, and restaurant.

The workshop dinner is on Thursday, 10 November from 7 pm.

You will be served a buffet with salads, Italian antipasti, cheese, bread, diced turkey breast with champignon cream sauce and 'Rösti', grilled Saltimbocca with whitewine-sauce, salmon fillet with braised vegetables and two varieties of rice, cannelloni with ricotta spinach filling, Tiramisu, Panna Cotta, and 'Kaiserschmarrn'. A selection of beverages is included.

The Bayerischer Bahnhof can be reached from UFZ by Tram No. 3 and 9 within 25 minutes.

Tickets for the dinner have to be purchased beforehand.

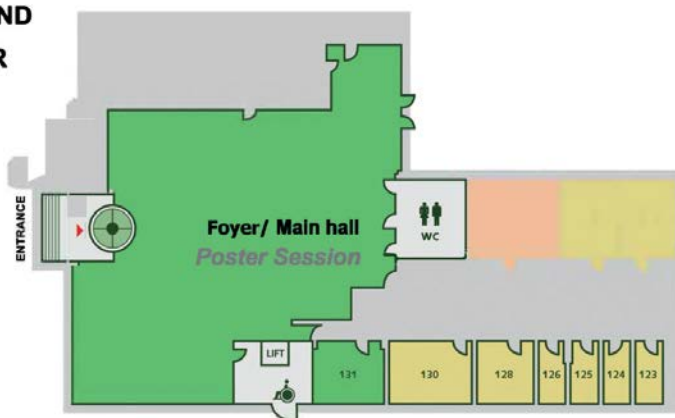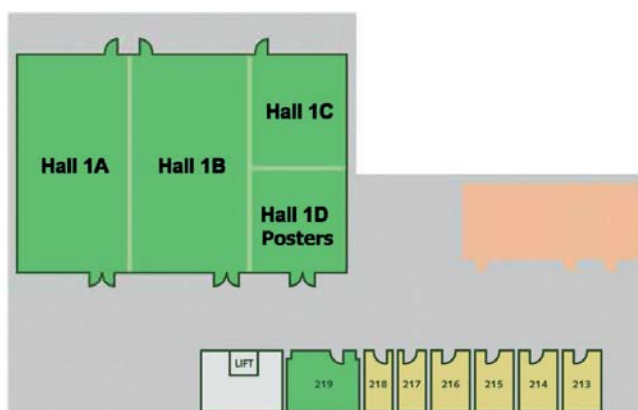# Plan of the venue

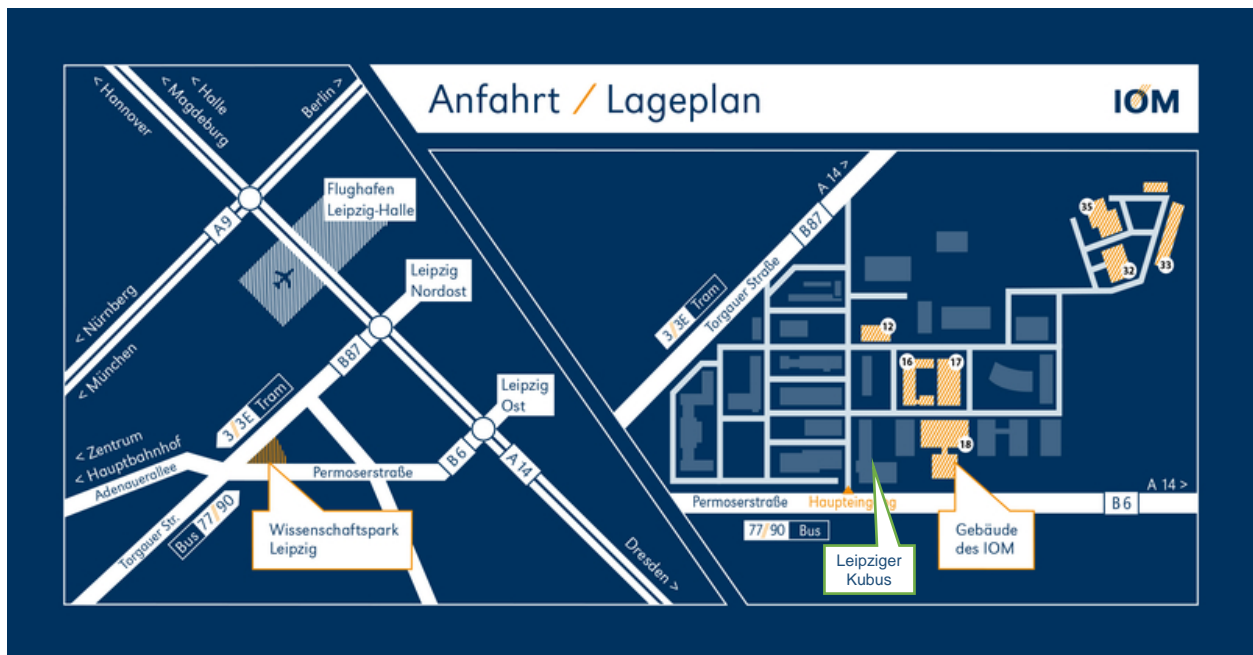## Leipziger KUBUS (UFZ).

How to reach the Kubus at UFZ.

Oral presentations on   **Wednesday, November 9, 2016 in Kubus Hall 1A-1B,**

Thursday, November 10, 2016 in Kubus Hall 1C-1D.

Friday, November 11, 2016 in the hall of the IOM

(see below).

Lecture hall at IOM

You find the lecture hall of the IOM on the Campus of the UFZ.

Workshop Program at a Glance

	Time		Wednesday 9 November 2016	
UFZ Kubus	10:00	12:00	Registration and Poster hang up	
Room AB	12:00	12:20	Kästner, Thiele-Bruhn: **Opening & welcome**	
Session 1:		Who are the relevant actors and drivers and in which micro-habitats or „hot spots" do they appear?		
Chair Kästner, Glaser	12:20	13:00	1st Keynote Teri Balser, Curtin Univ., Perth	Microbial community composition and functions in soil micro-habitats
A1	13:00	13:15	Cornelia Rumpel, CNRS-INRA-AgroParisTech	Microbial communities involved in root litter decomposition and stabilisation in top- and subsoil horizons: Evidence from a longterm field study
A2	13:15	13:30	Axel Don, Thünen Institute	Does microbial community composition affect the turnover of soil organic carbon in mineral soils?
A3	13:30	13:45	Ashish Malik, Centre for Ecology & Hydrology	Novel understanding of microbial soil carbon cycling mechanisms through metagenomics based assessment of central carbon metabolism genes
A4	13:45	14:00	Joerg Schnecker, Univ. of New Hampshire	Microbial foraging strategy is dependent on substrate concentration
Chair Poll, Spielvogel	14:00	15:00	Coffee break + **Poster session S1 Actors**	
Chair Harms, Tebbe				
A5	15:00	16:00	Johannes Rousk, Univ. Lund	Microbial control of biogeochemistry during drying-rewetting: The legacy of drought
A6	16:00	16:15	Margarida Soares, Univ. Lund	Bridging the priming effect into aquatic systems: does labile carbon stimulate the fungal decomposition of submerged plant litter?
A7	16:15	16:30	Stefanie Schulz, Helmholtz Center Munich	The effect of soil mineral composition on microbial community establishment and functioning - artificial soil mixtures as a simplified study system
A8	16:30	16:45	Gerd Gleixner, MPI for Biogeochemistry	Using isotopes to understand microbial action in soils
Chair Miltner, Woche	17:00	17:35	**Poster session S2**	
Chair Helgason, Reichel	17:35	19:00	**Poster session S3**	
	18:00	20:00	**Poster social**	all posters

Kubus, Room CD	Time		Thursday 10 November 2016 - Morning	
Session 2:		Significant boundary conditions, micro-habitats and micro-habitat properties, processes of succession, and systems fluctuations - what can we learn from the marine microbial pump concept?		
Chair Rumpel, Thiele-Bruhn	08:15	08:55	2nd Keynote Josh P. Schimel, Univ. of Santa Barbara	Ecosystem conditions and stress shape microbial community structure and activity
H1	08:55	09:10	Angela Straathof, Univ. of Manchester	Plant and soil successional stage modifies the impact of drought on rhizosphere C cycling
H2	09:10	09:25	Michaela A. Dippold, Georg-August Univ. Göttingen	Microbial metabolite recycling: an underestimated process contributing to SOM stabilization at mineral surfaces
Chair Richter, Poeplau	09:25	09:55	Coffee break **Poster Session S4 Systems Ecology**	
Chair Kuzyakov, Sleutel	09:55	10:35	3rd Keynote David J. Burdige, Old Dominion Univ.	Dissolved organic matter (DOM) cycling in anoxic marine sediments: General observations and the formation of refractory DOM
H3	10:35	10:50	Geertje Pronk, Univ. of Waterloo	Soil organic matter development during water table fluctuations in an artificial soil column incubation
H4	10:50	11:05	Carsten W. Mueller, Technical Univ. Munich	From plants to microaggregates – organic matter transfer at soil biogeochemical interfaces
H5	11:05	11:20	Peter Maenhout, Ghent Univ.	Is soil pore structure control on substrate decomposition manifested through N availability?
H6	11:20	11:35	Christoph Tebbe, Thünen Institute for Biodiversity	Particle size fractions provide distinct microhabitats for soil microbial communities
H7	11:35	11:50	Kathleen Lemanski, Univ. of Cologne	Soil nutrients and microbial activity in a post-mining chronosequence
	11:50	13:20	Lunch break	

Kubus, Room CD	Time		Thursday 10 November 2016 - Afternoon	
Session 3:			Molecular processes and components interacting with SOM and soil minerals - turnover steady state or residual `inert´ material?	
Chair Diehl, Guggenberger	13:20	14:00	4th Keynote Markus Kleber, Oregon State Univ.	Beyond "recalcitrance" – carbon flow through the mineral soils of a prokaryotic world
I1	14:00	14:15	Karin Eusterhues, Friedrich-Schiller-Univ. Jena	Interactions of extracellular polymeric substances (EPS) with Fe oxides
I2	14:15	14:30	Nikolas Hagemann, Univ. of Tübingen	Potential role of microbial electron shuttling in soil, biochar and biochar co-composting
I3	14:30	14:45	Stephanie Turner, Fed. Inst. Geosci. Nat. Resour. (BGR)	Microbial utilization of mineral-associated nitrogen in soils
I4	14:45	15:00	Nele Meyer, Univ. of Bonn	Microbial N and P mining from recalcitrant pools
I5	15:00	15:15	Evgenia V. Blagodatskaya, Georg August Univ. Göttingen	Microbial residues accelerate decomposition of soil organic matter: new mechanism, actors and thresholds
I6	15:15	15:30	Lukas Wick, UFZ - Helmholtz Centre for Environ. Res.	The mycosphere as logistic hotspot: Contributions of fungal bacterial interplays for soil ecosystem functioning
Chair Ebrahimi, Pagel	15:30	16:05	Coffee break **Poster Session S5 Modelling**	
Session 4:			What is the contribution of methods and modelling approaches from systems biology/ecology to understanding SOM in the soil system?	
Chair Rousk, Ruess	16:05	16:45	5th Keynote Mary Firestone, Univ. California	Mapping microbial transduction of root carbon using isotope-enabled molecular approaches
S1	16:45	17:00	Vanessa Bailey, Pacific Northwest National Laboratory	The soil C cycle as microbial metabolism: Integration of soil metagenomic and chemical data
S2	17:00	17:15	Jessica Ernakovich, CSIRO Agriculture and Food	The role of microbial biodiversity in soil C stabilization
S3	17:15	17:30	Christopher Poeplau, Thünen Institute	Effects of macro-nutrients on microbial metabolism driving soil organic carbon cycling
S4	17:30	17:45	Andreas Richter, Univ. of Vienna	Long-term versus short-term warming effects on microbial processes and soil organic matter storage
S5	17:45	18:00	Andreas Breidenbach, Georg-August-Univ. Göttingen	Composition and functions of microbial communities in top- and subsoils of degraded pasture ecosystems on the Tibetan Plateau
			Poster take down	
	19:00		**Dinner at Bayerischer Bahnhof**	

Room IOM	Time		Friday 11 November 2016	
Session 5:			Modelling approaches for the integration of process components	
Chair Franko, Garnier	08:15	09:00	6th Keynote Claire Chenu, INRA-AgroParisTech	Accounting for microbial habitats in modeling soil organic matter dynamics
M1	09:00	09:15	Stefan Trapp, Technical Univ. of Denmark	Simulation and prediction of biomass turnover and soil organic matter formation
M2	09:15	09:30	Patricia Garnier, INRA, AgroParisTech	Uncertainty of a soil organic matter model at the microscale: Influence of the micro-habitat structure
M3	09:30	09:45	Holger Pagel, Univ. of Hohenheim	Microbial control of SOM dynamics in the detritusphere: Insights from modeling coupled pesticide degradation and organic matter turnover
	09:45	10:15	Coffee break	
Chair Pot, Trapp				
M4	10:15	10:30	Sebastian Doetterl, Augsburg Univ.	Soil weathering as a control on the linkages between measured soil carbon fractions and modeled soil carbon pools
M5	10:30	10:45	Ali Ebrahimi, ETH Zürich	Mechanistic modeling linking thermal and hydration dynamics with microbial methane production and emissions from permafrost soil
M6	10:45	11:00	Helmer Schack-Kirchner, Albert-Ludwigs-Univ.	A first step to model SOM dynamics by stochastic self assembly
M7	11:00	11:15	Suphathida Aumtong, Maejo Univ.	Artificial neural network development for forecasting soil carbon sequestration of paddy soils in Thailand
M8	11:15	11:30	Sergey Blagodatsky, Univ. of Hohenheim	Environmental drivers and microbial activity: alternatives in modeling of soil organic matter decomposition
Chair Kästner, Thiele-Bruhn	11:30	13:00	**Final discussion & concluding remarks**	
			Optional Lunch	

	Time	Wednesday 9 November 2016		
UFZ Kubus	10:00	12:00	Registration and Poster hang up	
Session 1:	**Who are the relevant actors and drivers and in which micro-habitats or „hot spots" do they appear?**			
	14:00	15:00	Poster session S1 Actors	Chair Poll, Spielvogel
AP1	Bruno Glaser, Martin Luther Univ. Halle-Wittenberg	Microbial production of condensed aromatic structures in soil		
AP2	Su Ding, MPI for Biogeochemistry	Identification of novel 7-methyl branched glycerol dialkyl glycerol tetraethers in Chinese lakes		
AP3	Thomas Kuyper, Wageningen Univ. & Research	Epigeic earthworms change quantity and composition of dissolved organic carbon during composting of garden waste		
AP4	Gan Huei Ying, MPI for Biogeochemistry	Is there a link between land use and priming effect?		
AP5	Amit Kumar, Georg-August Univ. of Göttingen	Maize rhizosphere effects on soil aggregate stability and associated enzymes activities in field.		
AP6	Marie Uksa, Univ. of Hohenheim	Spatial variability of microbial key players and their activity patterns in subsoil and hot spots		
AP7	Ali Ebrahimi, ETH Zürich	Linking hydration status, carbon source and aggregate size distribution on soil GHG emissions: Laboratory column experiments using artificial soil aggregates		
AP8	Rüdiger Reichel, Research Center Jülich	Development of greenhouse gas emissions, organic C and total N related to fertilization regime and time since soil recultivation		
Session 2:	**Significant boundary conditions, micro-habitats and micro-habitat properties, processes of succession, and systems fluctuations - what can we learn from the marine microbial pump concept?**			
	17:00	17:45	Poster session S2	Chair Miltner, Woche
HP1	Christian Poll, Univ. of Hohenheim	Turnover of microbial carbon in microbial hot spots		
HP2	Somak Chowdhury, MPI for Biogeochemistry	Arbuscular mycorrhizal fungi colonization of the root and litter quality influence carbon use profile of soil microbial community		
HP3	Marc-Oliver Goebel, Leibniz Univ. Hannover	Role of bacterial biomass in water repellency development		
HP4	Ruth Ellerbrock, Leibniz-Centre for Agric. Landsc. Res. (ZALF)	Spatial distribution of soil organic matter composition at intact preferential flow path surfaces compared with surface properties		
HP5	Maki Miura, Univ. Bangor	Effect of freeze-thaw and dry-wet events on microbial activity in soils from the UK and Antarctica		
HP6	Marton Szoboszlay, Thünen Institute	Impact of land use change on microbial diversity in European soils		
HP7	Cahyo Prayogo, Univ. of Brawijaya-Indonesia	Impact of biochar on mineralisation of C and N from soil and willow litter and its relationship with microbial community biomass and structure		
HP8	Diana Hofmann, Research Center Jülich	Historical charcoal additions potentially improve stability of soil organic carbon due to altered particulate carbon fractions		
HP9	Jaroslav Kukla, Charles Univ. in Prague	The influence of traditional agriculture on soil organic matter in tropical ecosystems of Papua New Guinea		
HP10	Giulia Bongiorno, Univ. Wageningen	Biological soil quality indicators for agricultural management		
Session 3:	**Molecular processes and components interacting with SOM and soil minerals - turnover steady state or residual `inert´ material?**			
	17:45	19:00	Poster session S3	Chair Helgason, Reichel
IP1	Menuka Maharjan, Georg-August Univ. of Göttingen	Nutrient availability affects soil organic matter decomposition depending on land use		
IP2	Andrea Jilling, Univ. of New Hampshire	Insights into soil minerals as mediators of nitrogen transformation in the rhizosphere.		
IP3	C. Merino, Univ. Frontera, Temuco	Mineralogy can influence root preferences on different pools of native soil organic carbon mineralization through "priming effects"		
IP4	Laura S. Schnee, Univ. of Bremen	Impact of organic amendment on soil aggregation and microbial colonisation		
IP5	Cordula Vogel, Technical Univ. Dresden	The role of extracellular polymeric substances in aggregate turnover		
IP6	Stefan Dultz, Leibniz Univ. Hannover	Aggregation behavior of defined organic matter-goethite associations: implication for soil organic matter stabilization		
IP7	Markus Maisch, Eberhard-Karls-Univ. Tübingen	Approach to follow redox gradients and iron plaque formation in-situ over the vegetative development of a rice plant		
IP8	Anja Miltner, UFZ - Helmholtz Centre for Environ. Res.	Stabilization of microbial residues by co-precipitation with Fe and Al oxides		
IP9	Antonia Zieger, Technical Univ. Berlin	Mineral-associated carbon in an Andosol receiving massive carbon input		
IP10	Gabriele E. Schaumann, Univ. Koblenz-Landau	(How) do microbial exudates control interfacial properties and supramolecular structures in soil organic matter?		
IP11	Thorsten Reemtsma, UFZ - Helmholtz Centre for Environ. Res.	Formation of mobile bound residues of organic contaminants and detection by ultrahigh resolution mass spectrometry		
IP12	Sytske Drost, Netherlands Institute of Ecology	Microbial biomass and nutrient dynamics during decomposition of cover crop mixtures		
IP13	Rima J. Porre, Univ. Wageningen	Do cover crop mixtures increase soil fertility and promote soil organic matter stabilisation simultaneously?		
IP14	Pauline Winkler, Martin Luther Univ. Halle-Wittenberg	Fate of organic carbon in paddy soils with contrasting mineralogy		
IP15	Steven Sleutel, Ghent Univ.	Hydrolytic enzyme activities in soil: substrate supply or product demand controlled? Insights from assessment of soil N mineralization in two paddy field experiments		
IP16	Stefan J. Forstner, Univ. of Nat. Res. and Life Sci. (BOKU)	Vertical patterns of eco-enzyme activities in two temperate forest soils after 20 years of nitrogen additions		
IP17	Marie Spohn, Univ. of Bayreuth	Soil microbial carbon use efficiency and biomass mean residence times depending on soil depth and stoichiometry		
IP18	Marcel Lorenz, Trier Univ.	Are plants or microbiota regulating SOM stoichiometry in forest soils?		
IP19	Mauro De Feudis, Univ. of Perugia	Influence of the altitude on the water-extractable organic matter (WEOM) from rhizosphere and bulk soil in European beech forests of central Italy		
IP20	Parag R. Bhople, Univ. Kassel	Variations in fungal community structure along soil depth profiles and elevation gradients in alpine ecosystems		
	18:00	20:00	Poster social	all posters

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UFZ Kubus	Time	Thursday 10 November 2016		
Session 4:	**What is the contribution of methods and modelling approaches from systems biology/ecology to understanding SOM in the soil system?**			
	09:25	09:55	**Poster Session S4 Systems Ecology**	Chair Richter, Poeplau
SP1	Letizia Abis, INRA, AgroParisTech	Review: Microbial Volatile Organic Compounds (mVOCs) emissions by soil		
SP2	Christina Kaiser, Univ. of Vienna	Microbial physiology and self-organisation of microbial turnover processes at the microscale influence steady-state C and N content of the soil		
SP3	Julian Heitkötter, Ruhr-Univ. Bochum	Interactions between substrate and nutrient limitations for C-turnover in subsoil		
SP4	Sonja Leitner, Univ. of Nat. Res. and Life Sci. (BOKU)	Moisture sensitivity of soil respiration in the context of extreme dry-wet events		
SP5	Viridiana Alcántara, Thünen Institute	Topsoil burial through deep ploughing has contrasting effects on SOC turnover in croplands and forests		
SP6	Aurélie Bacq-Labreuil, Univ. of Nottingham	Influence of different cropping systems on soil structure visualised using X-ray computed tomography		
SP7	Susanne K. Woche, Leibniz Univ. Hannover	Bacterial contribution to wetting properties and SOM formation on particle surfaces as observed by X-ray photoelectron spectroscopy (XPS)		
SP8	Jennifer Herschbach, Univ. Bern	Combining position-specific 13C labeling with 13C-PLFA analysis to assess microbial utilization of free versus sorbed Alanine		
Session 5:	**Modelling approaches for the integration of process components**			
	15:30	16:05	**Poster Session S5 Modelling**	Chair Ebrahimi, Pagel
MP1	Delphine Derrien, INRA, Biogeoch. of Forest Ecosyst.	Energy balance associated with the degradation of lignocellulosic material by white-rot and brown-rot fungi		
MP2	Phil Sollins, Oregon State Univ.	Soil organic matter accumulation in relation to changing soil volume, mass, and structure: Concepts and calculations		
MP3	Florian Wilken, Univ. Augsburg	Modelling a century of soil redistribution processes and carbon delivery from small watersheds using a multi-class sediment transport model		
MP4	Yakov Kuzyakov, Georg-August Univ. Göttingen	Rhizosphere boundary		
MP5	Uwe Franko, UFZ - Helmholtz Centre for Environ. Res.	Interpretation of incubation experiments		
MP6	Gianna Marschmann, Univ. Hohenheim	Modeling microbial dormancy in soils		
	18:00	**Poster take down**		

Abstracts of oral presentations

Session 1:   Who are the relevant actors and drivers and in which micro-habitats or „hot spots" do they appear?

Keynote

K1   Microbial community composition and functions in soil micro-habitats

Balser T.

Curtin University, Perth

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KEYWORDS Soil carbon dynamics, microbial direct/indirect role, microhabitat

It has become increasingly clear that microorganisms play numerous roles in soil carbon cycling, and organic matter structure and genesis. We have long been aware of their functional/indirect role (decomposition activity/biomass/respiration), and during the past decade we have arrived at greater recognition of a direct role (microbial carbon pump, stabilization of microbial residues). Other work has been focused on the importance of microbial diversity or community structure. And still more work has been focused on soil micro-habitats. But soil reality is a function of all of these factors together – biomass, necromass, diversity, and architecture. This talk will seek to integrate and explore the possible consequences of microhabitat and diversity for soil carbon dynamics.

A1   Microbial communities involved in root litter decomposition and stabilisation in top- and subsoil horizons : evidence from a longterm field study

Sanaullah M.[1,2], Chabbi A. [1,5], Maron P.A.[3], Baumann K.[1,7], Tardy V.[3], Blagodatskaya E.[4], Kuzyakov Y. [4,6], **Rumpel C.**[1]

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KEYWORDS Wheat root; Top- and subsoil; Extra-cellular enzyme activities; PLFA; DNA

Contrasting microbial community composition and activity at different soil depths may affect root litter decomposition. These effects have up to now been investigated mainly in laboratory studies, which may not be able to take into account complex in situ conditions. Our study aimed to analyze the composition and activity of microbial communities after addition of ^{13}C labeled wheat root litter to a loamy soil under grassland at 30, 60 and 90 cm depths, during a three-year field experiment. We investigated the dynamics of bacterial and fungal abundances and community structures by DNA genotyping and pyrosequencing of 16S and 18S rDNAs. The genetic structures of bacterial and fungal communities were evaluated by automated ribosomal intergenetic spacer analysis. The functions of these communities were analysed by determination of extracellular enzyme activities and viable microbial communities involved in ^{13}C labeled organic matter decomposition studied by ^{13}C PLFAs.

The abundance of fungal and bacterial communities (16S and 18S rDNAs and PLFA) and the potential activities of enzymes involved in the C- and N-cycles were significantly higher at the top 30 cm compared with deeper soil throughout the experiment. Both were stimulated by fresh litter input. A trend to decreasing bacterial and fungal richness was noted after root litter addition at 30 cm, while richness of bacteria at 90 cm and those of fungi at 60 and 90 cm increased. Moreover, root litter addition caused a reduction of the Shannon Weaver Diversity index and a shift in microbial community structure at all three depths, which was more pronounced for bacteria at 30 and 60 cm and for fungi at 90 cm. The changes during litter degradation resulted in similar dynamics of most enzyme activities at all depths. Chitinase activity was enhanced after 29 months compared to initial conditions indicating the availability of high amounts of microbial detritus. The degrading microbial community as assessed by ^{13}C PLFA showed similar temporal dynamics at all three depths. Fungal contribution to this community decrease during later stages of litter degradation, while the contribution of Gram+ bacteria increased. We conclude that litter addition leads to convergence of microbial communities of top- and subsoil through stimulation of copiotrophic populations. Soil microbial community structures are thus connected with the amount of fresh litter input. Enzyme activities and ^{13}C PLFA reflect to some extent the changes occurring during degradation, i.e. exhaustion of fresh plant material and accumulation of detritus.

A2   Does microbial community composition affect the turnover of soil organic carbon in mineral soils?

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KEYWORDS microbial communities, carbon mineralisation, home-field advantage, biodiversity, community coalescence

Soil organic carbon (SOC) turnover is the most ubiquitous and ecologically fundamental process in soils and it is performed by microorganisms to meet their energy and carbon requirements. Microbial community compositions are highly complex and respond to a vast range of biotic and abiotic environmental factors. Considering the coevolution of soils and their microbial communities, it is generally assumed that SOC is utilized by functionally redundant soil-specific microbial communities which do not differ in their capability to mineralise soil organic matter. To challenge this assumption, the microbial communities in six topsoils from three locations and three land-use types, each location representing two of them, were analysed. With soil mixing and inoculation experiments community specific effects on SOC turnover were assessed. Comparisons of respiration by a native soil community and an alien community revealed significantly higher respiration (+29±18%) by the native community ("home-field advantage"). However, for one particular soil microbial community this home field advantage was overridden by the community´s capability to respire carbon. The capability of a community to mineralise SOC was determined as respiration rate of a single soil microbial community divided by the respiration rate of a mixed soil microbial community containing all communities of a sample set. Increased soil microbial community diversity was artificially generated by mixing several microbial soil inoculants but did not result in increased SOC mineralisation rates. Even under impaired conditions, in the presence of aged engine-oil as a less decomposable partly toxic substance, communities with higher diversity did not show higher respiration rates. Investigations on the effect of coalescence of two communities in a 50:50 mixture of two untreated soils showed, in fact, declining respiration in three out of six cases (by 23.9±5.9%) and increased respiration in only one case (by 57%), compared to the mean respiration of the two un-mixed soils. These positive and negative effects of coalescence were highly related to microbial community capability to respire carbon, with only weak microbial communities with

low capability profiting from mixing with a second community. While all experiments had certain drawbacks due to the inevitable disturbances of the soil habitat, all experiments indicated consistently that the microbial community composition but not their diversity had a significant role for SOC turnover in mineral soils. Thus, our results question the assumption of redundancy of microbial community's functionality for SOC turnover in soils.

A3   Novel understanding of microbial soil carbon cycling mechanisms through metagenomics based assessment of central carbon metabolism genes

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KEYWORDS Soil carbon, microbial physiology, metagenomics, central carbon metabolism

Genesis of soil organic matter is now thought be largely microbially mediated and a new paradigm that highlights the significant contribution of microbial biomass in soil organic carbon is now widely accepted. Yet the focus of soil carbon cycling processes still continues to be on the fate of plant organic matter in soil and microbial extracellular enzymes involved in litter degradation. We hypothesize that microbial physiological adaptation and the tradeoffs between anabolism and catabolism (referred to as carbon use efficiency) could be key in understanding the microbial contribution to soil organic matter formation. Such changes in microbial functional response due to environmental change could lead to changes in soil carbon. Here we analyzed 8 geographically distributed soils of low and high pH using whole genome shotgun metagenomics to specifically assess whether established patterns of taxonomic and functional gene diversity over soil gradients are associated with changes in central carbon metabolism genes. In terms of relative abundance of functional genes, those belonging to the groups glycolysis and gluconeogenesis, pentose phosphate pathway (PPP) and lactate fermentation were consistently and significantly higher in low pH soils; whereas those of the TCA cycle were higher in high pH soils. The relative abundances of genes involved in glycolysis and the TCA cycle (Gly: TCA ratio) can indicate altered physiological profiles. In high pH soils, Gly: TCA ratio is closer to one (1.25 ± 0.05) indicating that most of the glycolytic products are fed into the TCA cycle. This could be due to an increased cellular demand for energy and biosynthesis in more active high pH communities that drives the higher flux through the TCA cycle. A higher Gly: TCA ratio (1.65 ± 0.2) in low pH communities suggests that glycolytic products are fed into PPP and fermentation pathways in addition to the TCA cycle indicating a physiological adaptation of microbial communities yielding an efficient biosynthesis-driven metabolism of environmental carbohydrates. An observed strong correlation of the Gly: TCA ratio to soil carbon concentration and loss on ignition (LOI) index could be the corollary of an adaptive and efficient central carbon metabolism in low pH soils. Such tradeoff between anabolism and catabolism could be used as an indicator of changes in microbial physiology and subsequently soil carbon content. Thus, metagenomics can be used to gain new insight into microbial metabolic adaptations required to exist in soils of varying nutrient availability and edaphic conditions.

A4   Microbial foraging strategy is dependent on substrate concentration.

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KEYWORDS Spatial separation, dilution effect, enzyme patterns, non-linear responses

To efficiently break down and take up organic matter, soil microbes produce a substrate specific set of enzymes. Microbes might however only be able to do so if they are in close vicinity of the prevailing substrate. Spatial separation as a function of substrate concentration, might force soil microbes to

produce more general and less specific enzymes and lead to a less efficient degradation of organic matter.

To test this hypothesis we set up a lab incubation experiment. We amended a mixture of agricultural soil and sand with increasing amounts of one of three plant residues differing in their C/N ratio (clover C/N 14; rye C/N 23 and wheat straw C/N 110). Keeping the soil/sand mixture at a constant ratio, we obtained 9 levels of organic carbon (OC) content ranging from 0.25% to 5.7%. The sand-soil-residue mixtures were then incubated at constant temperature and water contents for a total of 63 days.

Our results show that across substrates microbes produced relative more oxidative enzymes and proteolytic enzymes at low OC levels while enzyme patterns became more specific with increasing OC content. After 15 days of incubation microbial enzyme patterns at high OC contents showed a relative high proportion of cellulose and beta-glucosidase activity, while after 63 days enzymes pattern shifted towards relatively more N-acetyl-glucosaminidase activity. This shift might indicate a change in the prevailing substrate for microbial growth from plant compounds towards microbial compounds and a corresponding shift in the microbial foraging strategy.

In addition to the adaptation in the microbial strategy to decompose organic matter, we also found that CO_2 production increased with increasing OC content following a sigmoidal curve function instead of the expected linear one. This non-linear relation might indicate a reduction of decomposition by spatial separation at low OC concentrations along with the more general enzyme patterns.

Our findings of an enzymatic adaptation of the soil microbes to substrate concentration rather than chemical composition of the substrate at low concentrations together with the observed non-linear decrease of CO_2 production with decreasing OC content indicate that spatial separation as an inherent property of SOM content is an important control on microbial foraging strategy and decomposition of soil organic matter.

A5   Microbial control of biogeochemistry during drying-rewetting: the legacy of drought

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KEYWORDS Microbial growth, respiration, drying-rewetting, soil moisture.

Drought and drying-rewetting cycles are frequent stressors for soil microbial communities; a stress that is predicted to grow increasingly severe with future climate change. Understanding how the microbial community controls biogeochemical cycles under these dynamic events is instrumental to enable predictive power for C and nutrient cycling in soils. We investigated the microbial growth dynamics underlying the dramatic soil C pulse induced by rewetting a dry soil at high time-resolution in a series of week-long studies in a range of soils. Second, we investigated how the duration of drought modulated the microbial responses to rewetting. Third, we investigated how the added perturbation of salt addition in addition to drying affected the response to rewetting. Fourth, we investigated how partial drying and repeated drying-rewetting cycles affected the response to rewetting. We also extended our analysis by investigating how the legacy of drought affected the actively growing microbial community and their biogeochemistry by assessing a cross-continental set of long term (>10 y) drought experiments including soils from ecosystems across Europe.

We found two principal types of respiration responses induced by rewetting a dry soil: Type 1: an immediate maximal peak followed by an exponential decline or Type 2: an immediate peak maintained for 20 h, followed by an intermittent period of exponential increase reaching a maximal peak rate only after > 24 h, followed by an exponential decline. Microbial growth contrasted sharply with the respiration dynamics of both types of rewetting responses. In the Type 1 response a linear increase starting immediately after rewetting from zero growth and gradually converging to similar rates as in a moist control soil occurred. In the Type 2 response microbial growth remained at zero for about 20 h, followed by an exponential increase, reaching a peak value many-fold times higher than that of the moist

control soils >24 h after rewetting. An extended period of drought prior to rewetting and the interaction between salt combined with drying could both change the microbial responses from Type 1 to Type 2. Partial drying and repeated drying-rewetting cycles could both change a type 2 response to a type 1. A legacy of field drought prior to a drying-rewetting cycle was found to consistently reduce the respiration per microbial growth induced, suggesting an economized microbial C-use efficiency.

A6   Bridging the priming effect into aquatic systems: does labile carbon stimulate the fungal decomposition of submerged plant litter?

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KEYWORDS Priming effect, fungi, bacteria, algae

The quality of organic matter (OM) is highly variable and covers a large gradient of resistance to degradation. OM can be 'activated' and thus involved in carbon (C) and nutrient cycling through the priming effect, which is the increased mineralization of recalcitrant organic matter triggered by inputs of labile OM. The effects of labile C on the decomposition of OM and C sequestration are of considerable interest for soil microbial ecology, especially in the rhizosphere where fluxes of labile C are high. However, less is known about the importance of labile C input for the turnover of OM in other systems. A situation similar to the rhizosphere can be found on submerged plant material in the presence of labile C input by photosynthetic algae. Within priming research, a central challenge is a relevant delivery of labile C. Most studies have used pulse additions at high concentrations, which may not represent a natural environment well. To achieve an assessment of the priming effect it is important to simulate a realistic delivery of labile OM, capturing a continuous but dynamic delivery of low concentrations.

We used pond water microbial communities where plant litter was submerged. We monitored the successional dynamics of fungal (acetate incorporation into ergosterol) and bacterial growth (leucine / thymidine incorporation), primary production (PP) activity, and respiration on litter under dark and light conditions. In a parallel experiment we used similar microcosms and mimicked the delivery of PP labile C by continuously adding ^{13}C-glucose at an identical rate using peristaltic pumps in dark systems, thus tracing labile C into respired CO_2.

We observed an increased fungal production in light treatments. The fungal growth response coincided with an increase in algal photosynthesis. Dark treatments showed a low fungal growth and no primary production. Bacterial production showed no differences between light and dark systems. Systems with glucose additions induced comparable effects to the light systems with active PP, and enabled the partitioning of sources for the respired $^{13}CO_2$. We observed that continuous glucose additions did not stimulate total litter decomposition, and therefore no priming effect was observed. Labile C, added as natural algal exudates or as glucose, resulted in an increased fungal contribution to litter decomposition relative to bacteria. The observed changes towards a fungal dominated litter degradation induced by labile C raises important questions with regards to C cycling since fungal products are known to be more resistant to degradation.

A7   The effect of soil mineral composition on microbial community establishment and functioning - artificial soil mixtures as a simplified study system

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KEYWORDS artificial soils, metagenome, microbial community, *alkB,* macronutrients

Soil organic matter (SOM) positively influences many different soil properties like structure, biodiversity, aggregation or fertility. The formation of SOM is mostly driven by the input and decomposition of plant material and the presence and activity of microbial biomass. In turn the stabilization of SOM depends on the mineral composition of the soil. Consequently, to understand the formation and stabilization of SOM one has to understand the interplay of microbes and mineral soil surfaces. Natural soils are highly complex systems, which form plenty of biogeochemical surfaces and niches. Therefore, we used a simplified artificial soil system to study the impact of the clay minerals montmorillonite (MT) and illite (IL), the metal oxides ferrihydrite (FH) and boehmite (B) and charcoal on the microbial community during soil formation and the response of the microbes to the addition of plant litter after 3, 12 and 28 months of maturation. To initiate soil formation all eight soil mixtures were inoculated with manure and microbial communities extracted from agricultural soils. Due to the different sorption, shrinking and swelling properties of the minerals used, we hypothesized that soil complexity and mineral composition strongly influenced community composition due to different niche formation and nutrient distribution, while the overall functionality of the system is resilient.

Based on the analysis of the diversity of the microbial community by targeting the 16S rRNA gene and specifically the alkane (litter) degrading community by targeting the alkane monooxygenase gene *alkB*, our data indicate that: (i) the impact of metal oxides was highest after 12 months and of clay minerals after 28 months (MT) of maturation, while the effect of charcoal decreased. (ii) The addition of litter led to an increase in microbial abundance and activity and a shift of the microbial community towards earlier soil development stages, where still easily degradable OM was available from the added manure. This goes hand in hand with a decrease of microbial network density and a masking of the effect of soil minerals and metal oxides. (iii) An in depths metagenomic analysis of two 28 months soils (MT and IL) revealed a highly conserved core microbiome with respect to nitrogen and phosphorous turnover. More than 90% of the reads were shared between both soils and functions, indicating that essential functions are conserved. Based on the P turnover it seems that microbes are adapted to P scarcity but deal with it differently for example in the IL soil P dependent mineralization dominated, while in MT P induced uptake is favored.

A8   Using isotopes to understand microbial action in soils

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KEYWORDS 13C, 2H, 14C, continuous vs pulse label, metabolite classes

In the past years we used stable (13C and 2H) and radioisotopes (14C) in several bulk fractions like SOM, DOC, DNA, RNA and CFE and metabolic fractions like individual compounds from carbohydrates, organic acids, alkanes, PLFA and NLFA to trace continuous and pulse labels into these compounds. We used the results to calculate turnover rates of the different compound classes and to identify food sources like organics from ancient rocks or direct uptake CO_2 by soil microorganisms. The results demonstrate that i) soil microorganisms are able to use several uncommon carbon sources, ii) the turnover of various metabolic fraction differ within and between organisms and that iii) careful experimental planning, i.e. the duration of the applied label, is needed as they strongly influence the experimental results

Session 2:   Significant boundary conditions, micro-habitats and micro-habitat properties, processes of succession, and systems fluctuations - what can we learn from the marine microbial pump concept?

Keynote

K1   Ecosystem conditions and stress shape microbial community structure and activity

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KEYWORDS Stress, extreme systems, microbial activity

Most studies of soil biology are done under conditions of optimal temperature and moisture, yet most ecosystems experience extended periods of conditions we consider stressful—notably drought, and freezing. "Optimal" is the exception. Stress alters microbial community dynamics but also how microbes process substrates, potentially shifting resources to optimize survival and productivity. Organismal acclimations to stress, however, are interwoven with physical and chemical processes which occur differently when liquid water is a limiting resource. As water becomes limiting, so too does substrate diffusion—microbes and resources become fragmented and disconnected. As a result, carbon flows differently through the microbial and soil systems. Microbes can shift from aerobic to anaerobic conditions when soils freeze, and can shift from N to C limited. Microbes seem remarkably tolerant of deep drought conditions, but dry/wet cycles can mobilize substantial amounts of C that was otherwise "stable." The mechanisms that drive these processes and how to capture them in biogeochemical models remain unclear, although developments are occurring rapidly.

H1   Plant and soil successional stage modifies the impact of drought on rhizosphere C cycling

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KEYWORDS Climate change; microbial respiration; alpine; rhizosphere; root exudates

Plant-soil interactions play a crucial role in determining the impact of drought, which is predicted to increase with climate change, on ecosystem functioning. Drought has strong and immediate effects on soil ecosystems, but there is still much uncertainty about how different soils and soil microbial communities respond to drought, and how this response might be modified by plants. It has been suggested that soil microbial communities might be more resilient to drought when they have access to inputs of plant-derived C. Similarly, slow-growing, resource-conservative plants might be more resistant to drought than fast-growing plants. Glacier forelands provide a unique study system to test these assumptions. They represent a successional gradient, with soils becoming richer in C, and plant communities becoming more dominated by slow-growing species with increasing distance from the retreating glacier. Here, we assessed the relative importance of plant and soil successional stage for determining ecosystem C cycling response to drought. We hypothesised that both soils and plant species from late-successional sites would more resistant to drought, and have the lowest overall C loss. We tested this hypothesis in a reciprocal transplant experiment, using both soil and plants collected from early and late successional sites of the Odenwinkelkees glacier. Two early and two late successional plant species were subjected to drought (or watered to 60% water-holding capacity) in the two soil types, alongside unplanted soils, in a fully factorial greenhouse experiment. Soil dissolved organic carbon, nitrogen, and respiration rates were measured. Rhizosphere C was extracted and added back to soils factorially in a substrate-induced respiration assay to test microbial physiological response to C from local vs external sources. Preliminary results show that, as hypothesised, drought reduced growth of early-successional plants most, and caused the greatest relative C loss in early-successional plant-soil systems. Substrate-induced microbial activity showed that rhizosphere communities were more conditioned to inputs from respective rhizosphere C than from the rhizospheres of different plants and soil. This indicates conditioning to drought is important for resilience of microbial function under drought. These results give insight into the mechanisms through which plants can modify soil C cycle response to drought, This knowledge is critical for predicting and mitigating the effects of climate change on the resistance and resilience of both natural and managed systems C cycling capacity.

H2   Microbial metabolite recycling: an underestimated process contributing to SOM stabilization at mineral surfaces

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KEYWORDSRecycling of metabolites, life on mineral surfaces, sorption, metabolic tracing, position-specific labeling

In the last two decades physico-chemical fractionation of soil organic matter (SOM) revealed mineral-associated organic matter as the oldest, and consequently most stable SOM fraction. Such results conflict with short-term incubation experiments demonstrating that microbial uptake outcompetes sorption and that even strongly sorbed compounds are microbially accessible and can be decomposed to a similar extend. Thus, the high apparent age of mineral-associated organic carbon (C) must result from additional processes that have yet to be identified.

Awareness of the important role that microbial metabolite recycling plays in terrestrial C transformations originated in the field of biogeochemistry within the last years. However, it is extremely challenging to differentiate microbial recycling from stabilization of untransformed organic matter by sorption based on ^{13}C or ^{14}C natural abundance and/or short-term pulse-labeling approaches. Long-term experiments based on uniformly-labeled glucose first indicated microbial recycling as a relevant process in soil C dynamics. Recently, 1) a position-specific labeling approach in terrestrial system and 2) moiety-specific isotope analysis in marine system demonstrated the relevance of lipid recycling for C turnover in soils and sediments. Novel metabolic tracing techniques provide the unique opportunity to observe metabolic cycling of sorbed organic matter and thus to assess the relevance of metabolite recycling at mineral surfaces. Therefore, position-specific labeling of sorbed versus free amino acids was combined with compound-specific isotope analysis of microbial biomarkers. Uptake of sorbed low molecular weight organic compounds was equal to non-sorbed compounds for nearly all microbial groups, which clearly opposes direct stabilization. Sorption shifted microbial metabolism from catabolic to anabolic use of the respective C – a clear indication that sorbed compound recycling partially explains the high apparent age of the mineral-associated organic matter.

Although quantitative assessment of recycled versus directly stabilized C is not yet possible, these results support the strong relevance of microbial organic matter recycling, especially within microhabitats located on mineral surfaces.

Keynote

K3   Dissolved organic matter (DOM) cycling in anoxic marine sediments: General observations and the formation of refractory DOM

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KEYWORDS Organic matter, marine sediments, anoxic

Dissolved organic matter (DOM) in marine sediment pore waters is a heterogeneous collection of compounds, ranging from large macromolecules (e.g., dissolved proteins or humic substances) to individual amino acids or short-chain organic acids. Most DOM that accumulates in pore waters appears to be refractory in a bulk sense, although DOM (in general) is also a key intermediate in the remineralization of particulate organic matter (POM) to inorganic end-products. To explain these observations we have developed a model in which the bulk of the carbon and nitrogen flow from POM occurs by processes that produce and consume labile intermediates of decreasing molecular weight, eventually resulting in the production of monomeric low molecular weight DOM compounds such as acetate, that are then utilized in terminal respiratory processes such as iron reduction, sulfate reduction and methanogenesis. At the same time a small amount of the carbon and nitrogen flow is also assumed to produce DOM intermediates that are refractory on the overall time scales of remineralization.

A fair amount of information exists about the concentrations and cycling of monomeric low molecular weight DOM compounds such as acetate in anoxic sediments. However far less is know about the dynamics and chemical composition of labile, higher molecular weight DOM intermediates, and even less is known about how refractory DOM forms, which is also largely uncharacterized at the molecular-level.

We have been examining these problems in sediment pore waters from Santa Barbara Basin (SBB) California, most recently using ultrahigh-resolution mass spectrometry. Among the ~9,000 unique chemical formulas we detected with this technique, 119 matched peptides with 2-4 amino acids, while 680 matched deaminated peptides (DeAPs), that is peptides in which terminal amine groups are removed leaving intact the remaining carbon skeleton and internal peptide linkages. Oxidative deamination by fermentative bacteria appears to be the dominant peptide deamination mechanism. This process produces H_2, which is likely then consumed by anaerobic microbes including sulfate-reducing bacteria, hydrogenotrophic methanogens, and acetogenic bacteria. The DeAPs we detected also fall within the region on a van Krevelen diagram occupied by carboxyl-rich alicyclic molecules (CRAM), considered to be a main component of refractory DOM in the oceans.

We hypothesize that DeAPs could represent an important component of refractory DOM found in sediment pore waters, and that their formation represents an important connection between oceanic and sedimentary carbon and nitrogen cycles as they relate to the existence of refractory DOM in the oceans.

H3   Soil organic matter development during water table fluctuations in an artificial soil column incubation

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KEYWORDS Water table, redox potential, soil organic matter

The depth distribution of moisture and the resulting redox potential have an important effect on the activity and development of microbial communities of soils. They can lead to the development of microbial communities specifically adapted to local redox extremes or to oscillating redox conditions. Furthermore, water table fluctuations, which cause flooding and drying of soils, have been linked to enhanced degradation of soil organic matter and release of greenhouse gasses (e.g. CO_2, CH_4) to the atmosphere. To improve our understanding of soil organic carbon degradation under changing moisture conditions, we carried out an automated soil column experiment with integrated monitoring of hydro-bio-geophysical processes under both constant and oscillating water table conditions. An artificial soil mixture composed of quartz sand, montmorillonite, goethite and humus was used to provide a well-defined system. This material was inoculated with a microbial community extracted from a forested riparian zone. The soils were packed into 60 cm high, 7.5 cm wide columns, to a height of 45 cm; three replicate columns were incubated under a constant water content while another three were dried and saturated monthly. The initial soil development, carbon cycling and microbial community development were then characterized during 10 months of incubation. Micro-sensors, installed at different depths below the soil surface in the columns, recorded oscillating redox potentials (E_h) between oxidizing (~+700 mV) and reducing (~-200 mV) conditions. Continuous O_2 levels throughout the soil columns were monitored using high-resolution, luminescence-based, *Multi Fiber Optode* (MuFO) microsensors. Pore water samples collected periodically with MicroRhizon® samplers at different depths were analyzed for pH, EC, dissolved inorganic and organic carbon and ion/cation compositions; headspace gas measurements were used to derive the effluxes of CO_2 and CH_4 during the experiment. In addition, small solid-phase samples were collected monthly from the saturated and unsaturated zones of the soil columns to characterize the microbial community. These measurements allowed us to track

major electron donor and acceptor availability in direct relation to carbon cycling within each column. A clear effect of the water table fluctuations on CO_2 release from the columns was observed, with lower CO_2 fluxes during flooding periods and enhanced CO_2 fluxes after drainage. Present work focuses on the characterization of microbial biomass and community, soil organic matter and mineral properties after incubation in order to link community dynamics to soil organic matter development under the local redox conditions and water dynamics at different depths of the columns.

H4   From plants to microaggregates – organic matter transfer at soil biogeochemical interfaces

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KEYWORDS rhizosphere, detritussphere, NanoSIMS, microaggregate, fungal hyphae, organo-mineral association

Rationale and objectives: The complexity of soils extends from the ecosystem-scale to individual microaggregates, where nano-scale interactions between microbiota, organic matter (OM) and mineral particles are thought to control the long-term fate of soil carbon and nitrogen. It is known that such biogeochemical processes show disproportionally high reaction rates within nano- to micro-meter sized isolated zones ('hot spots') in comparison to surrounding areas. However, the majority of soil research is conducted on large bulk (> 1 g) samples, which are often significantly altered prior to analysis and destructively analysed. Thus, it has previously been impossible to study elemental flows (e.g. C and N) between plants, microbes and soil in complex environments at the necessary spatial resolution within an intact soil system. By using nano-scale secondary ion mass spectrometry (NanoSIMS) in concert with other imaging techniques (e.g. scanning electron microscopy (SEM)), classic analytical analyses (isotopic and elemental analysis) and biochemical methods (NMR spectroscopy, GC-MS) it is possible to exhibit a more complete picture of soil processes at the micro-scale. Our main aim was to study how OM within the rhizosphere and from decaying plant materials is incorporated in the surrounding bulk soil. We had two main hypotheses. First, fresh OM gets directly incorporated into soil micro-aggregates and in parallel new organo-mineral associations are formed in the vicinity of litter and roots. And second, fungal hyphae play an important role as vectors for OM from the decaying plant material into the mineral soil.

Methodology approach: We will present two approaches, (1) an incubation study using an artificial soil mixture together with decaying plant materials to trace plant derived OM in OC free soil, and (2) a labelling experiment in the field using $^{13}CO_2$ to trace the fate of assimilates in the rhizosphere of wheat. Whereas the incubation experiment was used to trace the fate of the litter derived OM into the mineral soil, the labelling study focused on the fate of the assimilates in the rhizosphere. For in-situ analyses the samples were chemically fixed, embedded in epoxy resin and sections analysed using SEM and NanoSIMS. The imaging results are supported by classic bulk analyses (e.g. IRMS, NMR). In case of the incubation experiment we additionally studied the fate of bound fatty acids using GC/MS.

Results and conclusions: We were able to demonstrate in both experiments the new formation of organo-mineral associations in the direct vicinity to plant/soil interfaces. Especially in the detritussphere, fungal hyphae play an important role for the translocation of plant derived OM. After 42 days of incubation, the whole artificial soil matrix was penetrated by fungal hyphae which were growing from the

infested plant cells into the surrounding soil matrix. At the same time, there was a tremendous increase in OM within soil micro-aggregates but also at larger mineral surfaces, indicating the new formation of organo-mineral associations. For the rhizosphere system, we were able to demonstrate the flow of assimilate derived OC from the plant to the microorganisms and finally the mineral surfaces. This work clearly shows that litter surfaces and the rhizosphere are not just hot spots for microbial activity but also for the formation of organo-mineral associations and organic rich micro-aggregates.

H5   Is soil pore structure control on substrate decomposition manifested through N availability?

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KEYWORDS Organic matter, Microbial degradation, PLFA, Nutrient diffusion, X-ray CT

Rationale and objectives: Soil pore structure determines the location of OM particles, the distribution of O_2, water, micro-organisms and the diffusion of nutrients. Mineral N availability plays a crucial role in microbial degradation of N-poor substrates. To study these complex relationships between microbial community, C mineralization and soil pore structure we set up an experiment with microcosm soil incubations combined with pore network quantification. We hypothesized that fungi would dominate C-mineralization in soils with a porous structure and low water content. Second, we hypothesized that C-mineralization would be stimulated by increased N diffusion in soils with a more compacted structure and higher water content. We expect this innovative combination of methodologies to reveal new insights in the small scale carbon dynamics and to a better understanding of the microbial community functioning.

Methodology approach: We created mini-soil cores with an artificially reconstructed soil texture, namely a silt and clay (S+C) content of 50% or an S+C content of 20%, and a sand content of 50 and 80%, respectively. The soil cores were subjected to different levels of water filled pore space (WFPS of 25% and 50%) and amended with either easily degradable OM high in nitrogen (grass) or more resistant OM low in nitrogen (sawdust). Combined with or without KNO_3 application, these soil pore structure-substrate treatments allow to create contrasting microbial communities. Microcosm incubations under controlled conditions were set up for 128 days during which CO_2 was measured frequently via GC-TCD. After 2 weeks, state-of-the-art X-ray CT was used to quantify the soil 3D architecture and the microbial community composition at the end of the incubation was assessed using PLFA fingerprinting. For the first time, CT-based characteristics of the local porosity surrounding the OM particles will be correlated with C-mineralization and microbial community structure.

Results and conclusions: C-mineralization in the sawdust treatments was higher in the 50%_S+C soils than in the 20%_S+C soils at 25%WFPS, while such effect was not observed at 50% WFPS or for grass at both water contents. This interactive effect of soil structure and substrate type suggests that soil structural control on C-mineralization would be induced by differences in N diffusion, causing differing N availability. PLFA, however, did not reveal promotion of fungal over bacterial biomarkers in treatments with likely N-limited substrate decomposition. Ongoing CT-based local porosity quantification could confirm existence of localized elevated porosity surrounding substrate particles.

H6   Particle size fractions provide distinct microhabitats for soil microbial communities

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KEYWORDS Soil particle size fractions, microhabitat preferences, high-throughput sequencing

Organic matter (OM) associated with differently sized soil particles differ in quantity and quality, and range from free particulate organic matter (POM) associated with the sand-sized fraction to true organo-mineral complexes in fine silt and clay fractions. We previously found with arable soils that specific surface properties of different particle size fractions (PSF) select for distinct microbial communities (Neumann et al., 2013, Hemkemeyer et al., 2015). Here we show that PSF and long-term fertilisation affect communities also at a taxon and functional level.

Soil with similar texture and pH were retrieved from the Askov long-term field experiment using plots that had been kept unfertilised or dressed with mineral fertilisers or animal manure for more than a century, providing soil with different levels and qualities of OM. Soil was fractionated by gentle ultrasonic dispersion, wet sieving and centrifugation. DNA was extracted from each PSF and microbial domains quantified by qPCR. High-throughput sequencing of 16S rRNA genes was determined on the Illumina MiSeq platform.

On dry weight basis, microbial abundances increased with decreasing particle size by orders of magnitude. PSF from soil given animal manure showed the highest content of OM and highest microbial abundances. The responses to differences in OM content peaked in coarse silt. When based on OM content, differences between PSF and between fertilisation treatments diminished. However, bacteria remained more abundant in clay than in the coarser PSF, while fungi dominated the POM in the sand fraction. Phenol mineralisation during incubation followed the pattern of soil mass-based microbial abundance with one exception: Mineralisation rates were higher in the POM containing sand-sized fraction than in coarse silt with similar mineralogy. Mineralisation rates were generally higher in soil receiving animal manure. High-throughput sequencing confirmed the preferences of bacterial communities for distinct PSF. *Streptomycetaceae,* which are typically involved in early stages of decomposition, preferred the POM containing sand fraction while most other *Actinobacteria* preferred fine silt. Although preferences did not change due to the presence of OM, PSF differed in the responsiveness to the long-term fertilisation with coarse silt being most responsive. This study demonstrates the PSF provide distinct microhabitats for soil microbial communities with respect to structural diversity and potential to respond to environmental factors.

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H7   Soil nutrients and microbial activity in a post-mining chronosequence

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KEYWORDS Chronosequence, mining, microbial biomass, microbial nutrient limitation, microbial respiration

Rationale and objectives: Microbial activity governs all bio-geo-chemical cycles in soil, but microbial growth rates and functioning are strongly dependent on the relative ratios of growth-limiting elements, like carbon, nitrogen and phosphorus. Soil development in chronosequences of refilled open-

cast mines offer a unique opportunity to study changes in microbial nutrient-limitation during soil succession from a 'virgin' soil to old agricultural soils. We investigated changes in microbial nutrient limitations in a chronosequence of reclaimed agricultural soils after lignite mining as part of the Inplamint (Increasing agricultural nutrient-use efficiency by optimizing plant-soil-microorganism interactions) within the BonaRes (Soil as a sustainable resource for the bioeconomy) consortium. The main objective is to develop new strategies for improved fertility and sustainable management of agricultural soils.

Methodology and approach: The study site is a chronosequence of reclaimed agricultural soils, following the gradual relocation of the 'Inden' open cast lignite mine (RWE Power, Germany), approx. 50 km west of Cologne, Germany. Since 1964, new agricultural fields have been sequentially reclaimed into fertile agricultural soils. We investigated basal respiration, microbial biomass and nutrient limitation (C, CN, CP, CNP) in soils of 11 age classes, plus non-mined old agricultural land as control for pre-miming conditions. Samples were taken from intensively farmed fields, and adjacent grass margins as proxy for soil conditions at constant vegetation cover and non-mechanical disturbance.

Results and conclusions: Soil microbial biomass and activity of reclaimed soils reached pre-mining conditions approx. 5-10 years post reclamation. In contrast, soils under permanent grass cover required more than 10 years until recovery to former levels. Interestingly, the relative amounts of total C in soils remained constant, while total N strongly decreased after mining and did not converge to pre-mining conditions even 52 years after soil reclamation. Grass sites showed a steeper increase of total C and N over time, but had also higher pre-mining values. Microbial growth was strongly limited by N contents, in particular in soils under permanent grass cover. Younger soils showed a strong co-limitation of N and P, which exceed the effects of single N and P nutrient additions. Overall, soil microbial biomass and activity developed much higher values under a constant grass cover in absence of mechanical disturbance. Over time, more optimal soil nutrient conditions restored at a faster rate under grass than fields. However, the nutritional status of soils did not reach the pre-mining baseline even half a century after soil reclamation.

Session 3: Molecular processes and components interacting with SOM and soil minerals - turnover steady state or residual `inert´ material?

Keynote

K4 Beyond "recalcitrance" – carbon flow through the mineral soils of a prokaryotic world

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Keywords soil organic matter, carbon cycling, recalcitrance, oxidation state, continuous flow reactor

This contribution will center on two major aspects of the session theme: Molecular processes and components interacting with SOM and soil minerals - turnover steady state or residual `inert material?. I intend to discuss the merits of conceptualising the turnover of soil carbon as a process that involves the "formation" of a unique organic phase in soil. This notion will be contrasted with a more recent model that sees organic matter as a continuous "flow" of carbon atoms through the pedosphere. Due attention will be paid to the contributions of the mineral phase to both of these scenarios. The second item to be addressed is the adequacy of the concept of "inherent molecular resistance to decomposition" or "recalcitrance". Here I will present evidence and reasoning in favor of the view that

a) organic substrates are logically and mechanistically unable to "resist" decomposition and that

b) apparent resistance can, with superior logical strength, be explained as an evolutionary adaptation of the decomposer community to decompose different substrates in sequences and at rates determined by the capabilities, needs, preferences and logistic constraints of the ecosystem in question.

I1   Interactions of extracellular polymeric substances (EPS) with Fe oxides

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KEYWORDS AFM, C1s STXM, FTIR, C stabilization, adsorption

Extracellular polymeric substances (EPS) are produced by many microorganisms to perform diverse functions such as the initial attachment of cells to solid surfaces, cell-to-cell adhesion, scavenging of nutrients or protection from desiccation or toxic substances. EPS are composed of polysaccharides and proteins with minor contributions of nucleic acids and lipids, but the exact composition depends on the specific bacterial or fungal strain, the growth stage, and the physicochemical conditions of the environment. In addition, the composition of EPS is often studied after separating it from liquid cultures by extraction, a procedure which is prone to several artifacts.

We used carbon spectromicroscopy at the K-edge (STXM) and atomic force microscopy (AFM) to investigate composition and mechanical properties of EPS at high spatial resolution in intact biofilms of Bacillus subtilis. STXM allowed to quantify the contribution of proteins, non-aromatic proteins, polysaccharides, and lipids on EPS patches between bacterial cells at a resolution of 30 nm, while evaluation of force-distance curves gave Young`s modulus, deformation and tip-sample adhesion of the same patches.

In comparison to EPS extracted from a liquid culture, the EPS inside the biofilm were depleted in proteins and enriched in lipids. During adsorption of EPS on goethite we observed a preferential adsorption of proteins and lipids. When the biofilm was grown in the presence of goethite, the secreted (non adsorbed) EPS were also enriched in lipids. AFM images revealed that the biofilm-EPS is made up of domains of different mechanical properties. However, this was not reflected in the chemical composition as seen by STXM.

We conclude that lipids and proteins of EPS react preferentially with Fe oxide surfaces. Being bound to minerals may lead to the long-term stabilization of these compounds in soil.

I2   Potential role of microbial electron shuttling in soil, biochar and biochar co-composting

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Keywords electron shuttling, humics, compost, biochar,

Electron transfer reactions are the fundamental processes of all biogeochemical cycles. In soils, the exchange of electrons between microbes and soil components shapes the geochemistry and mineralogy, and determines the fate of nutrients and contaminants. In many cases, the accessibility of electron acceptors or donors are limiting microbial turnover of compounds. So-called "electron shuttles" were shown to promote certain microbially mediated redox reactions by facilitating or accelerating electron transfer. Dissolved and solid-phase humic substances are naturally occurring electron shuttles, while redox-active biochar, i.e. charcoal used in agriculture, is an anthropogenic soil amendment also capable of electron shuttling.

Electron shuttling by humic substances was shown to promote iron(III) mineral reduction in culture experiments with iron-reducing strains such as *Shewanella oneidensis* MR-1 as well as in natural environments such as freshwater lake sediments and soil. Here we present results that demonstrate that biochar has a similar capability to promote microbially mediated redox reactions, including iron(III) mineral reduction by *Shewanella oneidensis* strain MR-1. In cell suspension experiments, we showed that biochar can stimulate both rate and extent of microbial reduction of the Fe(III) oxyhydroxide mineral ferrihydrite, especially when the biochar was co-applied with anthraquinone-2,6-disulfonic acid (AQDS), a soluble model compound for quinones in humic substances. Related to our work, other studies have shown that biochar electron shuttling can also promote reductive dechlorination and soil nitrogen transformations.

In order to better understand electron shuttling by biochar, we analyzed the biochar spectro(micro)scopically. As biochar is usually added to soils with organic amendments (e.g. after aerobic co-composting with manure) to improve soil fertility, we analyzed such a pretreated biochar. We identified an organo-mineral coating on the biochar surface caused by co-composting. Suspending this coating in a 0.05 M NaOH solution showed that it is redox-active and has an elevated electron accepting and donating capacity compared to suspended initial pure/pristine biochar. However, while co-composting altered the surface properties of biochar, the biochar amendment did not alter the carbon speciation of the organic matter in mature compost, as evidenced by ^{13}C NMR and FTIR.

In summary, our work provides some mechanistic insights into electron shuttling by biochar and its potential effects on biogeochemical cycling in soils. This is of broad relevance since electron shuttling by biochar might partially explain the effects of biochar on agroecosystems, including the reduction of N_2O emissions. Natural pyrogenic organic matter found in many soils, might have similar redox properties.

I3   Microbial utilization of mineral-associated nitrogen in soils

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KEYWORDS Microbial nitrogen cycling; Net N mineralization; Functional genes; Mineral-associated organic matter; Priming

In soils, a large portion of organic nitrogen (ON) is associated with minerals and thus, possibly stabilized against biological decay. We therefore tested if mineral-associated N is an important N source for soil microorganisms, and which soil parameters control its bioavailability. Microcosm experiments with mineral-associated organic matter, obtained as heavy fraction (HF) via density fractionation, and bulk soil from mineral topsoil of the Franz Josef chronosequence were conducted for 125 days. We examined the effects of O_2 status, soil age (differences in mineralogical properties), as well as cellulose and phosphate additions on the turnover of mineral-associated N. Using a combination of activity measurements and quantitative PCR, microbial N transformation rates and abundances of N related functional genes (*amoA*, *narG*, *chiA*) were determined. Similar or higher values for microbial N cycling rates and N related functional abundances in the HF compared to bulk soil indicated that mineral-associated N provides an important bioavailable N source for soil microorganism. The turnover of mineral-associated N was mainly controlled by the O_2 status. Besides, soil mineralogical properties significantly affected microbial N cycling and related gene abundances with the effect depending on the N substrate type (ON, NH_4^+ or NO_3^-). In contrast, cellulose or phosphate addition hardly enhanced microbial utilization of mineral-associated N. The results of our microcosm study indicate that mineral-associated N is highly bioavailable in mineral topsoils, but effects of the mineral phase differ between N cycling processes.

I4   Microbial N and P mining from recalcitrant pools

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KEYWORDS substrate-induced respiration, nutrient limitation, microbial nitrogen mining, soil respiration

The effect of nutrient deficiency on microbial activity and related mineralization of carbon (C) is still debated. While common theories of stoichiometric decomposition predict limitations of C-mineralization under conditions of nutrient deficiency, the recent concept of microbial nitrogen (N) mining predicts a maintenance or even increase of C-mineralization. This is explained by enhanced decomposition of recalcitrant soil organic matter (SOM) for the acquisition of N contained therein.

In this study we are focusing on two major knowledge gaps of mining theories. 1) Is mining restricted to N acquisition or does it also apply to phosphorus (P)? 2) Under which conditions does mining occur in soils? We hypothesized that mining of either N and P can occur but that the efficiency is constrained by several factors, e.g., by a too small pool size of recalcitrant SOM and by multiple nutrient deficiency. To unravel these gaps, we conducted substrate-induced respiration (SIR) measurements on topsoil samples taken repeatedly from a site which was up to 7 years under bare fallow (Selhausen, Germany) and from up to 4 m deep tropical soils (Kalimantan, Indonesia) under secondary rainforest and rubber plantations. Thus, sites showed strong gradients in N and P availability either with time or with depth. SIR was measured with different combinations of nutrient manipulation (glucose, glucose+N, glucose+P, glucose+N+P additions). We also conducted a ^{13}C labeling experiment to trace the source of CO_2 (sugar vs. SOM derived CO_2). Repeated glucose addition should indicate whether the availability

of N and P increases due to microbial mining.

Mineralization of glucose was limited by a lack of available N in the bare fallow soil but microbes were able to slowly acquire N from previously unavailable pools. Hence, N was immediately available when samples received glucose a second time which resulted in a rapid mineralization of the added glucose. The subsoils of the tropical sites were limited by both N and P, but alleviation of either N or P deficiency was sufficient to stimulate mining and the mineralization of glucose. No indications for nutrient mining were found in the tropical topsoil (high nutrient contents make mining unnecessary) and in very deep subsoil (too less SOM for mining available).

Our results suggest that mining of both N and P potentially occurs but is constrained by multiple nutrient limitations, by the absence of SOM which contains the required nutrients, and by full nutrient supply which makes mining unnecessary.

I5   Microbial residues accelerate decomposition of soil organic matter: new mechanism, actors and thresholds

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KEYWORDS ^{13}C-labelling, Plant residues, Priming effect, Enzyme activity, Carbon sequestration

Soil organic matter (SOM) is mainly plant-derived and is microbially processed. After microbial death (as a result of starvation or environmental stress), microbial necromass is re-utilized and undecomposed cell debris is stored in recalcitrant SOM fraction. Therefore, microbial necromass is considered as significant source of SOM (Miltner et al., 2012). We hypothesized, however, that soluble cytosolic compounds of the necromass serve as labile substrates for living microorganisms and, therefore, affect decomposition of SOM causing priming effect (PE).

To reveal the role of microbial residues as SOM primers, we applied ^{13}C-labeled wheat (*Triticum aestivum* L.) residues (leaves, stems, roots) to the soil at low (5.4 g kg^{-1}) and high (10.8 g kg^{-1}) rates. The carbon sources (native SOM and residue-originated C) were partitioned in CO_2 and in microbial biomass; specific enzyme activity (involved in C, N and P acquisition) was estimated to reveal the mechanisms of PE during 120 days incubation. We hypothesized an increase in PE after starvation of residue-decomposing microorganisms.

During intensive residue mineralization (ca. 2 weeks), the PE was low or even negative due to preferential substrate utilization mechanism. Thereafter, the strong increase in primed CO_2 was accompanied by up to 60% decrease of microbial biomass and by increased specific enzyme activities. Surprisingly, no incorporation of SOM-derived C into MB during 15-60 days was detected. Such PE increment, therefore, was mainly explained by re-utilization of microbial necromass. This suggests a new mechanism of real PE where microbial residues serve as SOM primers. Remarkably, the PE and enzyme activities were mainly correlated with residue-metabolizing microbial biomass. We proposed a unifying logistic model describing a specific PE as a function of mineralized fraction for all types of plant residues. The model enabled estimation of threshold value of mineralized residue fraction above which a PE

increment was maximal, i.e., 20-22, 29-44 and 39-51 % of input of roots, stems and leaves, respectively. Thus, the PE is a power function of plant residue mineralization, whereby root decomposition has a lower threshold to a strong increase in PE than stems and leaves have. Our study emphasized the role of residue-feeding microorganisms as active players of PE induced by microbial necromass. Such a PE can reduce a contribution of microbial debris to SOM for about 15-20%, therefore, it cannot be ignored by the studies on soil C budgeting and modelling.

I6   The mycosphere as logistic hotspot: Contributions of fungal bacterial interplays for soil ecosystem functioning

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KEYWORDS Bacteria-fungus-interactions, biotransformation, dispersal, mycosphere, transport

Rationale and objectives: The structural heterogeneity of soil results in an enormous variety of soil micro-environments forming hotspots of microbial diversity and activity. Microbial contributions to ecosystem functioning in such microenvironments often are thereby driven by the composition and surface properties of soil components or the accessibility and availability of water, nutrients and carbon to microbes. In this contribution we exemplify such dynamic interplay by the example of the biodegradation of chemicals in soil.

Methodology approach: Prediction of a given ecosystem's ability to degrade a chemical needs to interlink knowledge on a molecule's chemodynamics with spatio-temporally emerging mechanisms of ecosystem functioning during microbial attenuation. Biodegradation thereby is a 'logistic' problem as optimal transformation of a contaminant will evolve only if the chemical is sufficiently available to degrading microbial communities. Efficient degradation is aggravated by a patchy distribution of contaminants, nutrients and degrading microbial communities as well as by ever fluctuating (e.g. disturbance) conditions. In order to cope with heterogeneous environments mycelial soil fungi have developed a unique network-based growth form. Unlike bacteria, hyphae spread efficiently in the soil, penetrate air-water interfaces and cross over air-filled pores.

Results and conclusions: Here we demonstrate the role of mycelial networks for preferential bacterial colonization of subsurface interfaces and discuss its effects on contaminant degradation. In particular, we show that mycelia (i) act as hotspots for horizontal gene transfer, (ii) shape predator-prey interactions and concomitant compound turnover, and (iii) enable the functionality of microbial ecosystems when stressed by low osmotic and matric potentials. Given the ubiquity and length of up to 500-1000 m g^{-1} dry soil of hyphae, we conclude that transport and dispersal processes by mycelia not only play a significant role for the ecosystem service of biodegradation of chemicals but also for the turnover and formation of soil organic matter.

Session 4:   What is the contribution of methods and modelling approaches from systems biology/ecology to understanding SOM in the soil system?

Keynote

K5   **Mapping microbial transduction of root carbon using isotope-enabled molecular approaches**

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KEYWORDS Rhizoshere, microorganisms, AMF, minerals, isotopes

The rhizosphere is the nexus of plant-soil-microbe interactions. As plant roots transfer organic compounds to the soil, the characteristics of and processes mediated by soil microbes are central to the fate of this OM. We have been investigating (i) *who* utilizes the C (*i.e.*, which microbial taxa), (ii) the turnover rates of C in microbes, (iii) the interactions of these microbes with mineral surfaces, and (iv) the characteristics of the resulting OM-mineral interactions. Our goal is to understand and quantify the roles played by bacteria, fungi, phage, and fauna in the transformation and transfer of root C into soil. Our general approaches have involved growing a common Mediterranean annual grass (Avena b*arbata*) with highly enriched $^{13}CO_2$ and following ^{13}C-labeled carbon transfer into soil. We have determined the microbial consumers using a combination of density-gradient stable isotope probing, metagenomic analyses, and nanoSIMS visualization. We assessed microbial associations with three types of minerals (quartz, kaolinite, and ferrihydrite) added to soil near roots by total DNA and ^{13}C analyses, 16S and ITS analyses of mineral associated DNA. We have used STXM to image the distribution of specific C functional groups and overlay those images with NanoSIMS mapping of ^{13}C enrichment across the mineral surfaces. Our findings indicate that 1) microbial utilization of root C provides a pathway for C movement to and a means of C association with mineral surfaces; 2) microbial colonization of fresh minerals differs depending on mineralogy; 3) while mineral reactivity enchances SOM association, the presence of even relatively non-reactive surfaces allows for SOM accumulation.

S1   **The soil C cycle as microbial metabolism: integration of soil metagenomic and chemical data**

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KEYWORDS Metagenomes, High resolution mass spectrometry, pathways, metabolism

A reciprocal soil transplant experiment was initiated in 1994 in eastern Washington in which soil cores were transplanted between two elevations (310 m and 844 m); the lower site is warmer and drier, and

the upper site is cooler and wetter. After 17 years, the bacterial community structure did not change significantly, although microbial function (enzymes, soil respiration) did. We resampled the transplanted cores the following year to characterize the microbial community functional capability (metagenomics), biochemical potential of carbohydrate-active enzymes (assays), and the soil organic matter profile (Fourier-Transform Ion Cyclotron Resonance, "FTICR").

Integrated 'omics data can potentially improve our understanding of how climate and soil environments affect soil microbial C cycling processes. However, the complexity and heterogeneity of soil makes it difficult to separate treatment-specific signal from noise. Thus, robust inferences of direct environmental impacts on soil microbial processes from individual 'omics technologies have been elusive. Rigorous statistical approaches were applied to extract distinctive features from the FTICR and metagenomic datasets to identify features that are differentially abundant. We found specific empirical formulae that discriminated soils by treatment, and developed methods to mine KEGG pathways to link those formulae with the enzyme assay data and metagenomic features using Trelliscope, an interactive statistical tool for exploratory data analysis. In this way, we identified the critical metabolic pathways that were significantly associated with treatment differences in both the metagenome (microbial capabilities) and in the chemical profile, indicating execution of these processes. For example, we identified impaired lysine biosynthesis in the lower site, through missing enzymatic capabilities in the metagenome in conjunction with absence of the coordinating reactions in the chemical data. The ability to infer biological and chemical bottlenecks from disparate sets of shotgun data presents new opportunities for exploring soil C persistence and vulnerability through the lens of microbial metabolism.

S2   The role of microbial biodiversity in soil C stabilization

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KEYWORDS Microbial biodiversity, organo-mineral interactions, management

New insights into the mechanisms that control the stability of soil organic matter (SOM) have revealed the importance of microbial processes in the accumulation of SOM. Despite this, little is known about biodiversity-function relationships in microbial communities, particularly the role of microbial biodiversity in soil carbon (C) stabilization. In macroecology, diversity-function relationships indicate that increases in species diversity result in increases in ecosystem productivity. Similar trends have been found in microbial culture studies, but manipulations of microbial diversity directly in soils have found variable impacts on the magnitude and direction of various ecosystem functions.

We took advantage of a management-induced difference in microbial biodiversity between remnant woodland and perennial pasture on the same soil type on the Fleurieu Peninsula, South Australia. We varied the biodiversity in soil microcosms by sterilization (using gamma irradiation) and inoculation with a dilution-series of the native microbial communities. We tracked the fate of ^{13}C-labeled litter (mixed grasses and eucalypts; 20 at%) into $^{13}CO_2$ and mineral soil fractions at five time points during a year-long incubation. Biodiversity was explored using Ion Torrent sequencing of 16S and ITS genes. SOM chemistry was evaluated using NMR spectroscopy.

By 11 weeks, significant and opposing trends emerged between the two land uses; in the managed pasture soils, reductions in biodiversity resulted in greater SOM-derived CO_2 production, but in the woodland soils reduced biodiversity resulted in less SOM-derived CO_2. No significant trends were observed for litter-derived CO_2 for either land use at this early time point. Further work will probe the contribution of litter-C to the mineral stabilized soil fraction through time. NMR spectroscopy revealed

that for both land use types, SOM chemistry was more similar in microcosms with higher microbial diversity than those with lower diversity across the dilution series. Together with additional mass spectrometry and NMR data, we expect to find that microorganisms with higher microbial diversity process C more efficiently, resulting in greater litter-C accumulation in SOM. We expect results from this study to provide new insights into the contributions of microbial biodiversity to the turnover and formation of SOM, which will have implications for management practices.

S3   Effects of macro-nutrients on microbial metabolism driving soil organic carbon cycling

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The effect of macro-nutrients on carbon outputs such as heterotrophic respiration and the mechanisms involved are still not fully understood and thus difficult to predict. Our objectives were to quantify long-term effects of nitrogen (N) and phosphorus (P) fertilization on soil organic carbon (SOC) stocks in ten meta-replicated field experiments in Sweden. In addition, short- and long-term effects of contrasting N and P availability on CO_2 and heat production were determined in three of these field experiments to advance our understanding on how major soil nutrients influence microbial metabolism and SOC cycling.

For the incubation experiment, we sampled the following three management treatments in each of three selected long-term field experiments: i) no NPK (0NPK), ii) no PK but highest N level (N_{0PK}) and iii) no N but highest PK level (PK_{0N}). We combined each field-treatment at each field site with 8 laboratory-treatments, which were no nutrient addition (Con) as well as +N, +P, +NP, Glucose, Glucose+N, Glucose+P and Glucose+NP additions. Five grams of soil were filled into 20 ml glass reaction vials with an agar-cresol-red indicator dye in their headspace as CO_2 trap. Heat production was recorded during five hours in an isothermal calorimeter and the trapped CO_2 was measured in a spectrophotometer.

We found a significant negative effect of PK-fertilization on long-term SOC stocks in the ten investigated experiments and the incubation experiment confirmed that this was most likely related to stimulated microbial metabolism due to P fertilization: While Glucose+N addition reduced CO_2 (-14%) and heat (-14%) production as compared to glucose addition alone, Glucose+P addition increased CO_2 and heat production by 17% and 9%, respectively. Similar results were found when comparing the contrasting long-term field-treatments: PK_{0N} had a higher Glucose-induced CO_2 and heat production per unit SOC as compared to 0NPK, while both were suppressed in N_{0PK} fertilised soils. For N, we found a clear interaction of the short-term response to N addition and long-term fertilisation history: Only in N-deficient soils, N-addition led to reduced CO_2 release, which may indicate microbial N mining when glucose was added without N in these soils. We conclude that nutrient effects on microbial metabolism do strongly drive SOC cycling.

S4   Long-term versus short-term warming effects on microbial processes and soil organic matter storage

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Rapid warming in northern ecosystems is predicted to drive massive losses of carbon from soils to the atmosphere, raising concerns that it will create a positive feedback to climate change. There is increasing evidence, however, that the soil heterotrophic microbial community can acclimate to temperature change at time scales from months to years, resulting in attenuating responses of soil organic matter decomposition. Despite this, virtually nothing is currently known about long-term warming effects on the activity and physiology of microbes, and, through this, the longevity of carbon losses from northern ecosystems. This study was conducted at a unique research site that makes use of natural (geothermal) gradients in soil temperature that have been in place for over 50 years as a natural warming treatment (FORHOT, www.forhot.is). We determined long-term warming effects (+0.5 °C, +1.5 °C, +3 °C and +6 °C) on soil carbon dioxide release, and explored microbial carbon use efficiency, growth, turnover rates and community composition (sequencing of the bacterial/archaeal 16S rRNA genes and fungal internal transcribed spacer, ITS, regions) as mechanisms. We also performed a companion incubation experiment to compare longer-term warming effects on microbial processes to those caused by six weeks of warming of ambient soil to the same temperature increase (+3 °C and +6 °C). We show that while microbial respiration was consistently higher by up to 30% after six weeks of warming, this effect did not persist in soils exposed to 50 years of warming. Microbial carbon use efficiency was not affected by soil warming, neither in the short-term nor long-term, but for different reasons. In the short-term warming treatment, both microbial respiration and growth were increased, while in the long-term microbial respiration and growth were unaltered by elevated temperature. However, under long-term warming, microbial turnover (biomass specific growth) was higher at elevated temperatures compared to ambient controls. This demonstrates that a faster turnover of the microbial community with warming persists even after 50 years. We further explored the underlying mechanism of this response with a microbial C and N turnover model. Interestingly, by simply implementing a positive response of the efficiency of extracellular enzymes to increasing temperature we were able to reproduce the experimentally observed pattern. We present further data linking such long-term thermal acclimation to shifts in microbial community composition, and discuss our findings in the context of warming-driven feedbacks from northern latitude soils to future climate change.

S5   Composition and functions of microbial communities in top- and subsoils of degraded pasture ecosystems on the Tibetan Plateau

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Kobresia pygmaea grasslands of the Tibetan Plateau provide a tremendous sink for organic carbon (OC). They form the basis for local pasture economy, prevent soils from erosion, and retain large amounts of water for SE Asia. Overgrazing triggers grassland degradation by altering plant species composition, and destroying the protective *Kobresia* root mats leading to massive OC losses and ecosystem destabilization. In this study, degradation of *Kobresia* mats were thereby classified into six degradation stages.

The aim of this study was to determine soil organic matter (SOM) composition in relation to degradation and to analyze the effects of altered SOM composition on microbial community. composition and functioning. Vertical gradients of δ^{13}C and δ^{15}N-values, neutral sugars, cutin and suberin contents, lignin phenol contents as well as microbial and fungal community compositions (t-RFLP analysis followed by MiSeq sequencing), and activities of six extracellular enzymes involved in the C, N, and P cycles were assessed.

Increasing degradation caused by intensive pasturing resulted in an increased OC decomposition demonstrated by decreasing δ^{13}C-, δ^{15}N-values and C/N ratio. The δ^{13}C shift towards more negative values reflects the relative enrichment of ^{13}C depleted macro-molecules such as lignin and suberin/cutin during OC decomposition in the strongly degraded soils. Translocation of topsoil material into the subsoil with advancing degradation was indicated by increasing contributions of cutin to OC in the subsoils. Enzyme activities involved in the degradation of more complex OC compounds (e.g. fungal phenoloxidases) increased with changing SOM composition and were highest in the subsoil of strongly degraded stages 4 and 5, whereas other enzyme activities decreased. Decreasing overall enzyme activities and increasing activity of phenoloxidases were associated with progressive alterations in microbial and fungal community composition, which were most pronounced in the subsoil, e.g. a pronounced decline in the phylum of Actinobacteria. Bacterial diversity (Shannon-Wiener index) was particular responsive to the degradation of *Kobresia* root mats and declined significantly along the degradation sequence, while overall diversity of the fungal community remained similar. As microbial communities play a central role in soil biogeochemical cycles, we conclude that the observed alterations of microbial community structure and losses in bacterial biodiversity with *Kobresia* degradation may strongly affect ecosystem processes.

Session 5:   Modelling approaches for the integration of process components

Keynote

K6   Accounting for microbial habitats in modeling soil organic matter dynamics

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KEYWORDS Microbial habitat, model, localization

The extreme heterogeneity of soils constituents, architecture and inhabitants at the microscopic scale is increasingly recognized. Microbial communities exist and are active in a complex 3-D physical framework of mineral and organic particles defining pores of various sizes, more or less inter-connected. This results in a frequent spatial disconnection between soil carbon, energy sources and the decomposer organisms and a variety of microhabitats that are more or less suitable for microbial growth and activity.

However, current biogeochemical models account for C dynamics at the macroscale (cm, m) and consider time- and spatially averaged relationships between microbial activity and soil characteristics. Different modelling approaches have intended to account for this microscale heterogeneity, based either on considering aggregates as surrogates for microbial habitats, or pores.

Innovative modelling approaches are based on an explicit representation of soil structure at the fine scale, i.e. at µm to mm scales: pore architecture and their saturation with water, localization of organic resources and of microorganisms. Three recent models are presented here, that describe the heterotrophic activity of either bacteria or fungi and are based upon different strategies to represent the complex soil pore system (Mosaic, LBios and µFun). These models allow to hierarchize factors of microbial activity in soil's heterogeneous architecture.

Present limits of these approaches and challenges are presented, regarding the extensive information required on soils at the microscale and to up-scale microbial functioning from the pore to the core scale. Accounting for microbial habitats in modelling soil organic matter dynamics can be based on an explicit representation for the microorganisms' environment.

M1   Uncertainty of a soil organic matter model at the microscale: Influence of the microhabitat structure

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KEYWORDS Dissolved organic carbon, Monod equation, Monte-Carlo approach, Lattice Boltzmann model

Rationale and objectives: How can be quantified the role of microscopic interactions occurring at the scale of microbial habitats in soils as these interactions are believed to be a major gap of knowledge to explain the lack of robustness of macroscopic models of soil carbon dynamics ? So far, models including spatial discretization of soil pore space have been parameterized with one set of biological parameters, for instance in Ingwersen et al., (2008) or in Resat et al., (2012). The question is to quantify the proportion of uncertainty on the outputs of these discrete models that is linked to uncertainty of

parameters describing micro-organisms physiology on the one hand and to uncertainty of parameters describing the soil microhabitats. In other words, is uncertainty linked to soil structure lost in too large uncertainty of the biological parameters?

Methodology approach: To answer the question, a global uncertainty analysis for microbial parameters has been performed in this study. We present a comparison between the variance of outputs of the carbon dynamics module obtained in homogeneous conditions, without soil structure explicitly assigned (named after homogeneous conditions) and the variance of outputs of the same carbon dynamics module used in a spatialized heterogeneous porous medium (named after heterogeneous conditions). In the latter conditions, outputs were obtained in a previous study [Vogel et al., 2015] using a Lattice Boltzmann model named LBIOS and scenarios built in a complete factorial design varying some physical microscopic descriptors while microbial parameters remained unchanged [Vogel et al., 2015].

Results and conclusions: The strong physical influence on biodegradation was betrayed by the concentrations of the dissolved organic carbon pool, which exhibited very distinct distributions whether examined in homogeneous or heterogeneous conditions, rather than by the CO_2 pool. We noted that extreme kinetic patterns observed when environment was not considered (extremely rapid growth, absolute storage in dormant biomass, insignificant cumulated respiration) did not appear when spatial heterogeneity was described. Although being contingent upon our model specificities, these observations encourage questioning generally how soil biophysical phenomena traditionally perceived in lumped space are actually shaped by the nature and kinetics of undescribed microscale processes.

M2   Simulation and prediction of biomass turnover and soil organic matter formation

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KEYWORDS Biomass; Non-extractable residues; Growth; Yield

Recent findings strongly indicate that soil organic matter is formed from bacterial decay products, and within the microbial food chain. We present a mathematical model for simulation and prediction of biomass turnover and soil organic matter formation. A key parameter for this prediction is the yield. The microbial yield is the ratio of biomass formation to substrate consumption. Common methods for the calculation of yield, derived in biotechnology, are based on balancing the *Gibbs* energy of formation of products and educts. We developed a new pathway-independent method dedicated for the estimation of yields from xenobiotic substrate that includes the *Nernst* equation and the availability of electrons to biological processes. Labelled substrate turns into metabolites, biomass, non-extractable residues (NER) and CO_2. Decaying microbes are the substrate for new microbes, which consume the necromass (or the necromass becomes stabilized e.g. by Fe incorporation or adsorption). Hereby, fatty acids and sugars are preferably consumed while amino acids (including DNA) are remarkably persistent and accumulate. We expect that this fraction eventually forms the soil organic matter pool.

We have set up a dynamic model that simulates biomass formation from carbon substrate, biomass turnover, and the formation of soil organic matter. It uses the common equations for enzymatic kinetics and microbial growth (*Michaelis-Menten* and *Monod* kinetics) and is expanded for the terms biomass decay, new biomass formation and biological non-extractable residue (bioNER) formation. The yield is pre-estimated, and for the decay rate default values can be used. Thus, only the initial biomass of the degrader population and the maximum growth rate remain as fit parameters. The simulation results are contrasted to studies with ^{13}C-labeled pesticides and pharmaceuticals degraded in soil mesocosms. The simulated living biomass is plotted versus phospho-lipid fatty acids (PLFA), while the sum of living and dead biomass is compared to the measurable total amino-acid fraction. An outcome of the equations is also that the knowledge of the yield allows to estimate bioNER formation from the CO_2 evolution. The presentation will describe the method and show simulation results.

M3   Microbial control of SOM dynamics in the detritusphere: Insights from modeling coupled pesticide degradation and organic matter turnover

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The detritusphere is a microbial hot spot, where interactions between transport processes and microbial dynamics strongly control organic matter turnover. Much faster rates of C cycling processes in this microhabitat compared to bulk soil significantly determine C cycling at higher scales up to the ecosystem scale and directly affect the formation and decomposition of SOM. Our objective was to quantify and unravel the microbial processing of litter-derived and pesticide-derived C in the detritusphere and its contribution to SOM dynamics.

We modeled pesticide degradation coupled to C turnover informed by physicochemical, isotopic and genetic data from a microcosm study and conducted a process analysis to better understand the underlying mechanisms of coupled pesticide, C and microbial dynamics in the detritusphere. The model considers dynamic feedbacks between specific microbial groups and their micro-environment. We used a combined data set of genetic information on abundances of bacteria, fungi and specific pesticide degraders and of biogeochemical dynamics of C and a pesticide (MCPA, 4-chloro-2-methylphenoxyacetic acid). A multi-isotope approach was utilized to trace the C flux from litter-C (^{13}C) and pesticide-C (^{14}C) to soil.

The model allowed exploring the temporal dynamics of C fluxes between the different system components (microbes and C pools) and analyzing the microbial control of SOM dynamics in the detritusphere. According to our simulations, input of litter-derived C triggered the successive increase of fungal control on C cycling in the detritusphere. Increased fungal growth in the detritusphere compared to bulk soil enhanced SOM decomposition and relocated insoluble soil-derived SOM to dissolved organic C. This led to increased availability of soil-derived C for microbes. Loss of insoluble SOM was partly compensated by the formation of litter and pesticide-derived SOM via death of fungi and specific pesticide degraders. Thus, the simulations show that accelerated microbial processes in the detritusphere strongly affect SOM decomposition and formation.

M4   Soil weathering as a control on the linkages between measured soil carbon fractions and modeled soil carbon pools

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KEYWORDS Soil weathering, Soil carbon stabilization, Geochemistry, Linking fractions to pools

Recent studies have linked measured soil carbon (C) fractions to modeled soil C pools. This is a major step forward in bringing experimental data on soil C turnover into a modeling framework. However, most studies on C turnover in soils are conducted on time scales ranging from 1 to 100 years, and in this context the soil mineral matrix, an important factor for C stabilization in soils, is often considered static. In contrast, soil weathering is traditionally studied at longer time-scales (centuries to millennia). In this study, we are trying to address this temporal discrepancy in the research between C sequestration (short-term process) and soil genesis (long-term process) to better understand the controls that explain C stabilization and turnover on the long-term.

Combining incubation and fractionation experiments with geochemical soil analyses, we show along a 3000 kyr fluvial terrace chronosequence that soil C content and the distribution of C among different fractions, as well as the potential turnover of these fractions, is highly variable as a consequence of mineral weathering. Generally, C content is lower in older than in younger terraces. In contrast, respiration per unit C increases with the age of terraces. While enzymatic activity and enzymatic residues are similar along the sequence, other microbial residues are depleted in older terraces, indicating changes in the microbial decomposer community and in the stabilization of its residues. Soils developed in younger terraces show an increased ability to stabilize C with the mineral phase. Silt and clay associated C, the fraction with the oldest measured ^{14}C signature, was insensitive to incubation temperature and geochemical changes. Interestingly, measuring reactive specific mineral surface area (SSA) revealed that C content is not correlated to SSA. However, soils developed in more weathered deposits lose the ability to form aggregates and to provide physical protection of C by occlusion leading to lower soil C content, higher temperature sensitivity and faster turnover. We relate the decreasing effectiveness of physical protection with time to weathering related mineralogical changes as aggregate stability relies critically on the geochemistry of soils.

We conclude that, at larger spatio-temporal scales, linking measured fractions to modeled pools in C turnover models needs to be considered very carefully with changes in the mineral matrix in order to accurately reflect C turnover on the long term. Linking fractions to pool in models has to be treated dynamically through time with turnover time of some fractions potentially changing.

M5   Mechanistic modeling linking thermal and hydration dynamics with microbial methane production and emissions from permafrost soil

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KEYWORDS Soil permafrost, Temperature rise, Methanogens, Methanotrophs, Methane emission

The sensitivity of Polar regions to raising global temperatures is reflected in rapidly changing hydrological processes associated with pronounced seasonal thawing of permafrost soil and increased biological activity. Of particular concern is the potential release of large amounts of soil carbon and stimulation of other soil produced GHG emissions such as methane. Soil methanotrophic and methanogenic microbial communities exhibit rapid adjustment in activity and spatial organization in response to permafrost thaw depth and hydrology driven by environmental factors. Soil structural elements such as aggregates and layering affect oxygen and nutrient diffusion processes thereby promoting methanogenic activity in temporal anoxic niches (hotspots). We developed a mechanistic individual based model to quantify microbial activity dynamics in soil pore networks including transport processes and

enzymatic activity associated with methane production and fate in soil. The model was upscaled to represent processes at a soil profile where freezing/thawing provide macroscopic boundary conditions for different microbial activity with soil depth. The model distinguishes between microbial activity in aerate bulk soil and in aggregates (or submerge profile) essential for estimation of methane production and oxidation rates. Methane transport by diffusive fluxes and ebullition of bubbles show sensitivity to hydration dynamics. The model quantifies how seasonal dynamics of microbial community composition affect net methane emissions in good agreement with experimental data. An abstraction of physically based models for soil microbial activity in thawing permafrost soils are of interest for estimation the carbon decomposition rates and net methane emissions in such rapidly changing and sensitive ecosystems. The model provide a consistent framework for systematically assessing the impacts of key controlling factors (e.g., nutrient availability, enzyme activity, PH) on long term methane emissions and carbon decomposition rates with temperature rise in polar regions.

M6   A first step to model SOM dynamics by stochastic self assembly

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KEYWORDS cellular automaton, diffusional aggregation, structural stabilization

Traditionally SOM pools were ranked by biodegradability with the most recalcitrant high-molecular compounds forming the stable stocks. The current view on SOM emphasizes diffusion, adsorption and self-assembly of small molecules. Protection against microbial decay is attributed to accessibility and micro-environmental conditions. In contrast, established SOM-simulation models do not consider explicitly the mineral-matrix structure and the spatial arrangement of SOM. This probably limits their ability to predict environmental impacts on SOM pools. As an alternative we suggest a model that adds stochastic diffusional pattern formation to the classical first-order kinetics of decay.

The model was implemented as a 2-D cellular automaton consisting of mineral matrix and non-mineral cells that are either empty or filled with SOM. In each new generation empty cells become organic at a certain probability. Existing organic cells can diffuse or be degraded, again as a stochastic process. The probability of decay depends on the number of mineral or organic neighbors: the more solitary an organic cell, the more easily it is degraded. Main model parameters are the structure of the mineral matrix, the probabilities of appearance, diffusion, and decay of SOM micro cells; and the neighboring modification of these probabilities. The model behavior has been tested over a wide parametrization range. SOM concentration development, spatial arrangement, and age distribution have been analyzed with regard to SOM characteristics in soils.

Most parameter sets yielded model systems where SOM density approached a weakly fluctuating equilibrium. In mature model systems SOM is clustered in inter-particle spaces and on particle surfaces with particles close to each other forming aggregates. Final SOM concentration increased with increasing mineral surface area. The age distribution of SOM showed a two-peak tendency with a maximum in youngest and oldest SOM, the latter barely accessible and mostly in mineral pockets. The number of steps to reach quasi equilibrium can be high which could be interpreted as an evolutionary process of structural stabilization. Rearrangement of the mineral matrix by "mixing" lead to a fast decrease of SOM density and a new spatial stabilization cycle. Mature model systems were independent of the initial distribution of SOM cells, e.g. spiking with "free" SOM had only ephemeral effects. We conclude that the cellular automaton simulates typical SOM processes not possible in classical models. The future challenge will be in relating the lumped stochastic parameters to soil parameters. First calibration tests could be done with SOM micro-imaging.

M7   Artificial neural network development for forecasting soil carbon sequestration of paddy soils in Thailand

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KEYWORDS Artificial neural network , Carbon sequestration, Paddy soils, Thailand

Rice organic farming is a method of using organic substances to increase soil fertility for crop production. This study was aimed to investigate the effects of soil management for 10 years conversion from conventional rice faming (CRF) into organic rice farming (ORF) with focus on the amount of organic carbon fractions and organic carbon storage as maintained in the soil. For this study, the experiment was conducted in rice plots of farmers who were divided into two groups: organic and conventional, with 11 farmer plots in each group and which consisted of 132 data respondents for each group that resulted from 11 farmer plots, each plot having 3 replications and each replication consisting of 4 soil depths (e.g.0-5, 5-10, 10-15 and 3=15-30 cm.) Carbon fractions analysis in soils included total organic carbon (TOC) and labile organic carbon fractions (LOC); they are water soluble carbon (WSC), hot water soluble carbon (HWSC), permanganate oxidized carbon (POXC), carbon in coarse particulate organic matter (CPOM-C) and carbon in fine particulate organic matter (FPOM-C).
ANN model design: learning algorithm is Levenberg-Marquardt (LM), number of hidden node is 5 hidden nodes and all datasets are divided into two datasets (one dataset is for learning and validation and another dataset is for testing model performance) with the ratio 11:3. In addition, for learning and validation set as random for 50 times and the result of testing is the average of all 50 runs. Experiment 1: Comparison different unit of input variables between mg/kg and g/m^2 as indicated *X* and *XX* respectively. Experiment 2: Investigation of using different input variables that can be classify into 4 models; The organic carbon sequestration by soil: At organic farm forecasting TOC (kg/m^2) model A and D, which have %clay as the extra input variable show the best performance (0.79) and model B that has no extra input variables (CEC and %clay) present the low R^2 value (0.55). The negative ME indicate that the models over estimated SOC stocks. In particular, AA model with a ME of −0.14 kg/m^2 had the highest over estimation in organic paddy soil, while BB model with ME of −0.50 kg/m^2 showed the highest tendency for over- estimation in conventional paddy soils.

M8   Environmental drivers and microbial activity: alternatives in modeling of soil organic matter decomposition

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KEYWORDS Microbial activity, model structure, temperature sensitivity

Incorporating of microbial biomass as a driving factor in ecosystem models describing soil organic matter (SOM) turnover became a mainstream in this research field reflecting a demand for improvement of large-scale earth system models (Wieder et al., 2015). The complexity of simulated biochemical and physico-chemical processes in soil presumes multiple alternatives in conceptual modeling schemes and ways of mathematical representation of microbial activity. A crucial task and one of future research directions is formulating of parsimonious description of environmental control of microbial biomass growth and turnover. We compared three model versions of SOM turnover driven by microbial activity

under different temperatures. The first case describes microbial response on temperature by direct inclusion of Arrhenius function in decomposition rate equation and in equation describing microbial turnover. In the second case, we assumed the temperature effect on microbial growth efficiency in addition to the dependencies described in model 1. In the third case, we added in the model microbial activity function r (Panikov, Sizova, 1995) and corresponding temperature effect on it (Blagodatsky et al., 2011). The model approaches were compared in respect to the dynamic behavior of all SOM pools, microbial biomass and respired CO_2 as well as model complexity (degree of freedoms and possibility to evaluate model parameters). Suitability of tested model approaches for incorporation in large-scale earth system models is discussed.

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Abstracts of poster presentations

Poster session 1:   Who are the relevant actors and drivers and in which micro-habitats or „hot spots" do they appear?

AP1   Microbial production of condensed aromatic structures in soil

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KEYWORDS Biological black carbon production, stable isotope labelling, pyrogenic vs. non-pyrogenic aromatic carbon, benzene polycarboxylic acids, black soils.

Black carbon (BC) is a complex continuum of partly charred organic matter predominantly consisting of condensed aromatic and graphitic moieties and it has high potential for long-term carbon sequestration in soils and sediments. There has been common agreement that BC is exclusively formed by incomplete combustion of organic matter, while non-pyrogenic sources are negligible. In this study, we investigated the stable carbon isotope signature of benzenepolycarboxylic acids (BPCAs) as molecular markers for BC to test if there is also a significant contribution of non-pyrogenic carbon to this fraction in soils. BPCAs were formed by hot nitric acid oxidation of different soils and analyzed by three different procedures: (i) elemental analysis – isotope ratio mass spectrometry (EA-IRMS) of bulk BPCAs and gas chromatography – combustion – isotope ratio mass spectrometry (GC-C-IRMS) of (ii) BPCA trimethylsilyl (TMS) derivatives, and (iii) BPCA methyl derivatives. Best accuracy and precision of isotope measurements were obtained by EA-IRMS of bulk BPCAs although this method has a risk of contamination by non-BC-derived compounds. The accuracy and precision of GC-C-IRMS measurements were superior for methyl derivatives (W0.1% and 0.5%, respectively) to those for TMS derivatives (R3.5% and 2.2%, respectively).

Comparison of BPCA d13C values of soil samples prior to and after laboratory and field incubations ranging from one month to 25 years with both positive and negative 13C labels at natural and artificial abundances revealed that up to 25% of the isolated BC fraction in soils had been produced in situ, without fire or charring. Commonly applied methods to quantify BC exclusively formed by pyrogenic processes may thus be biased by a significant non-pyrogenic fraction. Further research is encouraged to better define isolated BC fractions and/or understand mechanisms for non-pyrogenic BC production in soils.

AP2   Identification of novel 7-methyl branched glycerol dialkyl glycerol tetraethers in Chinese lakes

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KEYWORDS 7-methyl brGDGTs identification biomarker lake sediments membrane lipids

Branched glycerol dialkyl glycerol tetraethers (brGDGTs) are bacterial membrane lipids that are widely used as valuable paleoenvironmental proxies. The recently discovered 6-methyl brGDGTs improved the accuracy of the proxies for temperature "methylation branched tetraethers (MBT)" and soil pH "cyclization branched tetraethers (CBT)". However, the calibration uncertainties are still substantial for brGDGT-derived proxies (e.g., 5 °C for MBT). Here we report a series of novel 7-methyl brGDGT isomers that co-eluted with the known 5- and 6-methyl brGDGTs in normal phase high performance liquid chromatography (HPLC). The mean relative abundance of 7-methyl brGDGTs is ca. 5.9% of the total brGDGTs in Chinese lake sediments. In addition to the 7-methyl brGDGTs, we identified a novel tetramethylated brGDGT based on the HPLC/MS method. The relative abundance of uncommon hydrocarbons, which were generated from the ether cleavage of tetramethylated brGDGTs (m/z 1034), revealed two structural isomers with one cyclopentane moiety. The presence of the newly discovered brGDGTs in commonly applied HPLC separations may explain the high calibration uncertainty for brGDGT-based proxies.

AP3 Epigeic earthworms change quantity and composition of dissolved organic carbon during composting of garden waste

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KEYWORDS DOC fractionation, vermicomposting, carbon stability

Vermicomposting is an alternative composting method that is efficient at stabilising biodegradable waste. Dissolved organic carbon (DOC) content and composition (humic acid, fulvic acid, hydrophobic neutrals, hydrophilics) has recently been proposed as an indicator of compost stability. The objective of this study was to assess the earthworm effect on DOC content (quantity) and composition (quality), and on N_2O emissions; and link this effect to substrate quality. Earthworms reduced total DOC content compared to conventional composting, indicating higher stability of earthworm compost. CO_2 evolution of the compost was linearly related to the concentration of DOC. The concentrations of humic acid and fulvic acid were significantly reduced by earthworms, whereas there was no significant effect on hydrophobic neutrals and hydrophilics. The humic acid fraction was depleted more quickly than DOC, fulvic acid or hydrophilics, and the hydrophobic neutrals showed the lowest depletion rate upon compost maturation. Faster decomposition of humic acid than of hydrophilics could either be due to relatively fast lignin degradation in the compost and / or interactions within the various DOC pools, in agreement with recent perspectives on humic acids as supramolecular associations. Earthworms also reduced the fluxes of N_2O, another major greenhouse gas and reduced the ammonium : nitrate ratio of the compost, another indicator of compost stability. Our results suggest that measurement of DOC content and composition provides greater insight into the carbon stabilisation process.

AP4   Is there a link between land use and priming effect?

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KEYWORDS Priming effect, land use and management, stable isotope (13C), extracellular enzyme activities, nutrient availability

Microbial growth in soils can be limited by both carbon and nutrients like nitrogen (N) and phosphorus (P). The addition of labile carbon increases microbial activity and enhances the decomposition of native soil organic matter, a process termed priming effect. What is causing this priming effect, how it is affected by soil nutrient availability and if microbes use the extra carbon input also to acquire limiting nutrients is still poorly understood. Our study aimed to determine if land use (forest vs. grassland) and management (coniferous vs. deciduous forest, fertilized vs. unfertilized grassland) affect the direction and magnitude of priming effects, and if priming was driven by nutrient limitation. Composite topsoil samples were collected from 60 differently managed study sites in three regions in Germany. Samples were incubated with and without the addition of 800 µg glucose-C/g soil (100‰ 13C), and CO_2 evolution and its isotopic composition were monitored with gas chromatography coupled with isotope-ratio mass spectrometry for 48 hours. Four potential extracellular enzyme activities (ß-glucosidase, N-acetyl-glucosaminidase, sulfatase and phosphatase) were determined at the end of the incubation. Positive priming was observed in both land use types. Cumulative priming was significantly ($P<0.05$) higher in the grassland (2.2±0.3 mg CO_2-C/g OC) than forest (1.3±0.1 mg CO_2-C/g OC) sites in HAI but not in the other study regions. For management intensities, priming effect was not significantly different between coniferous and deciduous forests, but was higher for fertilized than unfertilized grasslands in all study sites, even though these results were not statistically different. Phosphatase activities increased significantly ($P<0.05$) in the ALB (30%) and HAI (65.3%) forest following glucose addition. This suggests that soil priming in the forest sites may be driven by P limitation, which is further supported by a negative correlation (Pearson) between priming and organic P in the forest samples (r = -0.71, p<0.001). Principal Component Analysis was used to link study region and soil abiotic properties to priming. In forest, priming intensity was positively correlated with pH and clay content, and negatively correlated with inorganic P and C:N ratio. In grassland, priming was positively correlated with pH and negatively correlated with organic and inorganic P. In summary, our results suggest that the controls for soil priming differ between forest and grasslands, and these differences could be driven by land use and management which were important controls for belowground soil organic carbon and nutrient availabilities.

AP5   Maize rhizosphere effects on soil aggregate stability and associated enzymes activities in field

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KEYWORDS rooted soil, root exudation, free microaggregates, plant density, specific enzyme activity

The alterations in soil C stocks have impacts on global C cycle. One of the important biotic drivers regulating soil C cycle is soil microorganisms. A reliable and sensitive proxy for microbial activity is the activity of extracellular enzymes (EEA). In the present study, we sought to comprehend how soil aggregates may affect EEA under three maize plant densities in field.

A modified optimal-moisture sieving technique was used to separate bulk soil for various aggregate size classes (>2000 µm large macroaggregates; 2000-250 µm small macroaggregates; <250 µm free microaggregates). Microbial biomass and EEA catalyzing decomposition of cellulose (β-1,4-glucosidase, BG), chitin (β-1,4-N-acetylglucosaminidase, NAG), proteins (L-leucine aminopeptidase, LAP) and organic P (acid phosphatase, acP) were measured in the rhizosphere of maize grown at three plant densities (low, normal, high) and bare fallow in field.

Microbial biomass C tended to decrease from macro- to microaggregates; however, it was similar between bare fallow and three plant densities. EEA and specific EEA (per unit microbial biomass C (MBC)) increased with decreasing aggregate size classes. In comparison with bare fallow, the specific EEA was higher up to 73% for BG, 31% for NAG, 26% for acP and 92% for LAP in free microaggregates in rooted soils. High plant density declined distribution of macroaggregates by 9% as compared to bare fallow, whereas other aggregate size classes were not affected.

Enhanced EEA in three aggregate size classes in rooted soils demonstrated activation of microorganisms by roots. Higher specific EEA in rooted soils suggested microbial demand for nutrient acquisition via enzymes production. Remarkable increase of EEA in free microaggregates isolated through the modified optimal-moisture sieving can be explained by the microaggregates' localization within the soil matrix. Being originally adhered to surfaces of macroaggregates, those microaggregates were preferentially exposed to energy and mass flows thereby promoting microbial activity.

AP6   Spatial variability of microbial key players and their activity patterns in subsoil and hot spots

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KEYWORDS Drilosphere, rhizosphere, subsoil, next-generation sequencing, DNA-SIP

Nutrient and SOM turnover processes in soil are highly dependent on the quantity and quality of organic matter and the microbial community composition, which determines the physiological and regulatory capabilities for degradation and transformation processes. Highly relevant changes in the nutrient and SOM composition are found at the small scale along soil depth gradients and in soil hotspots such as rhizosphere, drilosphere, and detritusphere. In these hotspots, easily degradable organic compounds are released from litter, earthworm cast and roots, whereas in subsoil oligotrophic conditions predominate.

To assess the spatial heterogeneity and key players of the prokaryotic soil community in different soil habitats of varying nutrient quantity and quality, 16S rRNA gene next-generation sequencing of bacteria and archaea was conducted in topsoil, subsoil, drilosphere, and rhizosphere. Furthermore, the activity pattern of root exudate-using bacteria was investigated via DNA-SIP and Illumina-sequencing of the wheat rhizosphere at different soil depth.

The studies reveal that at soil hot spots with high quality of organic matter such as rhizosphere and drilosphere, copiotrophic microbes of Proteobacteria, Bacteroidetes, and Firmicutes dominate the community. Within the rhizosphere, high variation among the active bacterial fraction is observed at different soil depth and root developmental status.

In contrast, oligotrophic conditions and low quality of SOM favor putative oligotrophic microbes, e.g. Acidobacteria. Especially at deeper soil horizons, a shift of the microbial community towards slow

growing microbes is observed. Interestingly, archaea respond less to the nutrient status of the soil habitat.

In further studies, the integration of "omics" approaches and SIP at different molecular levels are needed to understand microbial network interactions and cross-feeding during soil nutrient and SOM turnover. The quantification of active microbial pools at the small-scale is essential for prediction of SOM turnover at the field scale in carbon turnover models.

AP7 Linking hydration status, carbon source and aggregate size distribution on soil GHG emissions: Laboratory column experiments using artificial soil aggregates

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KEYWORDS Microbial activity, Soil aggregate, Hydration, Denitrification, Respiration

Soil hydration modifies the microbial community dynamics and shapes microbially-mediated biogeochemical processes (soil respiration, denitrification, methane production). Evidence suggests that anoxic conditions may persist in soil aggregates (long after bulk soil is aerated) thereby providing niches for anaerobic microbial communities. Despite their recognized role in mediating soil biogeochemical fluxes (hot spots), systematic studies of the impact of different environmental conditions (e.g., hydration and organic matter availability) on GHG emissions from soil aggregates remain rare. We have constructed artificial soil aggregates of different sizes and different carbon configurations (mixed, core, no addition) to study effects of hydration and carbon source on GHG emissions (CO_2, N_2O and CH_4). An assembly of aggregates of three sizes were embedded in sand columns (at four distinct layers) and the water level was varied periodically to quantify effects of wetting/drying and submersion on GHG fluxes. Results illustrate the critical role of water table level on GHG emission, for example, lowering the water table decreases CH_4 emission while increasing N_2O flux. We observe links between aerobic processes (e.g., nitrification) in promoting rates of anaerobic denitrification process presumably by promoting alternative pathways (e.g., ammonia and nitrite oxidizing processes. Methane production was activated under highly anoxic conditions. Production of N_2O was highest form aggregates with particulate carbon in the anoxic core whereas highest CO_2 production was obtained from mixed carbon source at rates that fluctuated with hydration conditions. Experimental results of artificial soil aggregates are of interest for improvement of physically- and processes- based models for realistic representation of biogeochemical gas fluxes from soil profile.

AP8 Development of greenhouse gas emissions, organic C and total N related to fertilization regime and time since soil recultivation

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KEYWORDS greenhouse gas, fertilization, nutrient, recultivation, field experiment

Soil organic matter (SOM) is a sink and source of C and N and critical for soil function and quality. SOM mediates nutrient storage, release, and balancing and thus also regulates nutrient losses by leaching or greenhouse gas emissions.

The project INPLAMINT, Increasing agricultural nutrient-use efficiency by optimizing plant-soil-microorganism interactions, is part of the German research initiative BonaRes. It looks for basic mechanisms

of nutrient fluxes between soil, microorganisms, and plants. It explores strategies to balance nutrient availability in the soil and to enhance nutrient-use efficiency in crop production. Linking the nutrient status, organic C and total N as part of SOM to the microbial biodiversity and activity patterns is part of this strategy.

Field experiments at the International Organic Nitrogen Long-term Fertilization Experiment (IOSDV) at Rinkenbergerhof (LUFA Speyer, Germany) and at the agricultural soil restoration chronosequence following open-cast lignite mining (RWE Power, Germany) in the region Niederrheinische Bucht, west of Cologne (Germany) will be presented. First results on greenhouse gas emissions, nutrient status, organic C and total N development are discussed as function of organic amendment, mineral N fertilization, season as well as time since soil recultivation.

Our strategies are directed towards "engineering" the soil microbial community, combined with targeted fertilizer and soil amendment application schemes, as the key to optimize nutrient use efficiency of crop production by avoiding stoichiometric imbalances, overcoming plant-microorganism competition for nutrients, and buffering nutrient surpluses. Knowledge about SOM surely is essential for such an initiative.

Poster session 2: Significant boundary conditions, micro-habitats and micro-habitat properties, processes of succession, and systems fluctuations - what can we learn from the marine microbial pump concept?

HP1   Turnover of microbial carbon in microbial hot spots

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Keywords detritusphere, decay rates, $^{13}C_{mic}$, ^{13}C-PLFA

Knowing the turnover of microbial C, i.e. the release of C from the microbial pool per time, is decisive for understanding and modeling the fate of microbial C and its contribution to the formation of non-living SOM. We hypothesize that microhabitat conditions strongly affect turnover rates of microbial C and that hot spots of microbial activity are particularly important in this context. In this study, we focused on the detritusphere and set-up a microcosm experiment to determine the turnover of microbial C recently assimilated from differently aged maize litter. 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 ongoing depletion of the ^{13}C signal in different biotic and abiotic soil C pools while maintaining the specific habitat conditions of the detritusphere. Pulse-labeling was done during the early (0-4d), intermediate (4-12d) and late stage (28-36d) of litter decomposition to account for specific microbial communities (r- and K-strategists) feeding on litter compounds of decreasing quantity and quality. Soil cores were sampled destructively directly before litter re-transplantation and after 4, 8, 12 and 20 days, respectively.

During the initial days of the experiment, up to 17% of the CO_2-C was maize-derived C. The ^{13}C value in the CO_2 decreased with continuous decomposition of the litter. The EOC pool showed a fast C turnover, especially when fresh litter was applied at the beginning of the experiment. The highest absolute amount of maize-derived C was found in gram-positive bacteria during the early stage of litter decomposition, whereas the turnover of maize C in gram-positive bacteria was the slowest in comparison to other microbial groups. For saprotrophic fungi, we found the highest incorporation of litter C during the intermediate stage of litter decomposition. 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. During the later stage of litter decomposition, maize-derived C was minor utilized by both bacteria and fungi.

Overall, this study underlines the importance of considering the dynamics of microbial C turnover in hot spots of microbial activity for understanding the formation SOM. In addition, turnover rates of microbial C of specific microbial groups in specific microhabitats are important for improving the structure and parametrization of C turnover models.

HP2   Arbuscular mycorrhizal fungi colonization of the root and litter quality influence carbon use profile of soil microbial community

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KEYWORDS litter, Decomposition, Priming, microbial ecology and pulse labelling

Rationale and objectives: Microbial communities in the rhizosphere are the first recipients of freshly fixed carbon from the atmosphere. The rhizosphere is essentially defined as the soil in immediate contact with plant roots and root symbionts. This habitat is home to a diverse group of microorganisms which help the plant in extracting nutrition trapped in complex organic matter in soil apart from serving other functions. The objective of this study was to characterise the flow of freshly fixed carbon into microbial communities associated with hyphae, mycorrhized roots and non-mycorrhized roots followed by a characterisation of key microbial players using molecular phylogeny in this interaction.

Methodology approach: We set up a greenhouse pot experiment with a fully factorial design to account for many variants of this key habitat. The pots were equipped with a central in-growth core containing soil guarded by nylon meshes allowing either roots or hyphae. We used a dual pulse labelling technique where a ^{15}N pulse was administered from the litter (microbial necromass, plant root litter and inorganic nitrogen) and ^{13}C pulse from the plant by manipulation of the atmosphere.

Results and conclusions: Soil microbial community associated with hyphae receive the ^{13}C label the quicker than mycorhizosphere and rhizosphere cores. The quantity of ^{13}C incorporated into microbial community was higher in case of cores with microbial necromass and inorganic nitrogen source. We also observe that microbial community associated with hyphae allocate more carbon to biomass as against respiration. Together the data indicates each habitat and organic matter input combination recruited. We are now attempting to link this behaviour of the organisms with their phylogeny based on 16S and ITS gene sequence.

HP3   Role of bacterial biomass in water repellency development

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KEYWORDS Bacteria, cell fragments, contact angle, interfacial properties, water repellency

Wettability is an important property of soil particle surfaces as it affects a wide range of physical, chemical, and biological processes. For instance, low wettability (i.e. water repellency) reduces the water infiltration capacity, thus promoting erosional processes and limiting the water availability for microorganisms and plants. Moreover, water repellency affects the distribution and continuity of the

liquid phase in the soil matrix which is crucial for the diffusion of dissolved organic substrates, nutrients and exo-enzymes, and hence, the conditions for microbial life. In general, pure soil minerals are well wettable, however, under environmental conditions they become easily covered by organic compounds which can modify particle surface properties considerably. Organic compounds identified to cause water repellency comprise waxes, alkanes, fatty acids, free lipids and amphiphilic molecules in general. Our study will focus on bacterial biomass residues as one important component of soil organic matter which has been neglected in the past regarding its role in water repellency development. Recent research indicates that increasing mineral surface coverage by bacterial cell envelope fragments is accompanied by increasing microbial lipid contents and water repellency. In addition, it has been shown that the chemical composition of cell envelopes and the surface properties of bacteria vary with respect to water availability. However, it is unclear so far to which extent bacterial cells and their fragments contribute to the occurrence and persistence of soil water repellency and whether bacterial adaptation to water stress plays a role in the frequently observed variation of water repellency in response to wetting and drying. Overall, we hypothesize that bacterial cells and their fragments significantly contribute to the occurrence and persistence of soil water repellency, eventually feeding back on their own living conditions. Our project aims at answering these questions by (i) studying the factors and conditions that contribute to the occurrence of bacterial surface hydrophobicity, (ii) investigating how bacterial surface properties are reflected by soil wettability, and (iii) testing the potential feedback of soil particle wettability on bacteria and their surface properties.

HP4 Spatial distribution of soil organic matter composition at intact preferential flow path surfaces compared with surface properties

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KEYWORDS Soil organic matter, Hot spots, Spatial distribution, Soil properties

In structured soils, soil organic matter is heterogeneously distributed. Surfaces of cracks, decayed root channels or worm burrows –assumed to represent hot spots in soils- are often covered by clay-organic coatings (i.e., cutanes), in which the outermost layer is mainly organic matter (OM). The composition of OM finally controls wettability, sorption, and transfer properties of the hot spots. However, the relation between the in-situ local distribution of OM composition and the spatial distribution of sorption properties along such surfaces is largely unknown. The objective of this study was to analyze the local mm-scale distribution and composition of the thin and vulnerable OM coatings at intact surfaces of earthworm burrows and cracks. Fourier transformed infrared spectroscopy in diffuse reflectance mode (DRIFT) was used to determine spectral information earthworm burrows, root channels, and cracks of structured subsoil horizons in 1 mm steps along transects of 15 up to 65 mm length (DRIFT-mapping technique). The distribution of OM composition was characterized by evaluating the ratios of the absorption band intensities of the alkyl- (C-H-) and carbonyl (C=O-) functional groups (CH/C=O) in DRIFT spectra, which represent a measure of the potential wettability of the OM of the surface. Samples of different soil types (Luvisol, Regosol, Stagnosol, Cambisol), of different geological provenance (till, loess, mudstone, limestone), and of different land use (arable, forest) were analyzed. The CH/C=O-ratio was generally higher for earthworm burrows and root channels as compared to crack surfaces and the soil matrix. Differences between flow path types could be observed with respect to soil type, parent material, and land use. The local distribution of the OM properties is potentially related to sorption properties like Cation exchange capacity and wettability.

HP5 Effect of freeze-thaw and dry-wet events on microbial activity in soils from the UK

and Antarctica

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Freeze-thaw and dry-wet events represent an important phenomenon in terms of soil hydrology and thermodynamics. The change in environmental conditions associated with these events may induce stress within the soil microbial community. Although the community has the potential to adapt to these stresses, their physiological responses remain poorly characterized. Previous studies have frequently observed a pulse of CO_2 from topsoils after freeze-thaw and dry-wet events. The enhanced release of CO_2 to the atmosphere may have important implications for soil carbon storage and 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 short term response to these two stressors, we investigated the effect of freeze-thaw and dry-wet events on microbial activity in two different types of soils using ^{14}C isotopic tracking. We observed a CO_2 pulse on rewetting and thawing from both soils, but the pulse of CO_2 on rewetting was greater than on thawing.

HP6   Impact of land use change on microbial diversity in European soils

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During the last 100 years, 25% of the land area in Europe was subjected to land use change (LUC). Changing the balance between the soils' input and output of organic material, LUCs lead to altered quantities and qualities of soil organic carbon (SOC). This study analyzes how LUC affects the diversity and composition of the soil microbial community, and to what extent this effect is explained by the changes in quality, i.e. the proportion of the different carbon fractions, and quantities of SOC.

Soil samples were collected from 30 paired sites covering the major European LUC types: cropland to grassland, grassland to cropland, cropland to forest, grassland to forest and additionally the new LUC type cropland to bioenergy plantation with *Miscanthus*. Changes in the quality and quantity of SOC were assessed together with physicochemical soil parameters. The population sizes of *Bacteria*, *Archaea,* and *Fungi* were determined by quantitative PCR and the structure of the soil bacterial communities was investigated with T-RFLP complemented by high throughput sequencing of PCR amplified 16S rRNA genes.

Comparing the different land use types, we found that the abundances of bacteria, archaea and fungi, as well as the soil bacterial community structure (as determined by T-RFLP), were significantly affected by land use type. Further, while abundances of bacteria, archaea and fungi depended on both SOC quality and quantity, the community structure of soil bacteria responded only to the quality of SOC. High throughput sequencing revealed that soil bacterial diversity is significantly different under different land uses being highest in croplands, and lowest in forests.

Assessing the factors contributing to the impacts of LUC, we found that changes in the abundances of bacteria, archaea and fungi, and in bacterial community structure were largely explained by changes in total soil nitrogen content and in pH. Changes in SOC quality and quantity affected bacterial, archaeal, and fungal abundance, while changes in the community structure of soil bacteria only depended on SOC quality but not quantity. The results from currently ongoing amplicon sequence analyses are now expected to identify the bacterial groups which respond to specific factors altered by the

LUCs, and these will be reported.

HP7   Impact of biochar on mineralisation of C and N from soil and willow litter and its relationship with microbial community biomass and structure

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Using a laboratory experiment, we investigated the effect of applying willow biochar to short rotation coppice soil on C and N dynamics and microbial biomass and community composition, in the presence and absence of willow litter. Application of biochar at a rate of 0.5 % had no effect on net CO_2 mineralisation in the presence or absence of litter. However at a rate of 2 %, net CO_2 mineralisation was reduced by 10 and 20 % over a 90-day period in the absence and presence of litter respectively. Biochar reduced N mineralisation when applied at both 0.5 and 2 % concentrations. pH was increased by application of 2 % biochar to soil. Phospholipid fatty acid analysis demonstrated that both concentrations of biochar affected microbial community composition, although the effect of biochar was not as great as the effect of time or litter application in shaping community structure. In particular, the amount of bacterial biomass was increased by biochar application to soil, and there was evidence for increased abundance of Gram-negative bacteria and actinobacteria following biochar application. The data is discussed in the context of microbial mechanisms underlying impacts of biochar on C cycling in soil, and the coupling of C and N cycles following amendment of soil with biochar.

HP8   historical charcoal additions potentially improve stability of soil organic carbon due to altered particulate carbon fractions

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Rationale and objectives: Improving the stability of soil organic carbon (SOC) and soil's capacity to store SOC are promising ways to mitigate climate change. Recently, several studies showed that additions of charred biomass (e.g. charcoal) elevated SOC stocks and stabilized natural organic matter; however, the mechanisms for C stabilization are hardly known.

Methodology approach: The SOC, dissolved organic matter (DOM) and particulate organic matter

(POM) from two different soils and their counterparts with former inputs of charcoal (kiln soil) were analysed by means of elemental analysis. Hot water extracts (HWE) of soils and applied charcoal were investigated by the ESI-FTICR-MS for molecular level details of thousands of inherent organic compounds, solid state NMR is made for soils and charcoal, respectively.

Results and conclusions: Charcoal additions increased substantially concentrations of black C, total C and total N in bulk soil, however, concentration of water extractable SOC and N remained unchanged. Pattern of the POM size fractions changed with a relative increase in the free POM fraction and a decrease in the occluded POM fraction and soil particles <20 μm. However, all POM fractions in charcoal enriched soils were augmented with C and N.

Organic compounds found in HWEs of soils and charcoal contained a broad range of molecules, which highly varied in their polarity and aromaticity. Highly condensed hydrocarbons were found however exclusive in charcoal HWEs. This is in contrast to molecular composition measured of Cambisols and Luvisols, which were generally less aromatic (lignin range only). Surprisingly, differences between molecular composition of soil and their charcoal enriched forms were negligible – in contrast to solid state NMR investigations.

This study confirmed previous findings that charcoal additions increase SOC long-lastingly. Further, an assumed abrasion resistance of charcoal particles may explain elevated free POM fractions, which thereby may act as sorbent of soil organic matter. This in turn will potentially stabilize soil organic carbon and increase the soil's carbon saturation capacity. A comparison to wildfire influenced soil samples complete the investigations.

HP9   The influence of traditional agriculture on soil organic matter in tropical ecosystems of Papua New Guinea

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Keywords Soil organic matter, Papua New Guinea, PLFA, Agriculture

Introduction: Previous studies have described negative effect of agriculture on tropical soil (McGrath et al., 2001; Dominy et al., 2002; Powers, 2004). Loss of soil organic matter (SOM) and soil carbon is common issue. We compared SOM, soil carbon and microbial biomass estimated by PLFA between succesion gradient of traditional agriculture and primary forest.

Methods: We investigated 13 study plots with different land use. The categories of study plots were gardens (recent), old gardens (less than 10 years since disturbance), secondary forest (10 – 20 years since disturbance) and primary forest (more than 50 years since disturbance). Soil samples were collected from two depths (0-5 cm and 5-10 cm). Samples for PLFA analysis were freeze-dried without delay in Wanang (PNG). The content of carbon and nitrogen in samples was determined using elemental analyzer EA 1108. Proportion of SOM fractions was measured according to Zimmermann et al. (2007). Phospholipid fatty acids (PLFA) biomarkers were identified by GC-MS.

Results and Discussion: In soil carbon concentration, there was a significant difference between depths ($p < 0.05$) but no significant difference was found between plot types (two-way ANOVA).

Soil carbon per unit area also did not differ significantly between plot types (one-way ANOVA, $p > 0.05$) As for carbon fractions, proportion of the passive fraction slightly increased in the 0-5 cm layer with the successional age of plots (GA<OG<SF<PF). In 5-10 cm layer, there is an apparent peak of active fraction in primary forest. This corresponds with the fact that two of the five PF samples show several orders of magnitude higher active SOM most likely due to the occurrence of hot spots such as termite nests. PLFA biomarkers did not differ between plot types.

Conclusions: Soil microbial biomass as indicated by PLFA and soil organic carbon did not differ between study plots. Amount of soil organic matter is similar across study plots as well as proportion of carbon fractions. Traditional shifting agriculture had no or little effect on soil organic matter.

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HP10   Biological soil quality indicators for agricultural management.

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KEYWORDS Soil quality, labile organic carbon, nematodes, microbial community, agricultural resilience.

Soil quality is defined as the capacity of a soil to perform multiple functions. Agricultural soils sustains a wide range of functions which are then translated into ecosystem services, defined as the benefits to human wellbeing derived from ecosystems. Soil capacity to function is established by soil chemical, physical and biological parameters. These parameters can be quantified and can be used as indicators of soil quality. The characterisation of soil quality is essential due to the negative pressure exerted by natural and anthropogenic-derived soil threats such as soil erosion, soil organic matter losses and soil compaction. However, there is no consensus yet about which combination of measurements is the most suitable for the assessment of agricultural soil quality. The specific objective of my PhD is to study the suitability of novel soil parameters as soil quality indicators. The soil parameters selected should be sensitive to agricultural management and well correlated with soil functions, consequently they should help to assess which soil management practices are sustaining multiple soil functions involved in production and environmental resilience. The new indicators will be assessed in ten European long term field experiments with different agricultural land use, management regimes and pedoclimatic characteristics. We will focus on biological and biochemical parameters, due to the unique role of soil biota in soil functions and to their high sensitivity to disturbances. We will measure labile organic carbon (DOC) quantity and quality through its extraction from soil and fractionation in hydrophobic and hydrophilic compounds. In addition nematodes, bacterial, fungal and mycorrhizal community diversity, composition and abundance of specific groups will be assessed with traditional (microscope, ergosterol content) and molecular techniques (sequencing and quantitative PCR). These parameters will be related to soil functions (nutrient cycling, humification and decomposition, pest and pathogen population control, soil aggregation) which will be measured with a minimum data set of chemical, physical and biological indicators. In addition, the capacity of soil to suppress disease will be assessed carrying out a bioassay with Pythium-cress pathosystem. The possible causal relevance of the soil parameters-soil functions-ecosystem services relationship will be investigated with structural equation modelling (SEM). We hypothesize that the selected soil parameters are sensitive to soil managements and can be quantitatively linked to a set of soil functions in agroecosystems. The novel soil quality indicators will be used to integrate existing minimum data set and will help to assess soil quality in European agroecosystems

Poster session 3: Molecular processes and components interacting with SOM and soil minerals - turnover steady state or residual `inert´ material?

IP1   Nutrient availability affects soil organic matter decomposition depending on land use

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KEYWORDS Land use; nutrients; soil organic matter decomposition

Land use and input of nutrients (N and P) strongly affect C dynamics and storage in soil. However, the magnitude and mechanistic understanding of the effects of labile C and fertilization input on soil organic matter (SOM) decomposition among land use remains incomplete especially for tropics. [14]C labeled glucose together with nutrients were added to soils (0 - 20 cm) from forest, organic and conventional farming systems. The [14]CO_2 and total CO_2 emission were measured over 44 incubation days and microbial biomass was measured at the end.

Labile C addition without nutrients strongly increased SOM decomposition in soil under organic farming (for 13%), while only slight increase (0.02 and 2%) were observed in soils under forest and conventional farming. Glucose addition with N decreased SOM decomposition by 3%, 12% and 21% compared to C addition alone in organic, conventional and forest soil, respectively. This decreased SOM-derived CO_2 emission may ascribe to the increased C use efficiency under high N availability, which is more pronounced in strong N limited soil (i.e. conventional and forest). In contrast to the negative effects of N, glucose addition with P increased SOM decomposition for 7%, 2%, 3% compared to C addition alone in organic, conventional and forest soil, respectively. Microbes are more limited by N than by P after P fertilization, thus, added glucose could be utilized to mine N from SOM and increased SOM-derived CO_2 emission. However, microbial biomass was not affected by N fertilization, but was increased by P fertilization ($P < 0.05$). Glucose addition with N and P increased SOM decomposition by 10% compared to C addition alone in organic farming soil, but decreased in forest and conventional soil by 7% and 12%. This mainly because of the effect of N fertilization, which led microbial shift from mining SOM to utilize added N and decreased SOM mining in forest and conventional soil. However, the P fertilization effect dominated in organic soil, where N was not strongly limited. Thus, positive effect of N and P fertilization on SOM decomposition was occurred in organic soil.

Overall, SOM decomposition is promoted by P and reduced by N fertilization in soils under forest and under organic and conventional management. The interactions of N and P fertilization were sensitive to nutrients availability and depended on land use.

IP2   Insights into soil minerals as mediators of nitrogen transformation in the rhizosphere

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KEYWORDS Mineral-organic interactions, rhizosphere, priming

Recent research on soil N dynamics has shifted in focus from net mineralization to SOM depolymerization as being the rate limiting step to N availability. To that end, Schimel and Bennett (2004) argued that plant-microbial competition for N-containing monomers drives N cycling. Here we present a new conceptual model arguing that while depolymerization is a critical first step, mineral-organic associations may ultimately regulate the provisioning of bioavailable organic N, especially in the rhizosphere. We argue that in rhizosphere hotspots, MAON is a potentially mineralizable and important source of N for plants. Several biochemical strategies enable plants and microbes to compete with

mineral-organic interactions and effectively access MAON. In particular, root-deposited low molecular weight compounds in the form of root exudates facilitate the biotic and abiotic destabilization, solubilization, and subsequent bioavailability of MAON. We believe that the competitive balance between the potential fates of monomers—bound to mineral surfaces or dissolved and available for assimilation—depends on the specific interaction between and properties of the clay, soil solution, mineral-bound organic matter, and microbial community. For this reason, the plant-soil-MAON interplay is enhanced in rhizosphere hotspots relative to non-rhizosphere environments.

To test this new conceptual framework, we conducted a laboratory incubation of silt and clay organic matter fractions to which we added simple carbon substrates in order to simulate exudation. We applied three solution treatments: ^{13}C-labelled glucose, to stimulate microbial activity and potentially the production of extracellular enzymes capable of liberating N; ^{13}C-labelled oxalic acid, which has been demonstrated to dissolve metal-organic bonds and possibly destabilize mineral-bound and N-rich organic matter; and water, to serve as a control. After two additions of exogenous substrates, we observed enhanced CO_2 respiration rates in both glucose and oxalic acid treatments. Hydrolytic enzyme activity increased in glucose treatments while activity either decreased or remained constant in oxalic acid treatments. Oxidative enzyme activity increased in response to both labile carbon treatments. These results are indicative of a microbial SOM-mining response which we will further test via ^{13}C-CO_2 analysis. We also predict that increases in respiration and enzyme activity will correspond with enhanced production of dissolved N and increased gross N mineralization rates. Results from this incubation will integrated with the proposed conceptual model as initial evidence for the potential N-supplying capacity of mineral-associated organic matter fractions.

IP3   Mineralogy can influence root preferences on different pools of native soil organic carbon mineralization through "priming effects"

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KEYWORDS Soil organic carbon mineralization, Nutrient status, Clay mineralogy, Priming effect.

Mineralogy can influence root preferences on different pools of native soil organic matter (SOM) mineralization through "rhizosphere priming effects" (RPE). However, the long-term direction, magnitude and intensity of SOC priming by root remain uncertain. Rhizosphere priming not only is affected by soil nutrient availability, but also by the influence of the environment in different organic fractions and mineralogy. We hypothesized that soil mineral assemblage, specifically short-range-order (SRO) minerals, influences roots responses to different quality of organic C in physical fractions. We evaluated the impact of root carbon influxes of C4 maize (*Zea mays*) plants on RPE on light (250-2000 μm), intermediate (53-250 μm) and heavy (< 53 μm) fractions isolated from forest kaolinitic and allophanic soils. Soil fractions were confined in small PVC capsules in contact with maize roots in a pot experiment. The three physical fractions of each soil interact in the same pot, to evaluate the preferences of root colonization. Soil C respiration and RPE were measured at flowering. The pot were harvested and, the capsules incubated for 24 h. In all fractions and soils there was a positive RPE. Clay *mineralogy* was determined by *X-ray* diffraction.The results supported the hypothesis that the intensity of RPE is reduced in heavy fraction of allophanic soil with the lowest C:N ratio. In contrast, in the heavy fraction of kaolinitic soil, the RPE was highest with lowest C:N ratio compared to the light fraction displaying the opposite. The more crystalline clay of kaolinitic soil mineralized twice the amount of C

measured in allophanic soil (14 % against 33 %, respectively). There was a negative and strong correlation between the amorphous Al content of allophanic soils and RPE. The same correlation was obtained for ^{13}C derived C. None of these results was obtained in kaolinitc soil. This study suggests a strong influence of the environment of soil organic fraction on C mineralization, controlled by the soil mineralogy. Our results also showed that the intensity of RPE might strongly depend on C:N ratio of different soil fraction triggering SOM-mining of microorganism for nutrient availability.

IP4   Impact of organic amendment on soil aggregation and microbial colonisation

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KEYWORDS Biochar, soil aggregation, soil microorganisms, tropical soils, remediation of degraded soils

Soil aggregate stability is a major predictor for the risk of soil erosion and an important feature of soil quality. Within aggregates, soil organic matter (SOM) is degraded and stabilised by microorganisms and stable organic carbon in turn positively affects soil aggregation. Compost amendment increases soil microbial activity and leads to soil organic matter stabilisation. Soil physical characteristics like hydraulic properties are also improved by compost amendment. Biochar causes inconclusive effects on soil aggregation. While some authors report improved soil aggregation due to favourable physico-chemical properties, other studies observed no or negative effects of biochar on soil aggregation. In most studies, biochar was found to contribute to SOM stabilisation in soils, but it is yet under debate whether this effect is caused by a stimulation or a sedation of microbial activity.

We examined the effect of compost and biochar amendment on physico-chemical and biological soil aggregation after three years of natural succession on the ReviTec demonstration site in Ngaoundéré, Cameroon. Jute bags filled with different substrates and plant seeds were installed for soil recovery. Soil samples from three treatments (mineral control, compost treatment and combined treatment with biochar and compost) were collected and sieved into four different aggregate sizes. Physico-chemical parameters were recorded and bacterial as well as fungi abundance were investigated applying fluorescence microscopy.

Soil conditions were generally improved by organic amendment, however antagonistic effects of biochar and compost were pronounced. Aggregate-dependent parameters such as cation exchange capacity and SOM content were mainly a function of soil texture. Microbial abundance increased in the compost treatment, but no significant differences between the biochar and the mineral substrate were observed. While bacterial abundance was sensitive to treatments, fungi responded to aggregate size. Moreover, dense bacterial colonisation of OM was found only in the presence of clay-sized mineral particles. Macro-aggregates were mostly relevant for physico-chemical parameters, micro-aggregates had the function of   reservoirs for SOM.

We conclude that biochar particles were barely incorporated into the soil body and did not fully participate in major soil processes such as hydraulic functions, microbial colonisation and soil aggregation. This view is supported by other studies that described increased erodibility and reduced microbial activity following biochar application to soils. We recommend that biochar must be ground to an appropriate size for the adoption by to soil processes or organisms, and should be effectively activated with nutrients and microorganisms for full incorporation into the soil body.

IP5   The role of extracellular polymeric substances in aggregate turnover

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KEYWORDS Aggregation, clay, decomposability, extracellular polymeric substances, microorganisms

Soil aggregation is critical for carbon (C) sequestration and microbial processes have been recognised as important control of aggregate turnover (formation, stability, and destruction). However, how microorganisms contribute to these processes is still a matter of debate. One crucial mechanism determining aggregate turnover and therefore C sequestration may be the excretion of extracellular polymeric substances (EPS) as microbial glue, but effects of the amount and composition of EPS on aggregation is largely unknown. Moreover, interdependencies between important aggregation factors like the amount of fine-sized particles (clay), the decomposability of organic matter and the microbial community (size and composition, as well as the excretion of EPS) are still poorly understood. Thus, our study reveals the complex interactions between these factors and their role in aggregate turnover. It is hypothesized that an increase in microbial activity, induced by the input of organic substrates, will stimulate EPS production and therefore the formation and stability of aggregates. To test this hypothesis, an incubation experiment has been conducted across a gradient of clay content (montmorillonite) and substrate decomposability (starch and glucose) as main drivers of the microbial activity. A combination of aggregate separation and stability tests will be applied. The results will be examined with respect to the obtained microbial parameters (amount and composition of EPS, CO_2 emission, microbial biomass, phospholipid fatty acid), to disentangle the mechanisms and factors controlling aggregate turnover affected by soil microorganisms. This study is expected to provide conclusive results on the role of EPS in the stability of aggregates. Thus, the results of this study will provide an improved understanding of the underlying processes of aggregate turnover in soils, which is necessary to implement strategies for enhanced C sequestration in agricultural soils.

IP6   Aggregation behavior of defined organic matter-goethite associations: Implication for soil organic matter stabilization

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KEYWORDS Microaggregates, organic matter stabilization, goethite, hidden places, interaction of molecular structures

Rationale and objectives: Microaggregates can increase the amount of organic matter (OM) stored in soils by limiting the accessibility of OM for soil biota. However, the effect of organic compounds in aggregate formation, especially those of microbial origin, is poorly understood. Organic matter sorbed to minerals can strongly modify their surface properties and thus particle interactions, making the prediction of aggregate formation difficult. Here we studied the aggregation behavior of goethite (□ FeOOH) in presence of defined organic substances, including model compounds of both microbial and plant origin as compared to dissolved OM (DOM).

Methodology approach: Synthetic goethite and galacturonic acid (GA), polygalacturonic acid (PGA), tannic acid (TA) as well as DOM from a litter (Oi-DOM) and a humified horizon (Oa-DOM) were used as model substances representing different sources of OM. At pH 4 and 6, the surface charge (SC) of goethite was adjusted by adsorption of variable amounts of organic acids and DOM to either equal positive and negative SC (e.g. +0.40 and -0.40 μmol_c m^{-2}). The resulting OM-goethite combinations with positive SC had low loadings of OM, while those with negative SC exhibited high OM loadings (e.g. TA-

goethite at pH 4: 0.15 and 3.83 mg C m^{-2} respectively). With this approach the effect of SC can be separated from other mechanisms influencing aggregation. The SC of goethite, OM, and OM-goethite associations were quantified by polyelectrolyte titration. After sonication, aggregation of goethite over time was traced by particle size analysis.

Results and conclusions: The principle behavior known for pure goethite with strong aggregation at the point of zero charge (*pzc*) and small aggregate sizes in presence of charged surfaces was only observed for OM-goethite associations formed at pH 4 and low OM loadings. Here, goethite associations with PGA, Oi-DOM, and Oa-DOM had final aggregate diameters of ~5 μm at *pzc* and ~0.35 μm for charged surfaces. This shows that independent from the amount of OM loading aggregation is controlled by SC. At higher OM loadings stable aggregates of larger sizes (5-6 μm) also formed in presence of TA at pH 4 and GA at pH 6 below the *pzc* of the respective associations, thus overcoming electrostatic repulsive forces. Consequently, the binding action of the polymeric plant polyphenol TA and the monomeric bacterial/plant sugar acid GA can offset the dispersibility of goethite particles. The presence of these associations in microaggregates may therefore increase structural stability and hereby protect the C deposit.

IP7   Approach to follow redox gradients and iron plaque formation in-situ over the vegetative development of a rice plant

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KEYWORDS Iron plaque, microaerophilic iron oxidation, rice, Moessbauer

Rice represents a staple food for more than half of world's population, with around 80 percent of worldwide rice production grown on water logged paddy soils. The rhizosphere is typically depleted in oxygen (O_2) and characterized by reducing conditions stimulating the release of iron(II) (Fe(II)) into the rhizosphere by Fe(III)-reducing microorganisms. Wetland plants, especially rice, exposed to these ferrous iron-rich environments have evolved a strategy to counteract toxification through high Fe(II) uptake. By radially releasing O_2 from their roots, Fe(II) is oxidized and precipitates as ferric iron plaque on the root surface. This radial oxygen loss (ROL) and zones with negative redox potentials create an ideal habitat for microaerophilic Fe(II)-oxidizing and Fe(III)-reducing microorganisms which implies a closed microbial iron redox cycle. Furthermore, redox processes that lead to the formation and dissolution of the iron plaque on the roots can have dramatic effects on the uptake of nutrients into the plant and contaminant (im)mobilization in the soil. To date, the geochemical gradients, mineral products and actual microbial processes that establish in the rhizosphere and lead to iron plaque formation over the life time of a rice plant are yet fully resolved.

In the present study we have developed an approach that allows us to follow the growth of a rice plant and the simultaneous visual and experimental observation of redox patterns in the rhizosphere and the resulting iron plaque formation on a high spatial and temporal resolution. We are able to track changes in redox conditions around the roots over the vegetative development of a rice plant. Moreover, the structural development, the composition and the activity of the microbial community associated with the roots and the iron plaque can be identified and quantified as a function of time. We found that the co-cultivation of rice plants and a well-described microaerophilic Fe(II)-oxidizing isolate revealed differences in iron plaque formation rates as well as in geochemical gradients around the roots compared to a plant grown without bacteria. In addition to that, we could observe a clear expansion of the iron plaque over various stages of plant growth. Mössbauer spectroscopy and μXRD revealed ferrihydrite as the dominating Fe(III) mineral formed. Comparing abiotic setup to co-cultured rice plants allowed a quantification of microaerophilic iron(II) oxidation rates decoupled from chemical iron(II) oxidation and the hypothesis that microbial iron(II) oxidation can affectively contribute to

short-term iron plaque formation on rice roots and influence long-term iron plaque accumulation.

IP8   Stabilization of microbial residues by co-precipitation with Fe and Al oxides

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KEYWORDS Microbial biomass residues, stabilization, soil minerals

Recent studies have shown that microbial residues contribute significantly to soil organic matter (SOM) formation. This material, however, is readily degradable and thus needs to be stabilized in soil. We hypothesize that the interaction with minerals, in particular co-precipitation with metal oxyhydroxides, plays an important role in stabilization of cell envelope material. We therefore analyzed the mineralization of ^{14}C-labelled Escherichia coli cells and cell envelope fragments during incubation of the cell materials alone or after co-precipitation with either Fe or Al oxyhydroxide by liquid scintillation counting of the $^{14}CO_2$ produced during incubation. We also tested the effect of environmental conditions, in particular oxygen supply and redox potential, on the stabilizing effect of the mineral phases. Co-precipitation with both Fe and Al oxyhydroxides decreased the mineralization of the cells and the cell envelope material significantly, indicating strong protection of biomass and biomass-derived fragments. Surprisingly, the mineralization of intact cells was higher than that of cell envelope fragments. This points to a higher recalcitrance of the cell envelope fragments, which therefore may be selectively enriched in SOM. Reductive conditions obtained after water-logging combined with excessive supply of an easily available carbon source resulted in a loss of the stabilizing effect of the Fe oxyhydroxides, due to reductive dissolution of the Fe minerals and thus loss of the stabilizing agent. We conclude that co-precipitation with and incrustation of organic material by Fe or Al oxyhydroxides is a relevant stabilization mechanism for microbial residues. The extent of stabilization is governed by environmental conditions affecting both microbial activity and mineral stability. The same mechanism also may apply for SOM in general.

IP9   Mineral-associated carbon in an Andosol receiving massive carbon input

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KEYWORDS Andosol, OC stock, saturation, sequential density fractionation, nano-crystalline minerals

Andosols represent the most carbon rich FAO-UNESCO soil unit, with an average of 254 Mg ha^{-1} organic carbon (OC) in the upper 100 cm. A current theory proposes an upper limit for OC stocks independent of increasing carbon input. This is assigned to finite mineral binding capacities for organic matter (OM). We tested the possible limits in OC stocks for Andosols under tropical rainforest with already large OC stocks (210 g OC kg^{-1} in the first horizon; 320 Mg OC ha^{-1} in the upper 100 cm). The soils received large inputs of 1800 Mg OC ha^{-1} as sawdust within a time period of 20 years. Adjacent soils without sawdust application served as controls. We determined total OC stocks as well as the storage forms of OM down to 100 cm depth. Storage forms considered were pyrogenic organic carbon, OM <1.6 g cm^{-3} with basicly no and little interaction with the mineral phase, strongly mineral-bonded OM forming particles with densities between >1.6 and 2.0 g cm^{-3} and >2.0 g cm^{-3}. The two fractions >1.6 g cm^{-3} were also

analyzed for aluminium-rich nano-crystalline mineral phases (Al-NCM) and imogolite type mineral phases (ITM) using ammonium-oxalate/oxalic-acid extraction and X-ray diffraction (XRD).

Pyrogenic organic carbon only contributed up to 5 wt% of OC, and thus, played only a marginal role for the accumulation of OM. In the uppermost two horizons, the fraction between >1.6 and 2.0 g cm^{-3} had 65-86 wt% of bulk soil OC and the mineral phase was dominated by Al-NCM. In horizons three to five (subsoil), the >2.0 g cm^{-3} contained 80-97 wt% of bulk soil OC and was dominated by a mixture of Al-NCM and ITM, with increasing proportions of ITM with depth. In response to the sawdust application, only the OC concentrations in horizon three increased significantly (P = 0.05); the increase was entirely due to increased OC in the two fractions >1.6 g cm^{-3}. Nevertheless, there was no significant increase in OC stocks within the upper 100 cm.

We assume, the topsoil is saturated in terms of OC concentrations, and thus, added OC tends to migrate downwards, where it becomes retained by OC-undersaturated nano-crystalline mineral phases. This indicates the possibility to sustainably increase already large OC stocks further, given that the subsoil still has binding capacity available and OC transport into deeper horizons is facilitated. The little additional OC accumulation despite the extremely large OC input over 20 years shows that long time periods of high input are needed to further increase large OC stocks.

IP10   (How) do microbial exudates control interfacial properties and supramolecular structures in soil organic matter?

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KEYWORDS extracellular polymeric substances, surfactants, molecular self-organization, swelling, interfacial properties

Microbial and plant exudates, especially extracellular polymeric substances and biosurfactants play are central role for the physicochemical environment of soil microorganisms. They are highly relevant for the microorganisms' and soil's water balance, but they also control interfacial properties and are involved in swelling-shrinking processes and in the stabilization of soil (micro)aggregates and soil structure. In addition, their properties control molecular self-organization processes in soil. Due to these unique characteristics, microbial exudates are central agents responsible for the flexible reaction of soil organic matter on dynamics in environmental conditions like moisture, temperature or pH. Vice versa, their origin, and formation and properties are controlled by the soil microorganisms and plant roots and under the current environmental conditions. This contribution tries to analyze and discuss the current knowledge and research need on the physicochemical aspects and the detection of exudate-mediated feedback-cycles in soil-microorganism interactions.

IP11   Formation of mobile bound residues of organic contaminants and detection by ultrahigh resolution mass spectrometry

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Keywords bound residues, FTICR-MS, emerging contaminants, organic matter

Rationale and objectives: The microbially mediated binding of anthropogenic organic contaminants to soil organic matter is an established strategy of decontamination in soil [1] and occurs besides mineralization. Products formed by this process are termed bound residue, which implies that these chemically masked residues would be largely immobile. However, bound residues formed in soil or in the aqueous phase may well be mobile, depending on the physico-chemical environment during formation as well as the chemical nature of the incorporating binding site.
Here we show that radical mediated formation of bound residues with natural organic matter (NOM) may result in a large suite of molecules which are potentially highly mobile, even in soils.
Methodology approach: Ultrahigh resolution Fourier transform ion cyclotron resonance mass spectrometry (FTICR-MS) has become the essential mass spectrometric technique to analyze NOM at the molecular level [2]. We used FTICR-MS to study bound residue formation of emerging organic contaminants with dissolved organic matter (DOM), first in laboratory studies. Artificial sunlight was used to initiate radical reactions in these systems. Detailed molecular information allows determining the potential bioavailability and mobility of these newly formed bound residues.
Results and conclusions: Benzotriazole is a corrosion inhibitor, widely found in the aquatic environment [3]. Upon photolysis of 1H-benzotriatole with DOM the formation of more than 100 new nitrogen containing molecules over a wide mass range (m/z 150-650) was observed [4]. Such reactions with DOM are, however, not limited to benzotriazole. Another example is the pharmaceutical carbamazepine (CBZ). Also for CBZ we detected hundreds of nitrogen containing molecules by FTICR-MS upon irradiation with DOM. Studies with isotopically labeled CBZ helped to elucidate reaction partners and the formation pathways.
FTICR-MS is an ideal technique to determine bound residue formation, as far as the products are water-soluble. Mobile bound residues may not only be formed upon photolysis but also in biological processes, in which one-electron-transfer occurs and radical intermediates are being formed, e.g. with peroxidases of fungi. Our results warrant further research looking at the extent to which bound residues formed by microbially mediated reactions are truly immobile and may contribute to and influence the genesis of soil organic matter in anthropogenically impacted areas.
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IP12   Microbial biomass and nutrient dynamics during decomposition of cover crop mixtures

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KEYWORDS Microbial ecology, agriculture, decomposition, SOM

Sustainable agriculture is needed to reduce losses of soil organic matter (SOM) and to ensure crop production with a minimum of negative impact on the environment. Due to land use change and intensive agriculture, SOM is reduced of the last century. This has a negative influence on the soil ecosystem and there is good evidence that this will lead to a reduction of soil functioning. Cover crops, planted in the fallow season, are commonly used to improve soil functions, such as soil structure, nutrient cycling, pathogen suppression and increasing SOM. Incorporation of cover crops in the soil in spring can increase the microbial biomass and activity. It is expected that turnover of the microbial community has a significant influence on nutrient dynamics in the soil. This can increase the nutrient availability and SOM.

The functional characteristics and stoichiometry of cover crops vary. The hypothesis is that cover crop mixtures with different functional traits will increase the belowground diversity by creating more niches in the soil leading to increased microbial functional diversity. We expect that this will result in more balanced nutrient dynamics with a more gradual delivery of nutrients to the cash crop, reduced leaching and greenhouse gas (GHG) emissions. The microbial community changes will depend on the quality of the incorporated cover crop remainders. The aim is to understand how cover crop mixtures alter microbial functioning and consequently carbon and nutrient cycling, and possibly disease suppression and yield of the cash crop. We expect that cover crop diversity will lead to increased microbial biomass. This will increase nutrient availability due to increased nutrient uptake by the microbes followed by release of plant available nutrients as a result of turnover of the microbial community.

To understand microbial turnover during litter decomposition, a pot experiment with litter of cover crop monocultures and mixtures will be used. During decomposition, the microbial biomass, GHG emissions and nutrient content will be measured over time. Preliminary results showed that the microbial community is active directly after litter incorporation in the pots. Further study is needed to determine if the turnover of the microbial biomass will indeed increase SOM and nutrient availability in the soil which can result in increased yield of the cash crop, leading to more sustainable agriculture.

IP13   Do cover crop mixtures increase soil fertility and promote soil organic matter stabilisation simultaneously?

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KEYWORDS Cover crop mixtures, SOM, Biodiversity

Intensive agricultural practices deplete the soil nutrient pool and organic matter content (SOM). Cover cropping is commonly used to prevent nutrient leaching as well as increasing the SOM content. Until now, cover crops are universally grown in monocultures and since biodiversity is declining worldwide growing cover crops in mixtures could potentially be a simple tool to increase biodiversity in agriculture. It is known from research in natural systems that increased species biodiversity can improve resource exploitation in the soil, which leads to an increased plant biomass and thus C and N accumulation in the soil. To be able to design cleverly chosen cover crop mixtures we aim to understand the

mechanisms involved in increasing cover crop biomass; improving soil quality through residue incorporation and in decomposition processes. To study if soil organic matter is increased, while not reducing soil fertility we will examine if cover crop residues increase both the labile and the stable fraction of the soil organic matter. The field experiment, as part of the project "Clever Cover Cropping: Synergistic Mixtures for Sustainable Soils", will run for 4 years (March 2016-Oct 2019) with cover crops in winter and a cash crop in summer. Three cover crop species (*Avena strigosa*, *Raphanus sativus* and *Vicia sativa*) were chosen with dissimilar plant traits, which constitute complementarity, based on a literature review. We aim to quantify any changes to the soil fertility by analysing the DOC content. To look for specific changes in DOC quality caused by the cover crops we will fractionate the DOC according to the method by van Zomeren and Comans. To get a better understanding of what plant properties drive the DOC content and quality we will analyse the plant and DOC material with py-GC/MS. Py-GC/MS allows us to see changes in SOM quality at the molecular level. To determine what effects cover crop have on SOM stabilisation we will compare labile and stabilised OM fractions with regards to their molecular fractions. The soil DOC content will be analysed each year before planting the main crop whereas we will examine the quality of the different fractions mentioned before only in the last year since it will take longer for the cover crops to have a significant effect.

IP14   Fate of organic carbon in paddy soils with contrasting mineralogy

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KEYWORDS paddy soil, redox oscillation, mineral-associated organic matter, Fe oxides

Submerged rice cultivation results in the formation of paddy soils. These soils often accumulate organic carbon (OC) during the initial phase of their development. However, it is unknown how the mineral composition and particularly the redistribution of Fe oxides affect OC storage. Two soil types with contrasting mineral assemblage (Alisol and Andosol) were exposed to 8 anoxic–oxic cycles over 1 year to mimic paddy soil development. Soils received rice straw labelled with ^{13}C (228 ‰) at the beginning of each cycle. A second set of samples without straw addition was used as control. Headspaces of the incubation vessels were regularly analyzed for CO_2 and CH_4 as well as their $\delta^{13}C$. In soil solutions, redox potential, pH, dissolved organic C ($DO^{13}C$), and Fe^{2+} were measured after each anoxic and each oxic phase. Soils were fractionated by density at the end of the experiment and the different organic matter (OM) fractions were isotopically analyzed. Samples of genuine paddy soils that developed from the test soils were used as reference.

During anoxic cycles, soils receiving rice straw released large amounts of CO_2 and CH_4, indicating strong microbial activity. Consequently, Eh values dropped and pH as well as Fe^{2+} concentrations increased. ^{13}C data showed that more than 90% of the added straw was respired. Concentrations of DOC were relatively small, indicating either strong consumption and/or strong retention of dissolved organic compounds. During oxic cycles, concentrations of dissolved Fe dropped in both soils while DOC concentrations remained constant in the Alisol and decreased in the Andosol. Density fractionation revealed increased contents of mineral-associated OC for the Andosol incubated with straw addition as compared to the parent soil. No changes were found for the Alisol. However, the mineral-associated OC fraction of both soil types contained ^{13}C of the added straw. Hence, fresh OM was incorporated

while part of the older OM has been released or mineralized. The increase of mineral-associated OC in the Andosol might be due to effective binding of fresh OC to minerals, which could be explained by the more reactive mineral composition of the Andosol than of the Alisol.

IP15   Hydrolytic enzyme activities in soil: substrate supply or product demand controlled? Insights from assessment of soil N mineralization in two paddy field experiments

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KEYWORDS soil N mineralization, enzyme activity, paddy soil, organic matter, fertilizer

Rationale and objectives: Microbial nutrient demand is determined by the elemental stoichiometry of microbial biomass in relation to environmental nutrient availability. The degradation of biopolymers to supply N requires the synergistic interaction of several classes of enzymes. Our aim was to assess the likeliness that selected enzyme activities would depend on either substrate availability or product demand, via modifications of N and OM supply. We also wanted to evaluate the role of these enzymes in mediating N mineralization based on their relative changes with soil N mineralization over field experimental treatments.

Methodology approach: Specifically, the influence of exogenous OM and fertilizer application on the activities of five relevant enzymes (β-glucosaminidase, β-glucosidase, L-glutaminase, urease and arylamidase) was measured in two long-term field experiments. One 18-years field experiment was established on a weathered terrace soil with a rice-wheat crop rotation at the Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU) having five OM treatments combined with two mineral N fertilizer levels. Another 30-years experiment was established on a young floodplain soil with rice-rice crop rotation at the Bangladesh Agricultural University (BAU) having eight mineral fertilizer treatments combined with organic manure.

Results and conclusions: At BSMRAU, N fertilizer and OM amendments significantly increased all enzyme activities, suggesting them to be primarily determined by substrate availability. Product-demand, in this case mineral N, would consequently seem to hold a lesser control on L-glutaminase, arylamidase and β-glucosaminidase activity because all were elevated at 220 kg N ha^{-1} compared to nil-N plots. At BAU, non-responsiveness of β-glucosidase activity suggested little effect of the studied fertilizer and OM amendments on general soil microbial activity. Notwithstanding the consequent probably equal microbial demand for N, β-glucosaminidase and L-glutaminase activities differed significantly among the treatments ($P > 0.05$) and followed strikingly opposite trends and correlations with soil organic N mineralization.

So enzymatic pathways to acquire N differed by treatment at BAU, indicating differences in soil N quality and bio-availability. L-glutaminase activity was significantly positively correlated to the aerobic and anaerobic N mineralization rates at both field experiments. Combined with negative correlations between β-glucosaminidase activity and N mineralization rates, it appears that terminal amino acid NH_2 hydrolysis was a rate-limiting step for soil N mineralization at BAU.

Future investigations with joint quantification of polyphenol accumulation and binding of N, alongside an array of extracellular enzymes also including oxidases and peroxidases for (poly)phenols, would enable verifying the hypothesized binding and stabilization of N onto accumulating polyphenols at the BAU site with SOM accumulating management.

IP16   Vertical patterns of eco-enzyme activities in two temperate forest soils after 20 years of nitrogen additions

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Keywords Nitrogen deposition, enzymes, soil carbon, temperate forest, soil profile

Rationale and objectives: Human-induced nitrogen (N) deposition to terrestrial systems is likely to increase over the next century with presumed consequences for ecosystem cycling of carbon (C), N and phosphorus (P). It has been shown that long-term N addition can slow down terrestrial decomposition rates so that more C is sequestered in soil, thereby contributing to climate change mitigation. The mechanisms behind this response remain elusive, however, N-induced changes in eco-enzyme activities that mediate soil organic matter (SOM) decomposition might be a major driver.
Methodology approach: We investigated links between eco-enzyme activities, soil depth and N availability in two long-term experiments where N has been repeatedly added to two temperate forests for approximately 20 years at rates of 35 kg N ha^{-1} y^{-1} (Klosterhede, Denmark) and 25 kg N ha^{-1} y^{-1} (Alptal, Switzerland), respectively. We hypothesized that ecoenzyme activities would decline exponentially with depth reflecting well-established trends in organic C and microbial biomass content. Concerning microbial nutrient limitation, we expected to see a shift from N- to C-limitation with depth which would be reflected in increasing ratios of C- to N-acquiring enzymes.
Results and conclusions: First results show that activity of hydrolytic enzymes generally decreases with depth. Oxidative enzyme activities, on the other hand, often increased with depth. We further observed site- and horizon-specific responses of ecoenzymes to N additions. At Klosterhede, enzymes involved in N-cycling increase with N in organic horizons whether C-enyzmes generally did not respond. Interestingly, N addition increased phosphatase activities over the whole soil profile, probably indicating a shift towards P limitation of soil microbes. At Alptal, N addition generally had less effect on hydrolytic enzymes. Taken together, this results suggest a response of microbial function to long-term N addition that goes beyond simple eco-enzyme C:N:P stoichiometry with unclear consequences for soil C sequestration.

IP17   Soil microbial carbon use efficiency and biomass mean residence times depending on soil depth and stoichiometry

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Keywords Soil microbial carbon use efficiency, soil depth, soil stoichiometry, ecophysiology

The ratios of bioavailable elements in soils hardly ever meet the nutritional demands of soil microbial communities. Yet, the microbial biomass stoichiometry is relatively constant. To maintain their biomass stoichiometry, microbial communities might adjust their carbon use efficiency (CUE), defined as the organic C taken up that is allocated to growth. So far, it is not well understood how microorganisms adjust their CUE and the mean residence time (MRT) of the microbial biomass to ratios of available elements in soil due to a lack of suitable methods. Microbial CUE has been measured by determining the incorporation and respiration of C from specific ^{13}C-labeled substrates. However, this approach confounds microbial CUE with the specific use efficiency of a given substrate. Moreover, the approach is associated with a large uncertainty since soil microorganisms do not only take up C from the labeled compound that is added, but also from the soil organic matter, and they may use both sources at very different rates.

We developed a method to determine both microbial CUE and MRT of the microbial biomass independently of substrate. The new method is based on the labeling of microbial genomic DNA with ^{18}O from ^{18}O-H$_2$O. Since genomic DNA is only synthesized when cells are dividing, the incorporation of ^{18}O into genomic DNA can be used to calculate the microbial growth rate. Based on the growth rate and the respiration rate, microbial CUE is estimated. Moreover, the method can be used to assess the MRT of the microbial biomass C in soil. We show results on microbial CUE and MRT of the microbial biomass in soil profiles and in grassland soils of a long-term fertilization experiment. With increasing soil depth, the rates of C uptake into the microbial biomass decreased, and the MRT of the microbial biomass increased. However, the microbial CUE did not change with soil depth. In the grassland experiment, we found that nitrogen but not phosphorus or potassium fertilization decreased microbial C uptake and increased microbial CUE, while the MRT was not affected by fertilization. We will discuss the implications of soil microbial CUE and MRT of the microbial biomass for C cycling.

IP18   Are plants or microbiota regulating SOM stoichiometry in forest soils?

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KEYWORDS SOM elemental analysis, recultivated soil, forest, dominant tree species.

The tree species influence on soil C accumulation and soil organic matter (SOM) stoichiometry is still not fully clear. We compared soil organic carbon (SOC) stocks, N, S, H, O as well as microbial (C$_{mic}$) and fungal C mass (C$_{fung}$) for the organic layer and three mineral horizons (0-5 cm, 5-10 cm, 10-30 cm) under five widely distributed tree species in the temperate region: Black pine (*Pinus nigra*), Common spruce (*Picea abies*), Douglas fir (*Pseudotsuga mienziesii*), European beech (*Fagus sylvatica*) and Red oak (*Quercus rubra*). The study was carried out at the spoil heap and recultivation area Sophienhöhe with an area of 10 km^2 and a height of about 280 m a.s.l., established after brown coal mining. There, boundary conditions including soil type, texture, climate, exposition were similar at the different forest stands.

First results of samples taken 35 years after recultivation show differences in organic layer C stocks among all five tree species increasing consistently in the order Douglas fir < beech < oak << spruce < pine. In mineral horizons the differences were significantly smaller with lowest C stocks under beech, whereas the highest amounts were reached under oak. C$_{mic}$ stocks showed similar trends; beech stands possessed the smallest stocks for both organic layer and mineral soil horizons. Highest C$_{mic}$ stocks were detected under pine (organic layer) and Douglas fir (mineral horizons). Element ratios such as C:N, C:S and O:C also showed clear differences among soil horizons and soils under different tree species.

Overall, significant differences were detected for a variety of soil parameters. Further data evaluation is planned, e.g. by using Van Krevelen diagrams and other statistical tools. Further litter and root analyses will be carried out to identify parameters and mechanisms regulating SOM stoichiometry in forest soils.

IP19   Influence of the altitude on the water-extractable organic matter (WEOM) from rhizosphere and bulk soil in European beech forests of central Italy

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KEYWORDS Rhizosphere effect; labile C pool; mountain soils; soluble phenols; climate change

The water-extractable organic matter (WEOM) represents the most active and mobile form of soil organic matter and it is linked to numerous biogeochemical processes. Although the litter floor is considered the main source of WEOM, roots release large amounts of soluble organic compounds through rhizodeposition processes which make the rhizosphere, the small soil volume in proximity of the root, a soil compartment enriched with WEOM. Since both the rhizospheric processes and the active organic C pool are highly sensitive to the environmental conditions, we evaluated the characteristics of WEOM from rhizosphere and bulk soil of European beech (*Fagus sylvatica* L.) forest soils of Apennines mountains (central Italy) at two altitudes (800 and 1000 m a.s.l.), using elevation as a proxy for temperature change. Specifically, we tested if 1) water-extractable organic C content is greater in the rhizosphere than in the bulk soil, 2) WEOM composition differs between rhizosphere and bulk soil, and 3) the quality of the rhizosphere WEOM is affected by altitude. Both at 800 m and 1000 m a.s.l., larger amounts of sugars were found in the WEOM from the rhizosphere than that from the bulk soil. Further, at higher altitude, the rhizosphere WEOM showed a greater content of organic C and soluble phenols, and abundance of tannins and condensed aromatics than the bulk soil. The clear influence of the altitude on the rhizosphere has been attributed to climatic and soil constraints, which enhanced the release of labile organics and secondary metabolites by rhizodeposition processes. Our findings suggest that the roots are able to influence the characteristics of WEOM, while the environmental restrictions, such as the temperature, increased the distinction between rhizosphere and bulk soil. This view confirmed the key role of the rhizosphere on the soil C cycle, and the importance of the rhizospheric processes when the environmental conditions become limiting. Hence, different environmental conditions should induce specific rhizosphere effects with implication on the quantity and quality of the active organic C pool and, as a consequence, on the soil organic matter cycle.

IP20   Variations in fungal community structure along soil depth profiles and elevation gradients in alpine ecosystems

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Plant and animal diversity patterns have been frequently monitored in many elevation gradient studies while knowledge on variability in fungal community distribution at such natural elevations remain sparse. Gaining insights on fungal community distribution would provide a comprehensive understanding of the global effects of changing climatic conditions. In our climosequence study at two Alpine forest ecosystems, we highlight soil fungal community distribution along soil depths over an elevation gradient of 900 to 2070 meters above sea level (m asl). Soil fungal communities were characterized using high-throughput Illumina sequencing (HTS) of internal transcribed spacer (ITS2) region. The species composition was significantly abundant at Hochschwab middle and Rauris lowest elevations respectively. Differences between community composition based on PERMANOVA analysis were significant between both sites due to differences in soil type ($p<0.05$) and highly significant ($p<0.001$) due to vegetation within elevations of each site. Total soil carbon (C) and nitrogen (N) contents followed by pH at different depths were apparently responsible for variations in major phylums. The diversity of soil fungi was majorly dominated by phylum *Ascomycota* followed by *Basidiomycota* and *Zygomycota* in our study. To our knowledge this is a promising metagenomics and climosequence study leading to better insights on variations in fungal community structure as affected by environmental and soil chemical properties at natural elevations and vertical soil profiles in alpine ecosystems.

Poster session 4: What is the contribution of methods and modelling approaches from systems biology/ecology to understanding SOM in the soil system?

SP1   Review: Microbial Volatile Organic Compounds (mVOCs) emissions by soil

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Volatile Organic Compounds (VOCs) have a central role in the chemistry and composition of the troposphere. VOCs are precursors of atmospheric aerosols (PM 2.5) and tropospheric ozone (O_3). Biogenic VOCs (bVOCs) are estimated to contribute up to 90% of the total VOCs emissions globally. One of the sources of bVOC is soil microorganisms, especially through sugar degradation but also through secondary metabolism processes. Microbial VOCs production in soils depends also on: nutrients, physiological state of the microorganisms, pH, temperature and oxygen availability. In particular, oxygen plays an important role because under anaerobic condition the diversity and the amount of VOCs emitted is increased.

The aim of this poster is to take an overview of the existing knowledge on VOC emissions by microorganisms in soil, with a special focus on the link between the VOC spectrum and the microorganism's metabolism. The diversity of micro-organisms and typology of metabolism in European soil is reviewed to identify the potentially most frequent pathways of VOC production. Furthermore, a focus on the most used techniques to detect VOCs in soils are recapitulate and in particular advantages of PTR-MS technique are shown. Finally, the effect of the interaction with the substrates in the soil is also reviewed, and a scheme of the VOC emissions pathways in soil micro-organism is proposed and discussed.

SP2 Microbial physiology and self-organisation of microbial turnover processes at the microscale influence steady-state C and N content of the soil

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KEYWORDS Microbial soil organic matter turnover, modelling, microbial physiology, self-organisation, microscale interactions

Recent research suggests that certain physiological traits of soil microbes, such as the efficiency with which they convert plant detritus into microbial biomass (microbial growth efficiency) or the efficiency of extracellular enzymes, influence C and N content of the soil at the steady state. We propose that feedbacks and self-organisation of microbial turnover processes at the microscale additionally influence C and N build-up in the soil. The latter phenomena are however rarely taken into account in microbial soil organic matter turnover models, and are difficult to observe experimentally.

We analysed possible mechanisms of microbial contributions to the build-up of soil C and N using an individual-based, stoichiometrically and spatially explicit computer model, which simulates the microbial decomposer system at the soil microscale (i.e. on a grid of 100x100 soil microsites). Soil organic matter dynamics in our model emerge as the result of interactions among individual microbes with certain functional traits (f.e. enzyme production rates, growth rates, cell stoichiometry).

Our model results show that resource limitation of microbes lead to µm-scale spatial pattern formation through spatial self-organisation of microbes and substrates, which can be explained by the Turing mechanism. Scenarios that exhibited pattern formation were generally associated with higher soil organic matter storage at the steady state compared to situations without pattern formation (i.e. at non-limiting conditions for microbes). Moreover, pattern formation lead to a spatial decoupling of C and N turnover processes (visible as a spatial decoupling of microbial N mineralization and N immobilization). A second type of pattern formation was induced by increasing microbial growth efficiency. These patterns also increased soil organic matter storage at the steady state, but mainly through substantially increasing the accumulation of microbial remains.

Our theoretical analysis shows that microbial physiological traits can influence the amount of C and N in soil at steady state. Pattern formation through spatial self-organization, which have also been observed on larger spatial scales in other resource-limited communities (e.g., vegetation patterns in arid or wetland ecosystems), may also occur at the soil microscale and additionally influence the amount of C and N present in the soil at the steady state.

SP3 Interactions between substrate and nutrient limitations for C-turnover in subsoil

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KEYWORDS Subsoil, Enzymes, Priming Effects, Nutrient limitations

Studies on factors controlling C-stability in subsoils are very scarce. Recent results suggest a lack of labile C substrates and nutrient limitations in subsoils as a reason for suppressed C-turnover. However, it is not known how different substrate qualities and in which way nutrients combined with labile C

affect C-turnover. The activity of soil enzymes plays an important role for the decomposition of organic matter in soils and can be a powerful tool to shed further light on substrate and nutrient limitations as a hypothesized controlling mechanism for C-stability in subsoils. We studied the impacts of ^{14}C-labeled citric acid (organic acid) and vanillic (phenolic acid) acid in combination with N or P supply and palmitic acid (fatty acid) alone on changes in soil organic carbon (SOC) mineralization and enzyme activities of dehydrogenase, peroxidase, phenoloxidase and 6 extracellular enzymes involved in C-, N-, P- and S-cycle. For this approach, we sampled a Cambisol in a forest at three different depths (2-12, 35-65 and 135-165 cm) and conducted a laboratory incubation experiment for 105 days at 20 °C. While N-additions showed no impact on C-turnover in the topsoil, highest SOC-mineralization was observed in both subsoil N-treatments, especially in 135-165 cm, resulting in about 2.5-fold higher mineralization compared to the control. Phosphorus showed no effect on C-turnover in all depths. Further, no substrate stimulates SOC mineralization in 35-65 cm, except in combination with N, but to a lower extent than pure N-additions. Substrate quality effects were observed in topsoil and lower subsoil, resulting in higher SOC-mineralization after vanillic acid additions in comparison to other added substrates. Interactive effects of N in combination with labile C were only observed in topsoil showing lower SOC mineralization compared to pure substrate additions. Most enzymes in the topsoil involved in C-cycle were not affected by additions of N or labile C. In contrast, dehydrogenase, peroxidase, ᴦglucosidase and chitinase were still highly increased after adding N to the lower subsoil compared to the control, indicating a long-term shift in the microbial community. Same patterns were observed for substrate additions in combination with N and pure palmitic acid addition to the lower subsoil, however, to a lower extent than N-addition alone. In contrast, N-additions to the upper subsoil (35-65 cm) only increased chitinase and ᴤxylosidase but reduced dehydrogenase activity. Our results clearly indicate that microbial N-limitation is the main factor for suppressed C-turnover in the subsoil at this site.

SP4   Moisture sensitivity of soil respiration in the context of extreme dry-wet events

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KEYWORDS Soil respiration, dry-rewet, extreme events, temperature sensitivity, temperate forest

Rationale and objectives: Climate change research predicts an increase in weather extremes like severe droughts and heavy rainfalls in central Europe. Because soil moisture is one of the major factors controlling microbially-driven soil processes, a changed moisture regime will impact soil organic matter (SOM) decomposition and soil respiration. This in turn can lead to feedback effects between altered precipitation and changed soil CO_2 fluxes which can intensify climate change. Soil respiration has been known to be temperature sensitive, often expressed as Q_{10} values. However, it is not clear how soil moisture controls soil respiration and whether the moisture sensitivity of soil respiration is affected by repeated extreme dry-wet cycles.

Methodology approach: To investigate the impact of repeated drought and heavy rainfall events on temperature and moisture sensitivity of soil respiration, a two-year precipitation manipulation experiment was conducted in an Austrian beech forest in 2013 and 2014. Experimental plots were covered with roofs to exclude rainfall, and an irrigation system was used to simulate heavy rainfall events. Treatments included "moderate drought stress" with 6 annual cycles of 4 weeks drought followed by 75 mm irrigation, and "severe drought stress" with 3 annual cycles of 8 weeks drought followed by 150 mm irrigation. Control plots received natural precipitation. Soil respiration was monitored 3-hourly with an automatic headspace chamber system connected to an infrared CO_2 analyzer, and soil temperature and moisture were recorded with a data-logger. Various statistical models were tested to

describe the relationships between soil respiration, temperature and moisture, as well as temperature and moisture sensitivity of soil respiration.

Results and conclusions: Our results show that repeated extreme events strongly reduced variation in soil respiration. Droughts significantly reduced soil respiration, and this reduction was stronger if the drought periods were longer. Cumulative soil respiration significantly decreased in dry-wet treatments compared to control plots, which indicates that the CO_2 pulses after rewetting did not outweigh the reduction in CO_2 efflux during drought periods. Temperature sensitivity of soil respiration was best described with a Gauss model. Furthermore, in severely-stressed plots when soil moisture dropped below a certain threshold, moisture became limiting for soil respiration and this "moisture threshold" effect overruled temperature limitation.

SP5   Topsoil burial through deep ploughing has contrasting effects on SOC turnover in croplands and forests

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KEYWORDS Buried topsoils, carbon mineralisation, subsoils

Soil organic carbon (SOC) storage capacity of subsoils is considered to be high. Nevertheless, measures for enhancing SOC stocks commonly focus on topsoils. We studied the option of actively burying SOC-rich soil material through deep ploughing to enhance SOC stocks on a long-term basis. Through deep ploughing, topsoil is buried in deeper soil layers (55 to 90 cm depth). The objective of this study was to assess the effect of soil depth on microbial activity, biomass and carbon turnover using this unique set up of buried SOC.

We sampled soil from five loamy and five sandy cropland sites and four sandy forest sites, which were dep ploughed 25 to 53 years ago. Adjacent, equally managed but not deep ploughed croplands and forests were sampled as reference.

Deep ploughed cropland sites contained 42 ± 13 Mg ha^{-1} more SOC than the reference down to 100 cm depth. On the contrary, at forests, SOC stocks of deep ploughed soils were on average 1 ± 10 Mg ha^{-1} lower than of reference soils. These contrasting results can be explained, on the one hand, by the slower SOC accumulation in the newly formed topsoils of the deep ploughed forest soil (on average 48% lower SOC stocks in topsoil than in the reference forests) compared to the croplands (on average 15% lower SOC stocks in topsoil compared to the reference croplands). On the other hand, the buried topsoils at the forest sites exhibited similar C mineralisation rates (determined in short-term *in-vitro* incubations) as compared to the reference topsoils. In contrast, at the sandy croplands, net C mineralization rates were significantly lower (67%) in the buried compared to the reference topsoil. Additionally, microbial biomass was not significantly lower in the buried than in the reference topsoils at forests indicating no negative effects of soil depth on microbial activity. At croplands, microbial biomass was 77% lower in the buried than in the reference topsoils. Respiration after glucose addition in relation to basal respiration was on average 2.3 times higher in loamy buried topsoils compared to the reference topsoils, at the sandy croplands 1.6 times higher and in the forests 7% lower in the buried than in the reference topsoils. This suggests that microorganisms in the buried topsoils at the arable sites are less adapted to using easily available substrates in contrast to the forest sites. Radiocarbon based turnover times will also be presented.

Our results show clear differences in microbial activity and resulting carbon turnover in buried topsoils at cropland and forests. This is most likely linked to the continuous input of easily available substrate in form of roots at forests, which is considerably lower at croplands.

SP6   Influence of different cropping systems on soil structure visualised using X-ray computed tomography

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KEYWORDS soil structure, cropping system, X-ray Computed Tomography, image analysis, porosity

Soil is a fundamental ecosystem which supports life on Earth by providing myriad functions. Soil delivers these functions via the interactions between soil structure, organisms living within the soil, water, gases and solutes. Soil structure is dynamic and modified by natural factors (e.g. the soil biota, wet:dry and freeze:thaw cycles) and also by management intervention (e.g. tillage, cropping system). The aim of this study was to investigate the effects of different cropping systems on soil structure at different spatial scales. Three systems were studied in replicated plot field experiments, involving contrasting degrees of plant-derived inputs to the soil, viz. perennial (grassland), annual (arable), and no-plant control (bare-fallow), associated with two types of soil texture (clay and sandy). The hypotheses were that the presence of plants results in a greater range (diversity) of pore sizes and that perennial cropping systems invoke greater structural heterogeneity, manifest as a wider range of pore sizes than annual or fallow systems. Accordingly, the nature of the pore systems was visualised by X-ray Computed Tomography and quantified in 3D. The results showed that the presence of plants did have an effect on the porosity of the clay soil at the mm scale, however at the μm scale, perennial and annual plant covers resulted in greater porosity, a wider range of pore sizes and greater connectivity compared to the bare-fallow soil. However, the opposite occurred in the sandy soil: here, plants decreased the porosity and connectivity within soil at the mm scale but had no effect at the μm scale. These data partly confirm the base hypotheses, and reveal the profound effects that plants have upon soil structure, however such effects are scale-dependent, and contingent upon soil texture and the nature and extent of plant inputs. Future studies will focus on the impact of different plant root morphologies on soil structural genesis mediated via interactions with the soil biota, and the functional consequences of the resultant contrasting soil architectures.

SP7   Bacterial contribution to wetting properties and SOM formation on particle surfaces as observed by X-ray photoelectron spectroscopy (XPS)

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KEYWORDS XPS, particle surface, SOM formation, microorganisms,contact angle

Rationale and objectives: Soil functioning (e.g., retention of colloids, organic matter decomposition) is strongly governed by surface processes and particle wettability. The latter, being decisive for all transport-related processes, is determined by the chemical structure of the outmost soil particle surface layer. Soil particle surfaces usually are coated by organic matter. Hence, the relevant part of soil

particles differs from the bulk in chemical composition. To relate the surface properties and processes to the chemical composition X-ray photoelectron spectroscopy (XPS) with a maximum analysis depth of about 10 nm is a promising analytical tool. Decreasing wettability (i.e., increasing contact angle, CA) along a soil chronosequence (soil age 0-120 yrs) has been previously explained by the concurrent increase in C and N content and decrease in O and mineral-derived cations as the result of increasing SOM formation on the mineral surfaces. Here we tested if these chemical changes can be linked to microorganism (MO)-related parameters (PLFA, coverage by MO necromass, and bacteria, fungi, and actinomycetes concentration) and if there is an MO contribution to soil particle wettability.

Methodology approach: For each of the eight chronosequence samples three XPS survey spectra (Axis Ultra DLD, Kratos Analytical, Manchester, UK) were recorded at three different spots (measured area 300x700 μm each) and quantified. A fitting scheme discriminating between polar and non-polar C species was applied to the C 1s peak.

Results and conclusions: All MO-related parameters showed a positive relationship with C and N and a negative one with the mineral-derived cations. Further, MO-related parameters were positively related to the thickness of the organic coating, indicating a continuous input with soil age. The extent of surface coverage by microbial necromass, like CA, showed a closer relationship with non-polar C species than with total C concentration, maybe hinting towards a greater contribution of dead cells to soil wetting properties than of living ones as bacteria concentration only showed a close positive relationship with total C. The results of this study clearly revealed a distinct contribution of MO to SOM formation on particle surfaces. The shallow XPS analysis depth thus allows directly linking the chemical composition of soil particle surfaces to the occurrence of MO associated with mineral surfaces as well as soil wetting properties.

SP8   Combining position-specific 13C labeling with 13C-PLFA analysis to assess microbial utilization of free versus sorbed Alanine

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KEYWORDS Isotope labeling, microbial utilization, PLFA, LMWOS, C fluxes

Microbial utilization is a key transformation process of soil organic matter (SOM). Sorption of low molecular weight organic substances (LMWOS) to soil mineral surfaces delays and changes microbial uptake and therefore mineralization of LMWOS to CO_2, as well as all other biochemical transformations. We used position-specific labeling, a tool of isotope applications, combined with ^{13}C-phospholipid fatty acid (PLFA) analysis, to assess microbial utilization of sorbed and non-sorbed Alanine in soil. Alanine as one of the quantitatively most important amino acid in soil and links C- and N-cycles and therefore is a model substance for the pool of LMWOS.

To assess changes in the transformation pathways caused by sorption, we added uniformly and position-specifically ^{13}C and ^{14}C labeled Alanine to the Ap of a loamy Luvisol in a short-term (10 days) experiment. The respired CO_2 was captured and its ^{14}C-activity was determined at increasing times intervals. Group specific microbial utilization of Alanine's functional groups was evaluated by ^{13}C-PLFA analysis.

Sorption delayed the release of labeled CO_2 and reduced initial respiration rate by 80%. Irrespective of sorption, the highest amount of C from the carboxylic group was respired, whereas C from the amino-bound group as well as from the methylic group were preferentially incorporated into PLFA. This is in

accordance with the basic microbial metabolism of C_3 molecules in glycolysis. Reconstruction of microbial transformation pathways showed that the C-2 position of Alanine was lost faster than its C-3 position regardless of whether the molecule was used ana- or catabolically. The highest incorporations of all positions in PLFA were accomplished by Gram negatives. Free Alanine was preferential used by highly competitive free living osmotrophs, while sorbed Alanine was more preferred by microbial groups that build larger amounts of biomass, e.g. biofilms and extracellular structures fixing hyphae. Remarkable is that both, those microorganisms that prefer free and those that prefer sorbed Alanine, do not belong to a common taxonomic or phylogenetic group, but they contain in each case both - pro- and eukaryotes and within the prokaryotes Gram positives and Gram negatives. Therefore, it is crucial to consider the ecophysiology of the microbial groups to give evidence about their behavior instead of classifying microbial communities solely based on phylogenic or taxonomic properties. These findings could only have been achieved with the position-specific labeling approach, therefore this method will strongly improve our understanding of stabilization processes and soil C fluxes.

Poster session 5: Modelling approaches for the integration of process components

MP1   Energy balance associated with the degradation of lignocellulosic material by white-rot and brown-rot fungi

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KEYWORDS Lignin - wood-rotting fungi – energy balance

Rationale and objectives: Forest soils cover about 30% of terrestrial area and comprise between 50 and 80% of the global stock of soil organic carbon (SOC). Lignocellulosic material, which is made of polysaccharides and lignin, is the major precursor of SOC in forested ecosystems. For this reason, its biodegradation plays an essential role in carbon cycling. Lignin has traditionally been considered as a recalcitrant polymer that hinders access to the much more labile structural polysaccharides. This view appears to be partly incorrect from a microbiology perspective, as substrate alteration depends on the metabolic potential of decomposers.

In forest ecosystems the wood-rotting Basidiomycota fungi have developed at least two different strategies to attack the structure of lignin and gain access to structural polysaccharides. White-rot fungi degrade all components of plant cell walls, including lignin, using enzymatic systems. Brown-rot fungi do not remove lignin. They generate oxygen-derived free radicals, such as the hydroxyl radical produced by a mediated Fenton reaction, that disrupt the lignin polymer and solubilizes amorphous and crystalline cellulose providing access to carbohydrate-degrading enzymes.

We developed a simple model to investigate whether the lignin relative persistence could be related to the energetic advantage of brown-rot degradative pathway in comparison to white-rot degradative pathway.

Methodology approach: The model simulates the changes in substrate composition over time, and determines the energy gained from the conversion of the lost substrate into CO2. It also estimates the

production of enzymes required to explain the observed substrate alteration. For brown rot fungus specifically, the production of OH radicals is included. The cost of production of the degrading agents is then determined.

The model was run, using data from the literature on litter degradation by *Trametes* versicolor, a white-rot fungus, and Gloeophyllum trabeum, a brown-rot fungus.

Results and conclusions: Our model demonstrates that the brown-rot fungus (*G. trabeum*) was more efficient than the white-rot fungus (*T. versicolor*). From an evolutionary point of view, this energy advantage could explain the emergence of the brown-rot degradative pathway from a white-rot degradative pathway and subsequently, the relative persistence of lignin in soil.

MP2   Soil organic matter accumulation in relation to changing soil volume, mass, and structure: Concepts and calculations

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Keywords volume-change, structure, porosity, pedoturbation, pedogenesis

Soil organic matter (SOM) stores change over time mainly as a result of microbial processing of plant and microbial metabolites and interactions with mineral surfaces. Such changes (ΔSOM) are critical issues for soil fertility, soil development, and the global C cycle. Measuring such change typically relies on sampling to constant depth (CD) which is well known to be inaccurate if bulk density (BD) has changed between sampling sites or times. The usual solution to this problem is to sample an equivalent mass (EM), but in most cases soil mass has also changed. Indeed, the whole point in measuring ΔSOM is to quantify a change in C mass. As SOM accumulates, soil volume must increase (dilation) unless all the added SOM fills in existing pores. Soil dilation as a result of root ingrowth is well documented in the geological literature but has rarely been considered in conjunction with studies of ΔSOM. Other processes that can alter soil volume include eluviation, bioturbation and dissolution/decomposition of both mineral and organic soil particles.

Here, we present a set of equations (the volume/mass corrected or VMC equations) for calculating potential effects of processes that alter soil volume and/or mass on calculated values for ΔC. We first present a hypothetical example to illustrate the expected differences in soil volume, mass, bulk density, and ΔC when measured via the CD, EM, and VMC methods. We then compare these approaches for assessing the changes in soil parameters for four soil-chronosequence studies in which change in soil volume (ΔV) and mass (ΔM) were also measured. Because ΔV was measured in these studies, the resulting values for ΔC can be calculated correctly.

The CD method yielded errors of −75% to +49% in ΔC and the EM method even larger errors (-87% to +54%). Where volume had increased (dilation) both CD and EM methods generally underestimated ΔC, whereas where volume decreased (collapse) or remained the same both methods overestimated ΔC. These results are discussed in light of the few laboratory, field, and simulation studies comparing effects of ΔV on ΔC measurements.

We hope that the VMC equations, by addressing the interplay between changes in soil volume, porosity, and structure, will provide the foundation for a new set of mechanism-based SOM models that take into account changes in these variables across the full range of spatial and temporal scales.

MP3   Modelling a century of soil redistribution processes and carbon delivery from small watersheds using a multi-class sediment transport model

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KEYWORDS Soil erosion modelling, SOC delivery, long-term, selective transport

Over the last few decades, coupled soil erosion and carbon redistribution modelling has received a lot of attention due to large uncertainties and conflicting results. The majority of modelling approaches addressing the long-term effect of soil redistribution upon carbon dynamics are based on conceptual erosion models, simulating annual mean erosion rates. In consequence, event-specific processes of preferential erosion, transport or deposition of soil organic carbon fractions is ignored. The aim of this study is to analyze the relevance of these carbon enrichment processes in delivered sediments. Therefore, we utilize an event-based and physically oriented erosion model (MCST) on a unique high resolution 100 year rainfall data set from central Belgium. The study area is a small agricultural catchment (3 ha) located in the Belgium loess belt about 15 km southwest of Leuven, with a rolling topography of slopes up to 14%. Our modelling results indicate (i) that enrichment of carbon in delivered sediments decreases in relation to event size and (ii) highest carbon enrichment ratios (max: 9) are found for events dominated by interrill erosion. (iii) Modelling 792 events over 100 years shows an average long-term carbon enriched ratio of 1.4. Overall, the study indicates the importance to account for event-specific erosion processes for coupled erosion and carbon dynamics analysis.

MP4   Rhizosphere boundary

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KEYWORDS Rhizosphere biochemistry, Microbial hotspots, Enzyme activities, Rhizodeposition

Estimation of soil volume affected by roots - the rhizosphere - is crucial to assess the effects of plants on properties and processes in soils and dynamics of nutrients, water and soil organic matter. The challenges are 1) the continuum of properties between the root surface and root-free soil, 2) differences in the distributions of various properties (carbon, microorganisms and their activities, nutrients, enzymes, etc.) along and across roots, 3) temporal changes of properties and processes. Thus, to describe the rhizosphere size and root effects, a holistic approach is necessary.
We collected literature data on the rhizosphere gradients of a broad range of physico-chemical and biological properties: pH, CO_2, oxygen, redox potential, water uptake, various nutrients (C, N, P, K, Ca, Mg, Mn and Fe), organic compounds (glucose, carboxylic acids, amino acids), activities of enzymes of C, N, P and S cycles. The collected data were obtained based on the destructive approaches (thin layer slicing), rhizotron studies and in situ techniques: optodes, zymography, sensitive gels, ^{14}C and neutron

imaging.

The root effects were pronounced from less than 0.5 mm (nutrients with slow diffusion) up to more than 50 mm (for gases). However, the most common effects were between 1 - 10 mm. Sharp gradients (e.g. for P, carboxylic acids, enzyme activities) allowed to calculate clear boundaries of the root effects. The first analyses were done to assess the effects of soil texture and moisture as well as root system and age on these gradients. The gradient based distribution functions were calculated and used to extrapolate on the whole soil depending on the root density and rooting intensity. We conclude that despite the specific effects of plants and soil on the rhizosphere size, the common distribution functions can be calculated and extrapolated for the whole soil profile.

MP5   Interpretation of incubation experiments

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KEYWORDS SOM turnover, modelling, model structure, incubation experiment

Interpretation of incubation experiments

Rationale and Objective: Typically, an incubation experiment will provide a result set about the net decomposition (treatment - control) of the added carbon in terms of emitted CO_2-carbon with a time course that suggests an exponential decay of the added organic matter. For a deeper insight it may be helpful to describe the results using the simplest model that is fit to explain the observations. In most cases the assumption of single pool decay is not sufficient. In literature we find different simple models that are set up to describe the turnover of different pools of soil organic matter (SOM) and/or fresh organic matter (FOM): two pool FOM decay (A) , two pool FOM interacting with one pool SOM (B), interacting with two SOM pools (C) and with a cascade flux and CO_2 emission from each SOM pool (D). This raises the question to what degree the selection of a model type is arbitrary.

Methodology approach: Simulation experiments were executed, using always one of the model types to generate a dataset, assuming the incubation process is controlled by a process of this structure. Then the dataset was disturbed with a small error (CV=5%) for each observation step. This was repeated (N=100) and for each sample the parameters of both pools were estimated by inverse modelling to identify the impact of the model structure.

Results and conclusions: If the generating process is of model type A all other models are not able to identify the original parameters, because they all assume a matter flux through a "native" SOM pool. Vice versa: model type A could not identify the original parameters if turnover includes SOM pools.

Assuming the assimilation of FOM in soil happens with only one SOM pool (model B) gives the models C and D some problems but they come more close to the "reality" than model A.

Assuming two SOM pools that are involved in the turnover gives problems only for model A - all other came close to the original parameters.

Therefore, to interpret the results of an incubation experiment, it is essential to use the proper model - having a pool architecture that will be used in the following application. Therefore the application of model type A to identify the half-life of added substrates is useless because it neglects that decomposers grow on a substrate as a first step of a food chain.

MP6   Modeling microbial dormancy in soils

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Keywords Ecosystem modelling, microbial physiology, nonlinear dynamics, steady-state response

Dormancy is a common survival strategy of soil microorganisms to cope with external stress, such as varying substrate and nutrient supply. Because rates of biogeochemical processes in soil are controlled by the active fraction of the microbial community, ecological models must account for dormancy. Dormancy is typically represented in models either by explicitly considering active and dormant biomass pools or by introducing a physiological state variable that describes the active fraction of the total biomass. Existing approaches mainly differ in the description of the transformation process between active and dormant states and disregard the classification into active, potentially active and dormant microbial states.

Dormancy is a reversible state, but despite very fast activation in response to substrate input – i.e. transition from dormant to active state within hours to days, the reverse process – fading from the active to the dormant stage, requires a much longer period of time and is different for individual cell components. This phenomenon, in which the actual steady state depends on the history of the system, is called hysteresis. Our objective was to compare state-of-the-art modelling approaches regarding their ability to reproduce hysteresis as a key feature of dormancy. This has not received much attention yet.

We set up a set of simple SOM turnover models differing in the representation of microbial dormancy as systems of ordinary differential equations. To understand and compare the dynamical properties of the different models, we applied dynamical systems and elements of control theory. This enabled us to analyze how the steady state behavior of the active microbial fraction qualitatively changed in response to substrate input which is an experimentally accessible characteristic and enables close collaboration between experimental and computational biologists.

We argue that hysteretic behavior of dormancy can only be captured by approaches with discontinuous steady-state response. We present criteria for creating such switch-like behavior and discuss how to improve existing mechanistic approaches to better reflect the hysteresis of dormancy.

List of participants

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