Soil bioindicators: how soil properties influence their responses and how choose them in function of the site issues?

Benjamin Pauget, Laurence Rougé, Annette de Vaufleury, Samuel Dequiedt, Isabelle Gattin, Cécile Grand, Marina Le Guedard, Mickael Hedde, Cecile Villenave, Guenola Peres

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Benjamin Pauget, Laurence Rougé, Annette de Vaufleury, Samuel Dequiedt, Isabelle Gattin, et al.. Soil bioindicators: how soil properties influence their responses and how choose them in function of the site issues?. 1. Global Soil Biodiversity Conference : Assessing Soil Biodiversity and its Role for Ecosystem Services, Dec 2014, Dijon, France. 702 p., 2014, The first global soil biodiversity conference, december 2-5, 2014, Dijon, France. hal-02740548

HAL Id: hal-02740548
https://hal.inrae.fr/hal-02740548v1

THE FIRST GLOBAL
SOIL BIODIVERSITY CONFERENCE
Assessing soil biodiversity and role in ecosystem services

GLOBAL
SOIL BIODIVERSITY
INITATIVE

Palais des Congrès, Dijon, France
2-5 DECEMBER 2014

THE FIRST GLOBAL
SOIL BIODIVERSITY
CONFERENCE

December 2-5, 2014, Dijon, France

Book of Abstracts

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PROGRAM
AND ABSTRACTS

THE FIRST GLOBAL
SOIL BIODIVERSITY
CONFERENCE

GLOBAL
SOIL BIODIVERSITY
INITIATIVE

December 2-5, 2014

Dijon – France

GLOBAL
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INITIATIVE

EcoFINDERS

December 2, 2014

Dear Colleagues,

On behalf of the organizing committee, it is our great pleasure to welcome each of you to the First Global Soil Biodiversity Conference - Assessing soil biodiversity and its role for ecosystem services - in Dijon, France.

The conference has been designed to meet and discuss current research efforts in the emerging scientific field of soil biodiversity and its links to earth processes, and to promote interdisciplinary collaboration. The goal of this meeting is promote scientific research on the role of soil biodiversity for soil functions and their translation in ecosystem services, and to integrate such understanding into international environmental agendas, sustainable policy and land management decisions.

Over the next three days we will hear keynote addresses from some of the top experts in soil biodiversity from across the globe. Papers chosen by the Scientific Review Committee from over 750 submitted abstracts will be presented in plenary sessions, with concurrent evening sessions. Posters will be displayed in two rounds to allow adequate time for presentation and discussion. On the final day, we will celebrate World Soil Day as we discuss the future of soil biodiversity research in connection with scientists, stakeholders and policy makers for sustainable soil management.

We hope that you enjoy the Conference and that by sharing your research and interactions with colleagues from around the world, ideas and collaborations will be formed to move the field of soil biodiversity and your own personal interests forward. Enjoy the beautiful city of Dijon, France in December.

Yours sincerely,

Diana H Wall

Philippe Lemanceau

Chair, EcoFINDERS
Institut National de la Recherche
Agronomique (INRA)
Head, UMR Agroécologie Department
Dijon, France

Diana H. Wall

Professor and Science Chair
Global Soil Biodiversity Initiative
University Distinguished Professor
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Colorado State University, USA

www.globalsoilbiodiversity.org

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International Union of Soil Sciences

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Convention on
Biological Diversity

With the Patronage of
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MILANO 2015
FEEDING THE PLANET
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et de la Maîtrise de l'Energie

TERRAGENOME

Agrale
DIJON

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GENERAL

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The conference will be held in the **Palais des Congrès, Dijon, France** (http://www.dijon-congrexpo.com/en/)**.**

Located in the centre of Dijon, the Palais des Congrès has grown with the city that surrounds it. The modern building is served by a direct tram service (Auditorium station, Line T1) from the train station.

The city of Dijon is capital of the Côte-d'Or 'département' and of the Burgundy region. Dijon has one of the best preserved medieval centres in France. It is easy to walk and see the sites, with lots of pedestrian walking streets. You'll sample some of France's finest cuisine and drink great Burgundy wines at dinner or at one of the many wine bars in town (http://www.visitdijon.com/en/).

Registration desk

The Symposium registration desk will be located in the reception hall of Palais des Congrès. The registration desk will be open from 13:00 at 16:00 on Tuesday 2nd December and from 8:00 at18:00 during the following days of the conference for queries and registration.

Badges & Security

For security reasons and for catering purposes please ensure that you wear your badge throughout the conference.

The color coding of the badge holder strips is as follows:
Grey : Chairs and Keynote speakers
Yellow : Scientific and Organizing Committee
Red : Staff
Black : Delegates

Language

The language of the conference will be English.

Speakers

Please upload your ppt file in the reception hall at the latest half a day before your presentation.

Session locations

The Conference sessions will be held in the Amphitheatre Romanée Conti and Morey St Denis (Video transmission) on the ground floor, beginning at 4:15 on Tuesday 2nd December. Please see the full program for oral sessions, poster sessions, and catering times.

Activities	Room Name
Registration	Reception hall
Conference Sessions	Amphitheatre Romanée Conti and Morey St Denis
Poster Sessions	Hall des Grands Echézeaux
Author Workshop	Santenay - Chablis
Evening sessions 1 and 3	Santenay - Chablis
Evening sessions 2 and 4	Morey St Denis
SBB editors meeting	Santenay - Chablis
Editorial Board of Soil Biology and Biogeochemistry	Santenay - Chablis

A lounge room, Mercurey, will be available on the first floor.

Cocktail, coffee break & Lunch

The registration fee includes the following catering arrangements:

Catering Arrangements	Dates	Times	Room Name
Cocktail	Tuesday 2 Wednesday 3	18:30-21:00	Hall des Grands Echézeaux
Coffee break	Wednesday 3 Thursday 4	Please see the full program for timings	Hall des Grands Echézeaux
	Friday 5		Foyer Reception Hall
Lunch	Wednesday 3 Thursday 4	13:00-14:00	Chambertin
Lunch - Author workshop - Michael Swift's workshop - Nina Koele - GSBI Committee	 Tuesday 2 Wednesday 3 Wednesday 3 Thursday 4	 12:30-15:00 13:00-14:00 13:00-14:00 13:00-14:00	 Santenay-Chablis Santenay Chablis Santenay-Chablis

Cocktails will be during the poster sessions, guided Tour of Dijon City and evening sessions.

Conference Dinner

The conference dinner will be held in 'Le Château de Marsannay' (http://www.chateau-marsannay.com/uk/).

The 'Château of Marsannay' is in the Côte de Nuits, in the heart of a very old winemaking village whose first traces date back to a thousand years ago.

The estate of the 'Château of Marsannay' begins 7 kilometers from the south of Dijon, at the gateway to the 'Route des Grands Crus' and leads down to Vosne-Romanée.

Posters

Posters of session 1 (P1.001 to P1.232) should be displayed at the latest by 4 pm on Tuesday 2nd and removed that same day at the latest by 9 pm.
Posters of session 2 (P2.001 to P2.232) should be displayed at the latest by 8am30 on Wednesday 3rd and removed that same day at the latest by 9 pm.

Wi-Fi

Wi-Fi will be available, free of charge in the Palais des Congrès during the conference hours, the password will be available at the registration desk.

Social Media Guidelines

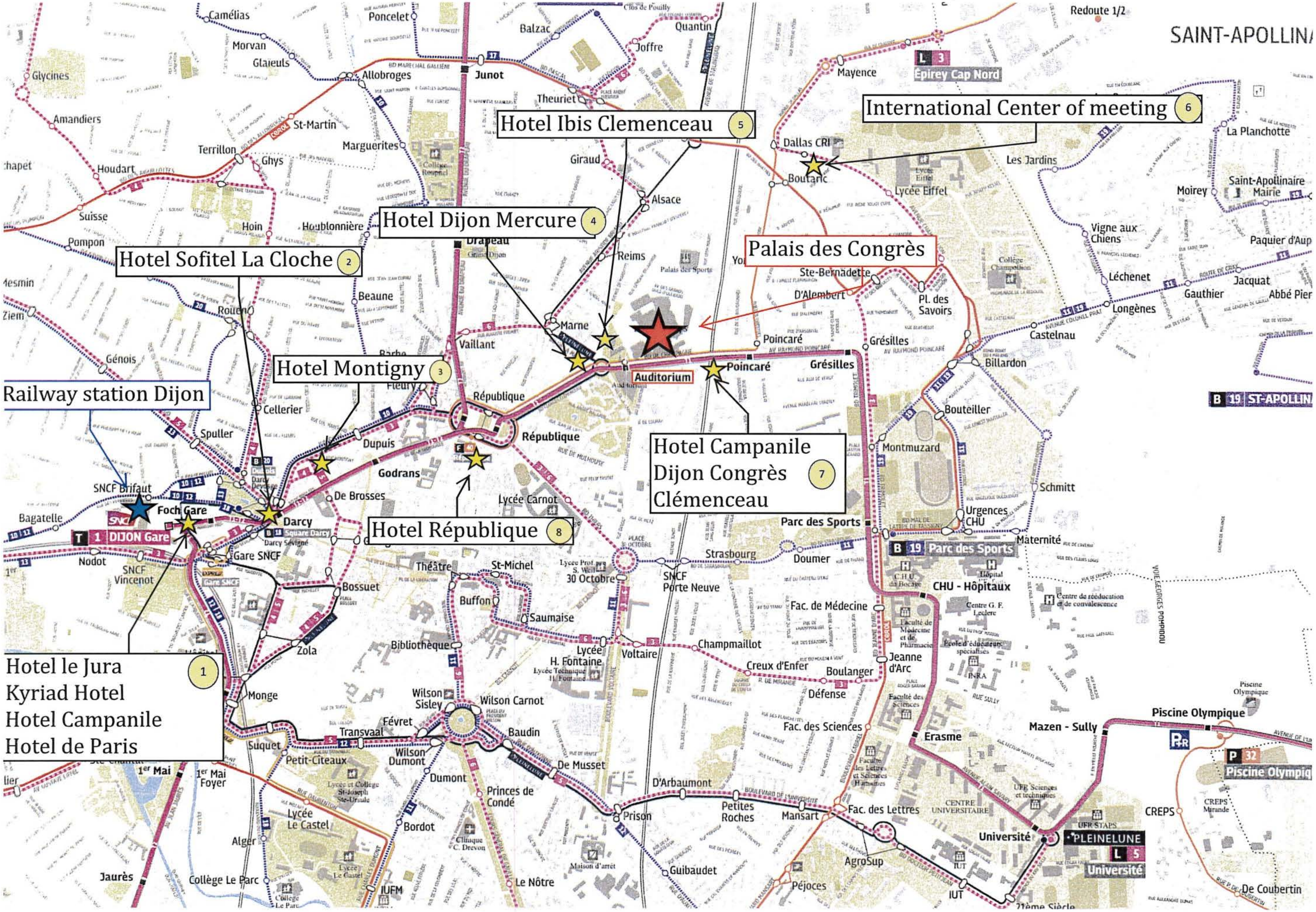
Please use #GSB14 as the event hashtag and include @theGSBI when tweeting about the conference. Social media is a great way to inform a wider audience about the conference. We request that you do not share details about a presentation if requested by the speaker and refrain from sharing information about unpublished data without permission. Do not share photos of slides or poster presentations without prior consent.

Certificates of attendance and presentation

Certificates of attendance are available at the registration desk.
Please ask to the registration desk on the final day of the conference if you require a certificate of presentation.

HOTEL MAP

GLOBAL
SOIL BIODIVERSITY
INITIATIVE


SAINT-APOLLINA
Railway station Dijon
Hotel le Jura
Kyriad Hotel
Hotel Campanile
Hotel de Paris
1
Hotel Sofitel La Cloche
2
Hotel Montigny
3
Hotel Dijon Mercure
4
Hotel Ibis Clemenceau
5
International Center of meeting
6
Hotel Campanile
Dijon Congrès
Clémenceau
7
Hotel République
8
Palais des Congrès
Auditorium
T 1 DIJON Gare
Foch Gare
SNCF Brifaut
Darcy
Square Darcy
Gare SNCF
République
Godrans
Poincaré
Grésilles
Parc des Sports
B 19 Parc des Sports
CHU - Hôpitaux
Erasme
Mazen - Sully
Piscine Olympique
Université
PLEINELUNE
L 5 Université
L 3 Épirey Cap Nord
B 19 ST-APOLLIN
P 32 Piscine Olympiq
Redoute 1/2
Dallas CRI
Boutaric
Mayence
Lycée Eiffel
Les Jardins
Saint-Apollinaire Mairie
La Planchotte
Moirey
Vigne aux Chiens
Paquier d'Aup
Léchenet
Jacquat
Gauthier
Abbé Pier
Longènes
Castelnau
Billardon
Bouteiller
Montmuzard
Schmitt
Urgences CHU
Maternité
Pl. des Savoirs
Ste-Bernadette
D'Alembert
Reims
Alsace
Giraud
Marne
Vaillant
Drapeau
Junot
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Balzac
Joffre
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Morvan
Glaïeuls
Glycines
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SNCF Porte Neuve
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Champmaillot
Creux d'Enfer
Boulanger
Fac. de Médecine
Jeanne d'Arc
Défense
Fac. des Sciences
Wilson Sisley
Wilson Carnot
Févret
Transvaal
Wilson Dumont
Baudin
Dumont
De Musset
Suquet
Petit-Citeaux
1er Mai
1er Mai Foyer
Lycée Le Castel
Alger
Collège Le Parc
Jaurès
Bordot
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Le Nôtre
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D'Arbaumont
Petites Roches
Mansart
Fac. des Lettres
Péjoces
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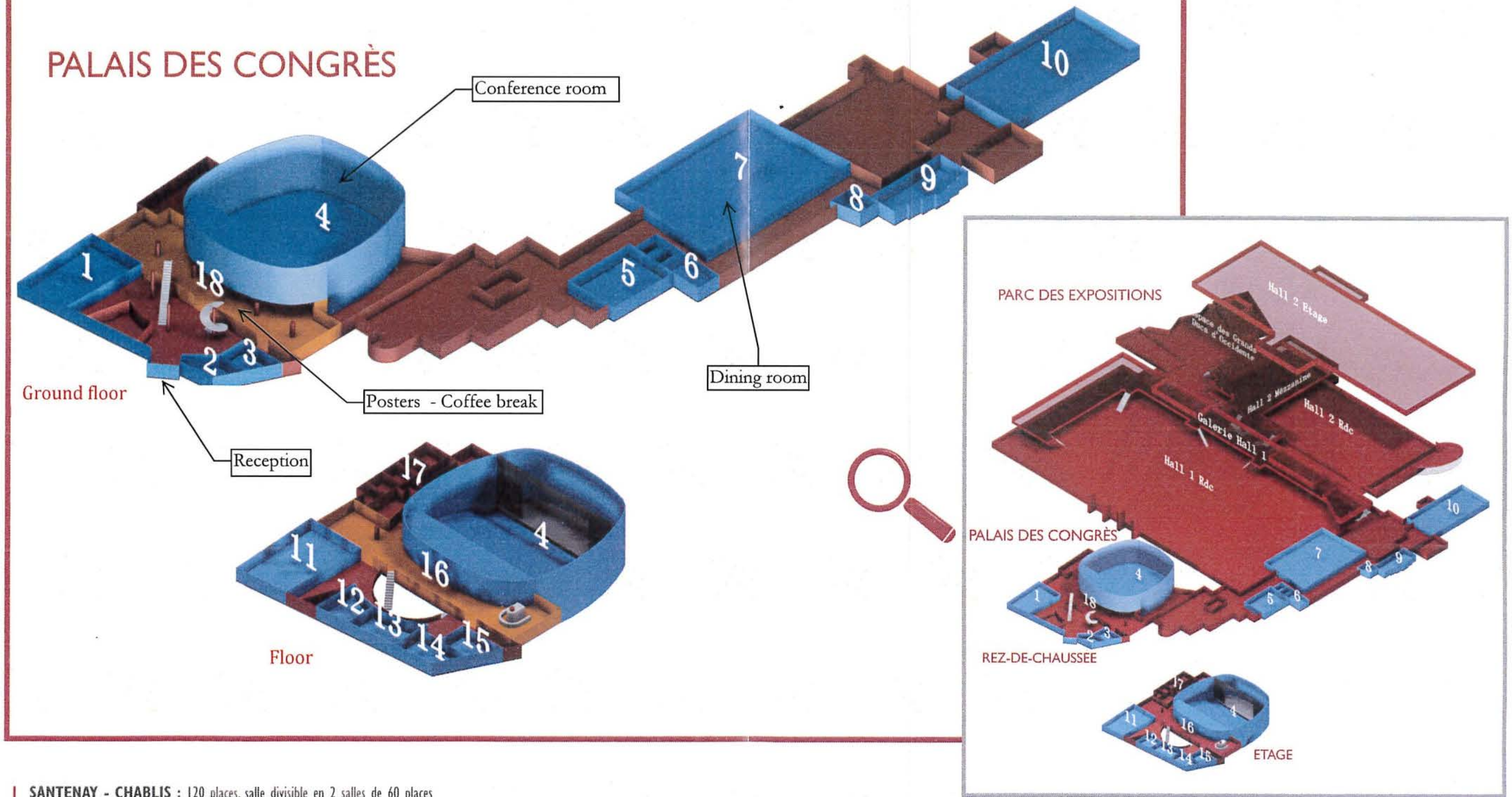
21ème Siècle
CREPS
De Coubertin
VOIE GEORGES POMPIDOU

PALAIS DES CONGRES MAP

GLOBAL
SOIL BIODIVERSITY
INITIATIVE

PALAIS DES CONGRÈS



1 **SANTENAY - CHABLIS** : 120 places, salle divisible en 2 salles de 60 places

2 **BUREAUX ORGANISATEURS** : deux espaces mis à disposition pendant la manifestation

3 **MONTHELIE** : 40 places

4 **AMPHITHEATRE ROMANEE CONTI** : 610 fauteuils avec tablette écritoire escamotable, 4 cabines d'interprétation simultanée, régie polyvalente, scène de 250m², arrière scène avec plateforme élévatrice monte voiture, grill technique, passerelles de lumière

5 **MUSIGNY - POMMARD - VOLNAY** : 200 places, salle divisible en 3 salles de 60 places

6 **MARCS D'OR** : 30 places

7 **CHAMBERTIN** : 670 places, salle divisible en 3 salles par rideaux

8 **MONTRACHET** : 25 places

9 **MEURSAULT - NUITS ST-GEORGES - CORTON** : 120 places, salle divisible en 3 salles de 40 places

10 **CLOS DE VOUGEOT** : 550 places

11 **MOREY ST-DENIS** : 190 places

12 **GIVRY** : 30 places

13 **SAVIGNY-LES-BEAUNE** : 30 places

14 **MERCUREY** : 50 places

15 **SAINT-ROMAIN** : 50 places

16 **FOYER BAR**

17 **4 LOGES**

18 **HALL DES GRANDS ECHÉZEAUX** : 760m²

PROGRAM

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Tuesday 2 December 2014	
12:30-3:00	Author Workshop: Soil Biology and Biochemistry workshop for early career scientists (only on pre-registration)
1:00-4:00	Registration
4:15-7:00	***Opening Session***
4:15-4:30	Introduction: **Dr. Diana Wall**, *Chair of GSBI,* **Dr. Philippe Lemanceau**, *Chair of EcoFINDERS*
4:30-5:30	Introductory lecture: **Dr. Ladislav Miko** Title: *Ugly and dirty friends for millennia - still little known and unrecognised*
5:30-7:00	Poster session from n° P1.001 to P1.265 (cocktail)
6:30-7:30	Editorial Board of *Soil Biology and Biogeochemistry*
6:30-7:30	*Optional*: Guided Tour of Dijon city (departure at 6:30 in front of registration desk)
7:00-9:00	**Evening Session 1: Soil Ecology Education** (10 minutes each) **Chair: Dr. Loren Byrne**, *Roger Williams University, United States*. 1. A happy families game on soil biodiversity - Chevallier, T. 2. Zizare Earthworm Lab: Soil ecology education at preschool - Albizu, O. 3. A K-12 activity using a homemade centrifuge to explore soil biodiversity - Emery, S. 4. "Don Erasmo's milpa": a short story about the below-ground of indigenous polycultures in Mexico - Negrete-Yankelevich, S. 5. Can soil organisms become our best teachers? Exploring soil biodiversity as an ecosystem service provider of excellent environmental education - Byrne, L. 6. Integrating the complexity of soil with interactive games: The soil web and the black box - Barois, I., Aranda-Delgado, E. Break (10 min) 7. Sharing knowledge about worms and aggregates on the transamazonian highway - Lavelle, P. 8. Using soil monoliths to teach soil ecology - Vancampenhout, K. 9. The ECOTROP field-school: integrating DNA barcoding into an education program for the census of soil invertebrate biodiversity in Lopé National Park, Gabon - Decaens, T. & the ECOTROP team 10. Enhancing soil biology education through service-learning and community engagement - Grossman, J. 11. A masterclass to train extension workers on best management practices for soil biodiversity - Hanegraff, M. **Evening Session 2: Living apart together** - linkages between plants and soil organisms and their impact on ecosystem functioning **Chair: Dr. Aurore Kaisermann**, *University of Manchester, England*. 1. Tree species diversity effects on soil microbial biomass, diversity and activity across European forest types - Carnol, M. 2. Hidden effects of large herbivores on plant competition through plant-soil feedbacks - Medina-Roldán, E. 3. Fungal role in carbon flow in the rhizosphere along a chronosequence of abandoned agricultural soils - Hannula, S.E. 4. Ectomycorrhizal symbiosis - cure or cause of forest nitrogen limitation? – Franklin, O. 5. How a native shrub affect soil nematofauna and microbial communities when growing millet in Senegal - Lardy, L. 6. How soil organisms interact with plant hormone signaling pathways – Blouin, M. Discussion

Wednesday 3 December 2014	
Session 1:* Discovery and observation**: Assessing soil biodiversity to determine status and trends ***Chair: Dr. Paul Eggleton, *Natural History Museum, England*	
8:30-9:00	Keynote lecture - **Dr. Wim van der Putten** Title: *Trends in Soil Biodiversity Research and Applications*
9:00-10:30	4 oral presentations (20 minutes each, including discussion) 1. Beta diversity and human impact in soil communities - Caruso, T. 2. Unearthing 'old growth' mycorrhizas in ancient ecosystems - Hart, M.M. 3. Unearthing ancient nematode DNA - possible proxy of past ecosystem features? - Vestergård, M. 4. Ethanol’s growing demand and belowground biodiversity: soil macroinvertebrate community responses to sugarcane expansion in Brazil - Franco, A.L.C.
10:30-11:00	Coffee break/Networking
Session 2*: Tracking and monitoring**: Understanding current, and predicting future distribution patterns of soil organisms ***Chair: Dr. Nobuhiro Kaneko, *Yokohama National University, Japan*	
11:00-11:30	Keynote lecture - **Dr. Noah Fierer** Title: *Predicting soil microbial responses to global change factors*
11:30-1:00	4 oral presentations (20 minutes each, including discussion) 1. A framework to synthesize global soil biodiversity data - Ramirez, K.S. 2. The Microbial Landscape in Soils - Biogeography of Soil Microorganisms in the German Biodiversity Exploratories - Kandeler, E. 3. Predicting and understanding the effects of land use on soil bacterial communities over large scales - Griffiths, R. 4. Evaluating soluble aluminum as a mechanism driving bacterial community structure in terrestrial soils from continental to microcosm scales - Welty-Bernard, A.W.
1:00-2:00	Lunch

Session 3:* Untangling the linkages:** Elucidating relationships between soil biodiversity and ecosystem functioning and ecosystem services ***Chair: Dr. Bobbi Helgason*, Agriculture and Agri-Food Canada, Canada*	
2:00-2:30	Keynote lecture - **Dr. Laurent Philippot** Title: *Linking soil microbial diversity, nitrogen cycling and greenhouse gas emissions*
2:30-4:00	4 oral presentations (20 minutes each, including discussion) 1. Functional microbial diversity, traits and interactions as modulating factors of methane and nitrogen cycling in soils - Bodelier, P.L.E. 2. Importance of community structure for GHG emissions - Lessons learned from genomes and metagenomes - Hallin, S. 3. Soil biodiversity as a driver of ecosystem sustainability - van der Heijden, M.G.A. 4. Resource pulse can alleviate the biodiversity-invasion relationship in soil microbial communities - Falcao Salles, J.
4:00-4:30	Coffee break/Networking
4:30-5:30	3 oral presentations (20 minutes each, including discussion) 5. Network architecture of rhizosphere bacterial community and ecological similarity with the pathogen predicts plant protection from an infection - Yang, T.J. 6. Absence of large soil predators lead to a decline of lower trophic levels and slower decomposition in temperate beech forests of northwest Spain - Melguizo-Ruiz, N. 7. The influence of soil macrofauna on soil aggregation in agro-ecosystems of sub-Saharan Africa depends on management intensity - Ayuke, F.O.
5:30-7:00	Poster session from n° P2.001 to P2.266 (cocktail)
6:30-7:30	*Optional*: Guided Tour of Dijon city (departure at 6:30 in front of registration desk)
7:00-9:00	**Evening Session 3: A New Research and Education Initiative:** The Global Soil Ecological Urban Network **Chairs*:* Dr. Rich Pouyat**, *US Forest Service* and **Dr. Katalin Szlavecz**, *Johns Hopkins Univ., United States* 1. Processes and Patterns of Nematode Biodiversity in Urban Soils - Grewal, P.S. 2. Filling the gap in the knowledge of urban soils organisms: ants and earthworms of urban parks - Vergnes, A. 3. Soil invertebrates as indicators of soil quality in urban vegetable gardens - Joimel, S. 4. A multi-city comparison of urban soil ecosystem function - Szlavecz, K. Discussion **Evening Session 4: Global harmonization of methods** for structural and functional diversity of soil organisms: A GSBI Initiative. (15 minutes each) **Chair: Dr. Jörg Römbke**, *ECT Oekotoxikologie GmbH, Germany*. 1. Standard methods for the assessment of structural and functional diversity of soil organisms: a critical overview - Römbke, J. 2. Soil invertebrate functional traits - Hedde, M. 3. Which bioindicators are suitable for soil quality monitoring and risk assessment? From relevance study to transfer tool development - Pérès, G. 4. A tiered approach for high-resolution characterization of the soil faunal community via DNA metabarcoding - de Groot, G.A. 5. Edaphobase - The online soil-zoological data warehouse – Russell, D.J. 6. Biomes of Australian Soil Environments (BASE): a dataBASE of Australian soil microbial diversity - Mele, P.M. Discussion

<table>
<tr><th colspan="2">Thursday 4 December 2014</th></tr>
<tr><td colspan="2"><i>Session 4</i>: Assessing the pressures and threats: Impacts of global change on soil communities, ecosystem functioning and ecosystem services
<i>Chair: Dr. Maria Iglesias Briones</i><i>, Universidad de Vigo, Spain</i></td></tr>
<tr><td>8:30-9:00</td><td>Keynote lecture - Dr. David Wardle
Title: <i>Aboveground-belowground responses to global change drivers: tales of islands, fires and invaders</i></td></tr>
<tr><td>9:00-10:30</td><td>4 oral presentations (20 minutes each, including discussions)
1. Predicting soil bacterial responses to multi-factor global change with trait-based modeling - Le Roux, X.
2. Future climate alters soil biodiversity and carbon storage of northern peatlands - Lindo, Z.
3. Impacts of global climate change on the leaf-litter arthropod community: effects of altered detrital input and rainfall extremes in two long-term field experiments in a deciduous forest - Wise, D.H.
4. Are there links between the responses of soil biota and ecosystem functioning to elevated CO_2, N deposition and warming? A global perspective - García-Palacios, P.</td></tr>
<tr><td>10:30-11:00</td><td>Coffee break/Networking</td></tr>
<tr><td colspan="2"><i>Session 5:</i> Strategies for management and conservation: Practices to maintain and enhance ecosystem services provided by soil biodiversity
<i>Chair: Dr. Edmundo Barrios</i>, <i>World Agroforestry Centre (ICRAF), Kenya</i></td></tr>
<tr><td>11:00-11:30</td><td>Keynote - Dr. Junling Zhang
Title: <i>Can nutrient management strategy improve diversity of arbuscular mycorrhizal fungi in intensive agroecosystems?</i></td></tr>
<tr><td>11:30-1:00</td><td>4 oral presentations (20 minutes each, including discussions)
1. Land use legacies and agrodiversity from the below-ground perspective: Los Tuxtlas case study - Negrete-Yankelevich, S.
2. Tropical pasture heterogeneity and soil arthropod biodiversity: bad plants also help - Andrés, P.
3. Biodiversity and ecological succession as indicators of compost maturity and quality - Neher, D.A.
4. Are sustainable agricultural practices sustaining larger earthworm populations? A quantitative review using meta-analysis - Schmidt, O.</td></tr>
<tr><td>1:00-2:00</td><td>Lunch</td></tr>
</table>

Session 6: **Extending the knowledge base**: The social and economic value of soil biodiversity ***Chair: Dr. Fatima Maria de Souza Moreira**, Universidade Federal de Lavras, Brazil*	
2:00-2:30	Keynote lecture - **Dr. Kate Scow** Title: *Assessing the economic and social values of soil biodiversity*
2:30-4:00	4 oral presentation (20 minutes each, including discussions) 1. Soil natural capital: Can we use it to close future yield gaps and reduce agricultural risks? - Hedlund, K 2. Farmer knowledge and use of soil biodiversity: a global synthesis illustrated with case studies - Pauli, N. 3. Measuring changes in agricultural land quality: The case of the Italian farms - Zoupanidou, E. 4. On the value of soil biodiversity and ecosystem services– Foudi, S.
4:00-4:30	**Distinguished lecture: Dr. Diana Wall** Title: *Soil Biodiversity: Big impact of small creatures*
4:30-6:30	Coffee break/networking
6:30	***Conference dinner*** (departure by bus at 6:30 in front of registration desk)

Friday 5 December 2014, World Soil Day		
Session 7: **Setting the agenda for the future:** Bridging scientific knowledge and applications for soil and land management ***Chair: Dr. Philippe Lemanceau**, INRA, France*		
8:30-8:50	*Summarising what science brings so far in terms of knowledge and what are the future challenges*	Keynote lecture - **Dr. Richard Bardgett** Title: *Digging into the future: future challenges for soil biodiversity research*
8:50-9:10	*Views and experiences on applications of soil biodiversity knowledge for soil and land management*	Keynote lecture - **Dr. Michael Swift** Title: Applying soil biological knowledge to the management of soil fertility and other ecosystem services: the *Tropical Soil Biology and Fertility* experience
9:10-9:30		Keynote lecture - **Dr. Ben Delbaere** Title: *Going underground – why soil biodiversity matters to stakeholders*
9:30-9:50	*Further knowledge required to overcome remaining bottle necks*	Keynote lecture - **Dr. Michael Stocking** *Title: Mainstreaming Soil Biodiversity to Deliver Both Global Environmental Benefits and Human Development*
9:50-10:10		Keynote lecture - **Dr. Antonio Bispo** Title: *Soil biodiversity: from science to bioeconomy*
10:10-10:45	Coffee break	
10:45-12:30	*Panel Discussion: How to translate scientific knowledge in soil policies and for soil management? What are the bottlenecks for such translation?* Moderator: **Kristin Ohlson;** Panelists: **Dr. Richard Bardgett**, (University of Manchester, UK), **Dr. Antonio Bispo** (ADEME, FR), **Dr. Pia Bucella** (Director of Directorate Natural Capital, DG Environment, EC), **Dr. Ben Delbaere** (ECNC, NL), **Dr. François Houllier** (President and Chief Executive Officer of INRA, FR), **Dr. Cyril Kao** (Ministry of Agriculture, Head of the Department of Research, FR**), Dr. Michael Stocking** (University of East Anglia, UK), **Dr. Mike Swift** (Former Director, Tropical Soil Biology and Fertility Institute, Kenya)	
12:30-13:00	Presentation of crowd sourcing video - **Dr. Ciro Gardi** Presentation of the Global Soil Biodiversity Atlas - **Dr. Alberto Orgiazzi**	

EARLY CAREER SCIENTISTS' STATEMENT

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Panel Discussion "*How to translate scientific knowledge in soil policies and for soil management?"*

Early Career Scientists' Statement

Current threats to soil biodiversity demand global scientific, political and economic actions to ensure the functioning of ecosystems for future generations

Biodiversity is now a well-accepted and understood concept of functional importance that is used ubiquitously! However, 'biodiversity' describes more than the organisms we can see aboveground - like plants, birds, and mammals. Biodiversity also includes the most diverse and complex ecosystem on the planet: SOIL! "*Soils contain over 98 per cent of the genetic diversity in terrestrial ecosystems*". Yet, most of this belowground biodiversity is not visible, and, therefore, it is often overlooked in discussions regarding conservation of global biodiversity or its contribution to ecosystem services.[1]

Belowground biodiversity is critical to maintaining ecosystem functioning and global sustainability, and deserves the same attention as aboveground biodiversity. To reach this goal, we will face bottlenecks at the scientific, economic, and political level. Questions that must be addressed include: are policy-makers aware of soil biodiversity's importance? Are scientists providing the evidence to support soil biodiversity's importance to stakeholders and policy makers?

The Early Career Scientists group proposes to use the First Global Soil Biodiversity Conference to give Soil Biodiversity a voice!

As a whole, the soil ecosystem provides myriad ecosystem services, both from its physical and chemical properties (e.g. nutrients, water, and texture), as well as from its biological properties (e.g. all the organisms living in the soil). Furthermore, the physical/chemical properties are intrinsically linked with soil biology. Soil biodiversity should be recognized as a crucial player in guaranteeing the functioning and the quality of soil. Taken together,

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[1] In fact, soil biodiversity is not addressed in the Global Biodiversity Outlook (GBO-3) from the UN Convention on Biological Diversity (Secretariat of the CBD, 2010), and is not referred to in the popular International Union for Conservation of Nature (IUCN) Red List of Threatened Species (IUCN, 2012).

the soil ecosystem with its biodiversity and concomitant ecosystem services provide a common denominator for all terrestrial ecosystems (e.g. agriculture, forests, grasslands, peatlands, deserts, and urban areas).

Numerous major anthropogenic pressures and threats are also exerted on soil and its biodiversity: from soil pollution and sealing to soil erosion and intensive human exploitation. As a consequence of these many pressures, soil-dwelling organisms are also under threat. In fact, the possible decline in soil biodiversity has been identified as one of the major issues that will need to be dealt with in the coming years. Yet, despite the clear threat, the overall relationship between pressures on soils and belowground organisms has been poorly investigated to date. A common framework and, consequently, suitable policies to protect soil biodiversity are still missing. This is mainly due to 1) the difficulty in disentangling how these real threats affect soil biodiversity, 2) the lack of standardized procedures, and 3) the lack of data on the distribution of soil organisms at large scale are crucial contributors to this gap in policy and management.

Further complicating efforts, soil processes do not occur within a time scale that is easily grasped by human society. For example, soil formation is a process that takes thousands of years, but it can take only a matter of minutes to degrade soil. Therefore, tangible, operational, strategic policies and goals must be established to ensure sustainable soil management, to guarantee long-term ecosystem functioning of soil and to preserve and value soils and soil biodiversity. This challenge is global and cannot be limited to countries or even continents. It must be a global collaboration.

We, a group of early career scientists from all over the world, would like to actively contribute toward identifying and overcoming these bottlenecks to establish policies and initiatives to preserve the invaluable resource that is the soil ecosystem as a whole. Given the strong link between soil biodiversity and ecosystem functioning and considering that functioning ecosystems are necessary for a sustainable human society, we hope that policy makers, research institutions, and other scientific and non-scientific stakeholders will support us in taking an active role and encourage us to express our passion and willingness to contribute toward the responsible use of soils for the sake of our generation and generations to come.

1. **Ali Rana Shahbaz (Pakistan)** – Institute of Soil Science and Land Evaluation, University of Hohenheim, Germany.
2. **André Franco (Brazil)** – University of São Paulo, Brazil.
3. **Apolline Auclerc (France)** – Université de Lorraine / ENSAIA, France.
4. **Ashley Shaw (USA)** – Colorado State University, Fort Collins, Colorado, USA.
5. **Catalina Sanabria (Colombia)** – University Pierre et Marie Curie, Paris 6, France.
6. **Emma L. Aronson (USA)** – University of California, Riverside, USA.
7. **Emmanuel Amoakwah (Ghana)** – CSIR, Soil Research Institute/Soil Science Department, University of Cape Coast, Ghana.
8. **Felicity Crotty (UK)** – Aberystwyth University, UK.
9. **Jasper Wubs (The Netherlands)** – Netherlands Institute of Ecology (NIOO-KNAW), the Netherlands.
10. **Jay Prakash Verma (India)** – Institute of Environment and Sustainable Development Banaras Hindu University, India.
11. **Kevin Mganga (Kenya)** – Department of Soil Science of Temperate Ecosystems, University of Göttingen, Germany.
12. **Kristin Aleklett (Sweden)** – University of British Columbia, Okanagan, Canada.
13. **Bonface Ombasa Manono (Kenya)** – Centre for Sustainability, University of Otago, New Zealand.
14. **Melanie Sapp (UK)** – Food and Environment Research Agency, England.
15. **Renuka N. Attanayake (Sri Lanka)** – University of Kelaniya, Sri Lanka.
16. **Rodrigo Mendes (Brazil)** – Brazilian Agricultural Research Corporation, Embrapa Environment, Ministry of Agriculture, Brazil.
17. **Runa Boeddinghaus (Germany)** – University of Hohenheim, Institute of Soil Science and Land Evaluation
18. **Santosh Swamy (India)** – ITC ltd, ABD-ILTD, Research Department, India.
19. **Seema Sharma (India)** – KSKV Kachchh University, Bhuj, Kachchh, Gujarat, India.
20. **Shi Ling Ling (China)** – World Agroforestry Centre (ICRAF) and Kunming Institute of Botany, Kunming, China.
21. **Simoneta Negrete (Mexico)** – Instituto de Ecología AC, Mexico.
22. **Stefan Geisen (Germany)** – Netherlands Institute of Ecology (NIOO-KNAW), the Netherlands.
23. **Vanessa Pino (Chile)** – University of Sydney, Australia.
24. **Yevgeniy Marusenko (Ukraine)** – Arizona State University and University of California, Irvine, USA.
25. **Leticia Pérez Izquierdo (Spain)** – Instituto de Ciencias Agrarias (ICA), Spain.
26. **Kostas Andreou (Cyprus)** – Department of Environmental Management, Cyprus University of Technology.
27. **Tandra Fraser (Canada)** - Colorado State University, Fort Collins, Colorado, USA.
28. **Kelly S. Ramirez (USA)** – Netherlands Institute of Ecology (NIOO-KNAW), the Netherlands.
29. **Alberto Orgiazzi (Italy)** – European commission, Joint Research Centre, Institute for Environment and Sustainability, Italy.
30. **Martha B. Dunbar (Italy)** – European commission, Joint Research Centre, Institute for Environment and Sustainability, Italy.

ABSTRACTS

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Keynote presentations

[K01]

Ugly and dirty firends fro millenia - still little known and unrecognised.Introductory lecture

L. Miko*
[1]*European Commission, Belgium,* [2]*Czech University of Life Sciences, Czech Republic*

Soil organisms were studied since the times of Charles Darwin, and despite the fact that their role for soil and ecosystem processes is generally known and recognised as crucial, study of soil ecosystems and their components remains to be an open challenge. Broad variety of soil living organisms remains unknown and unrecognised, due to the complexity of both soil system itself and it’s study, and often also because of lacking expertise and sufficient capacity. Absence of species-level information complicates ecological studies and interpretations. Despite of increasing interest in last few decades, both human and financial resources dedicated to study soil life are not sufficient.

Challenges related to soil health and functioning in globalised world, in connection to intensification of agriculture, forestry and growing urbanisation are growing. Human caused soil degradation affects the whole society in many ways, with ever growing impacts on food production and quality, resource efficiency, biodiversity and ekosystém function and consequently on human well-being and overal economy.

Yet, the transfer of available scientific knowledge to policy decisions, as well as recognistion of need to extend the study of soil ecosystem in order to adress the challenges, is difficult and slow. Despite of several global and regional initiatives, adopted documents and programmes, only little is translated into direct action at public policy level and implemented in practice. Nevertheless, individual farmers or farmers organisations, or some private companies, may serve as examples of growing interest and positive developments, which may pave the wayfor broader demand for soil biological studies and their practical application.

The lecture will address these problems, discuss the soil biology science-policy interface and analyse possible reasons. Using the experience from national and supra-national (EU-level) decision making, possible solutions will be proposed and analysed in terms of their feasibility and policy-attractiveness. Some opportunities and possible innovative solutions for future developments will be summarised in conclusion.

Keywords: soil biology - policy interface, challenges and opportunities, human and financial resources

[K02]

Trends in soil biodiversity research and applications

W.H. van der Putten*
Netherlands Institute of Ecology, The Netherlands

Soil ecology research has made enormous progress during the past ten or twenty years by revealing how soil biota contribute to plant community dynamics and the regulation of aboveground biodiversity. However, the role of soil biodiversity in these interactions has only rarely been examined. Unlike in plant ecology, where plant species, functional groups, or trait diversity may be varied relatively easy, such studies in soil have been constrained by the myriad of species, functional groups and traits present below ground. Still, much progress has been made by examining consequences of global change scenarios of changes in land use, climate, and introduced exotic plant species. These studies initially have been hampered by adequate possibilities to quantify and qualify belowground communities, but recent developments in molecular identification methods are facilitating these approaches enormously. Originally, in soil food web studies soil biodiversity has been organized into feeding guilds, which may be considered as a predecessor of the functional group, or trait approach in aboveground ecology. Currently, novel developments take place in network approaches, which may provide novel insights into transient states and key groups or interactions that may prevent, or promote transitions in soil community composition. Another novel development is to consider the role of soil biodiversity in eco-evolutionary dynamics, for example by studying the role of soil biota in controlling invasive exotic plant species. These are some major new trends in soil biodiversity research that may have important potential for applications, for example in enhancing sustainability of agriculture. Awareness is growing how soil communities can be made nutrient use efficient and resilient against extreme events and other environmental disturbances. However, new fundamental insights are needed in order to design soil systems for future agriculture that will yield high amounts of food, feed, and biomass from ecosystems with highly nutrient use efficient and resilient properties. Therefore, we may capitalize on recent advances in soil ecology research in order to further understand the organization and functioning of belowground biodiversity and use this knowledge for enhancing sustainability of life in a rapidly changing world.

Keywords:

[K03]

Predicting soil microbial responses to global change factors

N. Fierer*, J.W. Leff
University of Colorado, USA

It is relatively easy to demonstrate how global change factors can impact belowground microbial communities and processes at individual sites. It is far more difficult to predict the effects of global change factors across sites that represent a broad range of climates, soil types, and biota. Our limited inability to predict effects across ecosystems makes it difficult to build any broader understanding of how soils across the globe will change in response to future conditions.

To address this knowledge gap, soil microbial ecologists need replicated, cross-site investigations. As just one example, I will discuss an ongoing study being conducted across 25 international grassland sites with the goal of building a predictive understanding of how elevated nutrient inputs impact soil microbial communities and their functional attributes. Through marker gene sequencing, we demonstrate that elevated nutrient inputs to soils elicit substantial changes in bacterial, fungal, and archaeal community composition, changes that are largely consistent across the grassland sites. To better understand how these shifts in community composition relate to alterations in microbial function, we subsequently performed shotgun metagenomic sequencing on samples from replicated control and nutrient amendment plots from six of the grassland sites (72 samples in total). Although the functional attributes of the microbial communities differed most strongly between sites, N and P amendments also had significant impacts on the functional attributes of the belowground communities within sites. These results suggest strong concordance between shifts in soil microbial community composition and function with elevated nutrient inputs. Moreover, the results are consistent with the hypothesis that alterations of soil microbial community structure may be a key mechanism driving changes in soil C sequestration under elevated nutrient deposition.

Keywords:

[K04]

Linking soil microbial diversity, nitrogen cycling and greenhouse gas emissions

L. Philippot*
INRA, France

Microbial communities have a central role in ecosystem processes by driving the Earth's biogeochemical cycles. However, the importance of microbial diversity for ecosystem functioning is still debated. This talk will highlight how trait-based approaches can help understanding the role of microbial diversity in soil functioning. For this purpose, denitrification, a microbial process involved in N-cycling, was selected as a model functional trait. Denitrification is a microbial respiratory process during which soluble nitrogen oxides are used as alternative electron acceptor when oxygen is limiting. It is involved in ecosystem services such as filtering but also disservices. Thus, denitrification can results in considerable losses of nitrogen, which is the most limiting nutrient for crop production in agriculture. It is also responsible for emissions of nitrous oxide, one of the six greenhouse gases considered by the Kyoto protocol. Using both naturally assembled and artificially manipulated communities, I will show how the diversity of the denitrifier community relates to process rates and N2O emissions. This talk will also illustrate how the analysis of spatial patterns of traits can help bridging microbial community ecology and ecosystem process in terrestrial environments.

Keywords:

[K05]

Aboveground-belowground responses to global change drivers: tales of islands, fires and invaders

D. Wardle*
Swedish University of Agricultural Sciences, Sweden

Recent syntheses show that soil biotic responses to global change phenomena are highly context-dependent, with both their magnitude and direction being influenced both by the characteristics of the ecosystem and the global change driver under consideration. Here I show, through each of two field-based examples, how a major global change driver may impact on the soil biota, and the consequences for carbon sequestration and plant production. The first example involves fire, a major disturbance agent in many ecosystems worldwide and one that is strongly impacted by global climate change. I use results from studies on lake islands to show that reduced fire frequency leads to long term soil fertility decline, alterations in the abundance and diversity for many belowground groups, and feedbacks that impair plant growth and promote carbon sequestration. Importantly, reduced fire frequency causes shifts in the soil fungal community towards taxa that produce recalcitrant residues, contributing greatly to ecosystem carbon storage and related ecological processes. The second example involves invasive biota; while there is increasing recognition that global change is not causing consistent local-scale diversity decline, it is causing major shifts in community composition through biotic homogenization. Here I will use two examples from New Zealand forests, each showing how an invasive mammal (a herbivore, and a predator) has cascading effects that impact adversely on the soil food web. These also reveal that this reduction in soil biota does not have clear-cut consequences for either carbon sequestration or plant biomass production, because of partial decoupling of the soil biota from ecosystem processes. These examples show that global change phenomena can be powerful drivers of the soil community, but that the extent of effects and consequences for ecosystem processes are often not simple or straight forward, and therefore need to be considered on a case by case basis.

Keywords:

[K06]

Can nutrient management strategy improve diversity of arbuscular mycorrhizal fungi in agroecosystems?

J. Zhang*, W. Liu, Z. Fu, X. Li

China Agricultural University, China

Appropriate nutrient management is important to minimize nutrient losses from intensively managed agricultural ecosystems in China. Soil microorganisms are vital components of the rhizosphere. Exploring the community structure and function of arbuscular mycorrhizal fungi (AMF) in response to nutrient management is important for sustainable landuse management. We have undertaken a comprehensive comparison of the vertical distribution of the AM fungal community in soil and its temporal structure in maize roots among different N or P management treatments over a five-year period at a field experimental site located in an intensive agricultural area on the North China Plain. This region is an important agricultural production region in China which provides more than 75 % of the national wheat crop and 35 % of the maize production. A significant difference in AMF community structure was observed between the control and fertilizer treatments but less significant between the N or P application strategies. Soil pH, Nmin and/or Olsen-P contents were the major soil properties affecting the soil AMF communities while vertical distribution was influenced mainly by soil electrical conductivity. Crop phenology had a stronger influence on the temporal shifts of AMF communities in maize roots. Our results provide evidence for the importance of nutrient management in maintaining AM fungal diversity. Changes in soil chemical properties due to fertilization should be integrated in nutrient management strategies to reduce the negative impacts on AMF communities induced by fertilization. Excessive N inputs induced significant changes in soil physic-chemical properties, especially soil acidification, may have negative impacts on AMF communities. Furthermore, we also found that the indigenous AM are crucial for early seedling growth, particularly for plants with small seeds and low P reserves and when seedlings exhibit P deficiency. Our results have implications for the importance of maintenance of intact hyphal networks in intensive agroecosystems.

Keywords:

[K07]

Assessing the economic and social value of soil biodiversity

K.M. Scow*[1], S. Fonte[1], E. Dominati[2], L. Pincus[1]
[1]Univ of California Davis, USA, [2]AgResearch, New Zealand

Much of the natural capital of soils--with the ecosystem goods and services it produces--is inextricably connected to its biodiversity; thus valuing of soils is impossible without valuing soil biodiversity and vice versa. The social and economic value of soil biodiversity, per se, is beginning to receive the attention it deserves in ecosystem service frameworks. Farmers have long recognized these values; however, knowledge has become secondary or lost as agricultural management practices have become more reductionist. Interviews with farmers in California, Bolivia and Uganda indicate that, for at least some, the <u>social</u> and <u>economic</u> values of soil biodiversity are tightly linked; social values (e.g. spiritual, inspirational, educational) guide farmers in creating conceptual models of soil that help to define and evaluate their on-farm practices. Among scientists, recognition of the social (particularly educational) value of soil biodiversity is evident in the development of the concept of soil health, use of soil organisms/activities as bioindicators, and in helping to communicate the importance of soil biodiversity in the resilience of agroecosystems. Researchers are beginning to develop evaluations that explicitly consider the economic value of soil biodiversity in agriculture and other land management systems. We provide examples of estimates of economic costs to farmers in different regions of implementing practices that promote soil biodiversity, costs incurred from not considering biodiversity, and long-term pay off from biodiversity investments. Reconnection to and new understanding (for farmers and other land managers, researchers, policy-makers) of the social and economic value of soil biodiversity is leading to practices and systems that preserve/increase soil's natural capital and its services. And for society at large, the discovery and appeal of the <u>social</u> value (e.g., inspirational) of soil biodiversity--"soil is alive"--is expanding public support for soils far beyond what previously existed.

Keywords: economic value, social value, agriculture, soil biodiversity

[K08]

Soil biodiversity: Big impact of small creatures

D.H. Wall*, R.D. Bardgett, T. Fraser et al
Colorado State University, USA

Soils are living dynamic interfaces that are inhabited by millions of largely unseen and unknown microbial and animal species that are intimately interacting with life above-ground. Soil biodiversity is key to the maintenance of soil functioning and plant production, but is generally overlooked in global policies addressing food security, climate change, loss of biodiversity and desertification. Today, there is growing recognition of the integral role of soil biodiversity in ecosystems, such that the Global Soil Biodiversity Initiative (GSBI) was founded in 2011. By promoting interactions between scientists, policy makers, land managers and other end-users, the GSBI aims to increase the implementation of findings on the benefits of soil biodiversity and identify ways to restore and conserve it. Recent scientific advances in methods for studying soil biodiversity have accelerated knowledge on the identity of species, the factors determining their biogeographical patterns, and their key role in biogeochemical cycling in terrestrial ecosystems. Soil biological communities provide invaluable services to society such as decomposition, cleansing of water, regulation of pests, and nutrient cycling for food, feed and fiber production. Soil biodiversity, and consequently above-ground biodiversity and functioning, may be affected by land use change, tillage, agrochemical use, GMOs, nitrogen enrichment and climate change. In a rapidly changing world, restoration and conservation of soil biodiversity is, therefore, critical in order to sustain our soil resource and the rapidly growing world population. Moreover, the management of soil biodiversity for ecosystem services is relevant to the sustainability of global lands and has caught the attention of policy makers and all interested in sustaining biodiversity, healthy soils, people and global biogeochemical processes for our future earth.

Keywords:

[K09]

Digging into the future: future challenges for soil biodiversity research

R.D. Bardgett*
The University of Manchester, UK

The last two decades have witnessed enormous leaps in our understanding of how soil biodiversity is distributed and how it regulates the structure and functioning of terrestrial ecosystems. The question now is how to take this research effort forward. In this short talk, I will identify what I consider to be some of the major challenges facing soil biodiversity researchers in the future. Among these challenges is the need for a more theoretical approach to soil biodiversity research, developing new models to explain patterns of belowground community organisation and to improve understanding of how changes in soil communities impact ecosystem functioning. There is also a need to unpick diversity responses, in terms of the relative roles of genetic, species, and functional diversity in driving ecosystem processes, and to better understand how eco-evolutionary responses of soil communities to rapid environmental change impact ecosystem functioning and aboveground community dynamics. Finally, I argue that a key goal of soil biodiversity research should be to integrate this understanding into future management for sustainable food production and climate mitigation.

Keywords:

[K10]

Applying soil biological knowledge to the management of soil fertility and other ecosystem services: The TSBF experience

M.J. Swift*
Tropical Soil Biology and Fertility Institute, Kenya

This paper addresses the question posed to the final session of this conference - *How to translate scientific knowledge in soil policies and for soil management? What are the bottle necks for such translation? – by drawing on the experience of the TSBF Programme.*

The Tropical Soil Biology and Fertility Programme (TSBF) was created with the explicit objective of '*determining the management options for improving tropical soil fertility through biological processes*'. It should be noted that the philosophy was not necessarily that of organic agriculture - the exclusion of all industrial inputs – but that of optimising the use of biological resources where pragmatically possible. Thus the major approach to soil nutrient management at the scale of farming systems is that of the joint use of organic and mineral nutrient sources (Integrated Soil Fertility management, ISFM) with a focus on improving methods for organic matter management supported by research on biological processes and relevant soil biota. The purpose over the longer term and at higher scales of influence was nonetheless to correct the balance in tropical soil management away from practices and policies where the recommendations required an almost total reliance on industrial inputs to ones where biological resources were optimised. With the onset of public concerns about climate change and loss of biodiversity the TSBF programme evolved to address the soil-based aspects of these issues and broadened its targets to the management of ecosystem services beyond soil fertility and the conservation of below-ground biodiversity.

The objectives and context of TSBF nonetheless remain relatively specific. The paper will explore what useful insights the experience of TSBF and its national and international partners bring to the general issue of translating biological knowledge into practices for soil management and the policies necessary to support and implement them. – taking into account the varieties in content and scale of scientific knowledge, management practices and policies.

Keywords:

[K11]

Going underground - why soil biodiversity matters to stakeholders

B. Delbaere*
ECNC, The Netherlands

The notion that soil biota and the functional groups in which they are classified represent certain ecosystem functions that deliver ecosystem services in support of human well-being is receiving wide acceptance. The ecosystem services are provided to individuals and groups in society, to what is called the ‘stakeholders’. But who are they? And what do ecosystem services mean in practice to them? This presentation will illustrate a number of these essential connections. This is not based on scientific research or economic valuations. Rather it is based on observations from many years of work in the field of science-policy-society interaction for biodiversity conservation in Europe. This has involved a wide range of stakeholders, from scientists to European policymakers, from spatial planners to schoolchildren. Although most of this experience stems from experience with above-ground biodiversity, the presentation will demonstrate that the same principles hold for below-ground biodiversity, and that stakeholder engagement is essential to support sustainable management of soil biodiversity.

Keywords: stakeholders, science-policy-society interaction, ecosystem services

[K12]

Mainstreaming soil biodiversity to deliver both global environmental benefits and human development

M. Stocking*
University of East Anglia, UK

Mainstreaming' is the process of including a typically side-lined topic or item into commonly accepted thought – the 'mainstream' – with the view to influencing dominant institutions. Because environmental issues often have a low profile, they are widely by-passed in the development of policy and practice by local, national, regional and even global institutions. 'Soil biodiversity' is one such topic that is both elusive to grasp and difficult to include in wider policy; indeed it suffers double jeopardy in bringing two terms, 'soil' and 'biodiversity' that have little resonance with policy-makers and only scant evidence of importance to society. Mainstreaming 'soil biodiversity' requires not only demonstrating its utility but also identifying its value and central role in ecosystem services and human well-being. It is insufficient to expect policy-makers and the wider public to accept *de facto* our exhortations and rhetoric without satisfactory evidence and examples where soil biodiversity clearly brings societal and developmental benefits.

Mainstreaming *per se* is a core objective of the Strategic Plan of the Convention on Biological Diversity (CBD) and its Aichi Targets. Strategic Goal A is to "Address the underlying causes of biodiversity loss by mainstreaming biodiversity across government and society." By 2020, for example, Target 2 specifies that "biodiversity values have been integrated into national and local development and poverty reduction strategies and planning processes and are being incorporated into national accounting, as appropriate, and reporting systems." This is an ambitious objective.

As the financial mechanism of the global environment conventions such as the CBD, the Global Environment Facility (GEF) has been addressing the challenge in a variety of ways. Mainstreaming has been a component in at least 300 biodiversity projects, many of which adopt the relatively new integrated format of being multi-focal; that is, combining climate change, land degradation and biodiversity strategic objectives, along with co-benefits for human development. This coupling of biodiversity with issues of global relevance such as climate change that are well accepted, and issues of domestic relevance such as agriculture and land deterioration, is a major step forward for biodiversity. The current state of practice in biodiversity mainstreaming has recently been reviewed by STAP-GEF, from which lessons may be drawn on how to achieve a higher profile for soil biodiversity.

The most recent new programmatic format for the GEF is the creation of what are called Integrated Approach Pilots for the Sixth Replenishment phase of the GEF, 2014-2018. Prominent in the IAPs is the fostering of sustainability and resilience by addressing high-profile topics such as Food Security with a mix of investments that not only can be justified in delivering global environmental benefits but also support key developmental topics. In its present stage of planning, the Food Security IAP is seeking to safeguard ecosystem services for smallholder agriculture, which underpins food security for over 70 percent of the Sub-Saharan African population that is dependent heavily on assets provided by nature.

The paper will report on how the GEF is thus playing a prominent role in overcoming the most pervasive bottleneck for 'soil biodiversity'; its perceived lack of relevance to and demonstration of values for human society.

Keywords:

[K13]

Soil biodiversity: From research to bioeconomy

A. Bispo*
ADEME, France

We know for years that soils are living environments where all the principal taxonomic groups existing in terrestrial ecosystems can be found (Swift et al., 1979). Soil organisms probably represent as much as 25% of the 1.5 million described living species worldwide (Decaëns et al., 2006). The resulting activity of soil communities has a direct impact on the ecosystem services provided by soils such as food and fiber production, water purification or climate regulation (Gardi et al., 2010).

Knowledge on soil biota diversity and activity made significant progress in recent years thereby enabling laboratories to propose soil biology analyses, as it has been done for many years with soil physico-chemistry analyses (Lemanceau et al., 2014). At national, European and international levels several research projects succeeded in developing and testing methods to measure soil biodiversity and organisms activity (Bispo et al., 2009, Dequiedt et al., 2011, Peres et al., 2011, Lemanceau, 2011). Such protocols are now available (http://ecobiosoil.univ-rennes1.fr/ADEME-Bioindicateur/fiches-outils.php) and some are even standardized (see ISO 23611-1 to 6 and ISO 11063). However being able to measure does not mean that people will ask for such analysis unless results meet their concerns.

In the coming years, farmers' competitiveness will increasingly depend on their ability to reduce production costs and less rely on expensive commodity such as energy: they must learn how to substitute oil by soil. Measuring soil biodiversity and organisms activity should provide them with information which could help them to use less fertilizer and pesticides. At the same time soil biologists should also advise them on how to manipulate soil biota either by changing soil management practices (e.g. tillage) or crop rotations. Research should now concentrate on such issues to be able to give valuable information to farmers and start the "bioeconomy" of soil organisms. Information on soil biota (diversity and activity) may also be very useful for other fields as soil remediation, biotechnology and biocontrol turning soil into a new Eldorado.

Keywords:

Oral presentations

[O1.1]

Beta diversity and human impact in soil communities

T. Caruso*
Queen's Uniersity of Belfast, UK

Soil communities are astonishingly diverse not only in terms of species richness but also in terms of spatial and temporal changes in species composition and abundance, known as beta diversity. Beta diversity depends on several processes such as stochastic events (e.g. dispersal), environmental filtering and niche partitioning, and also biotic processes such as the complex network of direct and indirect interactions linking above-ground and below-ground systems. Surprisingly, soil beta diversity is poorly studied and I propose that the study of beta diversity can provide soil ecologists with a powerful tool to monitor community dynamics in response to disturbance, global change, and restoration strategies. I here show how the controversial neutral theory of biodiversity, which I use as a null model, and a quantitative, novel definition of beta diversity (BD) offer an innovative starting point. When levels of BD are compared to the predictions made by neutral models, three possible outcomes can be observed: BD equals neutral prediction or is larger (divergence) or smaller (convergence) than the neutral prediction. I show how different processes and sampling regimes can lead to these outcomes. For example, increasing the heterogeneity of soil spatial properties usually causes observed BD to be significantly higher than what predicted by neutral models. Also, species most responsible for the observed pattern can be detected. Understanding the mechanistic processes that underlie patterns of beta diversity in soil communities will be one of the future challenges of soil ecologists. Approaches such as community phylogenetics and a better understanding of the trophic ecology of soil species will be the key to tackle this challenge and understand the spatial and temporal structure of soil biodiversity

Keywords: beta diversity, disturbance, modelling, community dynamics

[O1.2]

Unearthing 'old growth' mycorrhizas in ancient ecosystems

M.M. Hart*

University of British Columbia Okanagan, Canada

Arbuscular mycorrhizal (AM) fungi associate with the roots of most plants and affect many ecosystem functions. Unfortunately, most of what we know about these fungi is based on studies from managed landscapes. Given that AM fungi exist in all ecosystems with a variety of plants, we may be underestimating their diversity and functioning. In particular, AM fungal communities in old ecosystems may represent late seral AM fungal communities. If so, they should contain more novel taxa compared to younger, more heavily disturbed ecosystems, which have been well, characterised.

I tested the effect of tree age, ecosystem age and disturbance on AM fungal community composition in a rarely studied and ancient system, the Cedar/Hemlock forests of the Pacific Northwest. I used Western Red Cedar as my target host because is the only exclusively AM tree in North American temperate forests and can live in excess of 1000 years. These forests exist along a chronosequence ranging from <200 years to >50 000 years old.

I found that older ecosystems contain significantly different AM fungal communities than younger stands. Within these stands, there is also evidence that the AM fungal community shifts from younger to older trees. Distance from disturbance was also highly significant. However, despite uniform climatic and host conditions, cedar stands differed significantly from each other, indicating high levels of beta and gamma diversity. I will discuss patterns in compositional changes and indicator taxa, as these data are currently being analysed.

Understanding the true biodiversity of AM fungi is essential if we are to preserve the immeasurable services they provide. Because old ecosystems and large trees are threatened globally, we must quickly work to identify and understand the role of these ‘old growth’ microbial communities, before they are gone.

Keywords: Arbuscular mycorrhizal fungi, Mycorrhizas, Community, Biodiversity

[O1.3]

Unearthing ancient nematode DNA – possible proxy of past ecosystem features?

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During the last decade major developments in retrieval and sequencing of DNA fragments from prehistoric sediments have prompted an entirely new field of DNA-based reconstruction of prehistoric ecosystems. Valuable information on ecosystem features can be inferred from soil nematode assemblages, and here we attempt to add analysis of ancient nematode-DNA from permafrost sediments to the palaeoecological proxy toolbox.

For decades, it has been debated whether dry, productive arctic steppe vegetation, or alternatively less productive and less palatable moist herb-tundra vegetation supported the large populations of iconic ice-age herbivores such as woolly mammoth, woolly rhino, wild horses and steppe bison that roamed ice-free landmasses of the Northern hemisphere during the Pleistocene.

In contemporary sub-Arctic ecosystems we identified soil nematode taxa that were indicators of either contemporary moist tundra vegetation or subarctic steppe. Subsequently, we extracted, amplified and sequenced DNA fragments for the identified indicator taxa from Arctic permafrost sediments ranging from 6.7-39 ky in age to demonstrate the past occurrence of these taxa in Pleistocene and Holocene sediments.

In accordance with reconstructions based on plant-derived DNA, tundra-affiliated nematode taxa were almost exclusively retrieved from sediments that were younger than 10 ky. Hence, both nematode- and plant-DNA based proxies indicate a transition after the last glacial maximum (15 ky ago) from steppe-dominated Pleistocene landscapes towards the moist tundra-dominated habitats that we find in the Arctic today.

Keywords: Ancient DNA, Soil nematodes, Palaeoecology, Arctic

[O1.4]

Ethanol's growing demand and belowground biodiversity: Soil macroinvertebrate community responses to sugarcane expansion in Brazil

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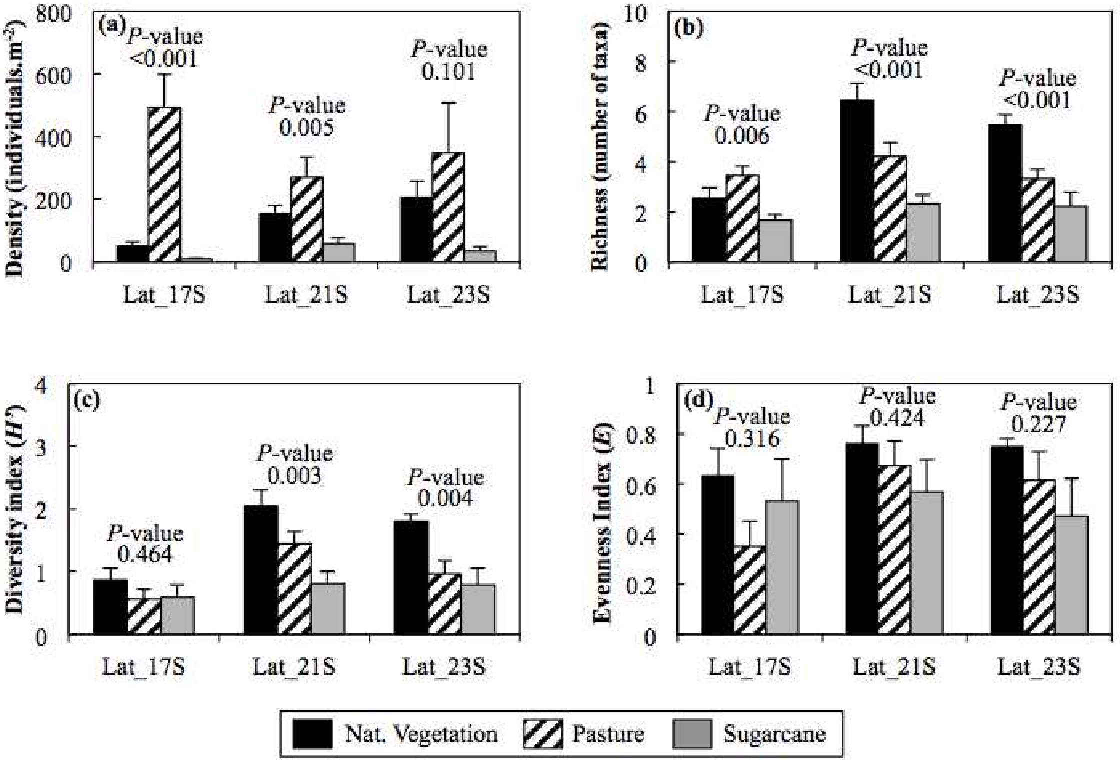
The ethanol's growing demand has driving the recent sugarcane expansion from pasturelands in Brazil. Potential direct impacts on biodiversity of aboveground organisms from this land use transition have been theorized as limited. Belowground, however, there are important changes in soil environment with the sugarcane crop establishment that can greatly alter the macroinvertebrate community composition, with potential effects on soil quality and multifunctionality, once these animals are key players of ecosystem engineering processes.

We addressed the soil macrofaunal community responses to the most common land use change in sugarcane expansion areas in Brazil, the world's largest producer.

We sampled 3 field sites to represent the northern, center, and southern region of the Brazilian sugarcane belt. In each field site was identified a chronosequence with the three land uses considered in this study: native vegetation (NV), pasture (P), and sugarcane crop (SC).

Termites and ants were the most abundant taxa. The mean density increased from NV to P and decreased sharply from P to SC in all sites. An average reduction of 89% in the size of the total soil macrofaunal community was observed when sugarcane replaces pasture (or a reduction of 74% compared with NV), besides a loss of 39% of soil macroinvertebrates taxonomic richness (total loss of 53% compared with NV). The overall diversity index dropped from 1.6 under NV to 1.0 under P, and to 0.7 in SC soils. The community of generalist predators was the mostly affected functional group with a reduction of 78%. About 6.4 Mha of land will be required by 2021 for sugarcane expansion in Brazil to achieve ethanol's demand.

Our results draw attention for an unpredicted biodiversity loss due to sugarcane expansion from pasturelands in soils belowground and warrant efforts to understand the implications of altering belowground communities on the performance of agroecosystems.



Soil macrofauna density (a), taxonomic richness (b), diversity (c), and taxa distribution (d) in the 0-30 cm soil layer as a function of the land use sequence native vegetation – pasture – sugarcane. *n* = 9, error bars denote standard error of the mean.

Keywords: bioenergy crops, environmental sustainability, land use change, macrofauna

[O2.1]

A framework to synthesize global soil biodiversity data

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Soils contain an immense amount of biodiversity; yet, with an estimated 10-100 million organisms belonging to over 5000 taxa in a handful of soil, our understanding of the spatial and temporal distribution of soil organisms, and the factors controlling distribution remains incomplete. While data is rapidly accumulating, there is a lack of coordination and networking among the different information sources characterizing soil biodiversity. Here, we present a proposal to bring together and synthesize soil biodiversity information for use in current and future research efforts, and for informing policy and management decisions. In April 2014, the Global Soil Biodiversity Initiative (GSBI) held a workshop at the Germany Centre for Integrative Biodiversity Research (iDIV) to propose a framework to link soil biodiversity data globally. The group outlined the potential practical applications and theoretical advances from such a synthesis, including research questions that could be answered, and proposed an action plan to link disparate soil biodiversity data. Briefly, the action plan addresses both the logistics of linking various datasets and impending challenges. The effort will be led by the GSBI, will link with the well-established Global Biodiversity Information Facility (GBIF) platform, and be structured to accept input from the scientific community and other biodiversity synthesis efforts (e.g. Edaphobase). Practically speaking, a global synthesis of soil biodiversity data will require participation and contribution from the entire soil biodiversity community. Here we present on the outcomes and products of the first planning workshop; future meetings will also need to address the resources necessary for such a large proposal and outline a clear timeline and precise goals to be reached. With the rapid influx of soil biodiversity information, now is the time to take the first steps forward in establishing a global platform to link data and make them available for use in ecological studies.

Keywords: biodiversity synthesis, global, biogeography, Global Soil Biodiversity Intiative

[O2.2]

The microbial landscape in soils - biogeography of soil microorganisms in the german biodiversity exploratories

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In the framework of an initiative to advance biodiversity research in Germany, three exemplary large-scale and long-term research sites were established to understand the role of land use and management for biodiversity and to understand the role of biodiversity for ecosystem processes across Germany (*www.biodiversity-exploratories.de)*. This platform is used to investigate the effects of land use intensity on single trophic levels, interacting organisms, as well as foodweb structures. We identified general relationships between abiotic soil properties and soil biota across spatial scales, ecosystems (forest and grassland) and different land-use intensities. Whereas abiotic soil properties and climatic conditions mainly explained differences in microbial community structure and function on the regional scale, on the local and plot scale differences were related to the land use intensity level. In 2011, we tested whether microbial biogeography of a grassland plot (10 m x 10 m) changes over the growing season. We sampled the plot (60 samples within a grid of 20 cm x 20 cm) six times within one season to cover the different stages of substrate release and nutrient demands of plant communities. Microbial community spatial structure (based on PLFA data) was positively correlated with the local environment in spring and autumn, while the density and diversity of plants had an additional effect in the summer period. Spatial relationships among plant and microbial communities were detected only in the early summer and autumn periods when aboveground biomass increase was most rapid and its influence on soil microbial communities was greatest due to increased demand by plants for nutrients. Individual properties exhibited varying degrees of spatial structure over the season. Finer phylogenetic resolution of microbial groups using next generation sequencing helped determine the importance of plant species density, composition, and growth stage in shaping microbial community composition and spatial patterns.

Keywords: microbial biogeography, ecosystem functioning, up scaling, long-term experiment

[O2.3]

Predicting and understanding the effects of land use on soil bacterial communities over large scales

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Bacteria contribute the largest proportion of the soil genetic pool, and along with other soil organisms are thought to be key drivers of various biogeochemical cycles. There is therefore widespread scientific interest in how bacterial biodiversity is affected by land use change and how this affects soil functionality and ecosystem services. From a policy perspective also, there is a need to provide relevant indicators of change in soils so as to establish target criteria to assess soil degradation and the efficacy of mitigation procedures.

This talk will discuss results from over one hundred local land use transitions on soil biodiversity and soil properties, using datasets from both large scale soil biodiversity surveys such as the UK Countryside Survey, and more recent targeted sampling within the EU funded EcoFINDERS project and other UK initiatives. We firstly show that bacterial communities are a particularly sensitive component of soil biodiversity for use as indicators of change in soils. Secondly we illustrate that bacterial communities in bulk soils are strongly driven by soil parameters, and that this knowledge of broad biodiversity gradients from large scale surveys can be used to predict and explain change within local land use transitions. In particular we show that the magnitude of variation in bacterial biodiversity is related to the specific land use transition context, and also relates to the relative change in soil parameters such as pH and organic matter. Finally we will discuss the results in terms of specific bacterial indicators of change, and demonstrate that similar bacterial taxa can be indicators of either intensively managed or pristine soils depending upon the specific context of the land use transition with respect to the wider soil biodiversity physical-chemical gradient.

Keywords: Soil, bacteria, land use, change

[O2.4]

Evaluating soluble aluminum as a mechanism driving bacterial community structure in terrestrial soils from continental to microcosm scales

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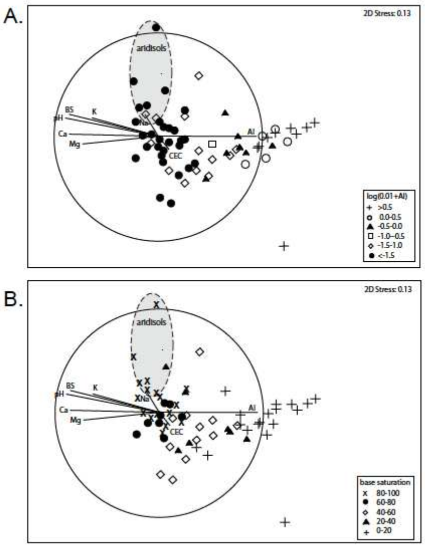
Soil pH has increasingly been implicated as the most effective predictor of bacterial community structure across a broad spectrum of soils. However, difficulty arises in ascribing hydronium ions as a mechanism because pH covaries with an exhaustive list of soil properties, some of which are not routinely measured. We evaluated Al toxicity, a soil parameter closely linked to pH, as a driver of bacterial communities at multiple spatial scales using molecular and culture-based techniques and predictive modeling. Al is a ubiquitous component of soils directly responsible for global declines in crop production and forest health over the past five decades. We used KCl-exchangeable Al as a proxy for Al^{3+}, the dominant, toxic Al species in soils below pH 6.

Across 67 soils from a previous cross-continental study in the Americas, we found that community structure as measured by UniFrac distances was significantly correlated with Al (*r*=0.94). We also found a significant linear relationship between phylogenetic diversity and Al (R^2=0.61). AIC model selection indicated that Al alone best explained variation although models incorporating Al and %base saturation, a measurement of soil nutrient status and buffering capacity, performed almost as well.



Unconstrained NMS ordination based on UniFrac distance metric showing dissimilarities between bacterial assemblages from 67 sites in the Americas. Sample exchangeable Al concentrations (A) and %base saturation (B) represented categorically on each plot. Aridisols were identified as outliers due of Na content and extremes in aridity and excluded from subsequent statistical analyses. Soil variables are plotted as a bi-plot using Pearson correlation coefficients. The circle radius represents a coefficient of 1.0. The cations and CEC were transformed using the function log(0.01+x) prior to analysis.

To further constrain the relationship between Al and pH and bacterial composition, we compared community fingerprints along a well characterized, regional gradient of pH and Al in *Pinus ponderosa* ecosystems in the southwestern USA. Approximately 90% of the most abundant orders, representing approximately half of the overall community, tracked the Al and Fe-oxyhydroxide content of the soils. Surprisingly, a culture-based study from the gradient using selective media (hydronium ion or Al additions) indicated that the abundance of culturable acidophiles did not correlate with pH whereas Al-tolerant bacteria varied predictably with Al and Fe content and pH.

These results suggest that Al is a highly plausible mechanism, which may supersede previous interpretations.

Keywords: diversity, aluminum, pH, soil microbiology

[O3.1]

Functional microbial diversity, traits and interactions as modulating factors of methane and nitrogen cycling in soils

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Despite intensive research there are still large uncertainties in global greenhouse gas balances and observed dynamics therein. Soils, including their inhabiting microbes and their traits, are major sources and sinks of atmospheric methane. The potential of microbial diversity, traits and interactions in improving our understanding of the dynamics in GHG balances is the aim of this study. Methane-oxidizing bacteria (MOB) are the only biological sink of methane globally thereby performing an important ecosystem service. Similarities in enzymology between MOB and ammonia oxidizing bacteria and archaea (AOB and AOA) enable these groups of microbes to simultaneously consume methane as well as ammonia thereby potentially modulating methane oxidation and nitrification. We assessed the functionally active MOB, AOB, AOA and nitrite oxidizers (NOB) in soil incubations by using a combination of stable isotope probing (PLFA, DNA, proteins) and molecular (QPCR, NGS) community assessment techniques to single out the active species at high resolution. Methane consumption was significantly related to MOB diversity. Next to this, active methanotrophs suppressed ammonia and nitrite oxidation in the studied soils by outcompeting the nitrifiers for ammonium. The active MOB were restricted to only one or two phylotypes whose relative abundance was affected by the amount of nitrogen applied. Similarly, active $^{13}CO_2$ incorporating AOB, AOA and NOB phylotypes were differentially affected by availability of nitrogen and nitrogen-consuming MOB. By assessing the biogeochemicaly active species we clearly demonstrate that important ecosystems functions and services are modulated by a very limited amount of microbial phylotypes and the way they interact. Predicting effects of climate change, land-use change or management may be facilitated by incorporation of their traits into process-based models. Incorporating traits into life-strategy frameworks as has been done for plants maybe a way to link functional microbial diversity to ecosystem functioning.

Keywords: methane oxidation, microbial diversity, nitrification, stable isotope probing

[O3.2]

Importance of community structure for GHG emissions - Lessons learned from genomes and metagenomes

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The only enzyme known to reduce the greenhouse gas nitrous oxide (N_2O) is the N_2O reductase, encoded by the *nosZ* gene among bacteria and archaea. Using *nosZ* as a proxy for the trait N_2O reduction, we compared 652 denitrifier genomes across 18 phyla to examine if this trait differed among taxa, preferred habitats or denitrifiers belonging to either of the two mutually exclusive *nir* types (*nirS* and *nirK*). To also determine if the *nir* subtypes reflect different ecological roles, the gene phylogenies were compared with the distribution of individual lineages in 11 environmental metagenomes.

Gene co-occurrence patterns were not randomly distributed across taxa and *nosZ* also displayed a higher frequency of co-occurrence with *nirS* than with *nirK*-type denitrfiers. The presence or absence of a gene coding for nitric oxide reduction largely explained this pattern. Thus, *nirS* denitrifiers are more likely to be capable of complete denitrification to N_2 than *nirK* types and thereby contribute less to N_2O emissions. A greater degree of shared evolutionary history between *nosZ* and *nirS* was detected; however 30% of the *nosZ* organisms did not possess any other denitrification gene suggesting an important role as N_2O consumers. We identified 9 *nirS* and 16 *nirK* lineages, which corresponded with contrasting metabolic requirements. In the metagenomes, these lineages differed significantly in relative abundance between habitats indicating physiological and ecological differences amongst the lineages. This implies that the lineages are not functionally redundant. Our results remark the need for physiological characterization of each lineage and a reinterpretation of their ecological role in the environment in relation to nitrogen cycling. Gene co-occurrence patterns were also non-randomly distributed amongst preferred habitat categories, with *nosZ* occurring more frequent than expected among aquatic organisms. We demonstrate that the denitrification pathway is highly modular, thus underpinning the importance of community structure for N_2O emissions.

Keywords: genomics, metgenomics, GHG emissons, nitrogen cycling

[O3.3]

Soil biodiversity as a driver of ecosystem sustainability

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Soil organisms can play a key role in ecosystems by enhancing nutrient uptake, plant productivity and plant diversity. The importance of soil biota for the sustainability of ecosystems is still unresolved. Here we show that soil organisms and soil biodiversity can enhance the sustainability of natural and agricultural ecosystems by reducing nutrient leaching losses after rain and promoting nutrient uptake. Experiments performed in indoor mesocosm and in outdoor lysimeters, showed that an increased abundance of mycorrhizal fungi and other soil biota, reduced leaching losses of nitrogen and phosphorus. The reduction of nitrogen leaching losses in outdoor lysimeters was substantial (a reduction of up to 80 kg N/ha/year) pointing to the key role of soil biota in nutrient cycling. Mesocosms experiments with experimental grassland further revealed that nutrient losses depend on the composition of fungal communities and were reduced in microcosms with enhanced soil biodiversity. Our results indicate that changes in soil communities and the loss of particular groups of soil biota threatens ecosystem multifunctionality and sustainability.

Keywords: ecosystem sustainability,, mycorrhizal fungi, soil biodiversity, nutrient cycling

[O3.4]

Resource pulse can alleviate the biodiversity-invasion relationship in soil microbial communities

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Invasive species have the potential to affect the functioning of ecosystems and the extent of this impact is tightly linked to the level of biodiversity at a local scale. There is no general theory that ties together all the factors influencing what is colloquially known as the diversity-invasion relationship, whereby more diverse communities resist invasion better than less diverse communities. The roles of species richness, resource use, and resource availability are central to many hypotheses explaining the diversity-invasion phenomenon but are generally not investigated together. Here, we created a large diversity gradient of soil microbial communities by either assembling communities of pure bacterial strains or removing the diversity of a natural soil. Using data on resource use capacities of the soil communities and the invader *E. coli,* gathered from 71 carbon sources, we quantified the niches available to the community by using the metric community niche, as well as the remaining niche available to the invader. A strong positive relationship between species richness and community niche across both experiments indicated the presence of resource complementarity. Moreover, community niche and the remaining niche available to the invader well predicted invader abundance (up to 96% of the variance), suggesting that increased competition in communities of higher diversity limited community invasibility and underscored the importance of resource availability as a key mechanism through which diversity hinders invasions. As a proof of principle, we subjected selected invaded communities to a resource pulse, which indeed allowed the invader to recover after nearly being eliminated in some communities and progressively uncoupled the link between soil microbial diversity and invasion. In summary, our results demonstrated that (i) resource competition drives invasion, (ii) biodiversity increases resource competition and decreases invasion through niche preemption, and (iii) resource pulses favour invasion even in diverse communities.

Keywords: biological invasion, bacterial diversity, resource use mechanism, diveristy-invasion relationship

[O3.5]

Network architecture of rhizosphere bacterial community and ecological similarity with th e pathogen predicts plant protection from an infection

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Host-associated microbial communities form an irreplaceable line of defense against pathogens with animals and plants [1,2]. While it has been shown that species rich communities are generally good at resisting pathogen invasions[3-5], there is a growing interest to understand the mechanisms linking community composition to pathogen suppression. Here we used a bipartite resource networks approach to examine which community characteristics of commensal rhizosphere bacterial communities (richness, nestedness, connectedness and niche overlap with the pathogen) best predict pathogen suppression *in vitro* and *in vivo*. We first used microcosm experiments to demonstrate that *Ralstonia solanacearum* pathogen is most suppressed when commensal trophic networks of the resident communities are weakly nested, highly connected and when their resource use niche clearly overlaps with the pathogen. We then used a greenhouse experiment with tomato plants to extend our predictions to actual host protection. Again, disease suppression was associated with nested and highly connected trophic networks overlapping with the pathogen. In addition, weak interspecific competition (high niche differentiation) within the commensal communities further reduced disease severity. No direct antagonism between *R. solanacearum* and biocontrol bacteria was found, which suggests that pathogen suppression was driven by resource competition. Together these results suggest that interaction network architecture of a commensal rhizosphere bacterial community, and its ecological similarity with the pathogen, robustly predicts host protection from pathogen invasion, providing an ecological approach to engineer microbial communities to improve plant health.

Keywords: Ralstonia solanacearum, Microbial biodiverity, Ecosystem function

[O3.6]

Absence of large soil predators lead to a decline of lower trophic levels and slower decomposition in temperate beech forests of northwest Spain

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Soil food webs are the result of complex interactions with variable controls from different trophic levels, which often has consequences for ecosystem processes. Bottom-up control occurs when higher productivity from lower trophic levels affects the density and biomass of top predators, whereas top-down control arises when generalist predators indirectly affect carbon and nutrient turnover through their impact on prey abundance. This study focused on the potential of top predators to structure the soil food web and leaf-litter decomposition in eight temperate beech forests sites of varying rainfall (1000-1500 mm) in northwest Spain. We tested if changes in the density of large predators affect prey density of different trophic levels, potentially cascading down to decomposition rates. We conducted a field experiment where we manipulated the presence of top-predators by removing or adding large arthropod predators in experimental plots, with simultaneous evaluation of leaf litter decomposition. After one year, predator removal had a surprisingly negative effect on the total abundance of soil fauna, particularly fungivore abundance, suggesting that the overexploitation of resources due to reduced predation, as well as the reduction of intermediate predators may have caused a strong decline in these prey populations. Springtails were significantly larger in predator removal plots, suggesting either a plastic response mediated by a growth-reproduction trade-off or that larger springtail species were favoured in the absence of predators. Finally, we found a significant reduction in litter decomposition with predator removal, which is consistent with the result that predator removal decreased fungivore populations and thus slowed decomposition rates and nutrient turnover. There was no interaction with site precipitation, suggesting that the effects of predators were similar and independent of rainfall. This study suggests a strong top-down control on the structure of the soil faunal community with important consequences for carbon and nutrient turnover in these forest ecosystems.

Keywords: soil food webs, top-down control, rainfall, decomposition rate

[O3.7]

The influence of soil macrofauna on soil aggregation in agro-ecosystems of sub-Saharan Africa depends on management intensity

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The effects of soil macrofauna on soil organic matter (SOM) and soil structure are rarely considered when developing sustainable management practices. We investigated the relative importance of earthworms and termites, in addition to soil- and climatic factors in influencing soil aggregation in 12 long-term field experiments in East and West Africa. Aggregate size distribution, SOM and soil texture, as well as the taxonomic diversity, abundance and biomass of earthworms and termites were measured in arable systems under contrasting management and a nearby fallow. Aggregate stability indices, SOM, and diversity, abundance and biomass of earthworms and termites were generally higher in the fallows compared to the arable systems. Factor analysis indicated that under fallow, 45.9% of the sample variation was explained by factor I, which was related to SOM, precipitation, clay content and earthworm indices, and 17.8% by factor II, which was related to termite indices. Under arable systems, 42.4% of the sample variation was explained by factor I, which related to SOM, precipitation and clay and 20% by factor II, which related to earthworms and termites. Regression analysis indicated that under fallow, the two factors explained 92.6% for total macroaggregates (TM) and 87.5% for microaggregates within macroaggregates (mM). Under arable cropping, the two factors explained 98% for TM and 100% for mM. We conclude that earthworms, and to a smaller extent termites, are important drivers of soil aggregation, together with climate, SOM and soil texture. However, the role of soil macrofauna in affecting soil aggregation is reduced with increasing management intensity and soil disturbance due to cultivation, whereas the relative contribution of SOM and clay is increased.

Keywords: Soil macrofauna, Agroecosystem, Soil aggregation, Management intensity

[O4.1]

Predicting soil bacterial responses to multi-factor global change with trait-based modelling

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The structure and functioning of ecosystems are impacted by human activities. Altered precipitation, elevated atmospheric CO_2 concentration, and rising nitrogen (N) deposition are occurring simultaneously and affect both resource availability and disturbance dynamics. Many studies have reported the effects of single global change factors on the functioning of the soil microbiota, and fewer have reported the effects of multiple, interacting global change factors, but descriptive studies of environmental change effects on soil bacteria remain insufficient to understand the mechanisms that determine their diversity and activity in soil and their responses to global change. However soils harbor a tremendous diversity of bacteria and breaking down the soil bacterial diversity into functional units and predicting their responses to multifactorial global changes remains intractable. In this context, trait-based approaches that reduce community complexity to key functional attributes (traits) are particularly promising. Despite recent progress, these approaches are still in their infancy in soil microbiology.

Here, we tested the hypothesis that classifying soil nitrite oxidizing bacteria (NOB) based on a few traits can identify the key controls over changes in the community composition and activity of these bacteria and predict their responses to global environmental change. First, we show that changes in N availability largely drive the *Nitrobacter*-to-*Nitrospira* ratio in soil under the 8 global change treatments tested. Second, a marked increase in the availability of organic carbon and nitrite, under relatively low oxygen tension, explains the emergence of mixotrophic *Nitrobacter* under the (high CO2 x high nitrogen x high precipitation) treatment. Third, at least three functional groups are needed to predict the response of NOB and their activity to the global change scenarios. Our results are a starting point for representing the overwhelming diversity of soil bacteria by a few functional types that can be incorporated into models of terrestrial ecosystems and biogeochemical processes.

Keywords: functional traits, global change factors, trait-based modelling, nitrifiers

[O4.2]

Future climate alters soil biodiversity and carbon storage of northern peatlands

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Northern peatlands are the world's largest terrestrial carbon (C) store, actively sequestering C due to slow decomposition rates under high water table, low temperature and poor nutrient conditions. Changes in temperature and moisture regimes are expected to directly alter decomposition rates in northern peatlands, alongside changes in aboveground (plant) and belowground (fungal, faunal) biodiversity.

In a large-scale mesocosm study, we subjected 100 intact, vegetated peat monoliths (25 kg) to elevated temperatures, increased atmospheric CO_2, and two water table levels over 18 months in a factorial design to determine the individual and synergistic effects of climate change factors on decomposition, and fungal and microarthropod soil biodiversity. We assessed the initial fungal and fauna communities in the top 5 cm peat, measured changes in soil biodiversity and assessed decomposition rates using litterbags over 12 months, and quantified the soil biodiversity in the top 5 cm peat after 18 months. Carbon dioxide flux (soil respiration) and dissolved organic carbon (DOC) loss were also measured as ecosystem-level variables.

During the experiment, increased temperature changed the aboveground plant community from Ericaceae and *Sphagnum*-dominated to graminoid-dominated systems. Lowered water table and increased temperature significantly increased decomposition rates, and increased the abundance and species richness of soil microarthropods. Temperature was the major driver of fungal community shifts, increasing the relative abundance of saprotrophic fungi under elevated temperature. At the ecosystem-level, CO_2 flux and DOC loss increased under all future climate conditions suggesting an overall reversal of carbon storage to carbon release concomitant with observed changes in soil biodiversity. Whether northern peatlands will continue to store carbon under future climate scenarios will depend on the direct effects of climate on ecosystem- and community-level responses, as well as the interaction between the two. Understanding changes in soil biodiversity is an important factor in predicting global carbon budgets.

Keywords: climate change, soil microarthropods, fungal communities, decomposition

[O4.3]

Impacts of global climate change on the leaf-litter arthropod community: Effects of altered detrital input and rainfall extremes in two long-term field experiments in a deciduous forest

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<u>*Introduction:*</u> By altering temperature and rainfall, global climate change will alter rates of detrital input and microbial growth, with likely impacts upon the detritus-based arthropod community of the leaf-litter horizon.

<u>*Methods*</u>*:* We investigated impacts in two 3-yr experiments in a deciduous forest. In Study 1 we altered rates of detrital input in open and fenced 4-m^2 plots. In Study 2 we simulated extremes of rainfall predicted by climate-change models in 14-m^2 fenced plots at two sites (dry and moist organic soil horizons). Perturbations occurred during the growing season, and arthropod densities were sampled by litter sifting and litter extractions 2x each season (summer and fall).

<u>*Results*</u>*:* In Study 1 effects of detrital manipulation on community structure were more pronounced in the fall, and the degree of divergence between experimental treatments increased over time (FIG. 1).

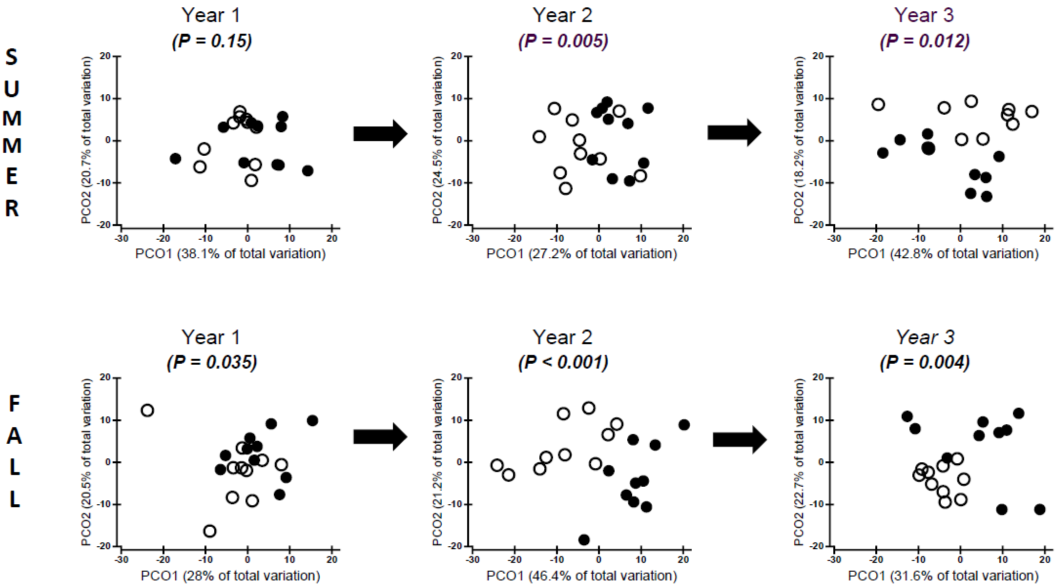

FIGURE 1. Effect of resource (detritus) supplementation upon arthropod community structure in Study 1 over time. Principal Coordinates Ordinations (Gower's Distance, 18 variables defined by taxon-sampling method combinations). The overall Resource x Year (R x Y) interaction is significant (*P* = 0.002, PERMANOVA). *P*-values for Resource Treatment from corresponding PERMANOVA's for each Year. The Resource x Year (R x Y) interaction is significant both seasons (*P*'s = 0.04, 0.003; Summer, Fall). Seasons are analyzed separately because (R x Y) x Season is significant (*P* = 0.04). Open and Fenced plots have been pooled because there were no interactions between Fencing and [(R x Y) x Year] or [(R x Y) x Season] (*P*'s = 0.22, 0.67).

○ **Control**
● **+ Detritus**

Densities of several taxa were positively correlated with resource supplementation in two consecutive years (entomobryid, hypogastrurid, onychurid and sminthurid Collembola; Diptera and Coleoptera). In contrast, Thysanoptera and larval Lepidoptera were negatively associated with increased detrital input. Web-building spiders were initially more numerous in supplemented plots, but by Year 3 were less dense in the resource-supplementation treatment.

In Study 2 the rainfall treatment altered community structure over time (FIG.2).

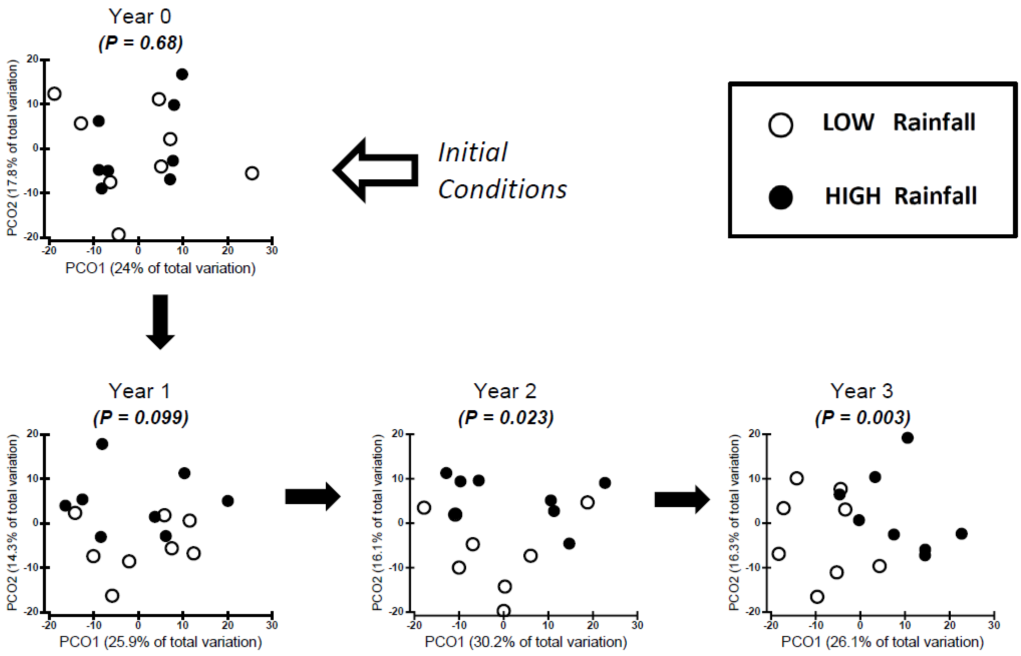

FIGURE 2. Effect of the rainfall manipulation upon arthropod community structure in Study 2 over time. Principal Coordinates Ordinations (Gower's Distance, variables defined by 55 taxon-sampling method combinations). The Rainfall x Year (R x Y) interaction is significant ($P = 0.002$, PERMANOVA). *P*-values for Rainfall Treatment from corresponding PERMANOVA's for each Year. Although Season and Site significantly affected community structure, these treatments have been pooled for these ordination plots because interactions between (R x Y) and both Season and Site are not significant (*P*'s = 0.71, 0.83).

Several taxa were consistently 2x more abundant in the High rainfall treatment: tomocerid Collembola, spiders, and Symphyla. Treatment x time interactions were less prevalent than in Study 1, with no indication of an altered response by web-weaving spiders over time. For most taxa the rainfall effect was greater on the drier site.

Discussion: Both perturbations substantially altered community structure, but temporal patterns were distinctly different. First, not all major taxa responded in a similar fashion to increased detritus or higher rainfall. Secondly, community equilibrium will be reached only after several years, especially for perturbations of detrital input.

Keywords: arthropods, leaf litter, detrital input, rainfall

[O4.4]

Are there links between responses of soil microbes and ecosystem functioning to elevated CO_2, N deposition and warming? A global perspective

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A comprehensive understanding of how the impact of global change on soil biota translates into altered ecosystem functioning is required for adequate predictions of future ecosystem states. A prerequisite for meeting this objective is a synthesis of relationships between global change effects on soil biota and ecosystem processes, which, however, is currently lacking. We used meta-analysis and structural equation modeling to assess whether effects of global change drivers (elevated CO_2, N deposition and warming) on soil biota abundance (total microbial community, fungi and bacteria) explain effects of these drivers on ecosystem functioning (plant biomass, soil C and N cycle). Across-taxa soil microbial abundance modulated the responses of ecosystem functioning to N deposition and warming, but not responses to elevated $CO_{2,}$ which were dependent on the soil taxon and ecosystem process in question. For example, fungal abundance responses to elevated CO_2 were positively correlated with those of plant biomass but negatively with those of the N cycle. In studies that simultaneously assessed global change, soil biota and ecosystem functioning, precipitation, soil fauna, P cycle and litter decomposition were clearly underrepresented. Future studies will need to address these research gaps, and use realistic global change rates and metrics of soil community composition, to improve current predictions of how global change will impact ecosystem functioning.

Keywords: global change, meta-analysis, ecosystem functioning, soil microbial abundance

[O5.1]

Land use legacies and agrodiversity from the below-ground perspective: Los Tuxtlas case study

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Land use intensification of naturally thin and nutrient poor soils has often been invoked as the prime explanation for reductions in food production in tropical mountains (Fig.1)

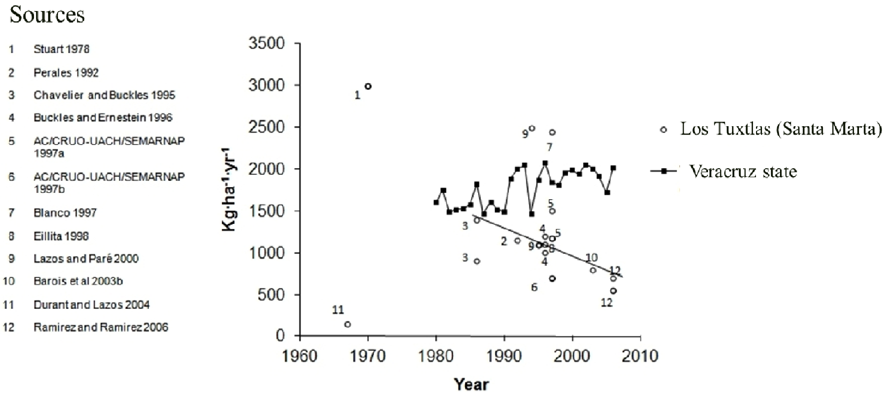

Fig. 1. Maize productivity decline in Los Tuxtlas

Little is known about the relative importance of land use legacies and current practices (like agrodiversity reduction) on soil functioning. For Los Tuxtlas, Mexico we (1) used the BGBD-Mex database to statistically model the cumulative effects of plot use history on soil fertility (10 indicators) and biodiversity (10 soil functional groups) and (2) experimentally investigated the consequences of aboveground crop diversity reduction (intra e interspecific) on the genetic diversity and function of native mycorrhiza and nitrogen fixing bacteria in indigenous maize polycultures (BioPop project).

The legacy of cropping years explained 8-22% of the variability in soil fertility and 5- 22% of belowground taxa richness (Mixed Models). The capacity of soils to establish mycorrhizal symbiosis diminishes with decreasing diversity of cultivated plants, while available P (Bray) increases with the diversity of crops (Fig. 2).

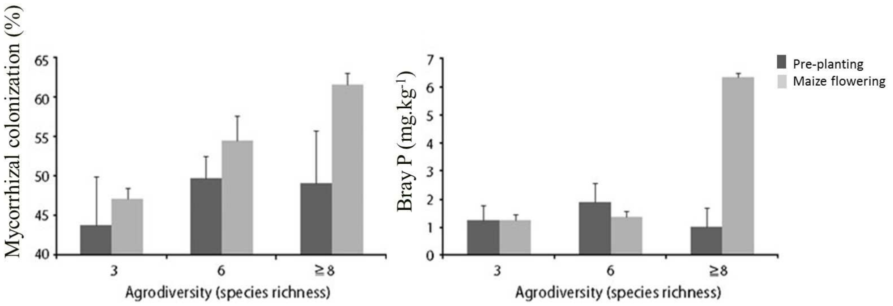

Fig. 2. Agrodiversity effect on mycorrhizal colonization and P availability

Compared to an introduced hybrid, some native maize landraces and their symbionts were much more efficient in obtaining P from very deficient soils (Fig. 3).

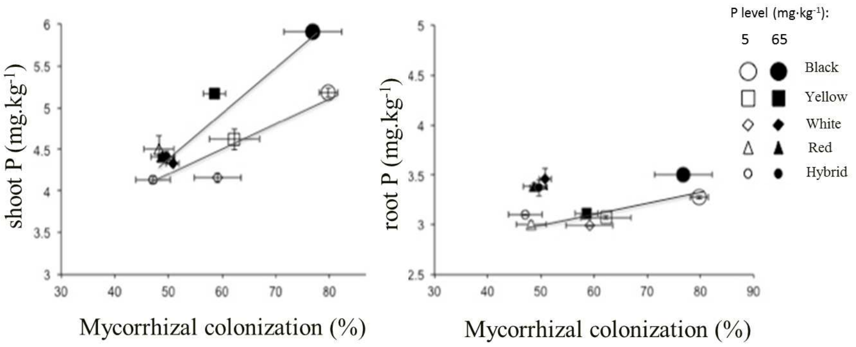

Fig. 3. Arbuscular mycorrhiza colonization and P uptake in native maize landraces and a hybrid

Many bacterial isolates from nitrogen-fixing nodules corresponded to bradyrhizobia closely related to native bradyrhizobia from the forest and novel groups were found. This being the first report of nodule bacteria from *P. lunatus* in its Mesoamerican site of origin and domestication. The interactions of land use legacies with current agricultural practices may be hampering the natural mechanisms that native polycultures have to cope with naturally thin and nutrient poor soils. The immense variety of locally developed crops benefits from symbiotic relationships with an equally diverse array of coevolved soil microorganisms. Understanding such a network is allowing us now to develop locally tailored technologies aimed at improving productivity and conserving an invaluable indigenous below-above ground heritage.

Keywords: Traditional maize polycultures, Arbuscular mycorrhiza, Nitrogen Fixing bacteria, phosphorus defficiency

[O5.2]

Tropical pasture heterogeneity and soil arthropod biodiversity: Bad plants also help

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Biodiversity and landscape heterogeneity usually correlate positively despite evidences of the opposite for particular faunal groups, and understanding the relationship between biodiversity and landscape structure is essential for proper land management.

We worked in dry tropical forests transformed to pastures to determine effects of soil cover heterogeneity on epigeic arthropod biodiversity.

During the rainy and dry seasons, we placed pitfall traps in three farms occupied by pastures except for some shrubs and monospecific stands of *Acacia pennatula* ("carbonales") and a small remnant of native forests. Arthropods were sorted and the most active groups were classified to species -springtails and ants- or to family -beetles-. Alfa diversity was characterized by Margalef and Shannon indexes and Beta diversity was defined as changes in indexes as several habitats are pooled. Spatiotemporal differences between communities and species contribution to differences were evaluated by MDS, ANOSIM and SIMPER analyses.

Unexpectedly, activity-density was only slightly depressed by drought. However, during rains arthropod activity was equitably distributed among all vegetation types while, in the dry season, pastures were deserted and more that 50% of the activity was sheltered under *A. pennatula*. There also was a seasonal shift in taxa relative activity, with water-dependent collembolans accounting for 75% of the activity during rains and several species of drought-adapted ants providing for 61% during drought. Species richness and biodiversity always responded positively to pasture diversification with shrubs and *carbonales* but with particular spatiotemporal patterns depending on bioindicators. *Carbonales* were the main contributors (even more than native forests) to global springtail biodiversity in the wet season and to beetle biodiversity during drought. Shrubs contributed more than *carbonales* to ant biodiversity.

Although fungicidal and allelopathic, *A. pennatula* is relevant for epigeic arthropod biodiversity in dry tropical silvopastoral systems, probably due to physical shelter provided by roots and fallen wood.

Keywords: Dry tropics, Landscape complexity, Arthropod epigeic biodiversity, Soil biodiversity management

[O5.3]

Biodiversity and ecological succession as indicators of compost maturity and quality

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Compost is an aerobic heat-producing process, during which organic waste is degraded by microorganisms to humus-like material. Compost has been touted as a solution for organic waste management, soil fertility, weed management, suppression of diseases, and promoting plant growth. For economic reasons, commercial composters have focused on the thermophilic phase to kill pathogens and weed seeds by maintaining a temperature between 55-77°C for a minimum of 15 days. However, biological control agents recolonize the pile in the subsequent curing phase. Nonetheless, literature is replete with inconsistent findings attributed to differences in recipe, composting process, and maturity. Chemical and physical indicators of maturity are imprecise. As a complement to these indicators, we empirically evaluated the composition of microbes and nematode communities as biological indicators of compost maturity and ability to suppress disease. At the end of the thermophilic phase, bacteria were dominated by thermophilic groups including Firmicutes, Actinobacteria, and gamma-Proteobacteria; fungi were primarily thermo-tolerant Ascomycota such as Dothideomycetes and Urotiales; and nematodes were mostly bacterial-feeding enrichment opportunists and fewer general opportunists. Mid-cure and end of cure are characterized by a different and more complex community. Bacterioides became more dominant than gamma- Proteobacteria and an increase of actinobacteria reflect reduced nutrient availability. Wood decay fungi were prominent. Nematodes shifted from dominance of bacterial-feeding/predators to increasing importance of fungal-feeding general opportunists. Based on these successional patterns and the advantages nematodes possess over microbes as indicators, a nematode based index for compost maturity is proposed. Our studies indicate that curing is critical for the biological compost component and its benefits. For example, in an on-farm experiment, mature hardwood bark compost reduced disease severity of early blight on *Brassica* crops. We propose that compost is disease-specific and, therefore, the recipe and maturity stage need to be tailored specifically by pathogen type and/or dispersal mode.

Keywords: compost, biological indicators, nematode communities, disease suppression

[O5.4]

Are sustainable agricultural practices sustaining larger earthworm populations? A quantitative review using meta-analysis

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Recognition is growing of the need for sustainable agricultural systems that encompass high crop productivity as well as the provision of ecosystem services. Thus, reducing the level of mechanical soil disturbance, either by decreasing ploughing depth (shallow tillage), loosening the soil without turning it (non-inversion tillage) or by direct seeding without any soil cultivation (no-till) are becoming increasingly adopted as alternative tillage practices worldwide. Earthworms are frequently used as indicators of soil quality under different tillage systems, and they have important functions in reduced tillage systems including a reduction in soil compaction and water runoff due to biogenic structures created by larger earthworm populations. However, earthworm abundance is also influenced by abiotic factors, such as soil texture, pH and temperature and moisture regimes and by food availability, which can override the effects of tillage and could explain the great variability in the observed responses across published studies.

Tillage effects on earthworms are of great interest in many research areas including agro-ecology, soil science, hydrology, agronomy and wildlife conservation, and many narrative reviews have been published. Here, we performed a quantitative review on the impacts of reduced and no-tillage practices on earthworm communities using meta-analysis, an analytical approach that gives different weights to published, collated studies based on replication and variability so that a statistically confirmed pattern emerges. Using data from published field studies (150 studies, 225 abundance and 124 biomass comparisons), we focused on the effects of different tillage practices on the abundance and biomass of earthworms. We also explored the modulating effects of rainfall, soil clay and C contents, pH, external chemical inputs, duration of experiments and earthworm sampling methods on earthworm populations under conventional and reduced tillage systems. This study provides the first global quantitative review of tillage effects on earthworm populations.

Keywords: Earthworms, Tillage, Meta-analysis, Review

[O6.1]

Soil natural capital: Can we use it to close future yield gaps and reduce agricultural risks?

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The soil natural capital, which is the capacity of soil biodiversity to generate ecosystem services is important for arable production systems. We ask here whether soil ecosystem services can be used in decisions to close yield gaps and reduce risk taking in production and market prices. Here we present novel models that can give the value of natural capital in decisions concerning agricultural management, that has effects on both farmers economy and may mitigate environmental problems from agricultural intensification. With a production function approach of data from long-term agricultural field experiments in Europe and the US were used to value changes in soil natural capital in relation to agricultural management. We demonstrate that dissipating soil organic carbon (SOC) and soil ecosystem services, will reduce both future attainable yields and fertilizer use efficiency, and thereby the value of soil natural capital. The reason for the lower fertilizer use efficiency with lower SOC, according to our results, is that additional fertilizer is needed to compensate for reduced levels of ecosystem services associated with lower SOC. We find that higher soil natural capital buffers yield variance against adverse weather and reduces reliance on external inputs. Further we address a view on how to use the value of soil ecosystem services when porposing strategies to close future yield gaps. We show the impact of soil ecosystem services and soil fertility on yields across the EU, using spatial econometric techniques by estimating yield functions in relation to fertiliser applications and climate. This allows for a comparison among policies and strategies that involves both private and social values of soil ecosystem services. Our approach makes it possible to quantify changes in soil natural capital and thereby value it in soil management decisions both on and off farm, which could help to promote globally sustainable agriculture through optimization of ecosystem services.

Ref: Cong et al 2014. Managing soil natural capital: An effective strategy for mitigating future agricultural risks? Agricultural systems DOI: 10.1016/j.agsy.2014.05.003

Keywords: valuation, agriculture, ecosystem services

[O6.2]

Farmer knowledge and use of soil biodiversity: A global synthesis illustrated with case studies

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The role of soil biodiversity and biological processes in on-farm management is receiving greater attention. This is a global trend, limited not only to management of smallholder farming systems, but also encompassing the drive to increase soil carbon stores in broadacre farming, and to improve understanding of the ecosystem services provided by soil biota. Underpinning this research and practice is farmer knowledge and use of soil biota and soil biological processes. To date, there has been relatively little research on this topic, and the research that exists has not been systematically reviewed. Our paper presents the first global review of published farmer knowledge of soil biota and soil biological processes. A thorough review of journal databases uncovered 44 papers on the topic; 42 of these reported original research, and two presented reviews (of largely inaccessible literature) for defined geographic areas. Study areas were drawn from 29 countries, including 21 studies from African countries, 10 papers from Central and South America, eight from Asia, five from North America and three from Oceania. No published studies on this topic were found for Europe. Almost half (20) of the papers addressed multiple soil fauna taxa, while 19 focussed on a single taxonomic group (commonly earthworms or termites). The ‘knowledge-practice-belief’ complex of framing local knowledge was used to critically analyse the main topics of the papers and identify key gaps in existing research. We illustrate our synthesis with case studies from a smallholder system in Honduras, and from broadacre grain farming in Western Australia, in order to highlight how local knowledge of soil fauna can be used in agriculture in a diverse range of settings. The results of the synthesis presented here offer insights for land management, agricultural extension and education, land use policy and future research on sustainable agriculture.

Keywords: Local knowledge, Biodiversity management, Agricultural management, Ethnoecology

[O6.3]

Measuring changes in agricultural land quality: The case of the Italian farms

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Soil is a vital pore for life and particularly for agriculture. Since the agricultural sector constitutes a large part of the economy of several countries, this indicates the need for land management practices. This study tries to address the link between soil biodiversity and soil services and particularly the contribution of soil quality to agricultural production. The main objective of the research is to estimate the economic value of soil biodiversity and its interplay with crop biodiversity. In the absence of precise data to measure farms soil nutrient stocks overtime, it is necessary to evaluate the intertemporal role of one period's yields affecting the next period's yields. By relying on a large panel dataset, we develop methods, using econometric techniques, to examine the interaction between soil biota functions, crop biodiversity and agricultural practices as well as to understand the factors that may influence the current and future use of soil ecosystem services.

This paper offers a preliminary examination of agricultural production with respect to fertility management within the Italian farms. We use dataset from a long-term study from the Italian Farm Accountancy Data Network (RICA). Farm selection is developed according to three variables of stratification: geographical location, type of farming and economic dimension. The preliminary findings indicate that crop diversification and soil fertility have a positive effect on farmer welfare and Crop diversification can be a potential strategy to improve or maintain soil fertility.

An important characteristic of this study is the use of a large panel dataset that allows the capture of changes over time and the consideration of past events that influence the current outcomes.

By further work this study aims to provide a reliable framework to secure farm crop production and encourage the development and new methods adaption by farmers, and contribute to the policymaking for future development of land resources.

Keywords: Sustainable agriculture, Soil quality, Crop diversification, Ecosystem function

[O6.4]

On the value of soil biodiversity and ecosystem services

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This paper provides a framework to understand the source of the economic value of soil biodiversity and soil ecosystem services and maps out the pathways of such values. We clarify the link between components of the economic value of soil biodiversity and their associated services of particular relevance to soils. We contend that soil biodiversity and associated ecosystem services give rise to two main additive value components in the context of risk and uncertainty: an output value and an insurance value. These are illustrated with examples from soil ecology and a simple heuristic model. The paper also point towards the challenges of capturing such values highlighting the differences between private (individual) and public (global) sources of value

Keywords:

[OE1.01]

A happy families game on soil biodiversity

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[1]IRD, France, [2]ADEME, France, [3]Ministère de l'Ecologie, France, [4]AgroParisTech, France, [5]AFES, France

Soil biodiversity is exposed to global changes, which may alter its functions and the services it provides for human well-being. Yet, soil biodiversity is largely unknown to children and the general public. While the size of soil organisms partly explains this situation, the paucity of awareness-raising activities targeted towards the wider public is responsible for such a lack of knowledge and interest.

In 2013, a game "the hidden life of soils" was designed by scientists and teachers for young audiences to discover soil biodiversity and understand soil ecological functioning. This Happy Families card game, in the style of Go Fish!, contains 42 playing cards (7 families with 6 representatives). Each card includes the name of the family, of the representative of the family, and of the other members of the family (Fig. 1). It also includes a large photo and description: the size of the representative, a short sentence on the diet of the organism or a short sentence to explain the photo. The simplicity of the rules makes the game accessible to virtually anybody while making players observe and memorize unknown organisms within their groups (mesofauna, microfauna...). Illustrations, texts and designs have been carefully selected to be both informative and attractive.

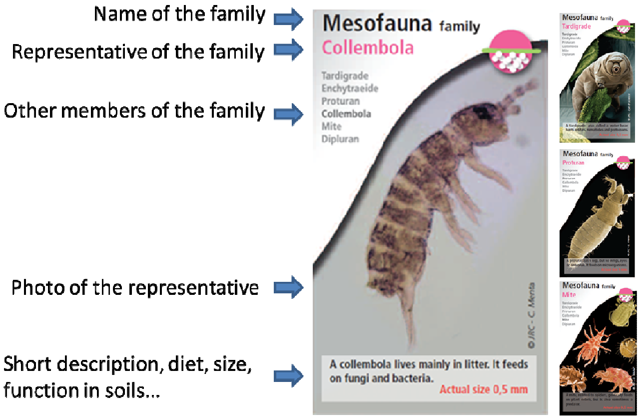

Fig. 1 Example of paying cards from the hidden life of soils

This easy-to-use and easy-to-transport pedagogic tool is used in different educational settings and for a large public from children to students. Illustrations, texts and designs of the cards and the supplemental educational booklet (Fig. 2) allow different uses at different level.

Fig. 2 The supplemental educational booklet either for parents of teachers describing the size distribution of the soil organisms and trophic networks

The game was distributed in schools and environmental associations. It is also available to free download on the internet (http://www.gessol.fr). Three months after the launch, the French webpage of the card game still received 2000 visits over a single week. We are developing an English version (available next December).

This game is a simple and efficient pedagogic tool to illustrate the astonishing levels of heterogeneity of life in soil and hint at the role of biodiversity on ecosystem functioning.

Keywords: Education, playing cards game, school, soil organisms

[OE1.05]

Can soil organisms become our best teachers? Exploring soil biodiversity as an ecosystem service provider of excellent environmental education

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Sustainable, thriving human societies depend on the conservation and management of biodiversity and ecosystem services. Those, in turn, depend on the actions of environmentally literate citizens who understand environmental issues and use ecological knowledge for decision making. Since soil biodiversity has critical roles for supporting human well-being, it should feature prominently in environmental education programs that seek to foster higher levels of people's environmental literacy. This should be easily accomplished because soil organisms have many characteristics that suggest their utility for environmental education: they are easy, quick and inexpensive to find in urbanized environments; many are fascinating, beautiful and fun to interact with. Also, their relatively small, less-well-known and underused stature can spark people's curiosity. Nevertheless, soil biodiversity is often overlooked in education programs, and most people's soil literacy is probably relatively low. This presentation explores opportunities to cultivate the recognized but under-examined ecosystem service of teaching with a focus on using "soil organisms as teachers" (a.k.a. educational service providers). Many possibilities exist to develop creative, hands-on education resources and activities that integrate soil organisms, such as living soil bins, scavenger hunts, and "outdoor classrooms" to dig in. A case study from Rhode Island, USA illustrates how a soil ecologist partnered with a local environmental education center to create soil biodiversity exhibits and teaching materials with outcomes that can be adapted in other places and contexts. Additionally, soil ecologists should help develop "soil surveys" (quizzes, questionnaires) to assess whether people's environmental literacy is improved by soil biodiversity education experiences. Such efforts by those who understand and love soil organisms the most is needed to cultivate the valuable ecosystem service of teaching by soil organisms. This enhanced service may help environmental education programs excel in fostering both the soil-specific and general environmental knowledge needed to support more sustainable soil-literate societies.

Keywords: Environmental literacy, Environmental education, Teaching, Soil exhibits

[OE2.1]

Tree species diversity effects on soil microbial biomass, diversity and activity across European forest types

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Increasing tree species diversity in forests might contribute to ecosystem-service maintenance, as well as to the reconciliation of regulating, provisioning and supporting services within the frame of multifunctional and sustainable forestry. Individual tree species influence biogeochemical cycling through element deposition (throughfall, litterfall), and through microbial activities in the soil. Yet, the influence of mixing tree species on these ecosystem processes is unclear, in particular concerning the microbial diversity and activity in soils.

Here we synthesize results from the Exploratory Platform of the FunDivEUROPE project (http://www.fundiveurope.eu/). This network of 209 comparative plots covering a tree diversity gradient of 1 to 5 tree species was established in existing mature forests in 6 European regions. These six focal regions represent a gradient of major European forest types from boreal to Mediterranean forests. We analysed the impact of tree species diversity and the role of other controlling factors on the metabolic diversity of soil bacteria (BIOLOG Ecoplate), soil microbial biomass (fumigation-extraction) and potential nitrification (shaken soil slurry) in the forest floor and the upper organo-mineral soil horizon.

Mean values of microbial biomass carbon ranged from 240 (Poland) to 1762 (Germany) mg kg^{-1} in the forest floor and from 4197 (Italy) to 11207 (Finland) mg kg^{-1} in the upper organo-mineral horizon. Tree diversity and soil water content were important controlling factors. Statistical models predict microbial biomass to increase in both horizons by 7-8% with each step increase in tree diversity. Metabolic diversity of soil bacteria (% of substrates used) showed high variability both within and between sites. Further results analysed with mixed linear models will be presented and discussed.

Keywords: forest soil, microbial biomass, nitrification, metabolic diversity

[OE2.2]

Hidden effects of large herbivores on plant competition through plant-soil feedbacks

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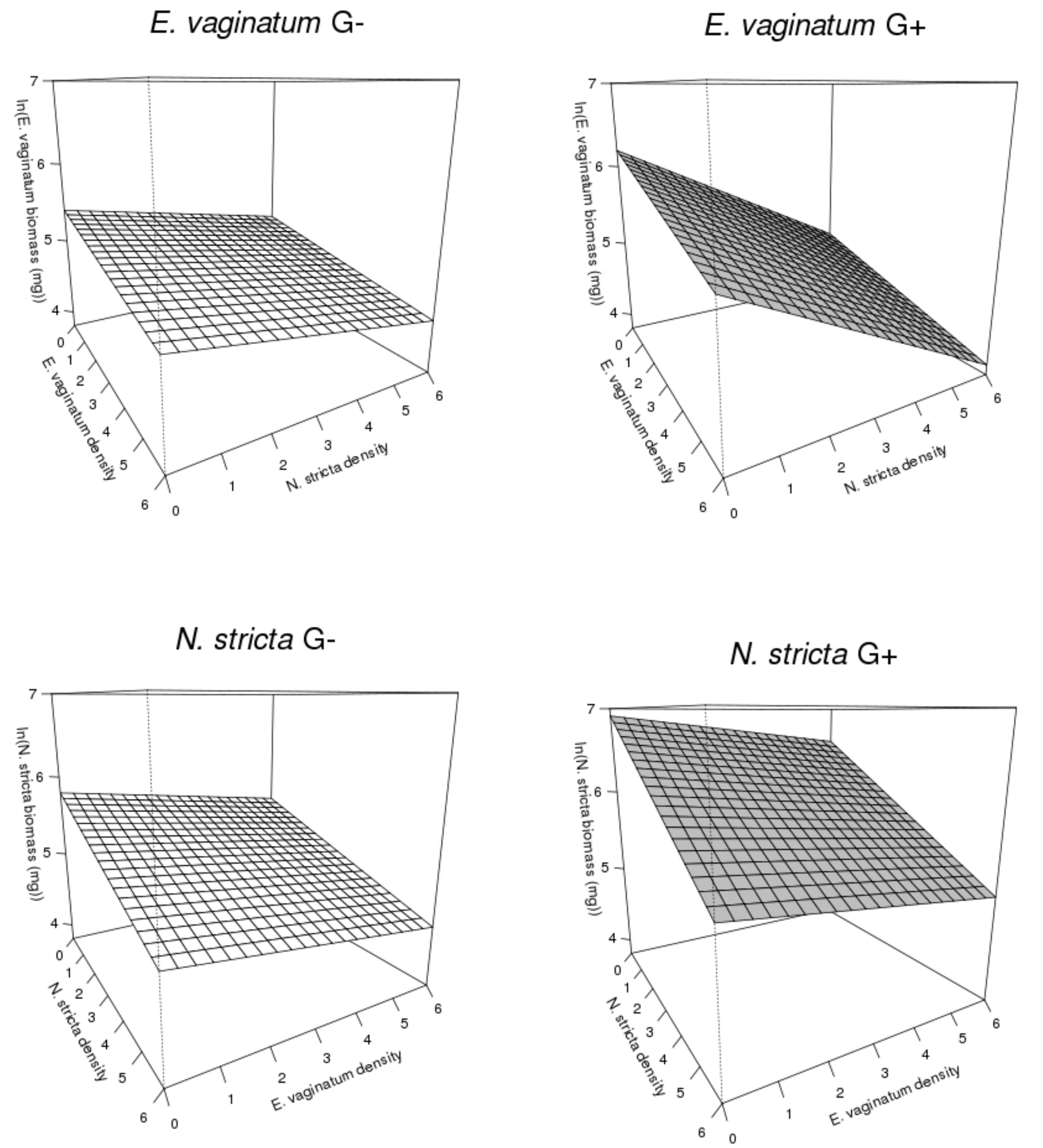
Large herbivores can influence plant community composition and thus ecosystem structure and function. One way is by affecting plant-plant interactions directly (trough grazing and/or trampling, for instance). However, it is less explored if large herbivores can modify plant interspecific competition indirectly through herbivores' effects on soil (by modifying soil microbial communities and/or soil processes; such plant-soil effects are known under the umbrella term of "plant-soil feedbacks"). We tested the hypothesis that herbivores would affect — via plant-soil feedbacks — the strength of interspecific interactions between two graminoids which occur at contrasting densities under grazed and ungrazed conditions in upland British grasslands (*Nardus stricta* L. and *Eriophorum vaginatum* L.). We grew *N. stricta* and *E. vaginatum* individuals in a controlled competition experiment using two soils with indications that their microbial communities and properties differed (a long-term grazed upland grassland where *N stricta* is dominant and a contiguous 6-years grazing exclosure dominated by *Calluna vulgaris* (L.) Hull. and *E. vaginatum*). Our design allowed us to exclude confounding effects due to variation in plant species densities and separate herbivore-driven plant soil feedback effects on interspecific and intraspecific competition in our target plant species. At the end of the experiment, soils from the long-term grazed grassland exhibited higher nitrogen (N) mineralisation rates and soil microbial activity in accordance with previous field measures, but soil microbial biomass Carbon: N ratio did not differ between grazed and ungrazed areas. Surprisingly, herbivores affect plant competition asymmetrically through plant-soil feedbacks by increasing the strength of interspecific competition of the superior competitor (*N. stricta*) over the inferior one (*E. vaginatum*) more than they increase intraspecific competition as a result of higher N availability (which coincides with field abundance of these species under grazing conditions). Our results are the first, as far we know, to show such an asymmetrical grazing-driven plant-soil feedback.



E. vaginatum G-

E. vaginatum G+

N. stricta G-

N. stricta G+

Keywords: Plant-soil feedbacks, Grazing, Density-dependent plant comnpetition, Upland grasslands

[OE2.3]
Fungal role in carbon flow in the rhizosphere along a chronosequence of abandoned agricultural soils

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Many of the ecosystem services provided by soils, such as plant growth, organic matter cycling, carbon sequestration and pathogen suppression occur through actions of microbes. Here, we present results on the structure of and the diversity within fungal communities active in soil along a chronosequence of ex-arable fields in The Netherlands (Veluwe LTO). These fields are typically managed by low-intensive grazing while undergoing a transition from an arable system into species-rich grassland. We hypothesized that the role of fungi in soil processes would increase with increased time after abandonment and that this would have further consequences to soil functioning. In order to assess the short term fate, turnover and retention of recent plant-assimilated carbon and study active soil communities in these systems, intact soil cores were collected and pulse labelled with $^{13}CO_2$. The fungal contribution to the processes was evaluated using PLFA-SIP and community structure and diversity was analysed using DNA-SIP combined with 454-sequencing.

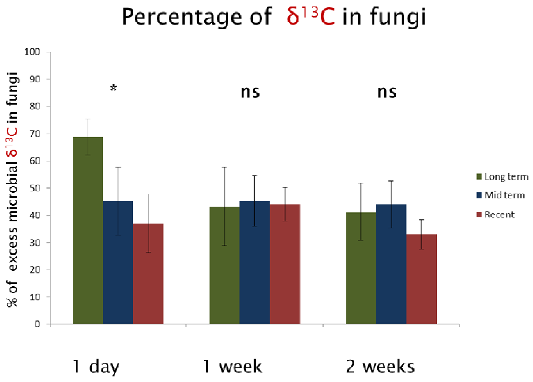

Figure 1. The percentage of the root derived labeled carbon incorporated into fungal biomass

Upon labelling, most of the root derived ^{13}C was found in fungal biomass. Interestingly, fungi in the cores from long-term abandoned fields received significantly more carbon from the plants than the fungi in the short-term abandoned fields in which bacteria dominated (Figure 1). We further observed that the changes in energy channels further affected the higher organisms. The active, ^{13}C labelled fungi, in the rhizospheres were analysed and interaction networks of species were constructed to entangle the reasons for the found differences. These results highlight the importance of fungi in the grassland rhizosphere and their role in the carbon cycling. We will discuss these results in relation to the soil biodiversity and ecosystem function.

Keywords: Fungal Ecology, Rhizosphere, Microbial Biodiversity, Ecosyctem funcion

[OE2.4]

Ectomycorrhizal symbiosis - cure or cause of forest nitrogen limitation?

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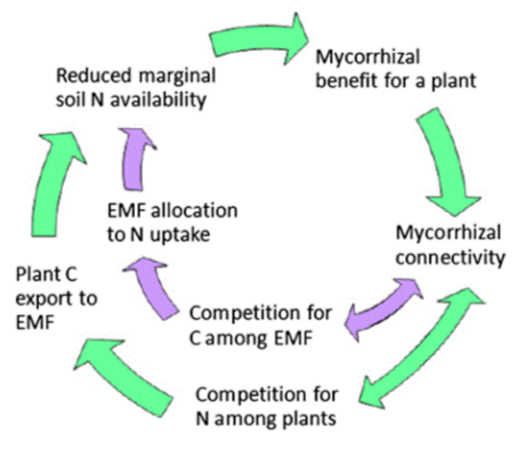
Introduction: Recent large-scale labelling experiments in the forests of Sweden have brought into question a long-held theory of biology: that the ectomycorrhizal fungi found on tree roots interact with trees in a symbiotic relationship that is always beneficial for both the fungi and the trees. These fungi, including many edible mushrooms, are particularly common in boreal forests where nitrogen limits tree growth. But in contrast to the current paradigm we showed that the fungi may be the cause rather than the cure for the nitrogen scarcity. In the experiments, we found that rather than alleviating nitrogen limitation in soil, the fungi maintain that limitation by transferring less nitrogen to the trees when nitrogen is scarce than when it is abundant in the soil.

Methods: A new theoretical model was developed to explain the experimental findings, by simulating the interaction between individual fungi and plants. It suggests that since each individual organism competes with others in trading carbon and nitrogen, the system as a whole may function more like a capitalistic market economy than a cooperative symbiotic relationship.

Results: The competition among trees makes them export excessive amounts of carbon to the fungi, which seize a lot of soil nitrogen and further aggravate the trees' nitrogen limitation. On the other hand, this self-sustained nitrogen limitation may prevent non-mycorrhizal plants from invading and therefore confers a competitive advantage of the mycorrhizal strategy despite hampered tree growth.

Discussion: Due to the dominant role of ectomycorrhizal symbiosis in boreal forest, these mechanisms may have large and unexpected consequences for forest growth under a changing climate. For example, the expected CO_2 fertilization of forest growth may be eliminated or even reversed.



Feedback loop stabilizing the mycorrhizal strategy, showing the interrelation between effects of ectomycorrhizal fungi (EMF; purple arrows) and plants (green arrows). Increased fungal-plant (mycorrhizal) connectivity enhances competition among both EMF and plants, which drives plants to increase C export to EMF and EMF to increase N uptake and N export to plants. These effects interact in depleting available soil N, which favours the mycorrhizal strategy compared to a non-mycorrhizal plant strategy, which in turn promotes mycorrhizal connectivity.

Keywords: boreal forest, ecosystem, market model, game theory

[OE2.5]

How a native shrub affect soil nematofauna and microbial communities when growing millet in Senegal

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Woody shrubs commonly co-exist with annual food crops in farmers' fields throughout the Sahel. Management strategies that deliberately include the native shrub *Piliostigma reticulatum* in Senegalese cropping systems results in better crop yields. This work focuses on soil microbial communities and nematofauna as potential key actors of the observed benefits.

Topsoils (0-10 cm) were collected in an existing experimental design at Nioro-du-Rip (Sénégal): (i) bare soil (treatment serving as a control, C), (ii) millet cultivation without external inputs (M treatment), (iii) shrub canopy (noted as P for *Piliostigma reticulatum*), and (iv) millet and *P. reticulatum* association integrating shrub pruning and mulching at crop seedling (M+P). The different trophic groups of soil nematofauna were characterized and related indices were used as indicators of the soil food web. Soil microbial communities were characterized by combined methodological approaches including PCR-DGGE of 16S rDNA and ITS gene, functional diversity (MicroResp^{TM}) analysis and enzyme activity measurements.

The structure and enrichment indices of the nematode community were significantly higher in M+P treatment. The abundance of the plant feeders (especially the Hoplolaimidae family) decreased when *Piliostigma reticulatum* was associated to the millet. Non-metric Multidimensional Scaling (NMS) of soil microbial community data revealed a shift in structure of both bacterial and fungal communities. Arylsulfatase and urease activities were significantly affected by the shrub. However functional diversity (MicroResp^{TM}) of microbial communities was not affected by the shrub.

The presence of *P. reticulatum* in millet cultivation provided more bacterivorous nematodes with indirect effect of nitrogen cycling and less plant-parasitic nematodes that further enhance millet productivity. The changes in structure and functioning of the soil microbial communities probably contribute to nutrient cycling as well. Further research should clarify interactions within the soil food web and impacts on soil fertility.

Keywords: Agroforestry, Piliostigma reticulatum, Nematode, PCR-DGGE

[OE2.6]

How soil organisms interact with plant hormone signalling pathways

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Plants interact with a large number of soil organisms. For a long time, these interactions have been the research area of soil ecologists and trophic relationships and physico-chemical modifications of the soil matrix were generally proposed as mechanisms underlying plant-soil organism interactions.

However, some specific symbioses and diseases have been well characterized at the molecular level by plant biologists and microbiologists. These interactions involve a physical contact between soil organism and plant. They are mediated through signal molecules that play upon the different plant hormonal signalling pathways, leading to modifications in plant development and defence. Nowadays, the role of signal molecules emerges as an important feature of interactions between plants and free-living soil organisms.

In this work we discuss genetic and physiological evidences of hormone signalling involvement in plant response to physically associated but also free-living soil organisms, for very different taxa ranging from the micrometer to the centimetre scales. The same hormone signalling pathways seems to be activated by very different kinds of soil organisms such as bacteria, nematodes, collembola and even earthworms, with common consequences on plant growth, development and defence.

Plant hormonal homeostasis appears to be the corner stone to understand and predict the issue of the multiple interactions that plants entertain with the community of soil organisms.

Keywords: plant hormone signalling pathway, plant development and defence, micro-, meso- and macro-fauna, microorganisms

[OE3.1]

Processes and patterns of nematode biodiversity in urban soils

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Little is known about belowground biodiversity in urban ecosystems. We have identified key processes that affect patterns of nematode species and functional diversity and structuring of nematode food webs in urban ecosystems. Results reveal that processes including land use, urban age, physical disturbance, chemical inputs (intended or unintended), and anthropogenic alterations in habitat structural complexity and heterogeneity influence nematode species and trophic diversity and structuring of nematode communities in urban ecosystems. Nematode communities tend to be less diverse and more disturbed in well-managed urban lawns compared to urban vacant lots and community or market gardens. Fertilizer applications negatively affect soil nematode biodiversity and food web structural complexity, whereas pesticides seem to have little effect. Nematode communities tend to be less diverse at the urban fringe compared to the urban core, likely due to more recent physical disturbance associated with urban development at the urban fringe. Nematode abundance and species richness increase with urban age and correlate positively with soil C, organic matter, and pH, which also increase along urban age. Nematode abundance and species richness however did not correlate positively with soil C, organic matter and pH along the distance to road gradient, suggesting a negative effect of contaminants associated with roads. Using multiple regression analysis we determined that a combination of heavy metals As, Cd, and Cr, and soil texture and organic matter are significant predictors of nematode abundance and community indices in urban soils. Bacterivore and fungivore nematodes were negatively correlated with As and positively with Cr and Zn; whereas plant parasitic nematodes were positively correlated with Cd, Cr, and Zn. Channel index was negatively correlated with Cd, Cr and Zn. Overall, the results show that soil nematode food webs in urban ecosystems are highly disturbed, less diverse, immature, and lack structural complexity compared to nearby forest ecosystems.

Keywords: soil biodiversity, soil food webs, nematodes, urban ecosystems

[OE3.2]

Filling the gap in the knowledge of urban soils organisms: Ants and earthworms of urban parksKey words: Urban soils, earthworms, ants, initial conditions, urban parks, community ecology

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Over half of the world's population lives in cities. Humans are the most in contact with urban soils but the biodiversity they shelter is paradoxically among the least known. The ecological drivers that shape soil organisms in the urban context are still to be addressed. Indeed, most of urban soils are man-made (technosols) and without most organisms. Colonization framework questions emerge such as the importance of age since their construction, initial conditions of soils or landscape properties.

We studied 20 patches of lawn located in parks around Paris (France) with different ages (from 2 to 64 years) and with two types of technosols: all with mineral anthropogenic backfill and with (TS) or (NTS) without top soil, which represent the initial conditions of the soils. Normalized Difference Vegetation Index (NDVI) around patches, management practices and soil physico-chemical properties have also been recorded (%C, %N…). We sampled soil macrofauna taxa that have major impacts in soil functioning and are considered as ecosystem engineers: ants and earthworms.

We collected 17 earthworm species and 12 ant species that are common. For earthworms, we highlighted a major effect of the interaction between the age and the type of technosols. Along time, we observed a decline of abundance and species richness in NTS patches whereas those indicators increased in TS patches. The difference in the initial conditions of the soils strongly affected earthworms. The NDVI showed a positive effect meaning that colonization was more efficient when habitats were present around the recently constructed technosols. For ants, no significant effect was observed which means that local process such as competition could be more important than colonization as they have high dispersal capabilities.

This study highlighted the importance of initial conditions for those key organisms and participated to fill the gap in the knowledge of urban soils.

Keywords: Urban soils, Earthworms, Ants, colonisation

[OE3.3]

Soil invertebrates as bioindicators of soil quality in urban vegetable gardens

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Do human activities systematically alter the ecosystems functioning by negative effects on soil biodiversity? Human activities are known to potentially alter physical, geochemical and biological properties of ecosystems. SUITMAs (Soils in Urban, Industrial, Traffic, Mining and Military Areas) are major supports of these man-modified ecosystems. Among these soils, some might play a key role in developing biodiversity in urban areas like vegetable gardens. Gardening is a very common practice in many industrialised and developing countries. However, the functioning and the ability of garden soils to provide support for biodiversity are underrated. What is the effect of urbanisation on taxonomic and functional biodiversity in vegetable gardens? A functional trait-based approach for soil invertebrate communities has been recently developed to understand the species responses to their environment (BETSI project funded by the Fondation pour la recherche sur la biodiversité).

This work was conducted to (1) compare springtail communities in France, using data collections from several national databases, along a gradient of land use (forest, agriculture, and urban vegetable gardens and (2) to assess the taxonomic and functional springtail biodiversity in French garden soils along an intensity gradient of gardening practices.

Fifteen gardens were selected using soil data, environment and gardening practices out of the 104 gardens of the French national survey on garden soils (JASSUR-ANR) conducted in contrasted climatic areas (Continental, Oceanic and Mediterranean). Correlations between characteristics of collembolan community (e.g. species richness, functional trait distribution) were established. Results showed that urbanization and changes in land use did not always translate to a lower taxonomical and functional structure of springtail communities. However, the functional structure tended to vary with changes of gardening practices.

Functional traits as indicators will allow a more precise understanding of the effects practice changes have on springtail communities in urban environments.

Keywords: functional traits, springtails, gardens, urbanisation

[OE3.4]

A multi-city comparison of urban soil ecosystem function

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Urban soils vary from relatively undisturbed in remnant habitats to highly disturbed in developed areas. As such, these soils form a continuum of human effects and provide excellent opportunities to study the impact of anthropogenic factors on soil ecosystem services.

We have recently initiated a Global Urban Soil Ecological and Education Network (GLUSEEN) to allow for a multi-city comparison to answer the following questions: (1) What is the response of soil community structure and decay rates in urban soils at local, regional and global scales? (2) Do differences in soil biodiversity among urban soil ecosystems relate to functional changes in the decomposer subsystem?

In a pilot study we conducted experiments in five cities: Baltimore, USA; Helsinki and Lahti, Finland; Budapest, Hungary; and Potchefstroom, South Africa. Four habitat types, ruderal, lawn, remnant and reference were selected, each replicated five times. We measured basic soil characteristics, and assessed the earthworm and microbial communities. To follow decomposition rates we deployed nylon teabags as a common substrate.

In cities with forest as the native habitat, we detected similar trends across the habitat types: soil organic matter concentration was lower, and pH was higher in the disturbed than in the reference sites. Among cities, absolute differences were higher in the reference sites than in the ruderal sites: for SOM 47.05% and 1.99% and for pH 2.1 and 0.7, respectively. NMS ordination of all 16S (Bacterial and Archaeal) sequences revealed a strong separation of Baltimore from the rest of the cities across the Atlantic. Both city and habitat type effects were significant. Within cities, microbial communities were strongly correlated both with soil organic matter and pH.

In both managed (lawn) and disturbed (ruderal) soils, anthropogenic effects dominate natural soil forming factors. Soil communities partially reflect this, but biogeographical factors still play a role in community assembly.

Keywords: urban soils, microbial diversity, decay rate

[OE4.1]

Standard methods for the assessment of structural and functional diversity of soil organisms: A critical overview

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Lack of standardized methods limits the ability to make comparisons across datasets and develop new global and regional experiments and assessments (such as the Global Soil Biodiversity Assessment (GSBI)). The main goal of this talk is to synthesize the current methodological approaches to measure structural and functional diversity of soil organisms and to identify gaps and ways to improve the methods to allow for comparable datasets. This exercise is urgently necessary because there are several ongoing regional and global soil biodiversity studies that are not coordinated with one another in terms of the methodological approach. Therefore, in a first step standard methods to sample, identify, determine and assess soil organisms currently in use or proposed all over the world will be critically evaluated, using well-accepted criteria such as ecological relevance, practicability of usage in terms of resources, time and costs, level of standardization etc. Methods addressing both soil organisms (population) structure and functions will be included, with a special focus on relatively new molecular methods based on DNA extraction. Soil microbes as well as soil invertebrates will be covered. In particular, the activities of the Technical Committee (TC) 190 of the International Organization of Standardization (ISO) will be highlighted, since ISO guidelines (= standard methods) are legally accredited by many national or international authorities when putting conservation laws and regulations into practice. Finally, detailed recommendations will be proposed regarding gaps in the available set of standards, to identify a list of new methods most urgently needed. Finally, we will discuss the ones that have to be developed from scratch and the ones which could be developed based on available methods, already used by the scientific community. We propose to organize this whole process under the umbrella of GSBI in order to ensure a truly global approach for the assessment of soil biodiversity.

Keywords: Standardisation, Structural diversity, Functional diversity, Harmonization

[OE4.2]

Soil invertebrate functional traits

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Soil invertebrates are assumed to play major roles in ecosystem dynamics. Functional traits represent one of the main opportunities to bring new insights in the comprehension of soil invertebrate assemblage against environment. They are properties of individuals which govern their responses to their environment. As no clear conceptual overview was done for soil invertebrate trait definitions, we first stressed that previously-described concepts of traits are applicable to soil invertebrate ecology after slight adaptations. A decade of literature on the use of traits for assessing the effects of environment on community assembly was then done. A major proportion of articles was dedicated to the effect of only one kind of stress in limited space scales. This review revealed that trait-based approaches contribute to improve predictability of community assembly against environment as it contributes to explain general patterns of assembly rules. But underlying mechanisms are far for being frequently assessed. Furthermore, literature allowed assuming that trait-based approaches are reliable whatever the environmental gradient considered. But it did not allow concluding over eco-regions. This review also highlighted methodological advantages and drawbacks. First, trait-based approaches provided complementary information towards taxonomical ones. Second, literature revealed methodological shortcomings. It could be for instance the heterogeneity of the trait names which can impede the data gathering or the use of traits at a species level which can impede the scientific interpretation. To overcome these shortcomings, the last part aims at proposing some solutions and perspectives. It concerns notably the development of a trait database and a thesaurus to improve data management.

Keywords: Community ecology, Soil fauna, Disturbance, Ecological preference

[OE4.3]

Which bioindicators are suitable for soil quality monitoring and risk assessment? From relevance study to transfer tool development

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Introduction- Considering the few number of bioindicators available for soil risk assessment and soil characterization, a national research programme has been set up in France by the French Agency For Environment and Energy Management (ADEME) to develop indicators able to judge about soil degradation and/or remediation of its properties and functions. Objectives of this “BioIndicator programme” are to (i) develop and validate methods for measuring soil biodiversity and soil functions, (ii) test the sensibility and complementarity of the bioindicators for the characterization of different perturbations (contamination, modification of soil uses), iii) identify relevant bioindicators or endpoints for different purposes (ecological risk assessment, monitoring of soil quality..), iv) transfer the results to stakeholders (policy makers, farmers, research board) by providing suitable tools.

Methods- 22 research teams are involved. 47 bioindicators are tested (microorganisms, fauna, flora) in a large panel of situations (47 situations including agricultural, industrial and forest sites) and sampled at the same moment by applying standardised sampling protocols. A common database allows the management of the high number of data (200.000).

Results- Bioindicator programme initiates a first national benchmark i.e. baselines values for the different biological groups. It provides relevant tools (battery of bioindicators, biological index) adapted to different environmental targets such as i) evaluation of the impact of agricultural practices (crop rotations, reduced tillage, organic and pesticides management), ii) evaluation of the bioavailability of industrial contaminants, iii) evaluation of the biological state of contaminated soils in order to orientate their future use, iv) soil monitoring of biological state at large scale. Moreover, it provides communication tools, such as bioindicator technical sheets and web-interface addressed to stakeholders (http://ecobiosoil.univ-rennes1.fr/ADEME-Bioindicateur/).

Conclusion- this10 years research programme, unique at the European Union scale, permits to improve the knowledge on soil biodiversity and its functioning, and provides tools to stakeholders for future soil management.

Keywords: Bioindicator, soil quality, risk assessment, monitoring

[OE4.4]

A tiered approach for high-resolution characterization of the soil faunal community via dna metabarcoding

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Characterization of the huge soil faunal diversity still relies heavily on the slow and expert-dependent morphological identification. This hampers our ecological understanding of spatial and temporal diversity of many faunal groups, as screening many samples at high taxonomic detail is not a realistic proposition. DNA-based approaches, especially high-throughput DNA metabarcoding assays, potentially solve this issue, but the development of such methods targeting soil fauna lags far behind that of soil microbes.

Within the EU FP7-project EcoFINDERS, we developed and tested a framework for automated identification of six different groups of soil fauna at high taxonomic detail, with a single integrated method. We adopted a tiered approach, in which a general eukaryotic marker is used to screen for the presence of different eukaryotic clades and a set of more specific markers is simultaneously analyzed to obtain high resolution data for six different groups: mites, collembola, enchytraeids, nematodes, earthworms and protists. New primer sets, as well as reference barcode datasets were established for several of them. Here, we show the results of two test runs based on 454 pyrosequencing.

In the first run, artificially created DNA pools of known composition were analysed to test to which extent the taxonomic composition could successfully be retrieved. Preliminary results show that for all groups the majority of species in the DNA pool were recovered by the metabarcoding approach. By comparing results for DNA pools that contained different relative amounts of DNA of the six groups, we could show that for most markers the number of taxa of the targeted group recovered depended on the presence of DNA from non-targeted groups. In the second run we moved towards the analysis of actual soil (e)DNA extracts, comparing the results of morphological identification by those of molecular identification based on the same soil samples.

Keywords: NGS sequencing, soil fauna, methodology, diversity

[OE4.5]

Edaphobase - The online soil-zoological data warehouse

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Edaphobase is a non-commercial data warehouse on soil organisms (up to now including Nematoda, Collembola, Oribatida, Gamasina, Chilopoda, Diplopoda, Isopoda, Enchytraeidae, Lumbricidae) publically available at http://portal.edaphobase.org/. Its data is furthermore regularly uploaded to the Global Biodiversity Information Facility (GBIF) network. Edaphobase combines data on taxonomy, zoogeography and ecology of these organisms in a comprehensive manner. Data are derived from publications, unpublished results of field studies (theses, reports), collection data from German museums and research institutions as well as raw research data. Data types (= entities) comprise modern taxonomic thesauri, geographical references, soil parameters, vegetation, meteorological data, sampling and extraction methods, quantity of collected organisms, identification methods, preparation techniques and behavioural data. The focus is presently on Germany and neighbouring countries, but some data from other European countries is included and can be incorporated more intensely in the future. Edaphobase offers a wide range of tools for data inclusion (data-input client, GIS-tool, semi-automatic literature analysis) and data exploration. Simple queries are possible as well as more sophisticated analyses of different data groups. Specific applications include, e.g., *the elucidation of species-specific habitat preferences (niche space), distribution patterns or environmental influences on population densities*.

Keywords: Data warehouse, Soil faunal biodiversity, Niche space, Biogeography

[OE4.6]

Biomes of Australian Soil Environments (BASE): A dataBASE of Australian soil microbial diversity

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The Biomes of Australian Soil Environments (BASE) initiative is a community effort to develop a publicly accessible database that encourages discovery and observation of soil microbial communities across Australia’s diverse natural and agricultural ecosystems. It represents an expanding “National Framework Dataset” that provides baseline information on microbial communities from Australian and Antarctic soils and allows exploration of the determinants of these microbial properties at a continental scale.

This dataBASE has been designed to capture the diversity of soil bacterial, archaeal and eukaryotic communities and so far has collected over 1000 individual soil samples. The data comprises 16S rRNA gene bacterial and archaeal sequences, fungal ITS sequences and 18S rRNA eukaryotic sequences and non-amplification derived metagenomic sequences (using a MiSeq sequencer). Each soil sample, collected according to a standardised protocol (www.bioplatforms.com.au/special-initiatives/environment/soil-biodiversity) also generates a rich suite of edaphic variables (moisture; texture; ammonium and nitrate content; total nitrogen, phosphorus, potassium, sulphur, total carbon, organic carbon, conductivity, pH, copper, iron, manganese, zinc and exchangeable cations and soil particle size) as well as non-edaphic site variables (elevation, slope, aspect), regional climate variables, overlying plant community composition and detailed land-use history. These samples represent diverse biomes (eg agricultural land, desert, rainforest, grassland, coastal heathland, savannah), different geographic regions (tropical, subtropical, temperate, polar) and a wide range of edaphic and climate characteristics. There have been few attempts to collect microbial data to populate diversity databases in such a systematic and controlled way with all chemical and molecular analyses carried out in a single laboratory, ensuring reproducibility and inter-sample comparability.

We will present the dataBASE and its repository and demonstrate how it is being used to model, map and ultimately to manage Australia’s diverse soil ecosystems.

Keywords: Biomes, Soil, Diversity, Metagenomics

Poster session 1

[P1.002]

Bioindicative assessment of soil quality in ecosystems of Mt. Kilimanjaro depending on land use

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Soil microbial biomass and microbial activity are crucial parameters of belowground processes in terrestrial ecosystems. A better understanding of soil microbial processes and activities enable to predict the long-term responses of ecosystems to changes in land use and soil management. Here, we measured soil microbial biomass (SMB), the ratio of microbial biomass carbon (C_{mic}) to total organic carbon (C_{org}), the mineralization quotient (qM) and the metabolic quotient, i.e. the specific soil respiration of the microbial biomass ($q\mathrm{CO}_2$) as eco-physiological indicators of soil quality. Soils from four ecosystems: savannah, maize fields, *Chagga* homegardens and lower montane forest presenting two natural and two agriculturally used ecosystems at Mt. Kilimanjaro, Tanzania. The percent C_{mic} in C_{org} ranged between 0.72% and 3.11%, and was lowest in lower montane forest soils and highest in maize fields. The C_{mic}: C_{org} ratio was higher in agroecosystems (maize fields and homegardens) compared to natural ecosystems (savannah and lower montane forest) located at the same elevation. Total SMB content was higher in soils from natural ecosystems compared to agriculturally modified ecosystems. In contrast, mineralization quotients were higher in agricultural soils compared to that in natural ecosystems. $q\mathrm{CO}_2$ values were higher in soils from ecosystems located at a lower elevation (savannah and maize fields) compared to those located at higher elevation (lower montane forest and *Chagga* homegarden). The high MBC content and correspondingly low $q\mathrm{CO}_2$ in lower montane forests and homegardens strongly suggests that these soil ecosystems are more stable and resilient. We conclude that the *Chagga* homegardens are offers the best compromise for sustainable agricultural land use in Mt. Kilimanjaro, Tanzania.

Keywords: Indicators of soil quality, Agroforestry, Soil microbial biomass, Mt. Kilimanjaro

[P1.003]

Review of Biodiversity in Sulphur Oxidizing Microorganisms

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Sulphur Oxidation Biotechnology is important in all parts of the world. Sulphur is using in different industries e.g. mining, Oil, Agriculture and any other industries. Many microorganisms are oxidizing sulphur for example *Archaea and Eubacteria*. They are chemolithotrophic or heterotrophic microorganisms. Fungi is one of Sulphur Oxidizing Microorganisms in ores.

Diversity of Sulphur Oxidizing Microorganisms in soil is studding based on DNA extraction, polymerase chain reaction and gen sequencing. In this paper, it were presented biodiversity of these chemolithotrophic organisms in acid mine drainage, hit spring and soils. Based on results, they are kinds of Sulphur Oxidizing Microorganisms in Iran. *For example, Thiobacillus spp*, is famous genus in every ecology. *Acidithiobacillus*, *Thermithiobacillus* and *Halothiobacillus* are found in acid mine drainage, hot springs and saline soil.

But other genus too, may be determined in these ecosystems. For example, *Sulfobacillus spp*. is sulphur oxidizing *archeae* in hot spring. *Thiomonas spp*, *Leptospirillum spp* and *Thiobacillus spp* are sulphur oxidizing bacteria in soil. The aim of this study was ecology diversity of sulphur oxidizing microorganisms in different ecosystems and compared them. We results that it was correlated between strains sources of isolated and strain diversity. This Sulphur Oxidizing Microorganisms biodiversity caused these growths in different conditions, e.g. temperature, acidity, salinity so; these can be suitable microorganisms for such conditions. These results will be applicable for better use from microorganisms in many industries now.

Keywords: Sulphur, Oxidizing, Microorganisms

[P1.004]

Germany x Brazil: GHG and microbiology - a comparative of soil under country - specific legume cultivation

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The conversion of land for cultivation of energy crops in Europe and the simultaneous demand for soybean (e.g. As animal feed) have an impact on land use and management in non-European countries, such as Brazil. Changes of land use come along with inevitably alterations in the carbon and nitrogen cycles of the soil. This consequently affects, among other things, the microbial activity in the soil and therewith the emission of greenhouse gases (GHG). In this study we compared microbial number and measurements of GHG emissions (CO_2-C, N_2O-N, CH_4-C) from two soils under legume cultivation in Germany and Brazil. The legumes were country-specific, which means pea cultivation (*Pisum sativum*) in Germany and soybean (*Glycine max*) in Brazil. In general, pea is a typical catch crop, but on the studied plot (Bad Lauchstädt, Saxonia-Anhalt) it was grown permanently, in Brazil soybean is the most important catch crop, is cultivate during October until February. Microbiology account and GHG measurements were made during an incubation experiment in the laboratory, in August 2013. Emissions from soil under soybean cultivation were measured in central Brazil (Campo Verde, Mato Grosso) from October/2013 until February/2014. First results do not show huge differences in the amounts of microorganisms number and emissions from both soils. The total bacteria was, in average, $1,1 \times 10^5$ in Brazil and $2,6 \times 10^6$ in Germany, and total fungi was $1,1 \times 10^4$ in Brazil $9,2 \times 10^3$ in Germany (CFU g $solo^{-1}$). As expected, emissions of N_2O-N were higher compared to soil under cultivation with winter rape. This can be explained by the ability of legumes to fix nitrogen in the soil. In terms of total microbiological number the soils were very similar, too, but it can be stated that in general the diversity of microorganisms is higher in Brazilian soils.

Keywords: C/N, land use, soil-plant-atmosphere

[P1.005]

Agroforestry systems in the north of mato Grosso (Brazil): The microbiological dynamic in the soil

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The adoption of conservation tillage systems and soil management and tillage systems integration have emerged as an alternative to contribute to the environmental sustainability of agroecosystems. The management systems that integrate crop-livestock-forest management (iCLF) aim to reduce environmental degradation and maintain sustainable productivity for a longer period of time. The aim of this study was to quantify the number of colony forming units of total bacteria and fungi in soil under iCLF system installed five years ago in the northern region of Mato Grosso state, Brazil. The samples were collected in 5 treatments in May 2012 and 2013, at a depth 0-10 cm. To determine the microbial community the method of serial dilution and plating on selective medium was used. The treatment under eucalyptus (double row) showed a higher number of colonies of bacteria and fungi in the two years evaluated, with 6.3×10^5 and 7.5×10^4 CFU g $soil^{-1}$ for bacteria and fungi, respectively. However there was a decrease in the number of microorganisms in all treatments in 2013 compared to 2012, regarding the same treatment (2.3×10^5 and 8.6×20^3 CFU g $soil^{-1}$ for bacteria and fungi, respectively). Since 2011 the treatments, except the forest, were grazed by cattle. Moreover, the amount of precipitation in 2011 was almost the double comparing the precipitation in 2012. These two factors could explain the high number of microorganisms in the year 2012 in all analyzed systems. We concluded that the amount of precipitation and the management are responsible for visible changes in the number of microorganisms in the soil and affected the microbial activity, as well.

Keywords: bacteria and fungi, integrated system, land use

[P1.006]

Protist diversity and function in soils

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I will review our modern conceptualization of protist diversity that I published for the Int. Soc. Protistology in 2012, focusing on lineages that occur in soil, with example of what these organisms are and their function in soils. I will review the discussion on why the published data indicate that protist species are not distributed everywhere, but consist mostly of rare local species. This highlights limitations of microscopic identification based on morphology and emphasizes extensive cryptic diversity within morphotypes. We published estimates of expected number of terrestrial protist species, and I will focus on where the estimates are inaccurate and how they will be improved. We tabulated all ~200 primers typically used in protist identification through SSU sequence analysis, to analyse their specificity and utility in environmental genomics. I will describe how this information can improve primer selection for different target lineages by considering the non-target lineages that are also amplified, when planning environmental genomics projects. I will show example environmental genomics data and the taxonomic resolution that can be obtained.

To understand what all this protist diversity does in the soil, we have used radioactive isotopes and stable isotopes to look at food web interactions. In published protocols and experiments we have described some of the interactions with nematodes and microarthropods. I will show example data to reflect on some of the conclusions. It is clear that feeding on protists is more extensive and widespread than previously known. Using functional response curves, we have detailed growth rates and feeding rates of many species on various bacteria or protists. This data allows us to estimate the contribution of protists to mineralization and nutrient transfer in soils. From these calculations the contribution of protist to soil respiration and bacteria turnover can be estimated, and extrapolated to biogeochemical scales.

Keywords: protist, food web, diversity, genomics

[P1.007]

Invasion by Conyza canadensis (L.) Cronq. alters activity of soil enzymes in Kashmir Himalaya, India

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Despite widespread occurrence and abundance of *Conyza canadensis* in Kashmir Himalaya, limited information exists about its impact on the soil microbial communities and activity of soil enzymes. Hence, we assessed the impact of *C. canadensis* invasion on activity of various soil enzymes across variable sites at three developmental stages (pre-flowering, flowering, and post-flowering). Results revealed that activity of all soil enzymes (protease, acid and alkaline phosphatases, urease and asparaginase) was negatively influenced by *C. canadensis*, invertase being the only exception. Soil microbial biomass as well as soil microbial activity also decreased in the invaded patches. These results allowed us to conclude that invasion by *C. canadensis* alters functional attributes of soil in Kashmir Himalaya.

Keywords: Alien plant invasion, Conyza canadensis, Soil enzymes, Soil microbial biomass

[P1.008]

Belowground carbon allocation by plant functional groups and soil type alter microbial community composition and nutrient cycling in tropical Eucalyptus plantations

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We studied the influence of plant functional groups on soil microbial community composition and nutrient cycling in a tropical Eucalyptus forest ecosystem with different plantation age and soil types by means of stem girdling (SG) and understory removal (UR). Fungal and bacterial communities were characterized using phospholipid fatty acids, and ectomycorrhizal fungi (EMF) colonisation was estimated visually. Total bacterial and saprotrophic fungal biomass was highest in soils treated with SG, followed by UR, through modification of plant belowground C allocation and N supply. EMF root colonisation, biomass of EMF, arbuscular mycorrhizal fungi (AMF) and the fungal-to-bacterial ratio were lowest in these soils. We found that EMF, AMF and the fungal-to-bacterial ratio were highest in sandy loam soils with a high C/N ratio and low pH. The fungal-to-bacterial ratio was higher in 5-year-old than in 15-year-old plantation. We propose that girdling of trees and removal of understory plants are important ecological components, due to their modification of plant belowground C allocation and N supply as key determinants of microbial community composition. Our results highlight the fact that soil abiotic factors play an important role in shaping the microbial community and nutrient cycling in tropical forest ecosystems.

Keywords: girdling, microbial community composition, mycorrhizal fungi, plant-soil relationship

[P1.009]

Effects of eucalyptus plantations in termite species richness

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The Brazilian Cerrado (savanna) biome is considered one of the 25 hotspots in the world with approximately 30% of the biological diversity of Brazil. In this biome, termites also have a great diversity. Moreover, the termites have ability to adapt to many different types of habitats, from humid forests to semi-arid environments. The objective of this study was to analyze the effect of eucalyptus plantation on the termites diversity in a new planting area, eucalyptus abandoned for 25 years, and native Cerrado (control). The study was carried out in the eucalypt plantations in the municipality of João Pinheiro (17º56'49.1" S; 46º05'50.5"W), Southeast Brazil, where the native vegetation consists of Cerrado, with average altitude of 889 m and annual average temperature of 24.3˚C. The modified transect sampling methodology of Jones & Eggleton (2000) was used in the systems; three transects of 20x2m in each system; with assessments at 90 days before and 90 and 180 days after planting the seedlings. We used generalized linear models (GLMs) to examine differences in richness per sampling points between systems. If significant, factor levels were compared through contrast analysis by aggregating level and comparing deviance change. All analyses were performed with R software. Fifty-three termite species belonging to the families Termitidae (96%) and Rhinotermitidae (4%) were found. The contrast analysis models showed that the observed richness did not differ among systems at the first assessment time (90 days before), but there were variation in subsequent times, between areas newly cultivated and uncultivated (eucalyptus abandoned for 25 years and Cerrado) (Figure 1). The results indicate no difference in the diversity of termites from Cerrado and 25 years after the abandonment of farming activities with eucalyptus, but the management for eucalyptus planting have impact in termite diversity.

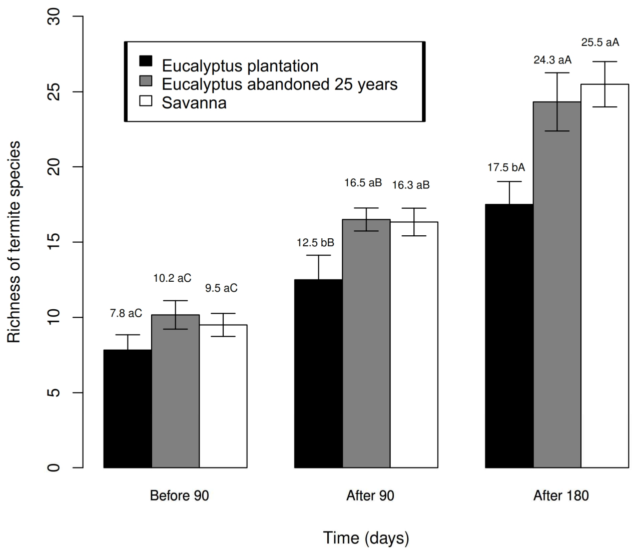

Figure 1. Richness of termites species at 90 days after, 90 days before and 180 days after planting in three systems (new planting area, eucalyptus abandoned for 25 years and native Cerrado). (Lowercase letters represent systems in the same time and capital same system in the time).

Keywords: eucalyptus, survey termite diversity, sampling termites, wood production impact

[P1.010]

Association of arbuscular mycorrhizal fungi on growth and nutrient assimilation of pioneering plants growing on nutrient-limited river bank soil

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An experiment was conducted to find out the effects of arbuscular mycorrhizal fungi (AMF) on the growth and nutrient absorption of pioneer plants growing in the soil collected from early succession area of Arakawa River bank, Kumagaya city, Saitama Prefecture, Japan. Three herbaceous plants, *Pharagmites japonica* (Gramineae)*, Miscanthus sacchariflorus* (Gramineae)*, Polygonum cuspidatum* (Polygonaceae) were selected for our experiment due to their vigorous growth and highly dense population in river banks. Spores (*Gigaspora margarita*) were collected from the commercial product namely 'Serakinkon' which was purchased from the central glass company, Tokyo, Japan. The initial colonizer *P. cuspidatum* showed very low level of AM colonization (0.2%-0.5%) whereas the average colonization level of *P. japonica* and *M. sacchariflorus* were 24-33% and 23-28% respectively. AMF colonization increased the chlorophyll content, plant dry mass, N, P, K, Mg, and Fe concentration of the *P. japonica* and *M. sacchariflorus* plant's roots, stems, and leaves when applied with natural and sterilized soil. In all cases, maximum values showed when *P. japonica* and *M. sacchariflorus* plants were applied with natural soil in combination with AMF, but Ca concentration decreased as colonization level increased. N retention of *P. japonica* and *M. sacchariflorus* plants from the soil were significant when colonization level was high. *P. cuspidatum* showed no or a negative response to AM colonization in all cases except chlorophyll content. So, AMF have some potential effect on river bank vegetation growth especially for *P. japonica* and *M. sacchariflorus*.

Keywords: Arbuscular mycorrhizal fungi, Phosphorus, Nitrogen, Primary succession area

[P1.011]

Assessing soil biodiversity: sampling and replication trade-offs

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Collecting soil biodiversity data is often expensive and time-consuming. Quantifying the trade-offs between the sampling effort and the quality of biodiversity assessment is an important part of research framework. Similarly, selecting an appropriate spatial scale when designing experiments is of crucial importance for soil biodiversity research, as many groups display spatial dependence and spatially structured diversity patterns at small and intermediate scales. Spatial autocorrelation in soil biodiversity data violates the assumptions in inferential statistics and affects the results of classical tests of significance and regression analysis. Correct replication, estimation of required sampling effort and knowledge of underlying spatial variability in community structure and abundance of soil fauna are essential for soil biodiversity assessment.

Using real data, we illustrate diversity patterns in communities of soil mites (Acari: Oribatida), and the implications of these patterns for trade-offs in biodiversity assessment. Sampling effort is discussed in relation to sample-based rarefaction curves from different environments. The distribution patterns at the metacommunity level are analyzed as the decay in community similarity with increase in intersample distance. The results are used to provide methodological suggestions for sampling effort, replication, and spatial layout of soil biodiversity studies involving Oribatida.

Keywords: biodiversity assessment, Oribatida, sampling effort, distance decay

[P1.012]

Diversity of methanotrophic bacterial transcripts in boreal mesotrophic fen using stable isotope probing of RNA with next-generation sequencing

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Boreal peatlands store about 30% of global soil carbon and are a significant source of powerful greenhouse gas, methane (CH4). When CH4 produced by methanogenic archaea in anoxic peat layers reaches the upper oxic part, methanotrophic bacteria (MOB) oxidize a part of it to carbon dioxide (CO2). Yet MOB are important biological brakes of climate warming, still little is known about the most metabolically active MOB and their diversity in boreal peatlands. In order to study the functional MOB, we took six peat core samples from the mesotrophic fen-type site of Lakkasuo peatland complex located in the middle of Finland. We cut cores into 10 cm sub-samples and determined the potential methane oxidation activity from them. Sub-samples from 0-10 cm layer (from the peat surface) that exhibited the most active oxidation rates were selected for stable-isotope probing (SIP) experiment. Samples were incubated with 13CH4 followed by nucleic acids extraction. DNase treated samples were subjected to isopycnic density gradient centrifugation with cesium trifluoroacetate (CsTFA) to isolate fractions that originated from metabolically active MOB which have incorporated 13C-label into their nucleic acids. Total RNA was isolated from chosen fractions by isopropanol precipitation. Samples from fractions were pooled and subjected to ribosomal RNA removal with Ribo-Zero Magnetic Kit for Bacteria. Transcripts were amplified and reverse transcribed with Ovation RNA-Seq System V2 kit followed by fragmentation and next-generation sequencing with Illumina's NextSeq 500 sequencing system. Results that we will obtain from NSG data will reveal transcripts and the diversity of metabolically active MOB in boreal peatland samples.

Keywords: methanotrophs, peatland, transcript, NGS

[P1.013]

Open invitation to methanotrophic bacteria by peatland Sphagnum mosses

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I will summarize the following publications

Larmola T, Tuittila E-S, Tiirola M, Nykänen H, Martikainen PJ, Yrjälä K, Tuomivirta T & Fritze H 2010. The role of Sphagnum mosses in the methane cycling of a boreal mire. Ecology 91: 2356-2365. doi.org/10.1890/09-1343.1

Putkinen A, Larmola T, Tuomivirta T, Siljanen H, Bodrossy L, Tuittila E-S & Fritze H 2012. Water dispersal of methanotrophic bacteria maintains functional methane oxidation in Sphagnum mosses. Frontiers in Terrestrial Microbiology 3:15. doi: 10.3389/fmicb.2012.00015

Larmola T, Leppänen S, Tuittila ES, Arva M, Merilä P, Fritze H & Tiirola M 2014. Methanotrophy induces nitrogen fixation during peatland development. Proceedings of the National Academy of Sciences of the United States of America 111: 734-739. doi:10.1073/pnas.1314284111

Putkinen A, Larmola T, Tuomivirta T, Siljanen HMP, Bodrossy L, Tuittila ES & Fritze H 2014. Peatland succession induces a shift in the community 1 composition of Sphagnum associated active methanotrophs. FEMS Microbial Ecology 88: 596-611. DOI: 10.1111/1574-6941.12327

to show the importance of ecosystem services, C and N acquisition to *Sphagnum* mosses, provided by methanotrophic bacteria in peatlands.

Keywords: Sphagnum moss, methanotrophs, C-cycle, N-cycle

[P1.014]

Tripmarks- is everything everywhere?

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Microbial biogeography has long been and is still influenced by the hypothesis of a microbial cosmopolitanism meaning that everything is everywhere, but, the environment selects. A number of studies were able to confirm the existence of globally occurring species. However, a general cosmopolitanism of microorganisms is arguable taking into account appearing geographical patterns and applying high resolving molecular and fingerprinting methods. High costs and questionable feasibility of global sampling cause many studies to be carried out based on models.

Here we benefit from the bicycle trip of an artist sampling soils on a route from Austria to Laos (www.tripmarks.at) and relate the communities of inherent fungi, ammonia-oxidising bacteria and actinobacteria to environmental as well as medium- and large scale spatial patterns.

We first generate spatial variables applying the large scale trend surface analysis and the finer-scale Principal Coordinates of Neighbour Matrices. Then we check for influences using variation Partitioning and combine all variables in the descriptive Canonical Correspondence Analysis.

Our results show that the variability in all investigated microbial groups is to the greatest extent owed to environmental and not spatial patterns. Clearly distinct communities in soils of far apart lying sampling sites are formed for AOB, but not for actinobacteria and fungi. Furthermore, cosmopolitan species with relative abundances as high as 80.5% (fungi) 74.0 % (actinobacteria) and 68.0% (AOB) have been detected. These findings show that Eurasian soil microbial communities are following environmental rather than spatial constraints, highlighting the unequal influence of all concerned variables on different organisms and sites and strengthening the assumption of a global distribution of microorganisms.

Keywords: microbial cosmopolitanism, PCNM, variation partitioning, trend surface analysis

[P1.015]

Using metagenomics to investigate microbial mechanisms underlying climate change-associated carbon release from peatlands.

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Peatlands contain a third of global soil carbon, but are threatened by anthropogenic climate change, including a potential increase in drought events. Drought leads to a well-documented release of carbon dioxide from peat, which is thought to result from increased activity of microbially derived phenol oxidase enzymes. Phenol oxidases degrade inhibitory phenolic compounds, which accumulate under waterlogged conditions. It is well established that drought affects microbial community composition, but so far, insights into the taxonomic and functional mechanisms underpinning the release of carbon have been limited by the approaches employed. Over the last 25 years, a number of DNA-based techniques for elucidating microbial community characteristics have been developed, including earlier ‘fingerprinting’ techniques (e.g. ARISA) and more recently, metagenomic and SSU rRNA gene amplicon-sequencing approaches. In particular, metagenomic sequencing can be used to identify functional genes and infer environmental metabolic pathways, potentially leading to a greater understanding of the functional mechanisms of ecosystem responses to external stressors. During this project, temporally-explicit drought manipulations will be carried out in different peatland habitats using controlled mesocosms and a field experiment. ARISA fingerprinting will be used to initially delimit radical shifts in microbial community composition, in order to identify key samples for amplicon and shotgun metagenomic sequencing. Replicated metagenomics will be complemented by biogeochemical assays to help understand the mechanisms underpinning the release of carbon. Here, results are presented from ARISA fingerprinting of bacterial and fungal components of the microbial community during drought in three peatland habitats, along with corresponding biogeochemical data. This will be the first time peat microbial communities have been monitored over the course of a drought experiment, and the first results to show the response of fungi to drought in bog and fen habitats.

Keywords: Peatlands, Drought, Phenol oxidase, ARISA

[P1.016]

Soil nematofauna as indicator of the effect of agricultural practices on soil biological functioning in apple orchards

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We present results of the Bioindicator French Program which assesses soil organisms as soil quality bioindicator (ADEME: http//www.ecobiosoil.univ-rennes1.fr/ADEME-Bioindicateur) and which reveals the interest of soil nematodes (www.elisol.fr).

The aim of this presentation is to show how the biological state of soil can be assessed by the soil nematofauna, using an example: French orchards.

The three orchards, planted in 2005, located in the Rhone valley, were trained as commercial orchards. They differed for plant protection and fertilisation, and were managed as follow:

(1) CV= Conventional (reference): chemical pesticides were mainly used to control pests, diseases and weeds with mineral fertilization;

(2) LI= Low-input: preference was given to other protection methods than chemicals (mating disruption, sanitation practices…) with mineral fertilization;

(3) OF= Organic Farming: no synthetic inputs.

Within each system, two cultivars were tested: (1) Smoothee: susceptible to scab (reference), (2) Ariane: scab resistant cultivar.

The nematodes were extracted by elutriation from soil samples taken in March 2010, according to ISO 23611-4 method. Abundances of nematode families, trophic groups and indices were calculated.

Significant differences in nematofaunal communities were observed between systems (P <0.001) and between cultivars (P <0.012) (PERMANOVA analysis). Phytophagous nematodes tended to be less abundant in CV than in the two other systems. Free-living nematodes tended to be less abundant in the Smoothee orchards than in the Ariane orchards for LI & OF. We can highlight for CV a trend towards higher abundance of bacterial-feeder (especially Rhabditidae). The enrichment index (EI) tended to be higher in CV (60) than in the other two systems (45-50). The structure index (SI) was higher in LI (55) than in CV (40).

The different practices linked with the 3 systems and the two cultivars led to different soil biological states, which can be described and analysed by the changes in the nematofauna composition.

Keywords: bioindicator, nematodes, agricultural practices, comunities

[P1.017]

Soil biodiversity and the stability of multiple ecosystem functions

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Soil microbes, although for the most part unseen, represent the largest portion of life on this planet and are crucial for the functioning of terrestrial ecosystems. But, soil community composition is dependent on soil history and may consequently alter the sensitivity of soil communities to biodiversity loss. Increased biodiversity supports ecosystem functioning as different organisms perform dissimilarly when abiotic conditions fluctuate over space and time. However, the ability of diverse soil communities to maintain multiple ecosystem functions in the face of a changing climate is not well known. We focused on understanding the link between soil community composition and diversity as a mechanism for stabilizing multiple ecosystem functions. To do this, soil was collected from three sites with varying soil histories. Within each we created a soil community diversity gradient based on species body size. Multiple ecosystem functions were traced over a one-year period for each soil community planted with a standard grassland plant community in self-contained microcosms. A reduced water regime was applied at regular intervals as a fluctuating environmental condition so that the stability in overall ecosystem performance could be assessed in relation to soil community composition and soil biodiversity loss.

Overall, greater soil biodiversity was found to improve plant productivity and diversity, decomposition of organic matter, C sequestration, and N turnover between above and belowground systems. Moreover, greater soil biodiversity improved the stability of many of these ecosystem functions. Our results are the first to link biodiversity stability theory in belowground communities with aboveground ecosystem stability. Understanding this relationship is a field of study that will become increasingly relevant, as variability in environmental conditions is predicted to increase around the globe.

Keywords: Soil Biodiversity, Ecosystem Functioning, Stability, Global change

[P1.018]

Fungi inhabiting decaying Norway spruce logs: species diversity and habitat preferences determined by 454 sequencing

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Fungi are the most important decomposers in boreal forests and they are used as forest biodiversity indicators. Along with tree decay, wood density decreases and fungal species change. Studies on fungal succession and habitat preferences have traditionally based on fruit bodies on logs classified to different decay stages and concentrated on polypores species, meaning that many species have escaped detection. Lately DNA-based high-throughput sequencing has enabled detection of basically all wood-inhabiting species.

We studied fungal community inhabiting decaying *Picea abies* logs by using pyrosequencing. Our aim was to model habitat preferences of common species in respect of wood density. Altogether 535 logs from five unmanaged forest sites in Southern Finland were sampled to represent the whole decay succession from recently fallen until heavily decayed trees. DNA was extracted from sawdust, amplified and sequenced by using 454 GS FLX System. Obtained raw data (500908 fungal-ITS1 reads) was processed by Mothur software. The responses of fungi on wood density gradient were modelled with generalized additive mized models.

Sequence data split to 932 OTUs (97% similarity) and fungal richness peaked in smallest density, i.e. in most heavily decayed wood. Most of the reads were identified as Basidiomycota (76%) and Ascomycota comprised 14% of reads. White and brown rotters both comprised 13% of reads whereas mycorrhizal fungi, which preferred heavily decayed wood, covered even 12% of reads. Observed species habitat preferences were mostly consistent with previous fruit body findings. Abundance of the most common identified species *Coniophora olivaceae* decreased with decreasing wood density, whereas *Xeromphalina campanella* peaked in most decayed substrate and *Phellinus viticola* had optima at mid-decay phase. Altogether we modelled abundance of 42 species or genera as function of wood density. These predictive models can be linked to wood decomposition models and forest stand simulators that are used in forest planning.

Keywords: wood-inhabiting fungi, decomposition, wood density, Picea abies

[P1.019]

Effects of irrigation, effluent dispersal and dairy conversion on soil quality and earthworms in New Zealand pastures

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New Zealand pastoral farming is undergoing intensification. This is notable in Waimate District, a drought prone region that was traditionally associated with extensive sheep farming, but which is now converting to intensive dairying supported by irrigation and effluent dispersal. We investigated the effects of this intensification on earthworms and soil quality across six treatments: (a) dairy pastures with (i) added effluent, (ii) added water through irrigation, (iii) effluent and water added together, and (iv) neither water nor effluent added; and (b) sheep/beef pastures (v) without irrigation, and (vi) with irrigation. Altogether 615 sites were sampled in 205 paddocks from 41 farms. Four earthworm species were observed dominated by *Aporrectodea caliginosa*. Maximum earthworm density occurred where both effluent dispersal and irrigation occurs. *Aporrectodea longa* appeared to be driven locally extinct in irrigated soils. Nutrients levels were highest in irrigated and effluent treated soils and lowest in the untreated ‘control’ soils. Irrigation and effluent dispersal reduced soil bulk density. There were reduced nutrient levels and more compact soils in land converted to dairy production but this effect is slight when irrigation accompanies farm conversion. Soils had higher water holding capacity where earthworms were abundant but there was no evidence of direct relationships between earthworm abundance and soil quality measures. This calls into question the utility of earthworm abundance as an indicator to guide sustainable soil management. Further, the comparative lack of anecic worms in irrigated soils calls for urgent research to assess its implications for farming sustainability.

Keywords: earthworms, soil quality, irrigation, effluent dispersal

[P1.020]

Impact of drought on soil microbial diversity with special reference to Phosphate solubilising microbes in different agro-ecosystems of Kachchh, western India

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Introduction

Phosphorus (P) is an essential plant nutrient. Although abundant in soils in both inorganic and organic forms, it is frequently a major limiting factor for plant growth as it is in an unavailable form for root uptake. Given that most soils are deficient in plant-available P and that P fertilizer represents a significant cost for agricultural production throughout the world, there is interest in using soil microorganisms as inoculants to mobilize P from poorly available sources in soil. Phosphate solubilizing microorganisms (PSM) can solubilize and mineralize P from inorganic and organic pools of total soil P and make it plant available. The present study was undertaken in Kachchh, western India which is a very unique ecological zone in terms of unique topography, seismic instability and erratic rainfall. These factors affect the agriculture in this area which is dependent mainly on rains.

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Methodology: Agricultural fields practicing different amendment practices were earmarked and for three years with different rainfall patterns the rhizospheric soils were analysed for TMC (total microbial count), PSM (Phosphate solubilising microbes), and available and total P status.

Results: The results demonstrated that organically amended farms were able to maintain good soil health in terms of PSM and beneficial soil microbes as compared to integrated farming systems which had a high dependence on chemical fertilizers and this holds true even for stressed conditions like drought. Moreover the organically amended soil exhibited good soil nutrient dynamics for all three years.

Conclusion: This study points to the idea that maintaining a good soil microbial diversity even during stressed conditions as drought can go a long way in maintaining a good soil health and eventually the yield and quality of produce. This study supports the central idea of organic based farming for a sustainable ecosystem.

Keywords: Phosphorus, microorganisms, soil, agriculture

[P1.021]

Nematode food web diversity as tool to assess soil processes and function

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Nematode assemblages in soil reflect substrate texture, climate, biogeography, organic inputs and anthropogenic disturbance. Nematodes use a wide range of resources and their diverse biological interactions result in a key role in soil food webs. By addressing the changes in horizontal as well as vertical food web diversity the nematode faunal analysis concept allows to determine soil conditions and health, e.g. major decomposition pathways, nutrient status or disturbance. Thus nematodes are an ideal group to assign ecosystem processes.

Changes in land use and its intensity are important determinants of biodiversity. Shifts in forest management, i.e. tree species identity and diversity, affect proportions of readily decomposable to recalcitrant compounds via related shifts in litter composition. Such resource diversity at the base of the soil food web is highly relevant for population dynamics and trophic complexity, and thus consumer diversity. However, the functional importance of biodiversity is often unclear due to the overriding effects of different management strategies. Therefor the nematode food web structure was investigated in: i) a large scale study on increased land use intensity, i.e. from natural to managed forest stands, and ii) a tree diversity experiment with six species representing different litter quality (ash, lime, beech, oak, spruce, pine) and arranged in five diversity levels (1, 2, 3, 5, 6 species mixtures). In this diversity manipulation study, nematode communities showed only weak interactions with tree diversity but distinct relation to the presence or absence of specific tree species. In the observational study, nematode faunal analysis revealed disturbance by land use as well as regional effects (e.g. local climate, soil type) on soil conditions. The observed changes within and across trophic levels likely shape decomposition processes and in turn energy flow and ecosystem functioning.

Keywords: food web diversity, forest tree diversity, decomposition pathways, nematodes

[P1.022]

Distribution patterns of fungi and bacteria in saline soils

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Saline soils are environments characterized by uneven temporal and spatial water distribution and localized high concentrations of salts. Spatial distribution patterns of fungi and bacteria in saline soils, and the link between microbial community dynamics and salts accumulation are critical issues throughout the world (Ettema, Wardle 2002).

This study was focused on spatial distribution patterns of soil fungi and bacteria in a saline soil located in *Piana del Signore* (Gela, Italy) where some ecological variables acted as shaping factors in aboveground and belowground communities distribution. Bacterial, archaeal, and fungal communities diversity and distribution in ten soil sites (A horizons, 0-10cm), were characterized by 16S rDNA genes with T-RFLP method. Pyrosequencing-based analysis of the V2-V3 16S rRNA gene region was performed to characterize the sites on the basis of bacterial groups distribution, diversity and assemblage. To better investigate the ecological niches of some of the main culturable species of this environment, it was carried out the isolation and identification of the fungal flora from soil, using Warcup plating within two different salt concentrations (NaCl 5% and 15%), combined with a metabolic screening of some representative isolates (Di Lonardo et al., 2013).

A natural gradient of soil salinity shaped the distribution of microbial species in the environment. The different concentration of salt (NaCl), and calcium sulfate (Ca2SO4) in soil influenced the structure and distribution of the microbial communities even when comparing neighboring areas within a 50 m scale.

Some bacterial phyla, together with some fungal species, appeared spread in the whole area, independently of the salinity gradient, thus highlighting the presence of organisms with a very different survival strategy in such an extreme environment.

In conclusion, the organization and diversity of microbial taxa at a spatial scale reflected the scales of heterogeneity of physical and chemical properties of the habitat under investigation.

Metabolic profiling reveals a functional succession of active fungi during the decay of Mediterranean plant litter. Soil Biology & Biochemistry 60, 210-219.

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Keywords: spatial distribution pattern, bacterial diversity, fungal diversity, Pyrosequencing

[P1.023]

Selecting cost effective and policy-relevant biological indicators for European monitoring of soil biodiversity and ecosystem function

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Introduction – There is a demand for reliable tools to design and implement strategies for sustainable management of soils, including the design of policy-relevant and cost-effective indicators for monitoring soil biodiversity and ecosystem function. Our goal, which forms part of an EU-funded project called EcoFINDERS, was to develop and evaluate novel approaches for monitoring of soil biodiversity and functioning across a broad range of European environments and land-use systems.

Methods – Eighteen existing and potential biological indicators were selected using a logical sieve approach, combined with meta-analysis of European soil monitoring schemes. All indicators were evaluated at six, long-term field sites offering replicated plots of different agricultural management scenarios. The sites covered the major European climatic zones and land use types, while the replicated treatments spanned a wide range of management intensification. Soil sampling was standardised and coordinated across all sites.

Results – The response of the indicators was analysed with respect to the intensity gradient of applied treatments. All the indicators tested were sensitive between the different sites, but showed variable sensitivity to the imposed management practices. Preliminary analysis showed greater effects of intensification on biodiversity and function in arable than grassland systems.. Cost-effectiveness of the indicators was assessed from their labour intensity, practicability and ease of interpretation.

Conclusion – Results clearly demonstrated strengths and weaknesses to each type of indicator, confirming that no single indicator will be appropriate for a large scale monitoring scheme. A scheme should aim for the lowest number of indicators in order to be efficient with limited resources, but with enough power to address the specific question. Some of the developing methods, especially next-generation sequencing and functional gene analysis, look increasingly favourable from cost-effective and ease of interpretation perspectives. The ‘toolkit’ of biological indicators can be adapted according to the priorities of the monitoring scheme.

Keywords: Monitoring, Indicators, Land use intensity, Sustainability

[P1.024]

Morphological diversity in the black garden ant: shifts in energy allocation along metal-pollution gradient?

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Morphological traits and body size of soil invertebrates can be affected by environmental metal pollution. In many already reported works body size decreased, in some species body size reminded unchanged, rarely it increased along pollution gradient. Ants are more morphologically diversified than non-social insects because different casts coexist in each colony. In this study we analyzed the relationship between the pollution level and the dry mass of pupae of workers, females and males as well as in the imago stages in the black garden ant *Lasius niger*. W assume that body size of each cast along the pollution gradient may decrease reflecting the toxic effect of pollution. It is also likely that each cast reacts differently that can be a part of colony-level tolerance. The analysis showed significant differences between the casts and developmental stages, but in each case the body mass reminded unrelated to metal pollution. We showed that pollution did not affected body size of any cast of *Lasius niger.* As no cast increased its body size, there is no evidence of shifts in energy allocation. Strong explanatory significance of colony factor supports previous works that showed strong genetic component of the body size of *Lasius niger*.

This study was supported by The National Science Center (NCN), grant 2011/01/D/NZ8/00167 and University of Agriculture, BM 4220.

Keywords: metal pollution, ants, morphology

[P1.025]

Functional diversification within bacterial lineages promotes wide functional overlapping among taxonomic groups in a Mediterranean forest soil

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We investigated the relation between taxonomy and functioning of soil bacterial communities in soils from a Mediterranean Holm-oak forest using a high throughput DNA pyrosequencing technique. We used non-parametric tests (U Mann-Whitney) to evaluate the sensitivity of each single bacterial genus within the community to the fluctuations of plant physiological and environmental abiotic variables, as well as to fluctuations in soil microbial respiration. Within-lineage (phylum/class) functional similarities were evaluated by the distribution of the Mann-Whitney standardized coefficients (z) obtained for all genera within a given lineage. We further defined different ecological niches and within-lineage degree of functional diversification based on multivariate analyses (Principal Component Analyses, PCA). Our results indicate that strong within-lineage functional diversification causes wide functional overlapping among lineages, which hinders the translation of taxonomic into a meaningful functional classification of bacteria. Our results further suggest a wide colonization of possible ecological niches as taxonomic diversity increases. While no strong functional differentiation could be drawn from the analyses at the phylum/class level, our results suggest a strong ecological niche differentiation of bacteria based mainly on the distinct response of Gram positive and Gram negative bacteria to fluctuations in soil moisture.

Keywords: taxonomic diversity, functional diversity, ecological niche, drought

[P1.026]

Arctic-alpine ectomycorrhizal fungi in Scotland: The ecology of unexplored fungal communities and threats to their survival

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Arctic and alpine habitats are experiencing rapid change under the influences of climate change, land use and elevated nitrogen deposition both in the UK and globally. They are inhabited by ectomycorrhizal (ECM) fungi which perform a critical role supplying a suite of obligately dependent shrubs with nutrients required for survival and growth, in what are typically nutrient poor and climatically harsh habitats. However, there is little data on ECM fungi in the montane zone of Scotland.

Communities of arctic-alpine ECM fungi were identified with DNA metabarcoding methods using high throughput sequencing of ECM plant root material and soil. To supplement the taxonomic resolution of these analyses, fungal sporocarps were also collected, described and sequenced to produce identified, habitat-relevant reference sequences. Surveys were conducted over 23 sites spanning the Scottish Highlands (hosts including *Arctostaphylos alpinus, A. uva-ursi, Betula nana* and *Salix herbacea*), an altitudinal gradient study, and an analysis of a long term experiment in a low-alpine heath testing the influences of heath burning, nitrogen addition and warming.

A total of 257 ECM fungal taxa were detected including 23 species new to science and 28 new species for the UK, which represents the highest degree of novelty of macro-organisms discovered in a terrestrial habitat in recent British history. At least 80 ECM species appear restricted to arctic-alpine habitats in Scotland, and ECM communities associated with alpine dwarf shrubs appear to be comparably or more species rich than those in native Caledonian Pinewoods. ECM fungi were found to have distinct altitudinal niches and biogeographies, with communities significantly influenced by oceanicity at a national scale. Extensive fragmentation and continued degradation of montane dwarf shrub populations through prescribed burning and over-grazing threaten the survival of these highly diverse fungal communities by reducing their resilience in the face of a changing climate.

Keywords: Mycorrhiza, Montane, Alpine, Habitat degradation

[P1.027]

Climatic versus biotic impacts on soil micro-arthropods

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Climate change is exposing organisms to more variable and extreme weather events. This causes direct stress for soil organisms potentially leading to increased mortality and therefore changes in the community structure. At the same time changes in the plant community, as a result of climate change, may lead to shifts in the belowground soil community but the relative strength of both climatic versus biotic changes is not often compared at the same time. Here we present data of a micro-arthropod (Collembola and Acari) community in response to extreme winter warming events followed by the impact of increased herbivory in a sub-Arctic heathland community.

The extreme winter warming events greatly reduced (50%) the abundance of the micro-arthropod community due to increased temperature fluctuations during winter. After 3 years of recovery the heath community was heavily grazed by the autumnal moth causing major mortality among the dominant dwarf shrub species (similar in extent to the extreme winter warming events). The micro-arthropod community did not respond to these changes in the plant community indicating that the direct effect of climate change are much greater for soil micro-arthropods than changes in the plant community. These conclusions are further supported by a plant removal experiment conducted in a northern boreal forest. In this experiment we quantified the effect of the complete removal of dwarf shrubs and mosses for soil micro-arthropod. Loss of the moss layers greatly reduced micro-arthropod abundance (76%) but loss of the dwarf shrubs did not affect the micro-arthropod community.

In conclusion, changes in the vascular plant community do not appear to have a strong impact on the soil micro-arthropod community in northern boreal forests and sub-Arctic heathland communities. Therefore, climate change impacts on soil communities will be felt through direct changes in climatic conditions and not through changes in the plant community.

Keywords: micro-arthropods, extreme events, diversity, herbivory

[P1.028]

Diversity of wood-decaying fungi is driven by habitat availability in managed and natural Norway spruce forests

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Temporal variation of the microbial diversity may affect the rate of decomposition and ecosystem functioning. In the boreal forests, decomposition of organic matter and nutrient cycling is based on activity of fungi. In the managed forests, timber harvesting and decreased amount of decomposing wood is a major driver of the diversity of fungi. Decline of dead wood in managed forests affects wood-inhabiting species that use it as their substrate, some now being listed as threatened while some are still thriving. Maintenance of the species diversity in the managed forests requires species-specific information about their occurrence probabilities and forest planning tools where this information is integrated to simulations of the stand dynamic.

We implemented an ensemble of habitat models of wood decaying fungi (polypores) to simulations of stand and dead wood availability. We asked how management of a boreal Norway spruce stand influences the dead wood availability and occurrence probabilities of wood-inhabiting species and their diversity. Simulation of multiple polypore species with stand management scenarios provided insight to dead wood dynamics and polypore species management.

Forest management has a clear and species-specific influence on occurrence of fungal species, as it directly influences resource these species are utilizing. In a managed stand, diversity thrived after final harvesting, but declined to low level by mid-rotation. Harvest residues and stumps, although low quality substrate for many species, were important for diversity in young managed stand due to their high quantities. Our study suggests that wise temporal management of dead wood supply could support presence of several species with different habitat requirements that are not frequently found in managed forests.

Keywords: fungal diversity, conservation, decomposition, sustainable management

[P1.029]

Assessing soil biodiversity and function across Europe

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Monitoring soil biodiversity and function across Europe is a huge task which requires an understanding of both the ecological niches and processes on-going in soils and the methodological constraints related to measurement of biodiversity and associated functions. In order to assess the feasibility of such a monitoring programme for European soils, the EcoFINDERS (Ecological Function and Biodiversity Indicators in European Soils) project implemented a monitoring campaign at 81 sites across Europe.

Spatial site selection was based upon EFSA spatial data provided by the Joint Research Council. Using spatial data on topsoil organic matter, pH (water), texture and Corine Land Cover Data sites were selected across Europe to provide a spectrum of soil properties, across five Biogeographical Zones (Atlantic, Continental, Mediterranean, Boreal, Alpine) and three land-uses (Arable, Grassland and Forestry). Samples were taken from 81 sites across 11 countries providing the selection of soil and land-use properties required for the specific biogeographical zones. All samples were prepared centrally and then distributed to the relevant laboratories across Europe to perform analyses of; bacterial, fungal and Archaeal T-RFLP, enchytraeids, mites and collembola species diversity and abundance, nematode feeding groups, ammonia oxider and denitrifier functional genes, phospholipid fatty acid analysis (PLFA), multiple substrate induced respiration (MSIR), BIOLOG, extracellular enzyme activity (EEA), nitrification potential. In addition soil baseline properties were analysed; pH, soil organic carbon, total nitrogen, cation exchange capacity and texture.

These measurements of biodiversity indicators and a range of ecological functional assays resulted in a snapshot of the current situation and have provided baseline information for further developments in monitoring of soil biodiversity in Europe. The data collected from this transect provides information on the logistical requirements, methodology constraints, discrimination potential of methods and finally an estimation of the Normal Operating Range (NOR) of the indicators tested.

Keywords: Normal Operating Range, Soil Biodiversity, Soil function, Monitoring

[P1.030]

N fixation in decaying Norway spruce logs

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Dead wood is a nitrogen poor substrate where N-fixing bacteria are thought to enable wood-decaying fungi to meet their N requirements for growth and decomposition activity. Wood-decaying fungi are capable to decompose complex lignocellulose compounds of wood, where initial C/N-ratio is >400. It is known that both N concentration and the total amount of N in decaying wood increase with decay phase and enhanced rate of decomposition. Biological N fixation may explain a part of this increase, but the N fixation in decaying wood of oreal forests is not quantified, yet.

We measured the rate of N fixation in decaying Norway spruce logs (n=33) that represented different decay phases and generalized the results to the stand scale with measured dead wood volumes. N fixation was measured with both acetylene reduction assay (ARA method) and by using ^{15}N label. We also studied composition of the N-fixing microbial community by analyzing *nif*H gene distribution in decaying wood.

The average rate of acetylene reduction was 7.5 nmol/g/d. In our data the N fixation activity was not clearly related to either wood decay phase or water content. Estimated annual N fixation activity was 13 g N per Mg of decaying wood (dry weight). In studied old-growth Norway spruce stand in southern Finland (Sipoo), where the total amount of dead wood was 100 m3/ha, the wood-inhabiting microbes fixed 0.38 kg N/ha/year. Our study showed N fixation activity and confirmed presence of diazotrophic microbes in decaying Norway spruce logs. Although the estimated annual fixation rate is relatively small, the cumulative amount is remarkable for a forest stand with long-living tree species without large annual losses of nitrogen. The amount of N fixed in 100 years is equivalent to one third of the N stock in standing stemwood of an average Norway spruce stand.

Keywords: nitrogen fixation, wood decomposition, boreal forest, nifH gene

[P1.031]

Soil bacteria and micro-eukaryote: Two domains with different seasonal and temporal variability of soil community structure and linkages to ecosystem functions in a restored floodplain

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Studies of soil biodiversity mainly focus on invertebrates, fungi or bacteria. However, a major component of soil diversity is composed by microbial-sized eukaryotes, among which protists have been particularly neglected. We studied the spatial and temporal (4 seasons) patterns of soil bacteria (T-RFLPs) and micro-eucaryotes (illumina sequencing of the SSU rRNA gene V9 region) in a dynamic floodplain ecosystem along a perturbation gradient (seven habitats from gravel bar to floodplain forest) to determine the relative importance of habitat diversity, soil environmental conditions (temperature, moisture and time elapsed since last inundation), seasons and external perturbation in shaping soil bacterial and eukaryotic communities and associated processes (ecosystem functioning proxies: basal respiration, enzymatic activity, microbial carbon and nitrogen).

Both bacterial and eukaryotic communities changed significantly among habitats and seasons. However, in bacteria, temporal variability was substantially higher than the spatial variability. Indeed, in a redundancy analysis, the spatial pattern was nested within the temporal effect. By contrast, in microbial eukaryotes, spatial effect was greater than temporal effects.

Microbial communities, environmental conditions and ecosystem functions were correlated, but link between communities and functions was seasonally inconsistent. External factors (e.g. floods) influenced ecosystem functions and microbial communities independently, possibly because of species functional redundancy.

The discrepancy between spatio-temporal patterns of bacterial and eukaryotic communities illustrates how fundamentally different these two broad categories of organisms are in their life history traits (e.g. dispersal potential, life cycles), functional roles and calls for more combined studies of the two groups.

Keywords: floodplain soil, bacteria, micro-eukaryotes, spatio-temporal patterns

[P1.032]

Investigation into the effects of elevated carbon dioxide on phosphorus and nitrogen cycling in a Eucalyptus woodland

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Despite the geographic and economic importance of native Australian *Eucalyptus* woodlands, relatively little is known about their responses to predicted increases in atmospheric CO_2 concentrations. The generally low nutrient status of Australian ecosystems suggests that nitrogen (N) or, in particular, phosphorus (P)-limitation could constrain tree responses to elevated CO_2 (eCO_2). In order to address this, we investigated the effects of eCO_2 on soil N and P availability, turnover rates, soil microbial biomass, soil extracellular enzyme activity (EEA) and dissolved organic carbon (DOC) in soil water as part of the EucFACE free-air CO_2 enrichment (EucFACE) experiment from September 2012 to March 2014. Three ambient and three eCO_2 ($[CO_2]$: ambient + 150 ppm) FACE rings (□ = 25 m) were installed in a native Cumberland Plain *Eucalyptus* woodland in Western Sydney, NSW, Australia.

We found seasonally dependent positive effects of eCO_2 on soil-ammonium and -phosphate and on DOC in soil water, but no effect on soil-nitrate, microbial biomass or EEA. Soil moisture was an important driver of seasonal fluctuation in soil-ammonium and -phosphate and EEA. These eCO_2 enhancements were observed especially in spring and summer (Oct-Feb). In particular the enhancement of soil-P cycling was distinctive. The eCO_2 treatment significantly increased Bray-P-extractable soil-phosphate and ion exchange resin (IEM)-adsorbed soil-phosphate by 12 % and 76 %, respectively, compared to ambient CO_2 treatment.

These results suggest that CO_2 fertilisation could increase DOC supply to the soil in warm seasons associated with CO_2-driven stimulation in photosynthetic rates. This could increase microbial decomposition of organic matter and supply plant accessible nitrogen and phosphorus into the soil. In this study, however, microbial responses and associated EEA to eCO_2 were not detected probably due to relatively small soil-plant interaction in bulk-soil. CO_2-driven increases in nitrogen and phosphorus availability could support increased plant demand associated with CO_2-driven fast growth rates.

Keywords: FACE, elevated atmospheric CO2, soil nutrient, phosphorus

[P1.033]

PLFA profiles of soil microbial communities subjected to addition stressors along two metal pollution gradients

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A study was undertaken to investigate how metal-tolerant microbial communities in metal contaminated soils would response to additional stressors. We hypothesized that such communities would be tolerant of additional stress such as more metal stress due to phylogenetic and functional adaptation. In microcosm experiments, lasting 60 days, phospholipid fatty acid (PLFA) profiles was used to compare profiles of communities in non-amended soils and those to which additional stressors (arsenic, salt, benzo[a]pyrene and flooding) were applied. This study sites is unique, as soil microbial communities residing in two distinct gradients have generally been characterized. Our results clearly showed that history of metal pollution did not affect stability of microbial biomass nor abundances of microbial groups and regardless to pollution level, stress treatments restructured the microbial communities in all soils and over the course of the experiment. Salt and flooding stress had stronger effect on communities structure than arsenic and benzo[a]pyrene stress. PLFAs relating to fungi, Gram-negative and Gram-positive bacterial declined relative to non-specific bacteria markers (belonging to general bacteria) in soils treated with salt and flooding stress. This may be a consequence of inhibition and/or killing of sensitive microbial groups and selection of tolerant by the stressors applied, but also of the proliferation of fast-growing species under stress condition. We observed a higher degree of saturation of the fatty acyl chains of the phospholipids extracted from soils exposed to arsenic, salt and flooding stress. Such a result was interpreted as an adaptive response resulting in higher membrane rigidity of the bacterial communities.

Keywords: stress, Metal pollution, PLFA, forest soil microbial communities

[P1.034]

A novel approach to restoring biodiversity and structural complexity in soil food webs

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The soil food web provides ecosystem services that form the basis of sustainability in all terrestrial biomes. However, soil food webs in urban and agroecosystems are severely degraded, short and dominated by opportunists at the entry level. Here we show how the structural diversity of the soil food web can be restored using nematode community as a bioindicator taxon. As nematodes occur at multiple trophic levels within the soil food web, we hypothesized that the missing trophic guilds (along with their associated suite of organisms) can be re-established by transplanting small intact soil cores extracted from a nearby undisturbed ecosystem. We found that opportunistic bacteria feeding (BF) and fungus feeding (FF) nematodes moved out of the transplanted cores and colonized a 60 X 60 cm arena containing autoclaved soil within 2 weeks, and the higher trophic level omnivorous (OM) and predatory (PR) nematodes began to spread out by week 5. Field trials also showed that OM and PR nematodes can be re-established in turf grass plots by transplanting forest soil cores, resulting in increases in structure index (SI) and maturity index (MI) of the soil food webs compared to plots receiving no core transplants or those receiving commercial topsoil. Experiments in urban vacant lots containing a low level of heavy metal contamination revealed that organic compost with a C:N ratio of 12:1 resulted in maximum increase in abundance of higher trophic level nematodes and SI and MI of the soil food web, as compared to the use of grass clipping (C:N = 20:1) or organic peat (C:N = 25:1). Organic amendments alone did not introduce any of the missing nematode trophic guilds into the soil ecology. This study provides a new approach for restoring the functional complexity of soil food webs and their associated ecosystem services.

Keywords: soil biodiversity, restoration, nematodes, technique

[P1.035]

A knowledge-based assessment of potential threats to different components of soil biodiversity

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Due to the numerous pressures exerted on soil, below-ground life is under threat. To date an effective and detailed assessment of the threat potential of these pressures on different components of soil biota remains to be carried out. Therefore, we proposed and presented a list of thirteen potential threats to soil biodiversity to experts from all over the world, with different scientific backgrounds (biology, ecology or soil science) in order to assess the potential of these threats in three major components of soil biodiversity: soil microorganisms, soil fauna, and functions provided by soil biodiversity. A meta-search of peer-reviewed publications dealing with each of the potential threats proved good representativeness of the participants. The scientific opinion poll approach allowed us to obtain knowledge-based rankings of potential threats to different categories of soil biodiversity.

	Microorganisms	Fauna	Functions
GMOs use	🟩	🟩	🟩
Habitat fragmentation*	🟩	⬜	🟩
Introduction of invasive species*	🟩	🟨	🟩
Climate change*	⬜	🟨	⬜
Nuclear pollution	⬜	🟨	🟨
Soil erosion*	🟨	⬜	🟨
Soil compaction*	🟨	⬜	🟨
Soil sealing *	🟨	⬜	🟨
Soil salinisation*	🟨	⬜	🟨
Industrial pollution	🟨	⬜	🟨
Land use change*	🟨	🟨	🟨
Organic matter decline*	🟥	🟨	🟥
Intensive human exploitation*	🟥	🟥	🟥

🟩	LOW POTENTIAL
🟨	MEDIUM POTENTIAL
🟥	HIGH POTENTIAL
⬜	UNCLASSIFIED POTENTIAL

Intensive human exploitation was identified as the most relevant pressure in all three categories. In contrast, the use of genetically modified organisms in agriculture was considered the threat with least potential. The potential impact of climate change showed the highest uncertainty. The obtained results show: (i) the effectiveness of the opinion poll for this type of analysis; (ii) the feasibility of ranking the potential of threats to soil biodiversity; (iii) a consensus among different experts on classifying the risks; (iv) the need to consider different components of soil biota and not soil biodiversity as a whole for this type of assessment. The obtained classifications represent a first attempt to evaluate the potential of a consistent number of factors threatening three different components of soil biodiversity and can be used in future research and decision-making as guidelines to localize areas of threat to soil biodiversity and, subsequently, to design appropriate strategies to monitor and protect soil biota.

Keywords: threats, opinion-poll, soil microorganisms, soil fauna

[P1.036]

Pesticide Interactions with N source and Tillage: Effects on soil biota and ecosystem services

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Pesticide effects on soil biota must be interpreted in the context of the specific management practice, including rotation, fertilization, tillage, and pest control. Tillage, foe example, has been shown to reduce earthworm populations by up to 80%, depending on timing and specific tillage technique. Such disturbances may fully or partly obscure the effects of pesticides. The direct effects of pesticides and other management factors and their interactions must, therefore, be quantified before integrated pest management strategies that protect soil biodiversity and maintain soil functions can be identified.

This study was planned to evaluate interactions between pesticide use and other soil management factors. The study was carried out within a long-term tillage experiment using two tillage practices (no-till (NT) and mouldboard ploughing (MP)), two contrasting N sources (manure and mineral fertiliser), and two pesticides (the fungicide mancozeb and the insecticide alpha-cypermethrin*)* in a split-plot design. Results on earthworms and microarthropods will be shown and discussed.

Keywords: Pesticides, Fertilisers, Soil management, Soil Invertebrates

[P1.037]

Assembly processes in soil oribatid mites: environmental filtering vs niche partitioning

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Competition for resources has traditionally been considered to be of minor importance in structuring soil animal assemblages but the relative role of environmental filtering and niche partitioning has not been analysed in the framework of recent theories. We used the stable isotopes ratios $^{15}N/^{14}N$ and $^{13}C/^{12}C$ to identify a set of species competing for shared trophic resources, and investigated patterns of community structure in this set of species. Multivariate analyses showed a clear gradient driven by soil variables such as organic C and N, and soil structure. Still, we did not find a negative correlation between the distance between species along the gradient and species trophic dissimilarity, which we expected under niche partitioning processes. Since the spatial scale of the study allowed us to rule out dispersal limitation, we conclude that environmental filtering plays a major role in structuring oribatid mite soil assemblages. In future studies, we will need to test other niche traits along which niche-partitioning processes could operate, alongside or in interaction with environmental filtering.

Keywords: niche partitioning, environmental filtering, oribatid mites

[P1.038]

Rehabilitation of microbial patrimony with Miscanthus x giganteus crops on polluted soils

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The discharge of urban waste water on farm land has led to a widespread introduction of pollutants into our environment, locally causing acute and diffuse contamination of soils. As a consequence, contaminated soils are unsuitable for crop production and need rehabilitation. One strategy is the establishment of energy crops such as *Miscanthus x giganteus*, a C4 grass used for biofuel production. Although the economical potential of this crop is known, its effects on soil biological properties remain unclear.

The aim of this study was to assess the effects of Miscanthus perennial cropping on the microbial properties in a contaminated soil. The work is based on an experimental real field site close to Paris irrigated for more than hundred years by raw wastewater (Pierrelaye, France). Soil microbial communities were characterized in terms of abundance, diversity and composition with molecular tools (soil DNA extraction, estimation of molecular biomass and high throughput sequencing of 16S and 18S ribosomal genes). The impact of perennial crops on microbial communities was assessed by (a) a synchronic study comparing communities between a field under Miscanthus for four years and a field managed under conventional cereal cropping (tillage, crop rotations); and (b) by a diachronic study monitoring communities during a two years-period of growth of Miscanthus following implantation.

Our results showed that the composition of the microbial community at the site was indicative of polluted state of the soil, with populations involved in PAH and hormone degradations. Perennial cropping significantly increased bacterial and fungal diversity, richness and equitability. Such perennial cropping stimulated bacterial and fungal *genera*, known to live in association with roots and/or to degrade easily organic matter via copiotrophic attributes. The establishment of Miscanthus appears as a good strategy to stimulate microbial resources in polluted sites and favorable for their rehabilitation.

Keywords: microbial diversity, rehabilitation, polluted soil, miscanthus

[P1.039]

Does forest floor heterogeneity modulate fungal dynamics in forest ecosystems?

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The forest floor of boreal mixedwood forests is a fungi-dominated environment composed of contrasting wood and leave litters of different decomposability and decay stages. Numerous studies have shown fungal translocation of C and nutrients between organic materials of contrasting quality (C/N) under controlled and simplified conditions. Whether these processes operate at larger scales and modulate fungal dynamics in forest ecosystems remains to be investigated. We tested the hypothesis that juxtaposing fresh (high C/N) and well decayed (low C/N) litters would increase fungal activity and decomposition rates of both litter types when compared with single litters. Fresh and well decayed litters of two origins (leaves, wood) from two boreal tree species (*Pinus banksiana* and *Populus tremuloides*) were incubated in microcosms (n = 96) under controlled temperature and moisture conditions for periods of 15 and 30 weeks. Mass loss, respiration, fungal biomass, C and N concentrations and enzymatic activity were then measured. Independently of litter juxtaposition and origin, well decomposed litters were characterized by higher fungal biomass, enzymes activity, C utilization efficiency and N losses than fresh ones. Independently of litter juxtaposition and decay state, leaf litters were characterized by lower fungal biomass but higher C use efficiency, higher laccase and lower Mn-peroxydase activity than wood. When litters were juxtaposed, fungal biomass and N were transferred from old to fresh litters increasing β-glucosidase and cellobiohydrolase activity in fresh litter. However, an increase in C mineralization was observed in well decayed litters only. Juxtaposing fresh and well decomposed litters increase C mineralization but decrease C use efficiency in wood while the reverse was observed for leaf litters. Our results indicate that the origin and decay stage were the main factors affecting fungal biomass dynamics. However, forest floor heterogeneity induces variation in fungal activity and C use efficiency.

Keywords: Decomposition, wood, leaf litter, enzymatic activity

[P1.040]

Cyanogen loading effects on terrestrial ecosystem and groundwater quality in agricultural soil.

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Cyanogens are important in inhibiting predation in various plant species; however, an increase in the concentration of these compounds in certain ecosystems (i.e. agricultural soil) can lead to soil degradation due the hydrolysis of these compounds to produce hydrogen cyanide (HCN). This paper focuses on cyanogenic glycosides' movement in soil and groundwater, as well as the effects of these compounds on terrestrial ecosystems and the environment. Cyanogens loading in agricultural soil, impact negatively on the soil's physical, chemical and biological properties. These compounds move from the subsurface through deposition, decomposition, infiltration, leaching and transportation into groundwater. Therefore, these compounds affect microbial activity, soil and groundwater quality. An unbalanced functionality of soil's organisms affects the texture and the structure of the soil, resulting in a dysfunctional terrestrial ecosystem and thus a reduction in produce during harvest.

Keywords: Cyanide loading, cyanogenic glycosides, terrestrial ecosystem, groundwater quality

[P1.042]

Indication of past climate humidity in the steppe zone from the state of microbial communities of paleosols of archaeological monuments

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Paleosols of ground archeological monuments (kurgans) of different ages in European steppe zone of Russia are unique objects to obtain information on peculiarities of environmental conditions and in particular, climate humidity, of past historical epochs. Microbial communities preserved until now in paleosols buried beneath kurgans together with physicochemical and morphological characterization of paleosols are studied. Adaptation peculiarities of microorganisms provide their survival under water and nutrient deficit, and the shift from humid to arid environmental conditions is fixed in a number of parameters of soil microbial communities. Among those are peculiarities of cell morphology, transition into nonactive/dormant state, and the changes in genetical diversity. Indicative parameters giving contrast patterns for humid and arid environmental periods were selected. They are the amounts of active and/or viable biomass and its share in total microbial biomass and soil organic carbon, ecological-trophic structure characterized by the ratio between microorganisms grown on soil agar and using dispersed nutrients, on nitrite agar and using humus, on rich organic substrate and decomposing plant residues, by the ratio between the number of microorganisms consuming readily available (plant residues) and resistant (humus) organic matter, and by index of oligotrophy. The dynamics of climate humidity in the region studied was analyzed on several pedochronosequences, which comprised paleosols buried beneath kurgans constructed in different historical periods, from the state and structure of microbial communities. Comparing microbial and physicochemical properties of paleo and modern surface soils the pattern of climate humidity within the Bronze, Early Iron, and Middle Ages was obtained demonstrating the sequences of arid and humid climatic periods of various duration.

(The work was supported by Russian Foundation for Basic Research and the Program for Fundamental Research of the Presidium of Russian Academy of Sciences)

Keywords: microbial communities, paleosols, steppes, climate humidity

[P1.043]

Functional assessment of soil fauna communities in perennial biomass cropping systems with the cup plant (Silphium perfoliatum)

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Efficient use of renewable energy requests high biomass yields. Currently, agroecosystems related to biogas production are subject to severe problems, summarized under the term maize overcultivation. Intensive soil management takes soil fertility and soil ecosystem services at risk on a large scale. Hence there is increasing demand for alternative energy crops able to keep up with maize. The cup plant *Silphium perfoliatum* is a perennial energy crop that delivers high biomass yields and requires only low management intensity in the long term. The aim of this study was the investigation of long term development and regeneration dynamics of soil fauna communities in agroecosystems with cup plant cultivation compared to maize. We sampled soil organisms according to the main size classes micro-, meso.- and macrofauna, e.g. nematodes, collembolans and earthworms. The study covered twelve cup plant fields representing an artificial timeline with fields planted in 2004/05, 2007, 2009, and 2011 (n=3). Maize fields (n=3) served as control. Sampling and extraction took place in spring and autumn 2012 and 2013 and followed ISO-guidelines. Earthworms were identified to species, collembolans and nematodes at family level and linked to their corresponding functional group. Results showed a trend towards higher functional complexity and biodiversity in old cup plant fields compared to young fields, which showed only small differences to maize fields. The perennial cropping system of *S. perfoliatum* seems to provide niches for a greater variety of life forms in soil of agroecosystems and consequently may facilitate decomposition cycles. Based on these findings positive effects on soil processes and services are expected by increased cultivation of *S. perfoliatum* in agricultural landscapes.

Keywords: energy crops, functional groups, long term, reduced management

[P1.044]

Detecting microbial patterns in relation to soil agricultural practices and the presence or not of plant roots

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Given the essential role played by bacteria and fungi in soil and regarding the recent introduction of multivariate analysis associated with the use of massive DNA (pyro)sequencing in microbial surveys, we can better understanding the relationships between microbial communities and environmental factors.

Here, we aim to detect microbial patterns in relation to soil agricultural practices and the presence or not of Vicia faba roots. Furthermore, rather than investigating microbial pattern at a high taxonomic level such as phylum or class commonly used in soil microbial surveys, we propose to exploit the available sequence information at the lowest taxonomic level attainable for each OTU, from phylum to genus.

Samples were taken at a depth of 15-20 cm from a silty soil in Belgium at seedling stage (without roots) and flowering stage (with roots), and to which two tillage practices (conventional and reduced tillage) and two crop residue management practices (residue retention and removal) had been applied in different combinations. After extraction of metagenomic DNA, massive 16S and 26S pyrosequencing followed by multivariate analysis was used to relate bacterial and fungal community patterns with soil management practices and the presence or not of plant roots. Furthermore, microbial taxa the most impacted by soil management and roots were detected. Analysis was performed at the lowest taxonomic level attainable for each operational taxonomic unit (OTU). The data analysis is ongoing and results will be presented at the conference.

Keywords: microbial community composition, pyrosequencing, conservation agriculture, taxonomical level

[P1.045]

Soil biodiversity and pedodiversity: Parallels challenges and synergies

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Soil biodiversity studies have grown dramatically in recent years with the ability to analyse functional, phylogenetic and structural diversity using gene-based technologies as well as bioinformatic tools[1-4]. Simultaneously, there has been a limited yet increasing recognition of the concept of pedodiversity – the diversity of soil properties, materials and classes. This talk focuses on the links between the two approaches.

Soil (microbial) biodiversity and pedodiversity seem at present to be emerging independently. Pedodiversity studies, because of their basis in soil classification, ignore the biological component; and soil biodiversity studies, do not readily recognise key soil entities such as aggregates, horizons or profiles and larger entities. Of course, at some level, soil biodiversity is an important component of pedodiversity.

Recent regional studies of soil biodiversity that have been done demonstrate strong geographic patterns as has been recognised for more than a century in pedological studies [5-9]. This suggests that we can expect co-spatial relationships between aspects of soil biodiversity and pedodiversity [10, 11]. Further because biodiversity can be measured at the finest scales it will have a four dimensional pattern (x, y, z, t) which can be related to the spatio-temporal distribution of soil materials.

The exciting challenge is to meld soil biodiversity and pedodiversity studies and understanding through studies at varying spatial and temporal scales to come to a joint consensus that helps that aids understanding of ecosystem functioning and consequently suggests enhanced management options. Results and discussion of a large global space-time soil carbon modelling exercise, comprising hundreds of thousands of observations for all continents and spanning over many decades, will be presented to focus the issues.

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Keywords: pedodiversity

[P1.046]

Molecular diversity of native arbuscular mycorrhizal fungi colonizing the roots of diverse cover crops and subsequent organic maize

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Arbuscular mycorrhizal fungi (AMF) are beneficial symbionts living in association with the roots of most plant species, including the large majority of agricultural crops. AMF deliver many essential agroecosystem services, such as nutrient and water uptake, crop tolerance to biotic and abiotic stresses and soil aggregation, representing key elements of soil fertility and productivity in organic farming systems. Though, scanty information is available on the impact of agronomic practices, in particular of cover crops, largely used in organic farming, on native AMF.

A field experiment was carried out to test the hypothesis that diversified cover crops increase the diversity of native AMF communities in the subsequent organic maize, in a Mediterranean agroecosystem. Maize was grown following two cover crop treatments: hairy vetch (*Vicia villosa* Roth) and a mixture of different species belonging to Fabaceae (*Vicia villosa*, *Trifolium alessandrinum* L. and *T. incarnatum* L.), Poaceae (*Avena* spp.) and Boraginaceae (*Phacelia tenacetifolia* Benth.). Partial SSU rDNA analysis was used to identify AMF in the roots of the cover crops and of the subsequent maize.

The sequence types detected corresponded to both known and unknown AMF species. A high diversity was retrieved, with sequences matching those of *Glomus*, *Rhizophagus*, *Funneliformis*, *Diversispora*, *Claroideoglomus*, *Acaulospora* and *Archaeospora* species. The cover crop species mixture hosted a higher number of sequence types than hairy vetch, which showed a low diversity when growing either alone or in the mixture. Consistent data were obtained from the subsequent maize crop, which hosted a higher sequence number when grown after the mixture than hairy vetch. Interestingly, sequences belonging to *F. mosseae* were detected only in maize roots. Our data highlight the important role played by cover crop identity in promoting AMF diversity and mycorrhizal symbiosis in organic maize systems.

Keywords: Arbuscular mycorrhizal fungi, Organic agriculture, AMF communities, SSU rDNA

[P1.047]

Specific bacterial communities are associated with spores of arbuscular mycorrhizal fungi isolated from geographically different areas

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Arbuscular mycorrhizal fungi (AMF), an important group of beneficial soil microorganisms, colonize the roots of most plant species and develop extensive extraradical mycelial networks that uptake and translocate nutrients from the soil to the roots, enhancing plant growth and increasing crop tolerance to biotic and abiotic stresses. The development and performance of mycorrhizal symbioses may be affected by bacteria living in the mycorrhizosphere, *i.e.* associated with mycorrhizal roots, spores, sporocarps and extraradical hyphae. Here, we studied the diversity of bacterial communities associated with spores of *F. coronatum*, *F. mosseae* and *R. intraradices* isolated from distant geographic areas.

The AMF isolates were maintained in pot-cultures with the same host plant, under the same environmental conditions and in the same soil substrate. Bacterial communities were analysed by PCR-DGGE of the variable V3-V5 region of the 16S rDNA. Cluster analysis (UPGMA) and Correspondence analysis were used to compare the DGGE profiles among isolates.

Results showed the occurrence of large bacterial communities intimately associated with AMF spores. The comparison of DGGE profiles revealed that each AMF isolate displayed a bacterial community specific pattern, unrelated with their taxonomic position. Such a specificity may be the result either of the diverse metabolic activity of the AMF isolates, exudating variable quantity and quality of chemical compounds, or of the variable composition of spore and hyphal walls. Sequence analysis of the major DGGE bands revealed that most bacterial sequences were affiliated with *Actinomycetales, Burkholderiales, Pseudomonadales, Rhizobiales, Bacillales* and *Mollicutes* related endobacteria. Among them *Actinomycetales* were widespread among all the isolates. The majority of the species identified are known as plant growth promoting and mycorrhiza helper bacteria. The isolation and selection of the most efficient strains could represent an important step for their utilization, in combination with AMF, as beneficial biofertilizers and bioenhancers, to improve the sustainability of agroecosystems.

Keywords: Arbuscular mycorrhizal fungi, Spore-associated bacteria, Mycorrhizosphere, PCR-DGGE

[P1.048]

Does soil functional diversity enhance organic P cycling and plant P nutrition? phytate mineralization as a case study

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Phosphorus (P) strongly limits plant productivity as plants can only absorb free inorganic orthophosphate (Pi) at very low concentrations in soil solution. However, soil contains high levels of poorly available P, especially phytate, considered as the most abundant plant-unavailable organic P source. Here, we investigated biological rhizosphere interactions involved in plant P acquisition from phytate. We hypothesized that the interactions between plant (*Pinus pinaster*), phytase-producing bacteria (*Bacillus subtilis*), mycorrhizal fungi (*Hebeloma cylindrosporum*), representing the more widespread strategy to improve plant P acquisition, and bacterial grazer nematodes (*Rhabditis* sp.) may improve plant P acquisition from phytate and thus P sustainability from soil organic P. We grew seedlings in microcosms containing soil with Pi or phytate, with or without the above-mentioned organisms for 100 days. With Pi, no significant differences were observed among inoculation or mycorrhizal treatments. In contrast, with phytate, nematode grazing was required for non-mycorrhizal plants to acquire P into their shoots. In mycorrhizal plants, bacteria alone improved net P accumulation and nematode grazing enhanced this positive effect. Our results indicated that the increase of phytase activity by nematodes grazing was the main pathway explaining the soil P microbial loop, while direct excretion of phosphates certainly not contributed much. To conclude, we found that organic P mineralization and plant P acquisition increased with increasing soil functional group richness. Trophic relationships should be considered as a sustainable strategy for plant P nutrition to enhance organic P availability in the rhizosphere.

Keywords: functional diversity, phosphorus cycling, trophic relationships, Plant nutrition

[P1.049]

Analysis of individual growth patterns in juveniles of *Eisenia andrei* grown on horse manure

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In this work we have evaluated individual growth of *Eisenia andrei* in two conditions: in mesocosm at similar initial densities and in isolated organisms. Our aim has been to identify growth dynamics with special emphasis on shift points from juveniles to sub-adults and its connection with density evolution. A sample of 51 individuals of *E. andrei* ranging from 34.66 to 1425.70 mg cultured in horse manure at 20°C and 80% RH, was selected for this study. Growth was monitored along 100 days and weekly determinations of biomass were undertaken. As regards to worms growing in mesocosm (n= 33) precise identification of individuals was achieved by tagging with fluorescent elastomers. Groups of 11 specimens were placed in 1100 cm^3 boxes with an average initial density of 7.3962 mg live weight/ g wet horse manure. The remaining 18 juveniles were individually cultured in 450 cm^3 boxes. Results obtained in both group and individual settings show that approximately 25% of the individuals presented an exponential growth pattern. Mesocosm specimens adjusted primarily to an asymptotic model (70%) whereas in isolated organisms a rectilinear pattern is defined in 44% of cases. Maximum weight achieved during the experiment correlates to growth model, being on average 552 mg and 1453 mg for group and individually cultured earthworms respectively. Maximum live weight recorded in individuals reared in group is associated to detection of clitellum ($Asymptotic\ live\ weight = 55.243 \times e^{(0.005 \times Live\ weight\ at\ clitellum\ detection)}$; $r^2=0.913$). Initial density increases along the experimental time according to an asymptotic function ($Density = 13.113 \times (1-e^{-0.830 x Time})$; $r^2=0.718$) indicating that 13.113 mg live weight / g wet horse manure would be the maximum density the population can support. When higher values are attained, death or weight loss of some of the individuals occur resetting density below hitherto referred threshold.

Keywords: Eisenia andrei, Growth pattern, Density, Mesocosm

[P1.050]

Strategy to manage AMF biological diversity within the cropping system

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Despite the great biological diversity of arbuscular mycorrhizal fungi (AMF) and its functional consequences on the host plant, a strategy to manage this diversity within the cropping system is still missing. The importance of this strategy is reinforced by the fact that commercial inocula are too expensive to be used in a large scale and only contain a single or few AMF species.

When high levels of botanical hierarchy are considered, such as grasses and forbs, there are evidences of strong preferential associations between some AMF and host plants, that can even superimpose the environmental conditions.

To investigate the AMF biological diversity associated to different host plants in a non-sterilized soil with a diverse indigenous AMF population, a 454 pyrosequencing technique was used. When spores and root fragments were the propagule source, the results showed that the AMF species present, in the two dicot plant species (*Ornithopus compressus* and *Trifolium subterraneum*) and in the two monocots (*Lolium rigidum* and *Triticum aestivum*) used in this study, were similar within each plant species group and clear differences could be detected between the two botanical groups. However, when a monocot was planted after a dicot or vice-versa, keeping the extra-radical mycelium (ERM) associated with the first plant intact in the soil, functioning as the preferential source of AMF propagule, the AMF community present in the second plant correspond to the one in the first plant of the succession, independently of their botanical group. Therefore in a succession of plants (cover crops or crop rotation) the choice of the first plant and the use of appropriate tillage technique in order to keep the ERM associated to the first plant intact can be used as a strategy to manage AMF biological diversity within the cropping systems.

Keywords: AMF diversity, cropping system, management, 454 pyrosequencing

[P1.051]

Functional diversity within indigenous AMF population in the bioprotection of wheat and subterranean clover against Mn toxicity

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The functional diversity of arbuscular mycorrhizal fungi (AMF) species is well demonstrated either for nutrient acquisition or the bioprotection against biotic and abiotic stresses. However most of the studies with these fungi have been conducted comparing inoculation of single AMF species or, at most, consortia of a very limited number of species.

The new generation sequencing techniques (NGS) allowed the perception of the high level of AMF species diversity associated with the host plant, either in natural or agricultural ecosystems. The integration of this information with the biological data of the host plant is still very scarce.

Mycotrophic tolerant plants (*Ornithopus compressus* and *Lolium rigidum*) were grown, in a soil with excessive levels of Mn, in order to develop an extensive extra-radical mycelium (ERM) from the indigenous AMF species. Wheat and subterranean clover were then planted without soil disturbance in order to enable the intact ERM to be the preferential source of AMF inoculum. Diversity of AMF colonizing the roots of wheat or subterranean clover was influenced by the plant from which the ERM initially developed and significantly influenced the nutrient acquisition and the growth of both crops. Correlations between AMF diversity and crop host plant biological data will be presented and discussed.

Keywords: AMF functional diversity, Bioprotection, Mn toxicity, New generation sequencing techniques

[P1.052]

Soil microbial structural and functional diversity across different agroecological zones in new south wales, australia.

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As an ecosystem, soil provides (food, fibre), regulates (water filtering) and supports (nutrient cycles) services for sustaining life[1]. Microbes working for those soil services include N-fixing bacteria (*nifH*) and ammonia-oxidizing archaeas (AOA) behind the N cycle[2]. It has been debated if loss of functional diversity affects soil functions [3, 4]. To support this relationship it has to elucidate the factors driving microbial diversity, which are still largely unknown[5]. We hypothesise environmental soil gradients are a strong factor controlling microbial distribution; we use this approach for uncultured-based microbial analysis for Australian soils. *Fingerprinting* and *NGS* methods will determine structural diversity of the major soil microbial taxa (i.e bacteria and fungi) and functional *nifH* and AOA across different agroecological zones in NSW. Forty-seven sampling sites were located along two transects: (1) a north-south transect along the 550 mm isohyet (900 km in length) from Queensland to the Victorian border; (2) an east-west transect perpendicular to the north-south transect (930 km in length) from Coffs Harbour on the coast to Wanaaring in western NSW (rainfall gradient >1500mm to <300mm). Within each site, two different land-use ecosystems, natural (forest or grassland) and agricultural (rainfed crop or pasture), were selected on the same soil class. In each land use ecosystem, soil samples were taken from 0-5cm and 5-10cm depth and stored at -20 °C. Soil physicochemical properties were estimated by Ku-pF apparatus and NIR spectrometer. Soil DNA was isolated and PCR-TRFLP (previously designed by BesTRF) yielded profile diversity of bacteria, fungi, N_2-fixing bacteria and AOA, based on 16S, ITS, *nifH* and *amoaA*_AOA genes, respectively. Based on T-RFLP results, will be run 454 pyro-sequencing to identify specific group of microbes. Preliminary results from the north-south transect suggest that structural and functional diversity in Australian soils are closely related to soil type, soil Carbon and soil pH.

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Keywords: microbial diversity, biogeography, nifH, ammonia-oxidizing archaea

[P1.053]

Risk assessment of GM crops on earthworms considering European biogeographical regions

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Within the framework of the EU project AMIGA, a laboratory test system for standard testing of the impact of genetically modified (GM) maize and potatoes of selected European biogeographical regions on earthworms as important non-target decomposers was developed.

The system bases on earthworm species of significant functional relevance in the European AMIGA sites (Ireland, Sweden, Spain), belonging to three biogeographical regions (Atlantic, Boreal, Mediterranean). By means of a literature survey, respective focal earthworm species (EFSA, 2010) were traced. The species *Aporrectodea caliginosa* (secondary decomposer) and *Lumbricus terrestris* (primary decomposer) were finally selected to be included in the test system.

Based on both selected focal species, microcosm feeding experiments were carried out with plant residues of GM and non-GM crops collected from AMIGA field sites. For risk assessment, biomass, cocoon production, cocoon size, percentage of cocoon hatching, as well as survival, biomass, growth and development of offspring as relevant performance traits to conclude on potential long-term effects and changes in ecological functions were analysed.

The results reveal lower hatching durations but higher developmental times of *L. terrestris* when fed with GM compared to non-GM potato tuber (Ireland). The species *A. caliginosa* showed slightly decreased cocoon production rates and an increased developmental time when fed with GM compared to non-GM maize leaves from Spanish AMIGA sites. When fed with Swedish maize material, performance traits of *A. caliginosa* did not differ between GM and non-GM treatments. However, the cocoon production of this species was twice as high when fed with Spanish compared to Swedish maize leaves.

Generally, the results indicate that differences between species and between biogeographical regions clearly exceed those between GM and non-GM treatments. Regarding the selected focal species, *A. caliginosa* might be preferred as indicator organism due to shorter generation times and higher reproduction rates compared to *L. terrestris*.

Keywords: earthworms, genetically modified crops, risk assessment, non-target organisms

[P1.054]

Title: Multi-SIR for monitoring changes in functional diversity of soil microbial communities

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The addition of relevant, low molecular and easily available C sources to soil, similar to root exudates or microbial decomposition products, followed by their mineralization to CO_2, has been used to describe differences between management (Nsabimana et al., 2004) or fertilization treatments (Buyer and Drinkwater, 1997; Romaniuk et al., 2011). Two main measuring methods exist for determining the community level physiological profile (CLPP) of a soil. Garland and Mills (1991) developed a micro-plate based method (Biolog), containing a tetrazolium dye plus substrate, which resulted in a CO_2-induced colour change after adding a serially diluted soil extract. The multi-SIR (substrate-induced-respiration) method of Degens and Harris (1997) is based on the SIR method of Anderson and Domsch (1978), but uses a large variety of different substrates and not only glucose. The “whole soil” method of Degens and Harris (1997) was combined by Campbell et al. (2003) with the advantage of a multi plate system of the Biolog method (Chapman et al., 2007; Creamer et al., 2009). In the multi-SIR method, the soil is weighed into a deep well plate and the CO_2 respiration of the soil is measured by a colour change in the NaOH and a pH indicator dye contained in the detector gel.

Keywords: Multi-SIR, Community level physiological profiling

[P1.055]

Flood conditions shape earthworm communities of conjunct floodplain and coastal meadows

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Monitoring of invertebrate fauna is necessary for implementing conservation strategies on semi-natural floodplain and coastal areas. ~7000 hectares of conjunct semi-natural meadows are situated in the Kasari River delta and around Matsalu Bay. The meadows with the gradients in the frequency and duration of floods as well as in salinity, and with smooth transition from the floodplain to coastal meadows provide a unique model system for testing the effect of inundations and consequent environmental conditions on soil biota. The earthworms were collected on 12 meadows using the mustard powder solution. Sampling sites were classified by soil salinity as follows: 1. fresh floodplains; 2. wet floodplains; 3. transitional meadows; 4. coastal meadows. The abundance of earthworm communities was the highest on fresh floodplains (86±23 ind m^{-2}) and decreased with increasing trend of soil salinity (9±2 ind m^{-2} on coastal meadows). Similar trend was observed in species number. Totally 11 species were found. Three species were present in all types of meadows – epigeic *Lumbricus rubellus,* endogeic *Aporrectodea caliginosa* and semiaquatic *Octolasion lacteum.* One half of community on fresh floodplains and one third on wet floodplains consisted of *A. caliginosa*, the number decreased to 8% and 5%, respectively, on transitional and coastal meadows. There were no anecic species in soils of transitional and coastal meadows.

There are two factors influencing the earthworms. Firstly, the duration of floods has strong but indefinite negative effect on earthworm communities in inundated soils. Secondly, the salinity of flooding water causes higher salinity of coastal meadow soils. The abundance and species number are influenced by salinity of soils and correlate with the soil electroconductivity. Consequently, the earthworms are good indicators of flood characteristics and the application of this finding in monitoring methodology is important in flooded areas where the border between fresh and sea water is undetectable.

Keywords: earthworms, semi-natural meadows, flood, salinity

[P1.056]

Diazotrophic community structure and function of soil crusts from two contrasting arid habitats in Mexico

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Microbial communities mediate many ecosystem processes, and changes in their function may have global impacts. However, it is commonly assumed that changes in microbial composition of communities are not relevant given the functional redundancy found in different microbial groups, but few studies have tested explicitly this assumption. In this study we investigated the functional (ecological) equivalence of different microbial communities from biological soil crusts by the characterization of the community structure and activity of N_2-fixing microorganisms from two arid ecosystems (Chihuahuan (CC) and Sonoran (BC) deserts) with contrasting temperature-precipitation regimes (summer and winter rain). Community structure was determined through a culture independent approach by fingerprinting the nifH gene diversity (TRFLPs). For N_2-fixing potential we measured nitrogenase activity by Acetylene Reduction Assay (ARA) in two contrasting temperatures (15ºC and 30ºC) for both types of communities, and used a two-way ANOVA to test for the effects of sample origin (proxy for microbial composition), the incubating environment and their interaction on functional response. We found significant differences between communities in diversity, composition and functional measures. On average, richness was lower for the CC crusts (3.9±1.2 OTUs) than for BC crusts (6.0±2.4 OTUs) (**Figure 1**), being most of the OTUs found in CC present in BC (**Figure 2**). Nonetheless, relative abundance of OTUs and identity of the most abundant OTU differed between sites (CC vs BC) (**Figure 2**). Results from the functional assay indicated that crust origin had a significant effect on nitrogenase activity ($F_{1,60}$=14.7, p<0.01), as well as the incubating environment ($F_{1,60}$=16.8, p<0.01), with no significant interaction between variables (**Figure 3**). We hypothesize that differences in nitrogenase activity between soil crusts microbial communities of contrasting habitats are driven by differences in identity of the abundant diazotrophic groups. Further research should focus in direct measure of activity of these groups via quantitative expression analyses.

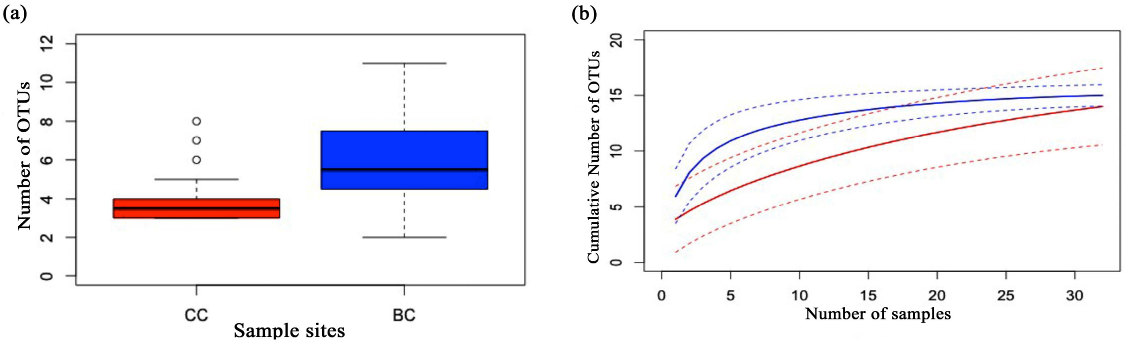

Figure 1. Richness differences between soil diazotrophic communities of the two contrasting arid sites (Chihuahuan desert = CC; Sonoran desert = BC). OTUs correspond to Terminal Restriction Fragments of nifH gene (a) Box plot for mean OTU richness (±SD) (b) Rarefaction curves of OTU richness for each studied site (CC=red; BC=blue). (n=32 for each site).

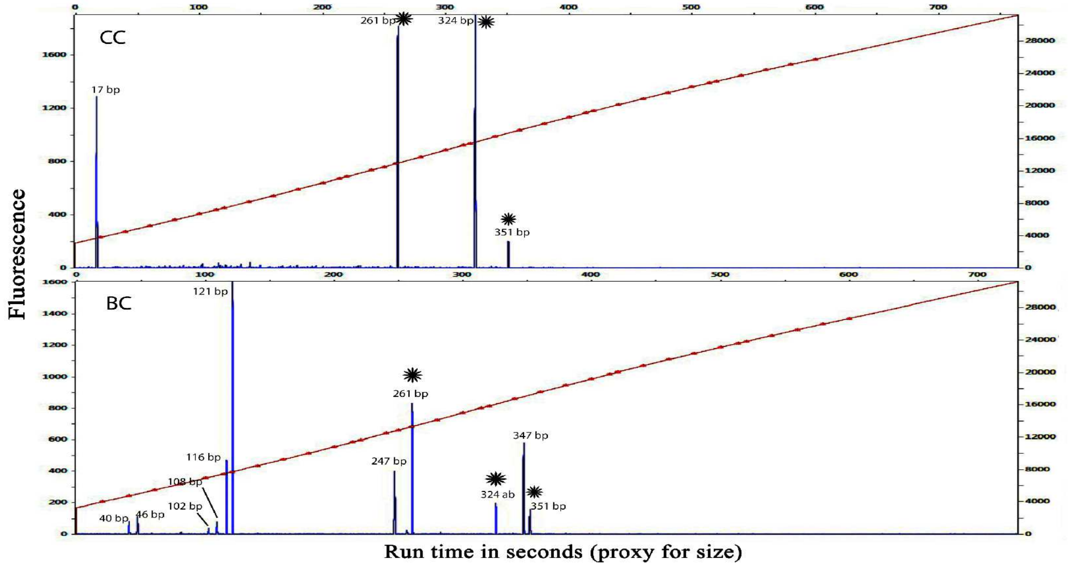

Figure 2. Exemplary *nifH* T-RFLP profiles of the crusts from the Chihuahuan desert site (CC) and the Sonoran desert site (BC). Asterisks highlight shared fragments (OTUs)

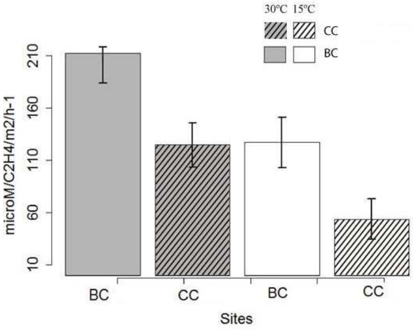

Figure 3. Mean nitrogenase activity (+SE) associated with soil crusts from two contrasting arid sites (Chihuahuan desert = CC, dashed bars; Sonoran desert = BC, solid bars). White and gray bars correspond to 15°C and 30°C incubation temperature respectively. (N=30)

Keywords: Biological Soil Crusts, Nitrogen fixation, Arid Habitats, microbial diversity

[P1.057]

The role of soil biota for sustainable nutrient cycling and N_2O emissions

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N_2O is a potent greenhouse gas involved in the destruction of the protective ozone layer in the stratosphere and contributing to global warming. Soils are a major source of N2O and the belowground interactions that affect its emissions are complex and not well understood. Here we present data, showing that soil biota from various taxonomic groups affect N_2O emissions.

First, we show that arbuscular mycorrhizal (AM) fungi, a dominant group of soil fungi, which form symbiotic associations with the majority of land plants and which influence a range of important ecosystem functions, regulate N_20 emissions from soil.

We manipulated the abundance of AM fungi using two different approaches and in two different soils in the greenhouse. N_2O emissions were increased by 42 and 33% in microcosms with reduced AM fungal abundance compared to microcosms with a well-established AM fungal community. This could partly be explained by increased N immobilization into microbial or plant biomass and reduced concentrations of mineral soil N as a substrate for N_2O emission. Moreover, AM fungal abundance was correlated with the abundance of key genes responsible for N_2O production, indicating that the regulation of N_2O emissions is transmitted by AM fungal induced changes in the soil microbial community.

We also use an outdoor experiment in lysimeters comprising a soil volume of 230 liters to compare effects of a reduced (microbially dominated) vs. an enhanced (soil organisms <4mm, including AM fungi) soil life on nutrient cycling, nutrient losses and N_2O emissions in an agricultural crop rotation. The results indicate that soil biota are a key factor for nutrient use efficiency in cropping systems by enhancing agricultural yields, reducing nutrient leaching losses and reducing N_2O emissions after fertilization.

Our findings suggest that intensive agricultural practices, which exert negative effects on soil organisms, may further contribute to increased nutrient losses and N_2O emissions.

Keywords: Arbuscular mycorrhizal fungi, Nitrous oxide, Sustainability, Agriculture

[P1.058]

Symbiont: a tool for assessing soil vitality based on soil analyses and expert judgement.

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Recommendations for soil and crop management are usually based on chemical and physical soil properties. Soil biology, and/or the interaction between soil organic matter and soil biology, is seldom taken into account due to the high level of complexity when living organisms are involved. The concept of soil ecosystem services may be useful for an integral assessment of the so-called vitality of soil. We describe a tool, Symbiont, that has been specifically developed for making an integral assessment of soil quality including the biological functions and the subsequent identification best management practices.

Symbiont is based on minimal data sets for ecosystem services with particular agricultural relevance, i.e. soil structure, nitrogen mineralisation, and soil health. A stepwise approach is used to analyse the available information and derive practical recommendations for the farmer. Firstly, soil analyses are carried out and the results visualised relative to target values with ‘spider webs’. Secondly, data on soil and crop management at the particular field is collected. This includes information on farmer’s experiences, which is essential for determining actual soil behaviour. Thirdly, interpretation is done by an iterative process between researchers, farmers and advisors. Data are compared with reference values and mirrored to findings from the field. This allows for deriving at recommendations as ‘best guess’.

Expert judgement thus plays an important role in all parts of the assessment, from the selection of indicators for the minimal data sets to the identification of appropriate measures. Other features of the tool include guidelines on: sampling (when, where), number of replicates vs. costs, and technical aspects of best management practices in terms of impact on soil biology, and, eventually, crop yield.

Keywords: tool, agriculture, recommendation, expert judgement

[P1.059]

Soil biodiversity and nutrient cycling in a chronosequence of abandoned agricultural fields

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Land abandonment is considered an effective tool for restoring biodiversity and ecosystem functions. Thus far little attention is given to the role of soil biodiversity. Here, we present results of a soil biodiversity and ecosystem functioning study from a chonosequence of ex-arable fields in The Netherlands (Veluwe LTO). These fields are typically managed by low-intensive grazing while undergoing a transition from an arable system into species-rich grassland. We present a method to investigate the soil biodiversity in the Veluwe chronosequence from the EcoFINDERS field sampling campaign in 2011. Abandoning agricultural fields triggers a change in the species composition and possibly the way species interact. We were able to reconstruct the full soil food web (from microorganisms to earthworms) at 10 fields that were taken out of production at different points in history. In total ~18000 species were found. The co-occurrence of species at different locations was compared by several network presentations. We also present the results of a mesocosm experiment where we have employed 13-C-CO2 pulse labeling and 15-N labeling to assess the short term fate, turnover and retention of recent plant-assimilated carbon and nitrogen in cores with field soil. Samples have been collected of aboveground and belowground plant tissues, soil bacterial and fungal PLFA biomarkers, nematodes, enchytraeids, mites, collembola, earthworms, and other soil fauna. Our aim was to investigate how the carbon and nitrogen is sequestered in the different components of the soil food web in relation to time since abandonment. We used the data from these cores on biomass and carbon-nitrogen contents of the feeding guilds within the soil food web to run an existing carbon/nitrogen flow model for grasslands. We discuss these results in relation to the soil biodiversity network analyses in order to predict the change in ecosystem processes during land abandonment and secondary succession.

Keywords: soil biodiversity, C and N cycling, pulse labeling, network analyses

[P1.060]

Soil biotic interactions and phosphorus availability: from knowledge to agronomic application. Examples from Madagascar

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Agroecological cropping systems are based on an intensification of soil ecological processes. The knowledge of these processes is thus necessary to propose and develop cropping systems in a way that enhance ecosystem services (crop production, carbon sequestration, nutrient cycling, control of soil erosion). These processes depend on biodiversity and more specifically on the complex trophic or non-trophic interactions existing between soil organisms. In the Highlands of Madagascar, the production of rainfed rice on Ferralsols is strongly limited by P (phosphorus) sorption. In traditional systems, soil is tilled, residues are generally exported and P fertilizers are rarely applied; soil biota are strongly depleted and plant production is low. In recent conservation systems, the absence of tillage, and the presence of a cover (crop or mulch) and of legumes ensure a better soil biodiversity and a better plant production.

Recent experiments have shown that earthworm activity results in higher amounts of soil phosphorus available for plants. This improvement is based on different mechanisms: (i) transformation of slowly exchangeable Pi towards quicker Pi pools of exchange (ii) increase of basal soil respiration, fresh organic matter mineralisation and priming effect, (iii) increase of microbial enzymatic activities in gut and fresh casts.

Using this knowledge, we tested in field experiments the effect of earthworm introduction on plant growth. A first trial with *Dichogaster saliens*, a small epi-endogeic earthworm living in the roots of grass has shown an improvement of the number of rice grains reflecting a better P absorption by plants. A second trial with Pontoscolex corethrurus, a true endogeic earthworm has been set up few month ago and first data are under analysis.

The presence of earthworms alone (even if numerous and active) will probably not eliminate the inorganic P deficiencies but their introduction in systems dominated by organic P could improve crop yield.

Keywords: Crop production, Agroecology, Earthworms, Tropical crops

[P1.061]

Response of soil AMF diversity to land use change in a grassland ecosystem

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Arbuscular mycorrhizal fungi (AMF) are ubiquitous plant root symbionts and are known to have essential effects on plant community assembly in most terrestrial ecosystems. Especially during succession presence or absence of fungal symbionts can accelerate or inhibit shifts in plant communities. Plant communities change in response to altered land use practices, and symbiont microbial communities change as well. The patterns of AMF community change in calcareous grasslands and whether they are in concordance with plant community changes remain however, still unknown.

We investigated plant and AMF communities in three successional stages of seminatural calcareous grasslands exposed to land use changes: I. permanently managed, open grassland, II. abandoned, partly overgrown grassland, III. completely overgrown by pine, and one heavily disturbed ecosystem (limestone quarry) in West Estonia . AMF communities in soil and roots were characterised by 454-sequencing of the SSU rRNA gene. Fungal taxa were identified by BLAST matches against a custom-made annotated sequence database (MaarjAM). AMF abundance was estimated from lipid acids.

Plant communities and AMF communities change during the land use driven succession in a similar manner. Species richness is highest in open grassland sites and decreases with shrub and tree encroachment. AMF communities seem to react less quickly to changes from an early (I.) to a mid-successional stage (II.), compared to plant communities. At the latest successional stage under consideration (III.) both - plant and AMF communities - differ strongly from earlier successional stages.

Symbiotic AMF communities in grassland soil undergo substantial changes under changing land use. This information is also significant for grassland restoration. Restoration in medium stages of overgrowth is highly recommended, as the AMF community is still intact and reopening of the landscape sufficient. In later stages of overgrowth reopening paired with inoculation with the grassland AMF community might enhance the restoration success.

Keywords: arbuscular mycorrhiza, plant-fungal interaction, biodiversity, succession

[P1.062]

Effect of winter wheat genotypes on soil health in Australia

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Under increased pressure from climate change and soil pathogens, there is an urgent need to breed towards more sustainable wheat production focussing on root traits. However, little attention has been given to the effect of breeding lines on soil parameters and for this reason here we examine the impact of different wheat lines on the chemical, biochemical and biological soil properties.

We selected 24 wheat lines (*Triticum spp.*) with variable levels of sensitiveness to the fungus pathogen *Fusarium pseudograminearum*. The different lines were planted in a randomized block design in NSW, Australia. At stem elongation plants, roots and rhizosphere soil were collected. Root architecture was characterized using WinRhizo. Soil microbial biomass carbon (MBC) and nitrogen (MBN), dissolved organic carbon (DOC), total dissolved nitrogen (TDN) and inorganic nitrogen were measured. Soil bacterial community structure was characterized by terminal restriction fragment length polymorphism (T-RFLP), while the microbial activity was assessed by fluorescein diacetate (FDA) hydrolysis.

A negative correlation between specific root length and specific root diameter was found ($P < 0.001$, $R^2 = 0.70$), with varieties 249 and Scout having the most contrasting root structure. Line 249 had longer and thinner roots and was associated with the highest MBC (125 µg C g^{-1}) and MBN (12 µg N g^{-1}), while Scout had shallow and thicker roots and was associated with significantly lower MBC (82 µg C g^{-1}), MBN (5 µg N g^{-1}) and with the highest values of nitrate in the soil (1.8 µg g^{-1}). We observed no wheat line effect on the structure and diversity of the bacterial community ($P > 0.05$).

Overall, our results suggest that belowground wheat traits can affect soil parameters; in particular long thin roots may promote microbial growth and nitrogen retention. For this reason we suggest that soil parameters should be considered by plant breeding schemes.

Keywords: Wheat, Soil health, Plant breeding, Root traits

[P1.063]

Soil bacterial and fungal diversity in the most rapidly warming region of Antarctica

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The Antarctic Peninsula and its associated islands constitute the most rapidly warming region of Antarctica. Throughout this region, ice-free terrestrial environments are dominated by vegetation-free soils that harbour microbial communities responsible for ecosystem functioning. Here, in the most extensive survey of maritime Antarctic soils to date, we report patterns of bacterial and fungal diversity and their relationships with latitude, pH and soil organic carbon and nitrogen contents (Fig. 1). Our comprehensive dataset provides a baseline for the future monitoring of maritime Antarctic soil bacterial communities and highlights populations that may represent sentinels of environmental change.

We observed a 42% reduction in the richness of bacterial communities with increasing latitude between the South Orkney Islands (60ºS) and southern Alexander Island (72ºS) (Fig. 1). We also detected small but significant changes in bacterial community composition associated with latitude and pH. Patterns of fungal diversity are still emerging.

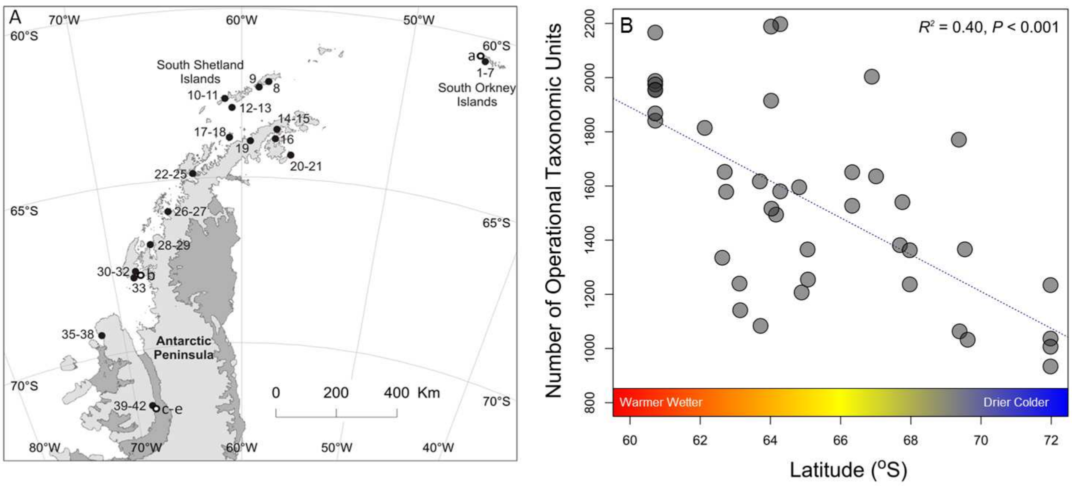

Fig. 1 (A) Location of sampling sites and (B) changes in the richness of soil bacterial communities between 60-72ºS.

It is well established that Maritime Antarctic terrestrial ecosystems become cooler and drier with increasing latitude; therefore, lower temperature and precipitation are likely to be the main drivers for the reductions in soil bacterial diversity at higher latitudes. We predict that the composition of Maritime Antarctic soil bacterial communities will change and the number of taxa will increase as the region continues to warm over future decades.

Keywords: Community ecology, Sequencing, Extreme environments, Climate change

[P1.064]

Plant pathogene repression by soil faunal communities as an ecosystem service for soil health

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Mesocosm-based field studies were conducted to assess the functional linkage between soil faunal communities and plant pathogenic fungi (*Fusarium culmorum*) in crop residues. The hypothesis was that *Fusarium* biomass and the content of its mycotoxin deoxynivalenol (DON) decrease in the presence of soil faunal activity (earthworms: *Lumbricus terrestris,* collembolans: *Folsomia candida* and nematodes: *Aphelenchoides saprophilus*) in a cropping system under on-farm conditions. In 2013, mesocosms were established in the topsoil of a winter wheat field located in Northern Germany. Soil fauna in different combinations (earthworms (E), E + collembolans (C), E + nematodes (N), E + C + N and a non-faunal treatment) was exposed to artificially infected wheat straw (*Fusarium* biomass content: 25.93 mg kg^{-1}) contaminated with DON (40.97 mg kg^{-1}). Wheat straw with a low concentration level served as control. After 4 and 8 weeks, *Fusarium* biomass and DON concentration in residual straw and in soil were determined by using ELISA-method. After 4 weeks the initial *Fusarium* biomass and DON concentration decreased in all treatments, whereas the highest reduction was determined throughout the faunal treatments (*Fusarium* biomass: 47-54%; DON: 78-90%). The reduction of *Fusarium* biomass and DON concentration in the non-faunal control treatments were significantly lower. After 8 weeks a further decline of *Fusarium* biomass and DON concentrations was measured in all faunal treatments (*Fusarium* biomass: 76-82%; DON: 67-85%). However, DON contents in residual straw increased in the non-faunal treatments during the final four weeks. *Fusarium* biomass and DON concentrations in soil were below quantification limits (<0.074 mg kg^{-1}, 0.037 mg kg^{-1}) throughout all treatments, respectively. Our results clearly demonstrate that earthworms, collembolans and nematodes contribute to a sustainable control of fungal phytopathogens and *Fusarium*-related contaminants in wheat straw thus reducing the risk of plant diseases and environmental pollution as an important ecosystem service for soil health.

Keywords: Plant pathogen repression, Mycotoxin degradation, Functional soil biodiversity

[P1.065]

Impact of ancient manuring on soil microbial diversity

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Ancient manuring practice was traced in soils and cultural layers of Alanic sites (Kislovodsk basin, Northern Caucasus, Russia) using peculiarities of microbial communities. Objects of studies were: (i) cultural layers of early Alanic site (AD II-IV) and vicinal soils presently abandoned or used as pasture and (ii) soils around late Alanic site (AD V-VIII) in site-watershed transect (about 2 km). Both sites studied were under one step of occupation in ancient time presently out of exploitation that allowed us to relate all anthropogenic changes of soil properties only with the impact of Alanic population.

Soils in close vicinity to the sites contained large amounts of pottery fragments due to ancient manuring. To trace the fact of manuring urease activity and abundance of thermophilic bacteria in soils were studied.

Urease activity in cultural layers of early Alanic site was significantly higher than in soils on vicinal territory, and on the area around late Alanic site it decreased with distance that correlated with the pattern of pottery distribution in soils along the transect.

The abundance of thermophilic bacteria in soils around the sites decreased as well with distance from 135×103 cells g^{-1} in soils most close to the site to 1×103 cells g^{-1} in soils on the watershed. Basing on this data we can conclude that for 1500 years viable spores of thermophilic bacteria preserved and soils did not undergo total self-purification. The data obtained two orders exceeded the level of thermophilic bacteria in modern manured agricultural plot abandoned for 30 years. High abundance of this group of microorganisms corresponded to the level of presently contaminated soils. The patterns of urease activity and distribution of thermophilic bacteria point to the large amounts of manure and duration of fertilization within the Alanic time.

(Supported by RFBR and Program of Presidium of RAS)

Keywords: microbial communities, urease activity, manuring, anthropogenic soils

[P1.066]

The biodiversity and function to monitor soil pollutant toxicity of electrogenic bacteria in soil

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Introduction: Soil has diverse electrogenic bacteria which are known to be widely distributed in soil. Soil electrogenic bacteria degrade organic compounds and generate electrical power. Our previous study showed that electrical signals generated by soil electrogenic bacteria monitored soil microbial activities continuously and in real time. We therefore hypothesized that the electrical signals can monitor soil pollutant toxicity. We aimed to develop a novel method of low cost and low labor but high sensitivity to detect soil pollutants.

Methods: Soil spiked with different amount of Cu (0 as control, 50, 100, 200 and 400 mg kg^{-1} Cu) and amended with glucose to create a final concentration at 5% glucose (*w*/*w*) was packed into anode chamber of MFCs. Voltage and current of MFCs was monitored every 10 min for 150 h. After MFCs operation, cyclic voltammetry was conducted to determine electrochemical activity of soil micro-organisms in anode chamber. The 16S rRNA gene from anode and soil was subjected to PCR-DGGE, sequencing and phylogenetic analysis.

Results: The voltage reduced, the startup postponed and the quantity of generated electrons decreased with the increasing Cu concentrations. Cyclic voltammogram demonstrated that the electrochemical activity of soil micro-organisms became lower with increasing Cu concentrations. The 16S sequences of recovered anodic bacteria were assigned to *Firmicutes*, including *Bacillaceae*, *Acetobacteraceae*, *Clostridium*, *Bacillus* and *Sporolactobacillus*. The DGGE bands intensity of anodic bacteria decreased except for that of *Firmicutes* and *Bacillus* which increased with elevated Cu concentration.

Discussion: The electrogenic process comprises the degradation of organic carbon and the exocellular electron transfer which is carried out by membrane bound electron transport proteins, such as c-type cytochromes. Therefore the electrogenic bacterial diversity and activity is sensitive to heavy metal pollution. our results indicate that electrical signals generated by soil electrogenic bacteria could be novel indicators to evaluate the ecotoxicity of pollutants.

Keywords: electrical signals, voltage, heavy metal, DGGE

[P1.067]

Recovery of soil mesofauna (Collembola) communities of grassland after summer flooding

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A large part of Germany was affected by a summer flood in 2013. This irregular flood strongly impacted grassland invertebrate communities reducing diversity, abundance and biomass of virtually all groups with the effects increasing with duration of flooding and temperature.

In grassland of different diversity (Jena Experiment) we analysed the recovery of the soil animal community by focusing on Collembola and taking repeated samples after flooding for more than one year. Collembola communities virtually got extinct by the flood but started to recover shortly thereafter. The effect of flooding on Acarina was less severe but recovery was slower.

The ability of soil animals to survive flooding depends on behavioural, morphological and physiological proprieties. The results suggest that Collembola are sensitive to flooding but also able to recover quickly due to high reproductive potential and dispersal ability. Whether their recovery varies with the composition of plant communities is currently investigated and will be presented.

Keywords: grassland, Collembola, flood, impact

[P1.068]

Community structuring of a soil mite community at small scale: relative contribution of dispersal limitation, environmental filtering and biotic interactions

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Identifying what drives community assembly and the maintenance of biodiversity is an important topic in soil animal ecology. A key issue is the relative contribution of environmental filtering, biotic interactions and dispersal limitation. In a temperate deciduous forest of the Maoershan Ecosystem Research Station, Northeast China, we examined the relative importance of environmental filtering, biotic interactions and dispersal limitation on a soil mite community within a regulate sampling grid (50 m×50 m) in 2012 and 2013, respectively. Moran's eigenvector maps (MEM) and variation partitioning was used to disentangle the relative roles of environmental filtering and dispersal limitation. Null mode was used to identify the relative contribution of biotic interactions and environmental filtering. Results showed that spatial variables significantly explained the species composition variation in 2012 and 2013, respectively. Environmental factors relatively low but obviously contributed to the community composition, in which soil pH, soil water content, litter water content, litter dry weight and soil organic matter content were all significantly. Results of null models showed aggregated communities, more positive species pairs, random body size ratio and indicated non-significantly interspecific competition. The results indicated that the soil mite community structuring at fine scale of a temperate deciduous forest depends on both environmental filtering and dispersal limitation, and biotic interactions are relatively not important.

Keywords: environmental filtering, biotic interactions, dispersal limitation, soil mite community

[P1.069]

A meta-analysis of belowground biodiversity impacts on the soil carbon cycle

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Loss of biodiversity can impact ecosystem functioning, such as carbon (C) cycling. Soils are the largest terrestrial C reservoir, containing more C globally than the biotic and atmospheric pools together. As such, soil C cycling, and the processes controlling it, have the potential to affect atmospheric CO_2 concentrations and subsequent climate change. Despite growing evidence of links between plant diversity and soil C cycling, there is a dearth of information on whether similar relationships exist between soil biodiversity and C cycling. This is despite increased recognition that soil communities display high levels of both taxonomic and functional diversity and are key drivers of C fluxes.

We used meta-analysis to quantitatively assess how soil biodiversity affects soil C cycling pools and processes (i.e., soil C respiration, decomposition, and plant biomass). We compared the response of process variables to changes in diversity both within and across groups of soil organisms. Overall, loss of soil diversity significantly reduced soil C respiration (-26%) and decomposition (-18%), but did not affect plant biomass. Analyses separated by types of manipulations show that loss of within-group diversity significantly reduced soil C respiration, while loss of across-group diversity did not. Decomposition was negatively affected both by loss of within-group and across-group diversity. Further, loss of microbial diversity significantly reduced soil C respiration, while loss of soil faunal diversity did not. In contrast, decomposition was negatively affected by loss of soil faunal diversity, but was unaffected by loss of microbial diversity.

Although understanding the complex relationships between soil biodiversity and C cycling processes is currently limited by a number of methodological concerns, our findings show that loss of soil biodiversity can strongly impact on soil C cycling processes, and highlight the importance of diversity across trophic levels (e.g., primary and secondary consumers) for maintaining full functionality.

Keywords: Carbon cycling, Meta-analysis, Biodiversity-ecosystem functioning, Soil food webs

[P1.070]

Ants as indicators of soil-based ecosystem services in agroecosystems of the Colombian Llanos

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Ants, fulfill key roles in the maintenance of energy and material flow in soils they performed. many functions like the constant rearrangement of soil particles, favoring the movement of organic matter and rapid mineralization of litter and organic residues. We tried to understand the impacts of agricultural management on ant communities in the eastern Colombian Llanos and to identify species that could be used as indicators of soil-based ecosystem services. 5154 ant individuals were collected and identified from the soil and litter layer within 75 fields (nine TSBF in each field) divided among five common agricultural land uses in the region: 1) annual crops (maize-soy-rice), 2) rubber plantations, 3) oil palm plantations, 4) improved pastures and 5) semi-natural savannas. As expected, land management was found to greatly influence ant communities. Improved pastures showed the highest species richness and semi-natural savanna the greatest abundance of ants. Within each of these fields a suite of soil and agroecosystem characteristics were measured and combined into synthetic indicators of five soil-based ecosystem services: 1) nutrient provision, 2) water storage and regulation, 3) maintenance of soil structure, 4) climate regulation services and 5) soil biodiversity and biological activity. Ant species were then associated with these synthetic indicators using the IndVal method to identify indicator species for each consolidated ecosystem services measured. In total, 14 indicator species were identified and found to be significantly associated with either the high or low provision of each of the five services. Our findings suggest that land use greatly impacts ant abundance and community diversity, and that an improved understanding of these effects could greatly contribute to biodiversity conservation and ecosystem functions at the regional scale. Also, the development of bioindicators offers a rapid and relatively inexpensive tool to facilitate land management and policy decisions in this region of Colombia.

Keywords: Agricultural intensification, Formicidae, Indicator species, Tropical savanna

[P1.071]

Soil biodiversity and disease suppression in relation to organic matter management.

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Soil biodiversity is considered a vital factor for several soil ecosystem services such as disease suppression. In general, disease suppression depends on the presence and activity of a wide variety of soil microbes, competing, consuming and otherwise antagonizing pathogens in their saprophytic phase. Presumably, rich and divers soil biota will harbour more antagonistic species than poor soil biota. In agricultural soils, the biodiversity is fundamentally reduced by monoculture and stringent soil management practices, like frequent ploughing, soil fumigation and other broad spectrum measurements for disease control. However, since the use of pesticides and fertilizers is increasingly restrained, growers need to rely more and more on the natural capacity of the soil to harvest a healthy crop. In order to sustain the productivity of agricultural soils, organic matter management has been put in the centre of attention, affecting physical, chemical and biological properties of the soil. In three long term field experiments with flower bulb crops on sandy soil, different organic matter management strategies were applied, including amendment of peat, compost and green manure crops. Effects of these amendments on biodiversity of the nematode and microarthropod communities and other soil parameters were assessed. Furthermore, disease suppression against four different soil borne pathogens, i.e. *Pythium intermedium, Rhizoctonia solani, Pratylenchus penetrans* and *Meloïdogyna hapla*, was measured using bioassays. Organic matter amendment significantly increased disease suppression against each of the tested pathogens in one or more experiments. Based on biplots and model selections, significant correlations were found between disease suppression and several biological-, physical- and chemical soil parameters, depending on the pathogen. Correlations between Shannon-Weaver diversity indices and disease suppression will be discussed including the relevance and practical implications of the results with respect to organic matter management.

Keywords: microbial biomass, nematodes, microarthoropods, flower bulbs

[P1.072]

The oribatid mite community of a German peatland in 1987 and 2012 - effects of anthropogenic desiccation and afforestation

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In many European countries more than 90% of the peatlands were destroyed through drainage for agriculture and forestry, but the knowledge about consequences for soil organisms is scarce. The current study presents a comparison of the oribatid assemblages recorded in 1987 and 2012 from a Sphagnum bog that has suffered from drainage between the two periods. Furthermore, the oribatid mite fauna of seven sampling sites in adjacent peatland habitats (Molinia meadow, spruce afforestation, birch wood) was recorded in 2012. The study addresses the following questions: 1) which environmental factors determine the oribatid species composition in the peatland complex? 2) how do anthropogenic desiccation and afforestation influence the oribatid assemblage? CCA indicates that species distribution was closely related to cover of herb-leaf-litter and needle-litter, soil moisture and vegetation temperature index. All sampling sites in the spruce afforestation contained similar sets of common species and no Sphagnum bog-specific species were detected. In the Molinia meadow as a degenerated part of the Sphagnum bog, bog-specific species were scarce, but species richness was higher than in the Sphagnum bog due to a large number of species characteristic for forest habitats.

In the Sphagnum bog, species richness and density were heavily reduced from 1987 to 2012 due to ongoing desiccation. Several bog-specific species have apparently disappeared. The results indicate that at the beginning of desiccation in Sphagnum sp. oribatid species richness is reduced. However, after vegetational changes to, e.g., a Molinia meadow, oribatid species richness increases again due to immigrating species that are characteristic for forest habitats and euryoecious species. Oribatid mites can therefore serve as indicators of peatland quality. In a future German Barcode of Life-Project barcoding methods for oribatid indicator species will be developed.

Keywords: Oribatida, peatland, drainage

[P1.073]

Termite communities in preserved and regenerating miombo woodlands in Burundi

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Burundian miombo woodland is endangered due to the destruction of natural ecosystems consecutive to the high population pressure and the demand for farmland. This ecosystem, dominated by leguminous trees (mostly *Brachystegia* spp.), is characterized by the presence of large termite mounds (*Pseudacanthotermes spiniger* and *Odontotermes* sp., Macrotermitinae), which structure plant and animal communities. They may also influence the termite community itself, which is of utmost importance in nutrient recycling.

The goal of our study was to evaluate the role of the large termite mounds in structuring the whole termite assemblage in preserved miombo, and its recovery during miombo regeneration.

We compared a well-preserved area (Rumonge forest), a more disturbed miombo fragment on Nkayamba hill next to Rumonge town, and an adjacent area in regeneration since 2009 after clearing and cultivation. In each site, three grids of 7x7 quadrats of 5 m^2, 10 m apart, were searched for termites. Mounds were searched separately from the forest matrix.

We collected a total of 1070 termite samples, representing 24 species, of which 13 were soldierless soil-feeders. The richness and species diversity were slightly higher in termite mounds than in the forest matrix, and the Rumonge forest was richer than the Nkayamba sites. Only four species (one *Coptotermes* and three Macrotermitinae) were found in the regenerating forest. Large Macrotermitinae mounds were still at an early stage of construction, and soil-feeders were completely absent.

The overall termite fauna of the Burundian miombo is similar to that found in the same ecosystem in Malawi, particularly rich in soldierless species. Like other authors, we observed the very high sensitivity of soil-feeders to environmental disturbance. The direct contact with the preserved and regenerating parts of the Nkayamba hill should allow us to follow the dynamics of mound re-building by Macrotermitinae and the recolonisation by soil-feeders in the regenerating miombo.

Keywords: miombo, Macroterminitae, termite mound, termite assemblage

[P1.074]

Alternative cultural practices promote soil clitellate oligochaeta

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Earthworms and enchytraeids are of great importance in soil agroecosystem functioning. Whilst the impacts of agricultural management on earthworms have been widely studied, the ecology and response of enchytraeids to agricultural practices are far less well documented. The present study aimed at (1) improving our understanding of how the abundance and biomass of these soil organisms are affected by alternative cropping systems and cultural practices in two long-term experimental trials located near Paris, and (2) better defining the relationships linking earthworm and enchytraeid communities. The first trial compared fields with repeated inputs of fresh manure or sewage sludge to a system without organic fertilization. The other trial compared four cropping systems, differing mainly in soil tillage, crop rotations, pesticide use and mineral fertilization: a conventional, an integrated, an organic, and a living mulch cropping systems (with no ploughing and a permanent living cover crop). Earthworm and enchytraeid communities were sampled during spring 2014.We found an overall positive effect of alternative cultural practices on the studied terrestrial oligochaeta. Organic matter inputs promoted earthworm density but no differences were found for enchytraeids. Earthworm density was not significantly different between the four cropping systems but it was 1.5 to 2 times higher in the organic and the living mulch systems than in the two others. These systems also had a positive effect on enchytraeids, ascribed to effects of the permanent plant cover and no use of pesticides. No significant correlation was found between enchytraeids and earthworms. For a better understanding of the relationship between these soil organisms, more information should be collected at the species level.

Keywords: Earthworms, Enchytraeids, Cropping systems, Agricultural fields

[P1.075]

Promoting earthworm abundance by reducing pesticides in agricultural systems

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The loss of biodiversity in soils under conventional intensive agricultural land use is a major environmental issue that called for the design of new cropping systems, such as organic farming and low-input cropping systems. Earthworms may be affected by pesticide applications, especially species living close to the soil surface. Based on empirical data obtained from conventional and organic cropping systems in different sites near Paris, we established simple relationships between the Treatment Frequency Index (a phytosanitary indicator of pesticide pressure) and the abundance of three earthworm species (*Allolobophora chlorotica*, *Lumbricus castaneus* and *L. terrestris*) living in the soil's surface horizon. Insecticides had more negative influence on earthworm species than herbicides and fungicides. We also found that the more time an earthworm species spends on or near the soil surface, the more it is affected by pesticide application. If the Treatment Frequency Index was halved, as is currently required by some European regulations, the density of these three earthworm species could be multiplied by a factor 1.5 to 4. Our findings demonstrate that a reduction in pesticide application favors an increasing of earthworm population density in agricultural fields, representing a major functional benefit for agroecosystems.

Keywords: Treatment Frequency Index, Organic farming, Conventional cropping system, Insecticides

[P1.076]

Soil Biodiversity And Soil Texture Control Energy Crops Performance

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Replacing annual energy crops with perennial is a key strategy to improve sustainability in production of renewable agricultural biomass.

The aim of this study was to investigate the influence of earthworms and collembolans in the performance of conventional and alternative bioenergy crops (*Z. mays* and *S. perfoliatum*) taking into account two soil textures, silty sand soil (65%) and clayey silt soil (67%).

For this purpose, a soil-plant-animal system was installed under greenhouse conditions for 42 days and followed a randomized block design. In total, 80 phytocosms were prepared, considering five replicates for each treatment: one treatment inoculated with earthworms (*Lumbricus terrestris*), one treatment inoculated with collembolans (*Folsomia candida*), a mixed treatment and one without animals which served as control. All phytocosms were closed at the bottom with nylon-mesh (20 µm) to avoid earthworms and collembolans to escape. Furthermore, the top of the phytocosms were covered with similar mesh prevent collembolans from escape and to reduce evaporation.

During the experiment samples of percolation water were taken and analyzed for ammonia and nitrate. Population densities and biomass of earthworms as well for plant shoots and roots were determined before and after the experiment. For microbial biomass, post-incubation analyses with pure soil were performed via SIR method.

The results show a positive influence of earthworms on plant growth and differences between the two energy crops. The cup-plant performance is higher in sandy than clayey soil. Root and shoot biomass of maize crops from clayey soil had a stronger growth in the treatments with earthworms rather that control. Nutrient consumption was higher in growing of maize crops that cup plant. Crops rhizosphere and soil fauna enhanced microbial biomass. The results showed higher benefits of cup plant from silty sand soil rather than to clayey silt contrary to maize.

Keywords: earthworms, collembolans, Silphium perfoliatum, Zea mays

[P1.077]

Monitoring soil biodiversity in nature reserves in England - a role for metabarcoding

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Natural England is the statutory nature conservation body for England and undertakes monitoring on its National Nature Reserves to detect changes in biodiversity and ecosystem function, including soil properties. Baseline tRFLP data have characterised microbial communities among sites sampled, but extracts of soil mesofauna are proving challenging to identify using only trained volunteers. Metabarcoding provides a potentially rapid, cost-effective alternative for monitoring soil mesofauna and characterising their communities.

We explored metabarcoding approaches for characterising soil communities from three different types of chalk grassland: (i) species-rich,(ii) agriculturally improved and (iii) naturally reverting grassland. Metabarcoding analyses on COi and 18S RNA genes were conducted for bulk soil and Tullgren mesofauna extracts, and compared with morphological identification approaches. Community genetic information was cross referenced to international genetic databases (Greengenes and GenBank), and to a *de novo* COi (barcode fragment) database generated from some 200 vouchered specimens collected from the sites.

18S RNA sequencing from bulk soil extracts provided the broadest representation of soil communities, representing mesofauna, plants, algae, fungi and protists, but sequences could not be matched to ecologically appropriate species using the global database. Morphological identification, COi metabarcodes from Tullgren extracts and both 18S RNA approaches (bulk soil and Tullgren extracts) revealed distinct and congruent differences in soil communities between grassland types. All approaches except bulk soil extracts reported more collembola in agriculturally improved grassland and more acari in the species-rich grassland soil. Using the *de novo* database alongside GenBank significantly improved matching of COi metabarcode operational taxonomic units over attempts to identify taxonomies using GenBank alone, and described more ecologically realistic communities.

Metabarcoding approaches show good potential for characterisation and monitoring of soil mesofauna communities but there is clearly a need for increased effort to develop species barcodes to help identify realistic soil communities.

Keywords: metabarcode, mesofauna, grassland, monitoring

[P1.078]

Functional profiles of soil microbial populations under various climatic conditions and agriultural practices in Burkina-Faso

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BIOSOL is a multidisciplinary scientific program (soil science, agronomy, geography) which aims at understanding and promoting agro-ecological practices among peasant communities in Burkina-Faso.

In this work, the pedological, geochemical and microbiological characteristics of agricultural soils were investigated in order to make an inventory of soil fertility in contrasted pedo-climatic contexts. The effects of agricultural practices on biomass, community structure and activity of micro-organisms were investigated for 19 different soils in parallel with the determination of various pedo-physical and chemical parameters.

Two sites (villages of Sampiéri and Bandougou) with contrasted pedo-climatic conditions were selected. From 19 samples (top soils), we determined the microbial biomass and community level physiological profiles (CLPP) by using the MicroResp^{TM} system. The soil samples were also evaluated for soil physico-chemical characteristics such as the in-situ moisture content, organic carbon and nitrogen concentrations, conductivity and pH together with their structure and texture and other soil physical parameters.

Except for one site (test plot), it appears that the microbial biomass for all samples are low. Metabolic quotients (qCO2) are very different and compared to samples from Sampiéri, statistically higher for samples from Bandougou, reflecting disturbed soils for these latter. Shannon diversity index were quite similar for all the samples.

Results from this study showed that the soil ecosystem from Bandougou have significantly influenced the functions of soil microbial community and hence probably its composition. More generally, catabolic diversity of soil microbial community is variable under contrasted climatic and the influence of various cultural practices. This may indicate that the efficiency of soil quality restoration is under the control of many factors which could be further investigated.

Keywords: agriculture, Burkina, crops

[P1.079]

Soil microbial diversity and related soil functioning in urban parks

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Several ecosystem services are provided by ecosystem functioning and especially soil functions.

The main thrust of this work was to improve the knowledge concerning soil biodiversity and related ecosystem services in soils from urban parks in several cities of the Région Centre, Orléans. The biodiversity of urban soils and the drivers that control this biodiversity are in fact poorly known. Moreover information on the functioning soils of urban parks is rare and even poorer concerning the link between these soils and their biodiversity.

In this work, the pedological, geochemical and microbiological characteristics of surface soils were investigated in order to make an inventory of soil fertility in several urban parks of te major cities of the Région Centre, France. The effects of agricultural practices on biomass, community structure and activity of micro-organisms were investigated in these soils in parallel with the determination of various pedo-physical and chemical parameters.

We determined the microbial biomass and community level physiological profiles (CLPP) by using the MicroResp^{TM} system in topsoils. The soil samples were also evaluated for soil physico-chemical characteristics such as the in-situ moisture content, organic carbon and nitrogen concentrations, conductivity and pH together with their structure and texture and other soil physical parameters.

Except for one site it appears that the microbial biomass for all samples was high. Metabolic quotients (qCO2) were in contrast variable for the different parks whether Shannon diversity index were quite similar for all the samples.

Results from this study showed that the soil ecosystem have significantly influenced the functions of soil microbial community and hence probably its composition. More generally, catabolic diversity of soil microbial community is variable under the influence of various cultural practices and geological contexts.

Keywords: Urban, Parks, Soil function

[P1.080]

Study of changes in the characteristics of an olive grove soil after irrigations with compost tea

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Sewage sludge is generated as a result of conventional treatments of wastewater treatment plants (WWTPs). This sludge is used to make compost and compost tea. The use of these products is beneficial to the soil in several ways, as they have been demonstrated. For this reason compost tea could be used as amendment in olive grove soil, soils with serious degradation problems.

In this context, the aim of this experiment was study, in pots conditions, the evolution of physic-chemical and microbiological parameters of an olive grove soil, incubated under controlled laboratory conditions, watered with different doses of sewage sludge compost tea.

For this, 56 pots were made using olive grove soil (<2mm) and watered with sewage sludge compost tea, following 4 treatments varying the amount of compost tea added. All the pots were incubated at 21 ºC and at 35 ºC, for a period of 90 days. The samples were destructively collected at 4, 8, 15, 30, 45, 60 and 90 d for chemical and microbial analyses: Count of viable microorganisms, enzymatic activities and biodiversity using qPCR and DGGE techniques.

Our results showed that the addition of compost tea increased the number of microorganisms present in the soil. However, no significant effect on the enzymatic activities was observed as consequence of the addition of compost tea into the agricultural soil. Finally, AOB and AOA populations showed similar characteristics in amended soil suggesting a important stability under our experimental conditions.

Keywords: COMPOST TEA, MICROCOSMS, ENZYMATIC ACTIVITIES, BIODIVERSITY

[P1.081]

Effect of tree species mixture on earthworm communities on a continental scale

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The belowground food web represents a major part of associated biodiversity in forest ecosystems, and plays a significant role in the ecosystem processes of litter decomposition and nutrient turnover. Past research has demonstrated overwhelming evidence of strong tree species identity effects on earthworm communities. It has been proposed that increased plant community diversity would be beneficial to the abundance and diversity of the belowground food web, but effects of tree species diversity on earthworm communities have seldom been reported, and are inconclusive.

In this study at continental scale we evaluated whether tree species diversity positively affects earthworm biomass and diversity. For this purpose the FunDivEUROPE Exploratory Platform was used with 209 plots in 6 regions well spread over Europe with a low within-region site variability, but a within-region tree species diversity gradient from monocultures to 3 or 4 species plots. In every plot earthworms were sampled using a combined method of mustard extraction and hand sorting of litter and a soil monolith. Data are being analysed with multivariate tools and mixed effects models.

First results suggest only limited influence of tree diversity on the biomass of earthworm communities at continental scale. Tree diversity effects are weak, context specific and interacting with tree identity. In nutrient poor soils we found a negative tree diversity effect on earthworm biomass when deciduous monocultures are enriched with coniferous species, while in rich soils we found a positive tree diversity effect which could be related with the food security this provides to the earthworm community.

Keywords:

[P1.082]

Variations of soil microbial diversity and communities' assembly history: what matters for ecosystem functioning?

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Microbial communities have a central role in ecosystem processes by driving the Earth's biogeochemical cycles. However, the importance of microbial diversity for ecosystem functioning is still challenged, notably because of the "functional redundancy". We recently showed that a reduction in denitrifier diversity resulted in a significant decrease in potential denitrification activity. However, our comprehension of the rules governing the assembly of bacterial populations and determining their structure is limited. In this study, we aimed at understanding how communities of different levels of diversity assemble when colonizing a sterile soil, how invasions with exogenous populations impact their structure and composition, and if these changes in population structure and diversity are causing changes in N-cycle activities.

Therefore, we experimentally manipulated the soil microbial community structure and the history of communities' assembly. We separately inoculated sterile soil microcosms with two different microbial communities extracted from native soils (Epoisses in France and Ulleråker in Sweden) at four different dilution levels in triplicate. After 44 days of colonization, flasks were reinoculated with one or the other community at two different dilution levels in triplicate mimicking an invasion process, while control microcosms for each soil and at each dilution were either sampled after 44 days or kept unchanged until the end of the experiment. The invaded and the control microcosms were finally sampled after 105 days.

For each microcosm, the abundance of different N-cycle microbial guilds was measured by qPCR and total bacterial diversity was determined by *16S rRNA* gene amplicons sequencing. NH_4^+, NO_3^- pools, and total mineral N content were quantified as a proxy for global N-cycle activities.

Our results revealed that the dilution/colonization experiment impacted drastically the structure and the activity of the soil microbial communities with either nitrification or denitrification favoured depending on the initial dilution. Invasions of established populations with a 2nd one had various effects on microbial community structure and activities depending on the origin of the established populations and the level of diversity of the invading ones. Altogether, our work suggests that changes in microbial community diversity resulting from erosions of diversity and/or invasions of exogenous populations can have dramatic consequences on N-cycle functioning in soils.

Keywords: Functional redundancy, microbial community structure, assembly, N-cycle

[P1.083]

Environment or space - What matters for snail community composition

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Soil macro-invertebrates are part of a highly diverse soil fauna and have been recognized to play an important role in key ecosystem functions, such as decomposition. However, relatively little is known about factors controlling the abundance and distribution of soil fauna. Besides biotic and abiotic factors, spatial heterogeneity plays a key role in soil ecosystems. In order to understand how communities are structured it is therefore crucial to investigate the relative importance of these factors by including spatial components in the analyses. We used long-term broad scale data on terrestrial snails collected in South Sweden by the Gothenburg Natural History Museum to examine the relative role of environmental and spatial variables in explaining community composition. Instead of species composition we analysed trait composition because traits directly link organisms` performance to environmental conditions. The data were analysed using variation partitioning based on redundancy analysis. We hypothesized that both, environmental and spatial components, would play an important role, but that environmental variables would have a stronger influence on community composition. The variation in community trait composition was jointly explained by environmental and spatial variables (total 41.1%) whereby the environmental component (represented by local conditions, such as type of habitat, pH and wetness) contributed considerably more than the spatial component. Including spatial components into our analysis enabled us to disentangle the true trait-environment relationship (niche-based process) from processes creating spatial pattern independent of the environment.

Keywords: variation partitioning, functional traits, PCNM, Gastropoda

[P1.084]

Edisp : Lessons learned from a four years project on earthworm biodiversity and dispersal

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Dispersal is a central process in the maintenance and recovery of biodiversity. However dispersal patterns and their determinants are still poorly documented, particularly in soil organisms. As a consequence, a large part of the determinants of soil biodiversity is still not understood.

We present the results of a four years project on dispersal in earthworm, a key organism in the maintenance numerous soil ecosystem services. With a combination of (1) a multi-scale field approach, (2) laboratory work, (3) a meta-community analysis and (4) and a landscape genetic study, we identify central mechanisms influencing earthworm dispersal in a typical agroecosystem, and we show the importance of dispersal for the maintenance of specific and genetic biodiversity.

Our capture-recapture experiment in homogenous environment shows that earthworms can disperse at maximum 35 m per year. The landscape genetic approach, focused on two species, *Allolobophora chlorotica* and *Aporrectodea icterica*, shows a significant relationship between landscape structure and genetic structure, suggesting that dispersal is a limiting factor for earthworm genetic diversity. Interestingly these two species responded to landscape structure at different spatial scales, showing that dispersal rules are species specific. The metacommunity approach suggests that passive dispersal plays a significant role in the maintenance of species diversity, whereas the role of competition on community structure of earthworms seem to be restricted to the plot scale and plays no significant role at the landscape scale. Finally behavioural experiments show that active dispersal is strongly determined by environmental conditions such as habitat quality, conspecifics density and the degree of soil modification by earthworm activities.

Overall the results of this project suggest that mechanisms of earthworm dispersal strongly differ according to the spatial scale considered. At the local scale, earthworms track optimal conditions and thus active dispersal – and biodiversity - are strongly determined by local conditions. At larger scales, such as landscape scale, passive dispersal – highly constrained by human activities - plays a fundamental role in the maintenance of earthworm biodiversity.

Keywords: spatial distribution, biodiversity, dispersal, earthworm

[P1.085]

Hierarchization of environmental factors inducing spatial variations in microbial diversity and functions involved in C cycle in Mediterranean forest soils

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Since the 1850s, an increase of 30% of carbon in the atmosphere has been showed to induce a greenhouse effect. Storage of carbon in soils can be considered as a valuable strategy to mitigate climate changes. Several studies have investigated how sylviculture may influence carbon-storage potential of forest soils. However, neither the ecological factors controlling carbon storage nor their spatial hierarchization have been clearly identified.

Plant debris are transformed in soil via humification and mineralization, leading either to carbon sequestration or emission of CO_2. Bacterial and fungal communities are involved in these transformations *via* the various extracellular enzymes they produced. In the current study, our main aim was to disentangle the influences of forest stand, edaphic and climatic conditions structuring at different spatial scales the microbial communities and their activities. We hypothesized that environmental factors considered at a regional scale (climate and forest stand of Meso-Mediterranean and Supra-Mediterranean bioclimates) influence microbial communities and thus C cycle more strongly than exposition, soil properties or forest stand at the meso-local and local scales respectively. We used a spatially structured experimental design in the Provence-Alpes-Côtes d'Azur region to assess variations in soil microbial enzyme activities and catabolic functions through the three spatial scales.

Venn diagrams showing the part of variance explained by the different environmental factors studied, indicated that forest mixity at a local scale influenced more strongly enzyme activities (11.3 % of variance, $P<0.05$) than forest stand at regional scale (5.6%, $P<0.05$) and exposition at meso-local scale (3.9%, $P>0.05$). At a local scale and for both bioclimates, in soils of pinewoods, a higher aromaticity ratio and lower nitrogen contents were associated with low cellulase activities, while in oakwoods, cellulose mineralization was favored. Our results also highlighted that the environmental conditions in the Meso-Mediterranean bioclimate seems to favor carbon storage in soils.

Keywords: Microbial functions, Bioclimate, C stocks, Variance decomposition

[P1.086]

Do afforestation and fly ash-aided phytostabilisation of highly contaminated soils affect soil fauna communities?

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A large scale pilot study of soil remediation was set up around a former smelter 14 years ago in Northern France. A former agricultural parcel, near the past Metaleurop-Nord plant, was divided into three plots: a reference plot with no amendment (R), the second amended with silico-aluminous fly ashes (F1) and the third with sulfo-calcic fly ashes (F2). These 3 plots were then planted with a tree mix. Although this aided phytostabilisation (trees+ashes) is efficacious in reducing metal bioavaibility to plant species, no studies were performed to determine the effect of this remediation on soil fauna communities.

The aim of our study was to determine whether fly ash-aided phytostabilisation of highly metal contaminated soils influenced *in situ* earthworms, carabids and soil mesofauna (collembola and acari) communities. In order to assess the effects of both phytostabilisation and aided-phytostabilisation, surrounding plots with similar metal levels but differing by use and cover were taken into account as control.

Data obtained for earthworms, carabids and soil mesofauna were analysed through abundance or density, specific richness and specific functional traits. The afforestation with a tree mix was shown to increase both abundance and species richness compared to monospecific tree plots or unplanted plots for the three groups. Fly-ash aided-phytostabilisation did not appear to be more benefit than single phytostabilisation. However, R appeared to be the plot with the best conditions for acari and euedaphic collembolans. Concerning earthworm species, fly-ash amendments decreased density of the epigeic worms *Lumbricus castaneus*, more in contact with the soil/ashes mix, and increased density of anecic worms *L. terrestris.* These results may explain the greater abundance of the large carnivorous carabid species *Pterostichus madidus*.

Afforestation, using tree mix, appears to favour soil fauna communities and thus represents a valuable tool for a sustainable restoration of regional metal contaminated soils.

Keywords: Phytoremediation, fly ash amendments, soil metal contamination, soil fauna communities

[P1.087]

Microbial food web links uncovered - probing carbon fluxes in the maize rhizosphere

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Plants allocate a significant amount of their photosynthetically fixed carbon (C) to promote microbial associations in their rhizosphere. It has been assumed recently that these belowground C-inputs form the major energy source driving the entire food web in soils. However, only few studies to date were able to picture specific microbial food webs depending on fresh root C-inputs, even though great efforts have been made to understand rhizosphere microbiota. It is now well-known that each plant species strongly interacts with a distinct subset of the soil microbial community colonizing its roots, i.e. its rhizosphere “microbiome”, but a detailed understanding of the C flows from the microbiome through the fungal and bacterial energy channels into soil food webs is needed to comprehensively understand terrestrial C cycling.

In a plant labeling experiment using combined rRNA-SIP with ^{13}C-labeled rhizodeposits and pyrotag sequencing we traced the C flow from maize (*Zea mays* L.) roots through communities of rhizosphere fungi, bacteria and heterotrophic protists. We found a highly diverse active microbial community in rhizosphere as well as in bulk soil, but only specific subsets of distinct taxa actively relied on fresh root-C. Mycorrhizal fungi within the *Paraglomerales* were the determinant factor for the allocation of plant-derived C into soil communities, thereby connecting food webs of rhizosphere and bulk soil. We unravel the organization of the rhizodeposit-associated microbial soil food web, identify specific microbial key players also within rhizosphere bacteria (e.g. *Mucilaginibacter, Opitutus, Sphingobium*) and protozoa (e.g. *Thaumatomonadida, Bicosoecida, Leptomyxida*), and detect a highly dynamic succession of plant-derived C through the respective microbes. These insights are crucial to improve our current perspective of the plant-associated microbial functional diversity and of the trophic interactions at the basis of soil food webs.

Keywords: rhizosphere, carbon flow, microbial food web, stable isotope probing

[P1.088]

Soil biodiversity as a tool to restore heavy metal polluted salt marshes

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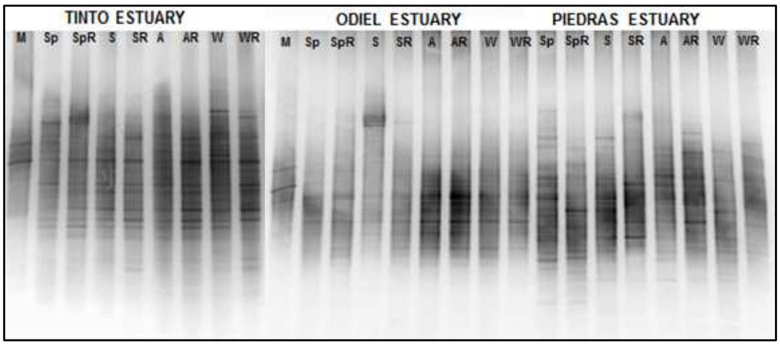
The joint estuary of Tinto and Odiel rivers in Spain is one of the most polluted areas by heavy metals in the world. It is a natural area protected by provincial and state policy plans that needs restorative intervention. By contrast, the Piedras estuary, 30 km away, maintains its environmental quality. In these estuaries, the indigenous cordgrass *Spartina maritima* grows naturally, making it useful for phytostabilization of estuarine sediments, which may be improved by inoculation with endogenous plant growth promoting rhizobacteria (PGPR). Within this scenario, bacterial estuarine soil biodiversity plays an utmost important role. It may allow the isolation of useful PGP strains. Moreover, studying the impact of pollution and environmental conditions on biodiversity is necessary to design *in situ* inoculations, as planned within regional projects agenda.

Cultivable bacteria were isolated from the rhizosphere of plants from polluted estuaries, characterized and tested in greenhouse experiments. Concurrently, Denaturing Gradient Gel Electrophoresis (DGGE) was performed for rhizosphere and bulk soil from the three estuaries in every season throughout an entire year.

Most of cultivable bacteria were different among the estuaries, despite colonizing roots of the same plant species. Regarding both cultivable and non-cultivable bacteria, the Piedras estuary showed the highest bacterial biodiversity, deeply affected by seasonal changes. On the other hand, in the Tinto and Odiel estuaries, neither plant roots nor seasonal variation had any marked effect on the bacterial populations observed. See the figure below.



M: Marker
Sp: Spring, bulk soil
SpR: Spring, rhizosphere soil
S: Summer, bulk soil
SR: Summer, rhizosphere soil
A: Autumm, bulk soil
AR: Autumm, rhizosphere soil
W: Winter, bulk soil
WR: Winter, rhizosphere soil

These results indicated that biodiversity in these soils is not completely related to the plant species they inhabit with, but to environmental conditions. This observation should provide for better management of resources in land decisions, as every estuary may need to be restored differently. This work is an important approach about the role of biodiversity in conducting restoration strategies in order to preserve native ecosystems.

Keywords: heavy metal, salt marsh, phytostabilization, PGPR

[P1.089]

Soil biodiversity as a major driver for the control of populations of the pathogenic bacterium Listeria monocytogenes in soil

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Untangling the linkages: Elucidating relationships between soil biodiversity and ecosystem functioning and ecosystem services

Disease regulation is one of the many services that ecosystems provide. Agroecosystems are dedicated to the provision of high quality, safe food and sustainability is a major issue. Biological contamination of the food supply may raise food safety issues. Prevention of contamination of the food supply requires a thorough understanding of the ecology of pathogenic microorganisms. Listeria monocytogenes is a food pathogen found in many habitats including soil, plants, water systems and food processing factories. We designed microcosm experiments to decipher extrinsic factors that drive the fate of this model of Human pathogen in soil.

We analysed population dynamics over 80 days after inoculation of a large set of 100 soils selected from the French Réseau de la Qualité des Sols (RMQS), a country-wide venture of monitoring of the quality of soils in France. The population of L. monocytogenes decreased over time but the survival ratio depended on the soil under scrutiny. Detailed information such as soil characteristics and land use were integrated into an analysis of variance. Chemical properties, especially the basic cation saturation ratio and soil texture were factors affecting survival of L. monocytogenes.

Analysis of the results collected under similar experimental conditions in the same set of soils but sterilised by ionisation indicated that the endogenous soil microbiota had a major impact on the decrease of the population of L. monocytogenes.

This prompted us to investigate the relationship between the biodiversity of the soil microbiota and the inhibition of the population of L. monocytogenes. By a dilution to extinction approach, we investigated the consequences of soil diversity erosion on the fate of a human bacterial pathogen in the telluric environment. Diversity analysis showed that both soil diversity and phylogenetic composition affected survival of L. monocytogenes.

Overall, our results demonstrate that soil biodiversity is a major driver that limit invasion of soil by pathogenic bacteria.

Keywords: agroecology, biological invasion, diversity erosion, pathogenic bacterium

[P1.090]

The decomposer food-web base impact on ecosystem biogeochemistry: revising the fungal-to-bacterial divide

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Resolving fungal and bacterial groups within the microbial decomposer community is thought to capture disparate microbial life strategies, associating bacteria with an r-selected strategy for carbon (C) and nutrient use, and fungi with a K-selected strategy. Additionally, food-web models have established a widely held belief that the bacterial decomposer pathway in soil supports high turnover rates of easily available substrates, while the slower fungal pathway supports the decomposition of more complex organic material, thus characterising the biogeochemistry of the ecosystem.

Three field-experiments to generate gradients of SOC-quality were assessed. (1) the Detritus Input, Removal, and Trenching – DIRT – experiment in a temperate forest in mixed hardwood stands at Harvard Forest LTER, US. There, experimentally adjusted litter input and root input had affected the SOC quality during 23 years. (2) field-application of ^{14}C labelled glucose to grassland soils, sampled over the course of 13 months to generate an age-gradient of SOM (1 day – 13 months). (3) The Park Grass Experiment at Rothamsted, UK, where 150-years continuous N-fertilisation (0, 50, 100, 150 kg N ha^{-1} y^{-1}) has affected the quality of SOM in grassland soils. A combination of carbon stable and radio isotope studies, fungal and bacterial growth and biomass measurements, and C and N mineralisation (^{15}N pool dilution) assays were used to investigate how SOC-quality influenced fungal and bacterial food-web pathways and the implications this had for C and nutrient turnover.

There was no support that decomposer food-webs dominated by bacteria support high turnover rates of easily available substrates, while slower fungal-dominated decomposition pathways support the decomposition of more complex organic material. Rather, an association between high quality SOC and fungi emerges from the results. This suggests that we need to revise our basic understanding for soil microbial communities and the processes they regulate in soil.

Keywords: Soil decomposer ecology, Fungal-to-bacterial dominance, carbon sequestration, nutrient cycling

[P1.091]

Home-field advantage: the role of specialized decomposers in accelerating decomposition processes

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The ‘home-field advantage (HFA) hypothesis’ predicts that plant litter is decomposed faster than expected in the vicinity of the plant where it originates from (i.e., its ‘home’) relative to some other location (i.e., ‘away’) because of the presence of specialized decomposers. However, HFA effects appear highly variable and context-dependent. Using a field experiment and a literature synthesis we evaluated if HFA effects were modulated by macroclimate, litter quality traits, and the dissimilarity between ‘home’ and ‘away’ plant communities. In our literature survey we found that decomposition was on average 7.5% faster at home than away, however HFA in our field experiment was limited. Both in the literature survey and the field study variation in HFA effects could not be explained by macroclimate and litter quality. The most significant drivers of home-field effects were the dissimilarity in plant community composition and litter quality between the ‘home’ and ‘away’ locations. Our study shows that rapid changes in plant community composition, particularly when new plants have very dissimilar litter quality, may disentangle plant species and specialized decomposer communities, resulting in altered decomposition processes.

Keywords: decomposition, home-field advantage, nutrient cycling

[P1.092]

Microbial growth upon rewetting: effects of long-term drought legacies

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Climate change is expected to increase the frequency and severity of drought and rainfall events, which increases the need to understand how soil microbes respond to fluctuations in water availability. Rewetting a dry soil is known to affect the carbon cycle, leading to a pulse of carbon dioxide release (respiration). The microbial decomposers, fungi and bacteria, must underlie this phenomenon. A decoupling between respiration and growth was observed in previous studies. However, the influence of historical drought conditions – the microbial legacy of drought – on the temporal response of microbes to a drying-rewetting event remains unknown. Here, we studied if exposure to decade-long experimental summer droughts in the field affected the response of soil microbes to a drying-rewetting cycle.

We collected soils exposed to multiple years of similar treated summer droughts from three field sites in Europe. Soil without a legacy of drought (control soil) and soil with a legacy of drought were exposed to four days of drought in the lab. The temporal responses of bacteria, fungi and soil respiration were measured upon rewetting during one week.

We observed that the legacy of drought was important for the temporal responses of soil microbial growth, but not for soil respiration. Bacteria reached higher maximum growth rates in soil with a legacy of drought. Fungal growth responses were site depended. Soil respiration rates did not differ between control and drought-legacy soils. Thus, the cumulative growth of bacteria was higher in soils with a legacy of drought while cumulative respiration was unaffected. These results suggest that soil bacteria may increase their relative allocation of carbon to growth during a drying-rewetting cycle when they were previously exposed to drought. This could translate to situation where a legacy of drought can enhance the microbial carbon-use-efficiency when exposed to more extreme fluctuations in water availability.

Keywords: Climate change, Fungi, Bacteria, drying-rewetting

[P1.093]

Functional diversity of soil microbial communities under different boreal forests

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Composition and diversity of plant assemblages may have a distinct effect on soil microbial communities. The objective of this study was to compare physiological profiles of soil microbial communities under four types of boreal forests differing in dominating tree species and plant diversity. The samples of O and A soil horizons were taken under pine (*Pinus sylvestris*), birch (*Betula* sp.) spruce (*Picea abies*) and mixed pine-birch-spruce forest stands in the Oulanka National Park, Finland. The community level physiological profiles (CLPPs) were measured with MicroResp^{TM} system using 22 different C substrates (9 neutral sugars, 5 amino acids, 2 amines, 5 carboxylic acids and 1 polymer). Chemical and physical soil analyses included determination of organic C (C_{org}), total N (N_t), pH, dissolved organic C (DOC), maximum water holding capacity and texture. The studied forest types differed in plant diversity with the pine forest being the least diverse and the birch and mixed stands being the most diverse ones ($p<0.05$). Despite this difference, the microbial diversity was similar in all studied forest types. Significant differences in CLPP between the studied forest stands were found in the O horizon but not in the A horizon. The largest contributions to dissimilarity of CLPPs between the studied forest stands were from carboxylic acids (D-malic, oxalic, L-ascorbic and α-ketoglutaric acid) and neutral sugar (D-cellobiose). Canonical correspondence analysis indicated that the use of these most discriminating C substrates depended on the contents of N_t and DOC in soils as well as on C_{org}-to-N_t ratio and soil pH. Our results indicated that the plant diversity of boreal forests has no effect on their soil microbial diversity. However, plant composition seems to be an important factor influencing the physiological profiles of soil microbial communities inhabiting soil organic horizons.

Keywords: boreal forests, community level physiological profiles, plant diversity, microbial diversity

[P1.094]

Faster is not always better: slow decomposition of litter produced by mature trees promote offspring nitrogen acquisition and growth by interacting with ectomycorrhizal fungi

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Nitrogen (N) is one of the most important limiting nutriments for plant growth in many terrestrial ecosystems. Recent studies have provided evidences for plant ecological strategies that involve specific leaf litter chemistry and mycorrhizal fungi both promoting plant N acquisition. In this study, we used an original experimental design in mesocosms to test the hypothesis that litter produced by mature beech (*Fagus sylvatica*) trees promote offspring N acquisition and growth by altering soil N cycling and reducing microbial N immobilization. After 6 months of growth in greenhouse, beech saplings (2 years old) exhibited higher N acquisition and growth in soil covered by litter from parent trees (90 years old), but only in presence of ectomycorrhizal fungi (EF). We did not find similar positive plant N feedbacks when the soil was covered by litter produced by young trees (15 years old), or when EF was absent. The chemical analysis of the soil showed higher particulate organic N retention, lower microbial biomass N, litter decomposition and N accumulation in presence of EF and when litter came from mature trees. The biomass allocation in beech shoot was maximal in presence of EF and litter from parents. These results validate our hypothesis and underline the importance of (i) age-related within-species litter quality variability, and (i) above-belowground biological interactions, especially those involving mycorrhizal symbiosis; in ecosystem function and productivity.

Keywords: Nitrogen cycle, Ectomycorrhizal fungi, Litter decomposition, Above-belowground relationships

[P1.095]

The effects of a natural carbon dioxide vent on soil microbial communities at Calatrava Volcanic Field (Spain)

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The effects of carbon dioxide (CO_2) natural seepages on soil microbial communities were evaluated in Calatrava Volcanic Field's (CVF), Spain, during two different seasons. The fluxes of CO_2 in the soil ranged from 14.64 (control) to 293,508 g m^{-2} day^{-1}. Soil samples were taken along a CO_2 gradient. Microbial activity, genetic profiles and number of *Bacteria, Archaea and Fungi* were evaluated through Biolog Ecoplates, DGGE and quantitative PCR respectively.

Regardless seasonal variations, results showed a dramatic impact on soil microbiota related to CO_2 increments: genetic diversity, metabolic activity and number of individuals were negatively affected by CO_2 emissions. At extreme CO_2 points (ca. 300 kg m^{-2} day^{-1}) opposite trend was observed, bacterial and archaeal numbers strongly increased and microbial activity was enhanced, probably in relation to higher soil organic matter content.

We concluded that CO_2 emissions severely affect soil microbial communities, drifting genetic and metabolic diversity and influencing numbers of edaphic microorganisms.

Keywords: Greenhouse gases, Edaphic microbiota, BIOLOG, DGGE

[P1.096]

Forest tree species shape their soil microbiome

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The impact of plant species on the soil microbial communities and the physico-chemical characteristics of the soil begins to be well documented especially for non-perennial plants. However, our understanding of the diversity and structure of the tree-associated microbial communities as well as the of tree species effect remains limited. Here, we investigated the archaeal, bacterial and fungal communities in replicate soil samples, using 16S rRNA, 18S rRNA and fungal ITS sequences, in the long term experimental site of Breuil-Chenue. We showed significant difference in abundance, composition and structure of the microbial communities associated to two contrasted tree species, *Fagus sativa* and *Picea abies* developed on the same soil. Our results highlighted a strong host effect on the soil microbial communities, with a stronger effect on the fungal communities. Although the pyrosequencing approach showed a limited rhizosphere effect, quantitative PCR revealed a significant enrichment of specific bacterial genera known for their ability to weather minerals in the tree root vicinity. At last, co-occurrence analysis revealed very different networks below the two tree species, suggesting a modification of the structure and abundance of the microbial communities, but also modification of the interactions established between microorganisms. In all the microbial communities considered we observed a host effect with variable intensity, suggesting that the tree host shapes its soil microbiome.

Keywords: forest, tree species, soil microbiome, rhizosphere

[P1.097]

Impact of soil type on the structure of the microbial communities: Insights from the Montiers-sur-Saulx soil succession

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In the present context, forest ecosystems are facing intensified exploitation, and the maintenance of both soil capacity for production and the quality of the environment is a central issue in sustainable forest management. Notably, a large part of the forest ecosystems in our temperate regions are developed on non-fertilized and nutrient-poor soils, making them very sensitive to nutritive perturbations. In this context, we can wonder how nutrient cycles are maintained in such forest soils and how trees collect the nutrients they need for their growth, and what is the relative role of the soil microbial communities. To decipher the potential relationship existing between soil properties and the functional and taxonomic structuration of the soil microbial communities, we initiated a set of analyses on the forest soil succession of the experimental site of Montiers-sur-Saulx. This site is characterized by a dominance of beech (*Fagus sativa*) trees developed on a range of soils with pH ranging from 4 to 7. In this site, we investigated the bacterial and fungal communities in using 16S rRNA and fungal ITS sequences, combined to the measure of the functional potential of the soil microbial communities. At last, a cultivation-dependent approach was initiated to determine the distribution of the mineral weathering bacterial communities along the soil succession. Our first results showed a strong impact of the soil characteristics on the taxonomic and functional structuration of both bacterial and fungal communities. Concerning the mineral weathering function, our first results highlight a significant enrichment of *Burkholderia* in the global soil in the most acidic condition compared to the soil with the higher pH. Together, our results suggest that the soil conditions impact the structure of the microbial communities and potentially of those selected by the trees in the vicinity of their root system.

Keywords: Forest, soil fertility, microbial communities, cultivation-dependent and independent approaches

[P1.098]

The effect of arbuscular mycorrhizal fungi (AMF) of the growth of rare plant species on abandonedfields

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Recent economic changes in the Czech Republic resulted in many regions in the increase of the number of abandoned fields. Such habitats were reported to have lower species diversity than surrounding grasslands due to secondary succession. Thus many projects try to influence the direction of this succession by sowing of target species into fields or transplanting of pre-cultivated plants. However, such species are frequently not able to efficiently grow on these habitats. The inability of species to persist on abandoned fields could be caused by changes in communities of arbuscular mycorrhizal fungi (AMF) as a consequence of long-term application of fertilizers, pesticides and fungicides. Agricultural fields are usually colonized by rapidly growing “ruderal” and cosmopolitan AMF species, slowly sporulating species are scarce. This could be the reason for the absence of obligatory AMF plant species or species adapted for native AMF. In contrast, non-mycotrophic or non-obligatory plant species would predominate on such habitats. In this project we tested whether the absence of grassland species field can be explained by the differences in AMF communities between these two habitats. Both AMF communities were characterized by molecular methods revealing significant differences in AMF species diversity, spore numbers and in ability of AMF to colonize roots. The differences in AMF communities and their effect on plant species diversity was tested at the community level as well as at species level in garden cultivation experiments. Seedlings of plant species were pre-inoculated by native AMF and transplanted into abandoned field. Seeds of plant species were also sown into the field inoculated by AMF from grassland. The results demonstrated that species composition is highly influenced by AMF community composition both in the field and in the garden experiments. In contrast, the effect of AMF community on each plant species did not show consistent results.

Keywords: abandoned fields, arbuscular mycorrhizal fungi (AMF), grasslands, succession

[P1.099]

Effect of fallows on species richness and abundance of macrodecomposer invertebrates in agricultural areas

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Intensification of agricultural management in Europe decreased the area of fallows (set-aside fields) during the last decade. In Hungary the establishment of sown fallows is a requirement in High Nature Value Areas by the local agro-environmental scheme.

We tested the effects of such habitats on the diversity of macrodecomposer Arthropods (diplopods, woodlice). Wheat fields and fallows of different ages (1, 2, 3 years) were paired and grasslands as controls were added. Altogether 38 areas were used. Pit-fall traps (5 per area in a distance of 20 m, for 2 weeks, 3 occasions) were applied for samplings during April-May, 2008.

We hypothesised a higher species number and abundance 1) in set-asides than in wheat fields; 2) in cereal fields neighboured by older fallows. In case 1) isopods (Oniscidea) showed a significantly higher species richness and abundance in fallows (Wilcoxon signed rank test), while millipedes (Diplopoda) proved hypotheses 2 (Wilcoxon rank sum test). Diplopods and isopods were influenced by habitat type (including plant species richness and vegetation cover): wheat fields differed significantly from other habitats (GLMM). These results were verified by one-way ANOVA. We found that plant cover also effected abundance of both groups, while plant diversity had significant effect only on the abundance of diplopods. At community level, field type (wheat, set-asides, grasslands) plant species richness and cover had a significant effect on assemblages of the studied taxa (RDA).

Our results highlighted the importance of fallows within the Hungarian agricultural landscape providing refuge for soil arthropods. The studied epigeic taxa are important members of the macro-detritophagous guild. They may play important role in decomposition processes providing ecosystem services and that way are important parts of nutrient recycling ensuring soil fertility.

Keywords: agrobiodiversity, fallow, millipede, woodlouse

[P1.100]

Role of plant rhizosphere and root exudates on microbial communities in polycyclic aromatic hydrocarbon (PAH) contaminated soil

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During the XXth century, the intensive coal and steel industries contributed to the chronic pollution of soils. Their dismantling left large areas of wasteland soils highly contaminated by recalcitrant organic compounds such as polycyclic aromatic hydrocarbons (PAH). We are interested in studying the potential for soil bioremediation using plants assisted rhizodegradation combining the potential of plant with those of rhizospheric microorganisms.

Our objectives were firstly to characterize the microbial diversity of an aged PAH-contaminated soil and secondly to evaluate the role of plant rhizosphere and root exudates on soil microbial communities and on the rhizodegradation potential.

Our work is one of the first to characterize the microbial diversity in such aged PAH-contaminated soil. The impact of plant rhizosphere on both bacterial and fungal densities and diversities was assessed using qPCR, TTGE and pyrosequencing (Cébron et al. 2009; Thion et al. 2012a; Bourceret et al. in prep). Plants favoured a higher density and diversity of microorganisms, with some OTUs being foster as *Arthrobacter* belonging to the phylum Actinobacteria, and *Fusarium*, *Bionectria*, *Acremonium* belonging to the Ascomycota.

Soil PAH-degrading microorganisms were identified using a combination of approaches and the impact of plant root exudates on their activity and diversity was assessed. As shown by qPCR targeting PAH-ring hydroxylating dioxygenases, the plant rhizosphere seemed to favour the PAH-degrading bacteria belonging to the Actinobacteria (Cébron et al. 2009). Stable isotope Probing using ^{13}C-labeled phenanthrene allowed showing that the presence of root exudates did not influenced the rate of PAH-degradation but modified the functional community. Two distinct populations were active, *Pseudoxanthomonas* and *Microbacterium* strains were the main PAH-degraders without exudates while *Pseudomonas* and *Arthrobacter* strains were the main PAH-degraders with exudates (Cébron et al. 2011). PAH-degrading microbes, one bacteria related to *Arthrobacter oxidans* and one fungus related to *Fusarium solani*, were also isolated and their physiology and PAH-degradation activity were studied in various conditions and in presence of plant (Thion et al. 2012b, 2013).

Cébron A et al. (2009) Applied and Environmental Microbiology 75:6322-6330.

Cébron A et al. (2011) Environmental Microbiology. 13:722-736.

Thion C et al. (2012a) FEMS Microbiology Ecology 82:169-181.

Thion C et al. (2012b) International Biodeterioration & Biodegradation. 68:28-35.

Thion C et al. (2013) Biodegradation. 24:569-581.

Keywords: PAH-polluted soil, bacterial diversity, fungal diversity, PAH-degrading microbes

[P1.101]

Effects of plant diversity and soil organisms within rhizosphere on the growth of Triticum aestivum (poaceae): a preliminary study

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The purpose of this preliminary study was to evaluate i) relationships between a genetic and specific diversified plant cover and soil communities and ii) how both affect the performance of *Triticum aestivum* L. We hypothesized that an increase in plant diversity affects soil organism communities and that interactions between aboveground and belowground diversity increase wheat growth. In a greenhouse experiment, we investigated effects of plant diversity on the rhizospheric fungal biomass and the nematofauna. We also tested whether plant and soil diversity has an effect on wheat biomass and N status.

We tested three levels of plant diversity (single genotype of wheat, mixture of three genotypes of wheat and the three genotypes mixed with *Trifolium hybridum* L.), and two soil treatments (sterilized soil and unsterilized soil); five endogeic earthworms were also added to unsterilized soils. N concentration in roots and shoots of plants were measured and the percentage of legume N derived from N_2 fixation was determined using the ^{15}N natural abundance method.

Higher fungal biomass characterized the modality of higher genotypic richness (figure 1) and the gradient of plant diversity positively increased the abundance of bacterial-feeding nematodes (figure 2).

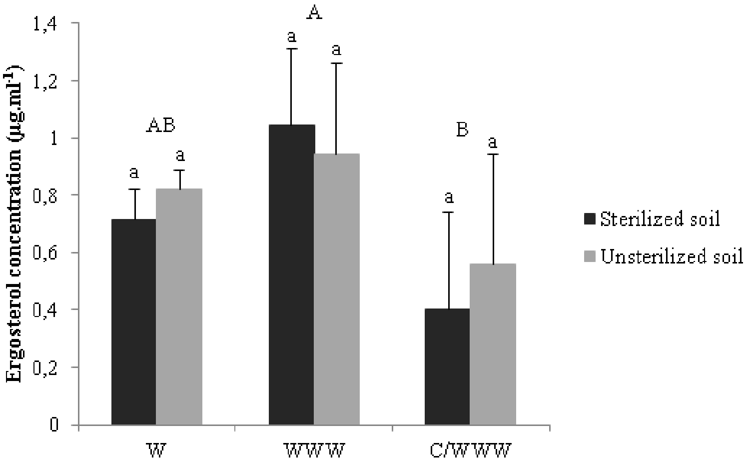

Figure 1. Effects of plant diversity on fungal biomass (ergosterol concentration) after 6 weeks. W: Wheat; C: Clover. Means with 1 SD bars showing the same letter are not significantly different (Newman and Keuls test, $p<0.05$)

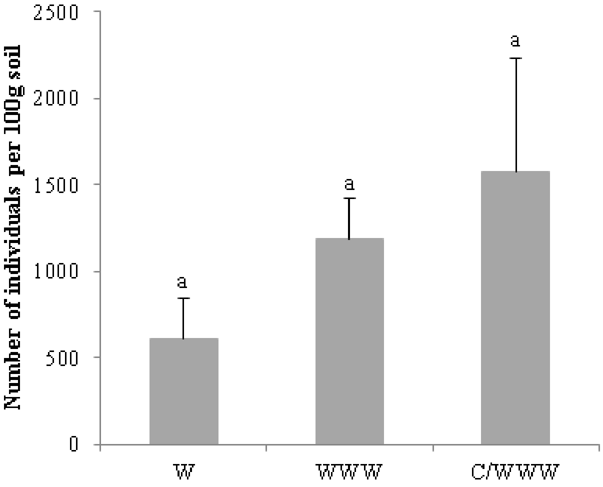

Figure 2. Effects of plant diversity on nematofaunal abundance after 6 weeks. W: Wheat; C: Clover. Means with 1 SD bars showing the same letter are not significantly different (Newman and Keuls test, p<0.05)

The increase in diversity within the wheat-clover mixture influenced the performance of wheat (biomass, nitrogen content) by higher nutrient availability thanks to complementarity effects (figure 3).

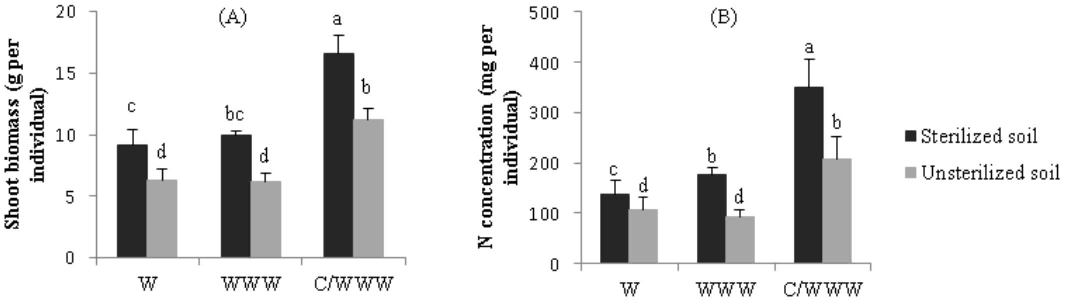

Figure 3. Effects of plant diversity on shoot biomass (A) and N content (B) of wheat in sterilized and unsterilized soil treatments after 6 weeks. W: Wheat; C: Clover. Means with 1 SD bars showing the same letter are not significantly different (Newman and Keuls test, p<0.05)

Overall, the results suggest that plant diversity enhanced soil organism abundance but the effects varied with the level of diversity and soil groups. Wheat alone seems to stimulate more fungal biomass than in the mixture with legume. Higher density of bacterial-feeding nematodes suggests higher bacterial activity with increasing plant diversity. In this study plant diversity seems to influence soil community structure however more information is needed. Moreover, the effect of soil communities on plant growth was difficult to assess and needs further investigations.

Keywords: plant diversity, fungal biomass, nematofauna, plant biomass

[P1.102]

Analyzing topsoil characteristics associated to vegetation types in Atlantic Iberian Peninsula: soil resistance to desiccation as related to organic matter

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A topsoil characterization involving collection of 66 samples (mean volume 869.1 ± 70.3 ml) from a variety of land covers was undertaken in Alonsotegi (Basque Country, Spain, 30TWN0088). Altitude gap goes from 20 m to 999 m a.s.l. with a slope average ~26% (maximum ~ 54%) and lithology appears homogenous (quartz sandstone).

Sampling took place at the beginning of October 2012 after an extremely dry and hot summer (total summer rainfall represented 70% of precipitation registered along the severe hot spell of 2003, temperatures being slightly lower), providing a baseline for maximum draught conditions. Following phytosociological criteria, topsoil from seven main vegetation units was surveyed: meadows, heaths, hygrophilous forest, climatophilous broadleaved deciduous and evergreen forests, coniferous, eucalypt and deciduous plantations. Field measurements taken were humidity, topsoil and air temperatures, ph, luminosity and canopy cover whereas laboratory determinations were pH, field capacity, field water content, and dry and organic matter.

Top soil temperature is related to air temperature and cover (two way ANCOVA $p<10^{-4}$) showing no difference at sun exposures below 50%; no significant differences appear between meadows ($T_{soil°C}$ = 23.6 ± 2.9) as fully exposed vegetation units and eucalyptus plantations ($T_{soil°C}$ = 22.9 ± 1.5) with 33% exposure. A common water field capacity of 30.3 ± 6.8% (vol %) appears but wide differences associated to vegetation profile are evident as regards of actual field water content: between 8.0 and 45.1% (weight %). Organic matter content (% dry weight) ranks from lowest for hygrophilous forest (5.0 ±2.3%) to highest for heath (15.9% ± 5.1%) indicating increased density in flooding areas. Organic content in top soil determines water retention capacity and a linear regression equation between field water (%) and organic content (%) indicating an isometric relation (slope 1.051 ±0.247 CL $_{95\%}$; $p<10^{-4}$) has been calculated.

Keywords: soil dehydration, soil organic matter, vegetation units, soil parameters

[P1.104]

Relating soil microbial diversity with GHG emissions: Taxonomic and spatial variability in a Mediterranean periurban forest

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In forests, relationships between above and below-ground communities and how they affect and regulate biogeochemical cycles, are of paramount importance. Here, the spatial variability and the interaction among soil features, soil microbial diversity with in situ measurements of CO_2 fluxes were investigated aiming at evaluating the role of soil microorganisms in regulating GHG emissions in a Mediterranean periurban Holm oak forest.

Soil was sampled randomly in three spots along six vertical transects (0-100cm) and was analyzed to determine the main chemical parameters and to characterize the structure, the diversity and the abundance of microorganisms through the T-RFLP and qPCR tecniques. Moreover, BaPS was used to quantify soil respiration, denitrification and gross nitrification rates. Eddy Covariance above the canopy was used to measure fluxes of CO_2 for the entire ecosystem. An additional EC system below the forest canopy was used to separate the contribution of soil from the ecosystem fluxes which also include canopies. CO_2 flux from soil within the EC footprint area was also measured to test spatial heterogeneity in CO_2 emission.

Results indicate that SOC was higher in the shallow layer (7.51%) and decreased along the soil depth (down to 1.20%) in all three spots. No changes in soil pH were revealed. A pronounced structural diversity of the microbial community occurred along the soil depth and spatially in all the spots in agreement with different rates of CO_2 fluxes. T-RFLP and qPCR highlighted marked differences in terms of structure, diversity, and total content of bacteria, fungi and archaea along both the vertical and horizontal distribution pattern. The same trends were confirmed by BaPS for gross nitrification and respiration rates, since the highest activities coincided with the most abundant microbial communities.

Current studies are preliminary to better investigate how soil microbial communities affect GHG emissions under changing environmental conditions.

Keywords: GHG emissions, Soil microbial diversity, soil respiration, forest

[P1.105]

Collembolan community trends under influence of flood and drought events

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Floodplains, either natural or seminatural, which commonly exhibit changes between flood and drought, are prime examples of sites with niche diversity and offer unique conditions and resources for both plants and animals. Such habitats have high conservation value and, due to the changing conditions, lead to high niche diversity. From the year 2002 hardwood and softwood floodplains of the Northern Upper Rhine Valley were investigated concerning the effects of drought and flood events upon collembolan communities. These communities are well adapted to periodic flood and drought events and show a wide range of morphological, physiological and behavioral (pre-) adaptations to the changing hydrological conditions. During 10 years of investigation different periodic and aperiodic flood and drought events affect the soil community with diverse impact qualities. Especially aperiodic events like irregular summer flood or long lasting drought events caused strong species shifts and disappearance of highly adapted species, whereas the abundance of opportunistic species increased. Changes of abundance and density values, biodiversity shifts and migration events were summarized in charts, which allow forecasts of the impact of different climatic scenarios for soil collembolan communities of this region.

Keywords: Collembola, floodplain, flood and drought, community changes

[P1.106]

Distinct soil microbial diversity under long-term organic and conventional farming

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Sustainable farming practices are essential to maintain ecosystem functionality, preserve biodiversity, and meet economic demands. Low-input organic farming systems aim at reducing the use of synthetic fertilizers and pesticides in order to improve sustainable production and ecosystem health. Despite the integral role of the soil microbiome in agricultural production, we still have a limited understanding of the complex response of soil microbial diversity to organic and conventional farming. Here we report on the structural response of the soil microbiome to more than two decades of different agricultural management in the DOK long-term field experiment using a high-throughput pyrosequencing approach of bacterial and fungal ribosomal markers. We recovered a total of 1,118,268 bacterial and fungal pyrotags from 80 soil samples across five different farming system, two different crop types, and two different years of sampling. Organic farming increased richness, decreased evenness, reduced dispersion, and shifted the structure of the soil microbiota when compared to conventionally managed soils under exclusively mineral fertilization. This effect was largely attributed to the use and quality of organic fertilizer, as differences became smaller when conventionally managed soils under an integrated fertilization scheme were examined. The impact of the plant protection regime, characterized by moderate and targeted application of pesticides, was of subordinate importance in this system. Stockless systems harboured a dispersed and functionally versatile community characterized by presumably oligotrophic organisms adapted to nutrient-limited environments. Systems receiving organic fertilizer were characterized by specific microbial guilds known to be involved in degradation of complex organic compounds such as manure and compost. The throughput and resolution of the sequencing approach permitted to detect specific structural shifts at the level of individual microbial taxa, which harbours a novel potential for managing the soil environment by means of promoting beneficial and supressing detrimental organisms.

Keywords: soil microbial diversity, organic and conventional agriculture, next-generation sequencing, indicator association networks

[P1.107]

Centimeter-scale spatial variability of bacterial diversity and PAHs biodegradation in a multi-contaminated rhizospheric soil

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Polycyclic Aromatic Hydrocarbons (PAHs) are organic pollutants mainly produced by industrial activities as coal derivative industry. This pollution causes environmental problem by heavy contamination of brownfield soils. In these historical contaminated soils the biodegradation of PAH is limited due to low bioavailability. Sowing plant that spread root exudates could enhance the pollutant bioavailability and increase microbial activity. However the spatial and temporal variability of rhizospheric phenomenon leads to contrasted effect of plant on the fate of PAHs. The aim of the study was to evaluate the spatial variability of PAH-degradation and bacterial diversity in two contrasted rhizospheres at the centimeter-scale.

In our study, the rhizosphere of alfalfa and ryegrass were compared in rhizotron devices that allow studying the spatial heterogeneity of the soil. Each plant was grown in an independent rhizotron (H: 30 cm x D: 30 cm x W: 2.5 cm), on soil from brownfield (Neuves-Maisons, Lorraine, France), recontaminated by a complex organic pollutant extract. After 37 days, the front faces of the both rhizotron were open to allow 56-core sampling (6 samples at 7 depth), on a grid pattern.

Multiparametric analysis, performed on the 56 samples per rhizotron had shown the establishment of a spatial gradient with depth (root density and PAH-degrading bacterial communities). A correlation was shown between the decrease of the total PAHs concentration and the increase of PAH-degrading bacterial communities density assessed using real time quantitative PCR. Moreover, the rhizosphere effect of alfalfa seemed to be more important on the degradation of 4-rings PAHs than ryegrass. These multiparametric data were further analyzed using geostatistical tools to illustrate and demonstrate the spatial variability. The bacterial diversity was analyzed through 454-pyrosequencing of 16S rRNA genes. After 37 days of plant growth, the relative percentage of bacteria belonging to Actinobacteria and Proteobacteria phylum increased in the rhizosphere of alfalfa and variability according to the depth was observed for different phyla. Another study is in progress to better understand the temporal variability of the alfalfa rhizosphere effect.

Keywords: PAHs, Rhizosphere, Bacterial diversity, Functionnal genes

[P1.108]

Soil protists: distribution and ecological roles

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Keywords: Protists, Diversity, (Plant) pathogens, Functioning

[P1.109]

Does afforestation of arable land with rubber tree improve soil biodiversity?

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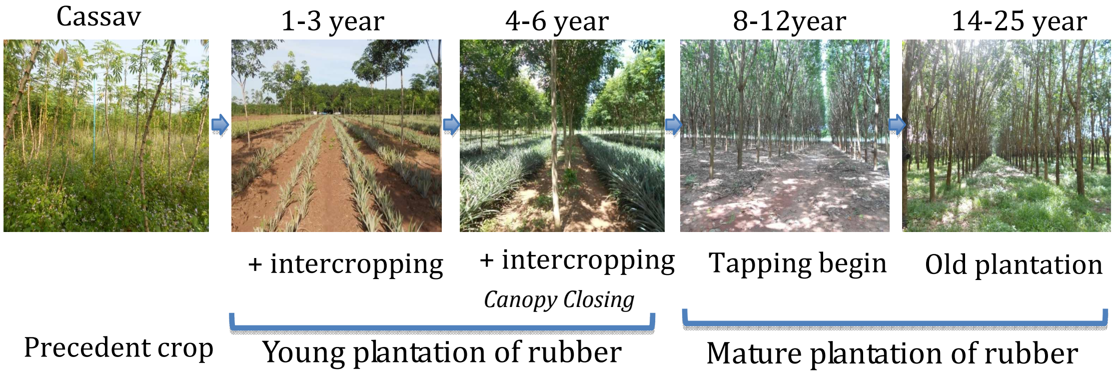
Tree plantations are often denigrated for their negative impact on natural resources particularly loss of biodiversity. This assessment is undeniable when tree plantation encroached natural forests. However, in the case of Rubber plantation, the main tree plantation in south East Asia, it often replaced intensively managed annual crops such as cassava. The impact of these land use changes on soil biodiversity remains unknown.

To address this issue, we investigated the impact of land use change from cassava to rubber trees on soil biological diversity (soil fauna, and soil microorganisms, using pyrosequencing approaches), biological activities (soil respiration and metabolic profiles) and soil organic carbon (SOC) content and quality. All these parameters were measured along a chronosequence of rubber plantations in Thailand from 1 to 25 years old compared to cassava fields, the most cultivated cash crop in the area.



Compared to cassava fields, activities and biomass of soil fauna and microbial communities showed significantly higher level in the old rubber plantations (>25 years). However, the soil species richness was lower (case of bacteria) or not significantly different (fungi and soil fauna) in older rubber plantations compared to cassava. The shift from cassava to young rubber plantations resulted in a decrease of most variables measured (activities, fauna density and diversity, SOC) except those related to bacterial and fungal diversity. The soil ecosystem started to recover from this shift after closure of the tree canopy with an important increase of earthworms unlike ants. Interestingly, soil fauna and microbial genetic structure were more impacted by the canopy closure, than by the shift from cassava to rubber plantation.

These results suggest that the replacement of a cash crop by a tree plantation like rubber trees, could represent a suitable alternative in terms of soil functional diversity and activities

Keywords: Tree plantation, Soil macrofauna, Pyrosequencing of microbial community, C sequestration

[P1.110]

Impact assessment of major pressures on soil biodiversity in Europe

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Soils provide a vital habitat to over one fourth of all living species on earth. Soil organisms provide numerous and essential services such as, supporting (nutrient cycling, soil formation, primary production and decomposition of organic matter), regulating (atmospheric composition and climate, water quantity and quality, pest and disease incidence in agricultural and natural ecosystems), controlling (environmental pollution), provisioning (directly benefits people by its chemical and genetic resources). Despite these important functions of soil biodiversity, there is still no regulating mechanism set in place at any level and soil biodiversity loss does not clearly figure as soil threat, putting this natural resource under high threats. Moreover, the lack of information on soil biodiversity and the difficulty of quantifying the impacts that major pressures exerted on European soils increase the complexity of the subject.

This study aims at putting together adequate knowledge and develops tools to spatially predict areas around Europe where soil biota could be impacted as a result of pressures' effects on the functional traits of soil biodiversity using tracing evidence from literature. A meta-analysis will highlight critical thresholds of studied pressures, being the level of a specific indicator beyond which the particular system of soil biodiversity is no longer sustainable. This evidence will support the quantification of their impacts on soil biodiversity.

Since, a single threshold value does not represent the boundary or cut-off between sustainable and unsustainable (high or low danger), a range of threshold values (due to the lack of information, only limited number of indicators such as soil pH, salinity and temperature) and temporal changing for particular indicators (land-use) are used in this study. A spatial identification of the pressures will be linked to the evidence on their impacts to develop spatial indicators. A spatial analysis of all developed layers derived from processed critical thresholds of the indicators are classified with SQL and then indexed. This method makes possible the observation of correspondences of the areas where have high risks and pressures on soil biota with the greater loss of biodiversity is envisaged in Europe as a first step of this broad study area. In conclusion, we searched our output how corresponds in high potential pressure map on soil biodiversity (Gardi et al, 2013).

Keywords: Impact assessment, Spatial prediction, Pressures, Quantifying

[P1.111]

The predictability of the functional diversity of soil macrofauna in temperate forest based on isotopic analyses

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Introduction: Belowground and aboveground food webs are tied by numerous links. Soil macrofauna form a substantial food source for a range of predators including amphibians, reptiles, birds and mammals. Stable isotope analysis (SIA) is used widely for reconstructing trophic links of vertebrate and invertebrate animals. Such reconstructions can not be done without knowledge on the full range of isotopic signatures of potential preys.

Methods: In order to estimate a typical range of the isotopic signatures of soil macrofauna we compiled published and experimental data on isotopic composition of plant litter and of soil macroinvertebrates in 11 temperate forests. We examined whether the baseline correction (i.e. subtracting $\delta^{13}C$ or $\delta^{15}N$ values of local litter) would decrease the between-sites variability in the $\delta^{13}C$ and $\delta^{15}N$ values of soil animals. The data set was subsequently used to estimate frequency distribution of $\delta^{13}C$ and $\delta^{15}N$ values in saprophagous and predatory soil animals.

Results: The baseline correction reduced the between-sites variability in $\delta^{15}N$, but not in $\delta^{13}C$ values of soil animals. Over 95% of taxa or individuals examined fell into an isotopic space with uncorrected $\delta^{13}C$ values ranging from –27.9 and –22.5‰, and litter-normalized $\delta^{15}N$ values from 0.8 and 9.6‰. Saprophagous and predatory soil animals were on average enriched in ^{13}C relative to plant litter by 3.5 and 2.7‰, respectively, which likely reflects the importance of saprotrophic microorganisms as a main energy source in soil food webs. The difference in $\delta^{15}N$ values between saprophages and predators averaged 2.8‰, which fits anticipated trophic enrichment per one trophic level.

Discussion: Our results indicate that the range of possible $\delta^{15}N$ values of soil macrofauna in temperate forest ecosystems can be roughly predicted based on the $\delta^{15}N$ values of plant litter. However, site-specific normalization seems impractical when predicting the range of $\delta^{13}C$ values of soil macroinvertebrates.

Keywords: ecological interactions, food webs, belowground – aboveground trophic links, stable isotopes

[P1.112]

Communities and populations of arbuscular mycorrhizal fungi (Glomeromycota) in agricultural settings: effects of short-term and long-term soil disturbance by tillage

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A large proportion of the well-documented deleterious effects of agriculture on arbuscular mycorrhizal fungal (AMF, Glomeromycota) communities may be due to tillage, depending on the tolerance of particular AMF species or genotypes to mechanical disturbance. Understanding the dynamics of AMF communities and populations in agroecosystems is a requirement for managing these beneficial symbionts in the context of moving towards sustainable agriculture. We studied the effects of tillage on the composition of AMF community composition in a long-term field experiment, as well as in combination with fertilization treatments in a small-scaled field trial over a period of three months. We used high-throughput sequencing of the marker gene rpb1, which was used for the first time in AMF community analysis. We detected a high diversity of molecular taxa in both experimental systems and no significant reduction of AMF diversity attributable to tillage. In fact, disturbance slightly increased AMF species richness in the short-term experiment. Significant shifts were detected in the relative abundance of sequences of molecular taxa. Intraspecific genotypes of *R. irregularis*, which are known to be differentiated between grasslands and arable soils, showed a partial transition away from grassland genotypes. Our results indicate that disturbance has the strongest impact on AMF communities over short periods of time, but that at the same time these effects are modulated by fertilization.

Keywords: arbuscular mycorrhiza, rpb1, mitochondrial large ribosomal subunit, Glomeromycota

[P1.113]

Methane- and nitrous oxide-cycling functional groups respond to site preparation and fertilization in waterlogged forest stands

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Forest site preparation and fertilization can improve productivity but can alter the efflux rates of greenhouse gases (GHGs), CO_2, CH_4 and N_2O, from waterlogged soils. This study took place in British Columbia (BC), Canada, in a hybrid white spruce stand subject to mounding and a western redcedar-western hemlock stand subject to drainage, and investigated management effects on GHG fluxes (using static closed chambers) and microbial functional groups (using quantitative PCR). Variation partitioning with redundancy analysis (RDA) was used to allocate abiotic and biotic sources of variation in GHG fluxes and functional gene abundances. Mounding reduced CO_2 fluxes due to organic carbon (C) removal, but created anaerobic hot-spots of CH_4 and N_2O fluxes. Ditch drainage increased soil C about 20% after 15 years and did not affect respiration rates, though CH_4 fluxes were reduced. Fertilization transiently increased N_2O fluxes up to 209 µg m^{-2} h^{-1}. Potential denitrification assays implicated ammonia-oxidizing bacteria (AOB) *amoA* genes, denitrifier nitrite reductase (*nirSK*) gene abundance and *nirSK* transcription as important for regulation of denitrification. In field studies, up to 84.4% of variation in CO_2 emissions could be explained, with almost 50% of explained variation allocated to soil temperature. CH_4 flux variation was explained by soil water content, soil temperature, methanogen (*mcrA*) and methanotroph (*pmoA*) functional gene abundance, indicating a CH_4-cycling microbial community regulated by soil physico-climactic variation. Variation in N_2O fluxes showed spatial patterns related to management practices and were significantly explained by soil water content, soil pH, NH_4-N concentration, AOB *amoA*, nitrate reductase (*narG*) gene and *nirSK* gene abundance. In addition to denitrification genes, these data highlight AOB as important determinants of denitrification. This study elucidates microbial functional groups influence on GHG flux rates in forest ecosystems.

Keywords: Denitrification, Forest, Methane, Nitrification

[P1.114]

Development of rhizobial inoculants to induce drought tolerance in cereals

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Drought is the major abiotic stress mounting up due to climate change and shrinking water resources. *Rhizobium,* which is usually known for nitrogen fixation in legumes has capability to tolerate drought stress and can enhance plant growth in non-legumes through different mechanisms. Therefore, a series of trials were carried out to study the prospects of various rhizobial strains to induce drought tolerance in maize and wheat. Thirty rhizobial strains, ten from each chickpea, lentil and mung bean were isolated. The isolated strains were screened for drought tolerance, using 10, 20, 30 and 40% polyethylene glycol. Eight best rhizobial strains were evaluated for their plant growth promoting activities at different drought levels (50, 75 and 100% of the field capacity) under axenic conditions. It was recorded that strain DRC-8, DRL-5 and DRM-3 significantly enhanced plant growth in wheat under drought stress. While strain CDR-6, CDR-4 and CM-1 performed better to mitigate drastic effects of drought in maize. Best performing strains and their combinations were evaluated in pot experiments at various moisture levels. Finally, three best performing combinations were tested in field conditions to further elaborate the role of rhizobial inoculants in inducing drought tolerance in wheat and maize. Drought was imposed by passing over irrigation at critical growth stages. The outcomes of the experiments revealed that biochemical, physiological and growth attributes of both crops were adversely affected by drought stress. However, rhizobial inoculants mitigated drought stress by improving photosynthetic rate, improved antioxidant levels and ionic balance in plants. Plant growth promotion was also endorsed by strong positive correlation between best performing strains in pot and field with their characterization like good root colonization, phosphate solubilization, exopolysaccharides, chitinase activity, siderophore production, IAA-production and ACC-deaminase activity. Study revealed that Rhizobial inoculants could be successfully used in cereals to mitigate drought stress.

Keywords: Drought, Rhizobium, Plant, Stress

[P1.115]

Bacterial consortium with ACC-deaminase activity for inducing salinity tolerance in cereals

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Soil salinity is one of the worst consequences of global climate change, which is declining the world agriculture production. Plant growth promoting rhizobacteria (PGPR) induce salinity tolerance in plants with their multiple mechanisms. Therefore in present study, rhizobacteria were isolated from rhizosphere of wheat and maize and initially screened on the basis of their salt tolerance potential (osmoadoptation assay) and ACC-deaminase activity. Further, selected salt tolerant rhizobacteria with ACC-deaminase activity were screened individually for their ability to promote wheat and maize growth under salt affected axenic conditions. Efficient PGPR strains were evaluated for their compatibility of growth, co-aggregation abilities and synergism with each other. Three PGPR strains having abilities to coexist were tested again under axenic condition in their possible combinations for inducing salinity tolerance in wheat and maize. Effective combinations (consortia) were evaluated in a series of pot and field trials to improve growth and yield of wheat and maize under salt affected conditions. The best combination of PGPR strains selected on the basis of evaluation was tested for their survival efficiency (shelf life) in different locally available carriers i.e. peat, press mud, compost, biogas slurry, biochar, crushed corn cob, saw dust and zeolite. These carriers were also evaluated for improving the efficacy of consortium inoculation to improve growth and yield of wheat and maize in salt affected pot and field trials. Multi-strain combination of PGPR with best suited carrier significantly improved the grain yield of wheat and maize upto 35 and 39% at salt affected fields, respectively, as compared to un-inoculated control. Better performance of consortium inoculation for improving yield of wheat and maize could be due to synergy of different PGPR strains which might have resulted in cumulative effect of various mechanisms adopted by PGPR.

Keywords: PGPR, ACC-deaminase, Salt Tolerance, Cereals

[P1.116]

Turning tailing pond into soil as revealed by metagenomic and ecological interaction network

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Industrial activities have led to the production of tailings that are stored in large ponds, resulting in significant unvegetated surfaces. Revegetation of such surfaces is needed to prevent dust storms and erosion. To evaluate the potential for such anthropogenic substrates to achieve soil functions such as fertility and plant growing, biodiversity support and specific habitat, we investigate microbial diversity between a tailing pond of a chlor-alkali industry and a nearby undisturbed soil (named natural soil).

A floristic inventory confirmed that revegetation of tailing pond had occurred rather rapidly, only 10 years after substrate deposit had ceased. We compared physico-chemical characteristics of topsoil in tailing ponds with topsoil from nearby natural soils and we found that pH, $CaCO_3$ concentration and exchangeable CaO were significantly higher in tailing ponds, while in natural soils, CEC was significantly enhanced.

We used a high-throughput DNA sequencing technology (16S rRNA and ITS sequencing using Ion Torrent) that generates large environmental datasets and further applied modeling of interaction network to investigate potential interactions between microbial taxa. We found that bacterial community of the tailing pond was more diverse and rich but with a global similar composition (63% of similar genera) as compared to nearby natural soil. Fungal communities showed only minor changes between tailing pond and natural soils. Interaction networks showed identical complex architecture with a few more specialized interactions between bacteria in the tailing pond, which could be correlated to soil characteristics.

The approaches we have used had allowed to access global community proxies, which lead us to conclude that a 10 year-recolonization of the tailing pond by microbes had allowed microbial community to achieve a community structure similar to that of natural soil. This is best illustrated by similar global diversity, sizes of common microbial pools and similar bacterial fungal ratios.

Keywords: Microbial communities, Tailing pond, High-throughput sequencing, Ecological interaction network

[P1.117]

Influence of connectivity and topsoil management practices of a technosol on pedofauna colonization : a field study

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Numerous sustainable urban projects based on the redevelopment of brownfields are currently scattering in France to deal with the urban sprawl issue. In the « Ecoquartier de l'Union », located in Roubaix (59) and characterized by highly polluted soils, it has been decided to create constructed soils, called technosols, consisting in a mixture of original silt and green-waste compost put on the top of a backfill layer made of demolition by-products.

The objective of the study is to identify the most suitable management practices of the technosol's upper layer for the establishment of a functional soil fauna community. Experimental plots consisting in 15m long and 3m wide strips have been set up on the Union brownfield to monitor the colonization by several soil invertebrates according to 8 different topsoil management practices. The influence of the connectivity to the surrounding ecological network is also evaluated by putting one experimental plot near a hedgerow whereas the other plot is disconnected from any ecological corridor.

Technosol recolonization is monitored via soil samples for Collembola and Acari, pitfall traps for Isopoda and Carabidae and the AITC technique for earthworms. A litterbag experimentation has also been conducted to assess litter decomposition.

First months results indicate that colonization by macrofauna is relatively slow and faster for Collembola. Furthermore, specific richness and abundance were higher in the hedgerow-connected plot, at least for Collembola and earthworms. More diverse and abundant soil fauna communities were found in strips sowed with flowering meadows or covered with ramial chipped wood (RCW). Litter decay rate was clearly higher in RCW strips suggesting a maximal biological activity for this differential management practice.

These results show that soil fauna communities can benefit from *in situ* restoration of brownfields using technosols even though the recolonisation of such constructed soils is a long-term process that imply an appropriate management.

Keywords: Technosol, Soil restoration, Colonization, Pedofauna

[P1.118]

Functional soil microbial diversity across Europe - estimated by EEA, MicroResp, and Biolog

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Soil microorganisms are abundant and essential for the bio-geochemical processes of soil, soil quality and soil ecosystem services. All this is dependent on the actual functions the microbial communities are performing in the soil. Measuring soil respiration has for many years been the basis of estimating soil microbial activity. However, today several techniques are in use for determining microbial functional diversity and assessing soil biodiversity: Methods based on carbon metabolism such as substrate induced respiration (SIR) on specific substrates have led to the development of MicroResp and Community Level Physiological Profiling (CLPP) using ECO-Biolog plates, while soil enzymatic activity are being assayed by Extracellular Enzyme Activity (EEA) based on fluorogenic labelled substrates. Here we elaborated and contrasted the three techniques of assessing soil microbial functional diversity in a European transect consisting of 81 soil samples covering five Biogeographical Zones and three land-uses in order to test the sensitivity, ease and cost of performance, and biological significance of the methods. Mechanistically, the techniques vary in how close they are to in situ functions; dependency on growth during incubation; and whether it is only bacteria or also fungi and /or extracellular enzymes. Practically, the techniques vary in the type and number of functions tested.

All three techniques were able to separate the soils according to land-use and biogeographical zone, however with different strengths. The MicroResp technique was the most labour intensive; both in terms of time spent in the laboratory and for data calculation, while CLPP based on ECO-Biolog plates required the shortest labour time.

The discrimination potential of the techniques and the ecological relevance and significance of the results will be discussed in lieu of the ability to determine soil biodiversity and quality.

Keywords: microbial functional diversity, MicroResp, Exo-enzyme activity, CLPP

[P1.119]

Occurrence of Fusarium oxysporum f.sp. passiflorae and Fusarium solani in soils cultivated with passionfruit, in the State of Mato Grosso, Brasil

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Among the phytosanitary problems that contribute to the low productivity of passionfruit in the State of Mato Grosso, fusariosis stands out, caused by the fungus *Fusarium oxysporum* f. sp. *passiflorae*, and collar rot caused by the fungus *F. solani*. In this study samples of soil and plants with symptoms of fusariosis and collar rot were collected from passionfruit fruit cultivation in the State of Mato Grosso. 65 passionfruit fruit cultivation areas were visited, covering the Cerrado, Pantanal and Amazon biomes, with *F. oxysporum* f sp. *passiflorae* being identified in 36 crops and *F. solani* in 8 crops.

It was found that of the seven environmental variables tested (organic matter, clay content and soil P, Ca, sb, t and v), only clay (χ^2 = 71.040, p = 0.002253) and organic matter (χ^2 = 80.371, p = 0.002804) exerted an additive effect on the probability of occurrence of *Fusarium* spp., through the model: Fusarium probability = exp(-1.587 + 0.05425267 * organic matter + 0.08204737 * clay)/(1 + exp(-1.587 + 0.05425267 * organic matter + 0.08204737 * clay)) (AIC = 77.04). The probability of occurrence of *Fusarium* spp. is favored with increasing soil clay and organic matter content (Figures 1 and 2). The clay and organic matter attributes directly determine the the water retention in the soil, favoring the permanence of soaking and low soil aeration, which may favor the fungus (Cavichioli, et al. 2011).

Keywords: Pathogen-environment relationship, Pantanal, Cerrado, Amazon

[P1.120]

Multitrophic interactions in the rhizospheres of range-expanding plant species

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As a consequence of climate change many plant species are expanding their range to higher latitudes and altitudes. As soil organisms are slow dispersers, the question rises how plant-soil interactions of range expanding plants develop in newly colonized areas assuming that the associated soil biota do not keep up with the fast expansion rate of their host plants. Range-expanding plants have been shown to be generally less negatively affected by soil communities in the new range than congeneric native plant species. This may be explained because fewer herbivores and pathogens are able to attacking the range expanding plants in the new range, either because of a lack of co-evolutionary history or by stronger direct or indirect defense mechanisms of the range expanding plant species compared to their native congeners.

We study how multitrophic interactions develop in the rhizosphere of range-expanding plants in their new range. We will show results of a greenhouse experiment in which we expose range-expanding plant species and native congeners from the new range to different generalist root-feeding nematode species and microbial communities, which contain nematode antagonists, both from the new range. We examine the control of the nematodes both bottom-up (by the plant) and top-down (by antagonistic microbiota) and compare the growth of the plants in response to the nematode species with and without microbial communities. We test the hypotheses that 1) if top-down control of root-feeding nematodes is plant-mediated, this will be stronger in native species than in range-expanders, as native plants have a shared evolutionary history with the soil community and 2) range-expanding plants are better defended against generalist root-feeding nematodes than congeneric natives, because of strong direct defense mechanisms.

Keywords: Range expansion, Novel interactions, Multitrophic interactions, Plant defense

[P1.121]

Soil microbial community response to a long history of oil contamination

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Oil contamination comprises a major environmental problem since the extensive use of fossil fuels started. Past oil spills have triggered much research on the microbial degradation potential, but it is still unclear how ecosystems respond to long-term contaminations.

Here, we investigate a natural oil seep located in Zakynthos Island, western Greece, called Keri Lake. In Keri Lake, hydrocarbon flow to the soil surface has been observed from belowground in a few natural escapes, first mentioned by Herodotus (484-430 BC), as well as several man-made drilling wells. We hypothesize that a well-adapted microbial community has been shaped under the long presence of oil hydrocarbons in soil. In order to study community structure as well as functions related to hydrocarbon degradation, soil samples were collected in October 2013 from 3 sites of different oil impact: non-contaminated, low and highly contaminated. Sample depths varied from ~0.1 to 6.5 meters. The influence of hydrocarbons and sampling depth on microbial communities was assessed using fingerprinting analysis and revealed a clear decrease in diversity with increasing sampling depth in all sites. A decrease in microbial diversity was further observed for contaminated sites versus the non-contaminated ones, but less pronounced.

Taxonomic and functional diversity was further investigated by metagenomic analysis using amplicon based barcoding approaches of ribosomal genes, as well as direct sequencing of extracted DNA. The obtained data was correlated to oil chemical analysis and the availability of alternative electron acceptors.

We will present detailed results on how microbial diversity is influenced by the long contamination of soils with hydrocarbons in the frame of the presentation.

Keywords: natural oil seep, Keri Lake, microbial diversity, long contamination of soil

[P1.122]

Soil Macroinvertebrates diversity in Mananged and Non Managed Fallow Lands in Calakmul, Reserve, Campeche, Mexico.

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Introduction. In Mexico, the Best preserved Tropical Rain Forest is found in Calakmul Reserve, where Fallow land management has been established since 2008, for promoting carbon sequestration. The aim of the study is to observe how the abundance and diversity of soil macroinvertabrates vary in managed and non-managed fallow lands in Calakmul.

Methods. Fallow lands were selected among the reserve according to the type and age of their plants. Plants were identified, counted and measured. 41 sites were sampled (5 Tropical Rain Forests, 2 maize crops and 34 Fallow lands). Soil macroinvertebrates were collected at the ending of the raining season by hand sorting according to TSBF method (Anderson and Ingram 1993) where 4, 25x25x30cm monoliths per site were done, soil samples and litter were also taken. Soil macroinvertebrates were counted, weighed and classified by order, and they were identified into morphospecies.

Results. As preliminary results we observed the highest macroinvertabrates biomasses and densities in Fallow lands and in Tropical Rain Forests (Figure 1 & 2). The highest number of morphoespecies was observed within the gasteropoda group (Figure 3). We wait for soil properties results in order to observe possible correlations between all variables.

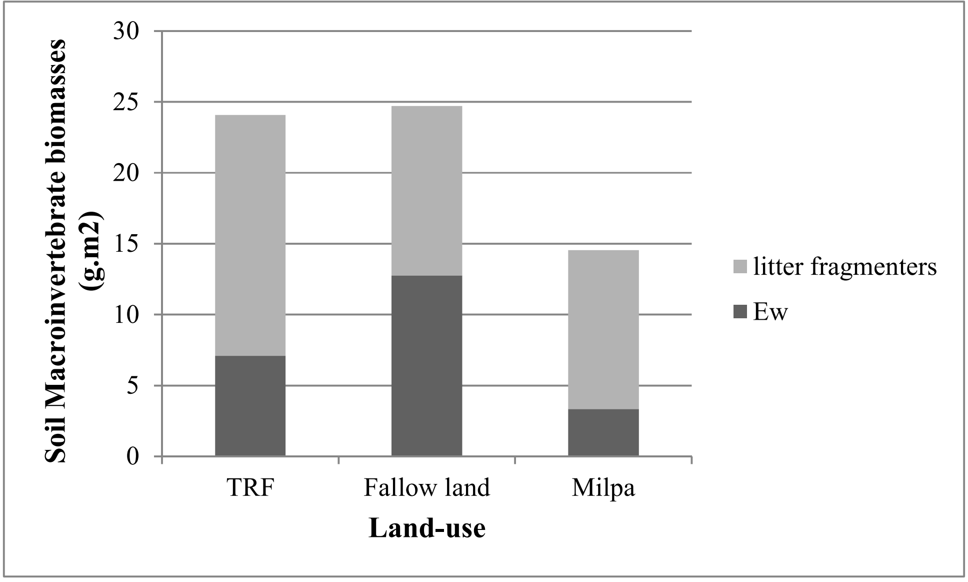

Figure 1. Soil Macroinvertebates biomasses (gm^2). TRF: Tropical Rain Forests, Milpa: maize crop with pepper and cucumber. Ew: earthworms.

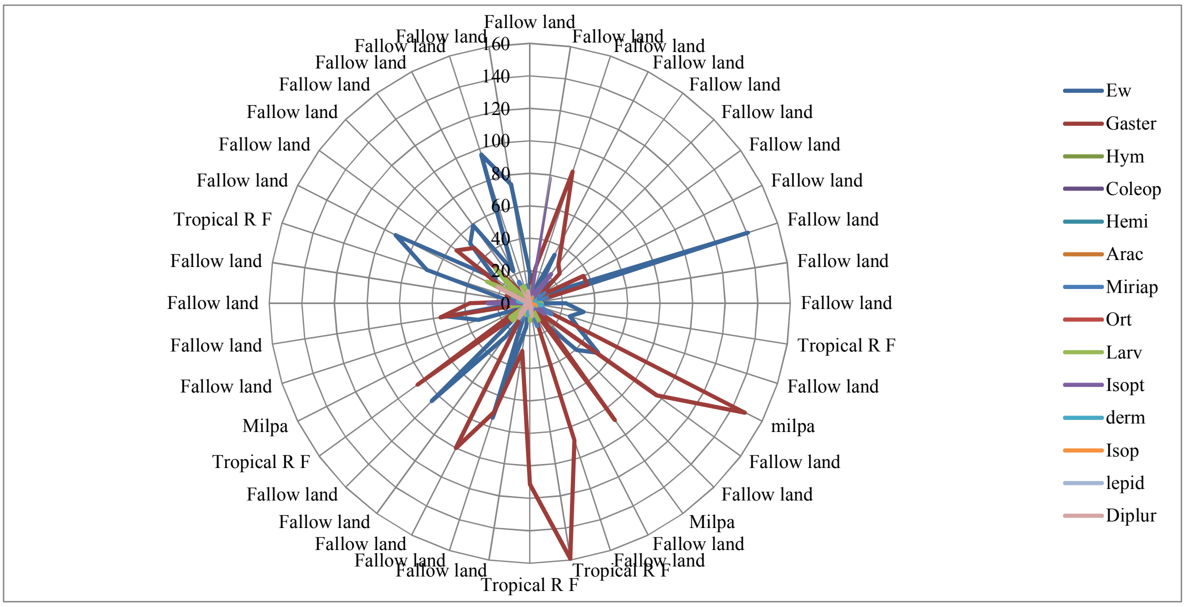

Figure 2. Soil Macroinvertebrates density (ind.m^2) per site. Ew: Earthworms, Gaster: gasteropodes, Hym: hymenoptera, Coleop: coleoptera, Hemi: hemiptera, Arac: Aracnida, Miriap: Miriapoda, Ort: Orthoptera, Larv: larves, Isopt: Isoptera, derm: dermaptera, Isop: Isopoda, lepid: lepidoptera, Diplur: Diplura.

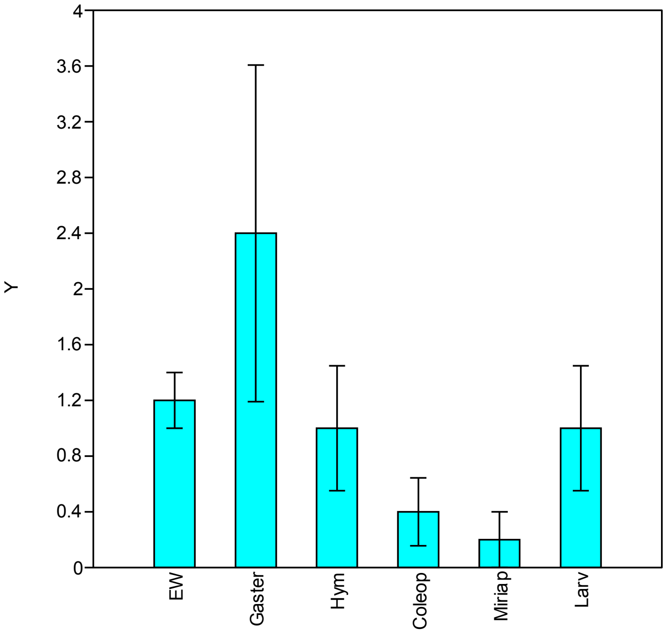

Figure 3. Soil Macroinvertebrates morphoespecies in Fallow lands. Ew: Earthworms, Gaster: Gasteropodes, Miriap: Miriapodes, Larv: Larves.

Discussion: Fallow land management in Calakmul seems not to disturb soil macroinvertebrates' abundance.

Keywords: soil macroinvertebrates, Fallow lands, Calakmul, diversity

[P1.123]

Predicting drought resilience of grassland plant communities through belowground functional traits.

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Plant communities have to cope with environmental changes that can cause dramatic reductions in the primary productivity and ecosystems' stability, among which biodiversity loss and drought events. In this study, we aim to determine the factors that make plant communities resilient to extreme summer drought by looking at the diversity in certain plant functional traits. We will mainly focus on morphological traits that are related to the resistance to drought or the recovery after drought, as resistance and recovery together determine the measure of resilience. Moreover, the focus will be on root traits, as little is known about the belowground traits, while they play an important role in the water and nutrient uptake, and are thus important for survival during water scarcity and nutrient acquisition under competition. In a common garden experiment, plant monoculture plots of 16 grassland species are established to measure the plant traits and responses to a simulated summer drought. In addition, 4-species and 16-species mixtures with different trait diversity levels are established and subjected to the summer drought. The extreme drought will be mimicked by catching the rain with roof installations for about 4 to 6 weeks in the middle of the growing season to reduce the precipitation with about 50%. Community resilience will be assessed by measuring productivity and species composition, and will then be linked to the community trait diversity and weighted means of the measured traits. These linkages between trait diversity and resilience are needed to be able to predict community resilience during droughts and to better understand the positive relationship between biodiversity, productivity and stability.

Keywords: Trait diversity, Drought, Resilience, Roots

[P1.124]

Isolation and characterization of bacteria able to degrade pesticides used in the fruit-packaging industry

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Diphenylamine (DPA) and ortho-phenylphenol (OPP) are used in fruit packaging plants for the protection of fruits during storage. However their application results in the production of high wastewater volumes which according to legislation should be treated in situ. Despite that, no methods for their detoxification are in place at the moment. We aim to develop biofiltration systems inoculated with tailored-made inocula for the detoxification of those wastewaters and their reuse by the fruit packaging plants. Towards this task, two pure bacterial strains able to efficiently degrade the fungicide OPP and the antioxidant DPA were isolated from a soil used as disposal site for pesticide-containing wastewaters in Greece. The isolation of such degrdingbacteria constitutes a first step towards the development of biopurification treatments.

The OPP and DPA degrading strains wereidentified as *Sphingomonashaloaromaticamans*and *Pseudomonas monteilii* respectively. *S. haloaromaticamans*was able to degrade up to 150 mg/l OPP within 7 days and use it as energy source for growth. Genome analysis revealed the presence of three main catabolic operons: a *bph* operon composed of genes with putative role in the initial transformation of OPP to benzoate and two *ben/cat* operons which control the conversion of benzoate to Krebs cycle intermediates via the *ortho*-cleavage pathway. The DPA-degrading strain was able to rapidly degrade 2 g/l DPA and to use it as a carbon and nitrogen source. Genome analysis revealed four main catabolic operons: a *bph* operon probably involved in the its transformation to catechol and aniline; a *tdn* operon involved in the transformation of aniline to catechol and two *ben/cat* operons which control the further transformation of catechol via the *ortho*-cleavage pathway. RT-q-PCR expression tests and proteomic analysis are currently running to verify the functional role of the identified catabolic genes in the two bacteria.

This work is part of the project “BIOREMEDIATO-OMICS” and is implemented under the "ARISTEIA" Action of the "OPERATIONAL PROGRAMME EDUCATION AND LIFELONG LEARNING" and is co-funded by the European Social Fund (ESF) and National Resources.

Keywords: bacterial degradation, pesticides, fruit-packaging industry, degradation pathway

[P1.125]

Species composition and distribution of oribatid mites (Acari: Oribatida) along an altitudinal gradient in Khibin mountains

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The study of patterns of spatial distribution of soil biota in altitudinal zones gradients is of great scientific interest. Here many habitat conditions, such as climate, vegetation, soil type and other, regularly change in relatively small area, allowing of the formation of unique biotic complexes.

Soils and litter samples were taken on Woodyavrchorr mountain's slope (Khibin Mountains, Kola Peninsula) in July-August 2010. Yernik tundra, lichen tundra, birch crooked forest and grass fruticulose spruce forest (*Picea* sp., *Geranium* sp., *Chamerion angustifolium*, *Milium effusum, Vaccinium mirtillus)* were investigated. Microartrodods were extracted from samples using Berlese funnels.

52 species of oribatid mites of 30 genera and 20 families were found. Maximum number of species (33) was found in mountain taiga forest (grass fruticulose spruce forest). The largest abundance of oribatids (above 190 000 specimens/m^2) was in tundra forest belt (birch crooked forest). In tundra belts, especially in lichen tundra, abundance and species number of oribatid mites were much lower. However, the largest indices of biodiversity (Shannon index 2.34) and evenness (Pielu index 0.7) of oribatid taxocene were recorded in yernik tundra.

Found oribatid fauna is represented mainly by widespread species: 51% golarcts, 23% palearcts, 10% European species and 16% are universally distributed. Most of found species (47) are widely distributed in forest zone of European part of Russia. Four species are strongly attracted by mountain areas: *Nothrus borussicus* Sellnick, 1929, *Camisia lapponica* (Trägårdh, 1910), *Neonothrus humicolus* (Forsslund, 1955), *Belba compta* (Kulczynski, 1902).

All found oribatids were divided into 9 morpho-ecological types: galumnoid, carabodoid, dameoid, oppioid, notroid, paleacaroid, hypochtonoid, tectocephoid, oribatuloid. Analysis of morpho-ecological types composition showed that quota of carabodoit type increases with altitude. Simultaneously there is a decrease of quota of Oppioidea superfamily and Eulohmanniidae family representatives.

This work was supported by RFBR (project №14-04-31754).

Keywords: oribatid mites, altitudinal belts, spatial distribution, mountain soils

[P1.126]

The effects of drainage and restoration of mires on peat-associated invertebrates

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Drainage is a major threat to peatland biodiversity. Finland has performed the world's most extensive program of mire draining for silvicultural purposes during the 1960s and 1970s. Mire restoration activities were started relatively recently. Still very little is known about the responses of peat-associated fauna to the rewetting of mires by complete ditch filling, which results in the regrowth of mire vegetation. Therefore, it is essential to evaluate the effectiveness of rewetting for the re-establishment of individual mire specialist species and their communities. We investigated nine pine mires with ditched, restored (3 years after restoration) and pristine (control) sites in Eastern Finland by evaluating the successional changes in peat-associated invertebrate (carabid beetle, ant, spider and crane fly) communities. Pitfall trapping was used as a method for collecting invertebrates. We also recorded vegetation changes and the water table level of these sites to determine how they influence the structure of invertebrate communities and individual species. Results indicate that drainage has a negative effect on peat-associated invertebrate biodiversity, while restoration has a positive effect on mire specialist species. Furthermore, wetness and openness related environmental features play important roles in predicting the responses of mire species and communities. It appears that ditch filling, as a mire restoration option, is successful in also restoring the peat-associated mire invertebrate community.

Keywords: mire drainage, peat-associated invertebrates, mire restoration, specialist invertebrate communities

[P1.127]

Do termites constitute a source or sink for atmospheric N_2O emissions?

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In tropics, termites represent a major soil fauna and play a significant role in C and N mineralization and greenhouse gas emissions as CH_4 but their role in N_2O emissions is poorly studied. Previous studies on termite N_2O emissions have focused on one trophic guild, soil-feeding termites, while they exhibit a wide trophic diversity (wood-, fungus- and litter feeders). This study addressed the extent to which termite feeding guilds would contribute to global N_2O and hypothesized that termites whose dietary N exceeds their needs emit higher N_2O than those with low nitrogenous intake. In-vitro N_2O emissions were measured from 15 termite species, belonging to different feeding guilds, collected from various tropical biomes. Their gut mineral N content and N-cycle functional genes abundance were also quantified to explore N_2O emissions' relationship with termite feeding guilds. Soil-feeding and fungus-growing termites evolved consistent levels of N_2O, ranging from 0.01−0.15 µg N_2O-N (g^{-1} dw termites d^{-1}) with a stimulation of N_2O emission (2−14 folds) during oxic incubation of termite individuals with their mound fragments. Whereas, wood-feeding termites demonstrated an intake of N_2O at rates ranging from -0.02−-0.04 µg N_2O-N (g^{-1} dw termites d^{-1}), setting the first evidence of N_2O reduction in soil invertebrates. No correlation was observed of termite N_2O emission with either their gut mineral N content or nitrifier and denitrifier genes abundance. Based on global termite biomass, potential contribution of soil-feeding and fungus-growing termites to total N_2O emission was low, around 0.2−1.0% in different tropical ecosystems. However, since these emissions are related to termite feeding guilds, a shift in their functional group assemblages due to climate and land-use changes might influence termites' contribution to atmospheric N_2O budget. Our results illustrate the importance of considering trophic diversity of termites and their feeding guild assemblages while estimating their global contribution to greenhouse gas emissions.

Keywords: termites, feeding guilds, N2O emissions, denitrification

[P1.129]

Obervation of ectomycorrhizal fungi (ECM) structures in Eucalyptus deep roots (São Paulo, Brazil)

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Many field observations suggest that ECM contribute to a number of key ecosystem functions such as carbon cycling, nutrient mobilization from soil organic matter and soil minerals, providing a link between trees through common mycorrhizal networks. In Brazil, the ECM form symbiotic associations with species of great economic importance, belonging to Eucalyptus. Until recently, most of the work on ECM functioning has been done in laboratory or in nursery conditions and field studies examining trees and their fungal associates in forest ecosystems are scarce. Furthermore, most of the studies are concentrated in the superficial soil layers and studies that assess root colonization by mycorrhizal fungi at depths > 50 cm are few. The ECM root tips can be morphologically described and classified into morphotypes or anatomotypes. This study aimed to determine the presence of ECM structures in deep roots of *Eucalyptus grandis* (2 to 4-year-old). Two types of observations were made down to a depth of 8 m: a-) minirhizotron were used in a deep pit to examine fortnightly the development of fine roots from 2011 to 2013; b-) fragments of roots were collected in March/2013 during the excavation of a deep pit and observed with a microscope. The study was conducted at the Itatinga Experimental Station (University of São Paulo) in a Ferralsol. ECM structures show by changes in coloration and morphology of roots, as well as fungal heath and hyphae were photographed. Similar ECM structures were found from the soil surface down to a depth of 3 meters. The genus *Cenococcum* was associated with roots at 50 cm and the determination of genus associated with very deep roots is in progress. These types of methodology (minirhizotrons and observation of root fragments) allowed us to verify the presence of morphological alterations in very deep roots associated with ECM.

Keywords: deep roots, ectomycorrhizal fungi, Ferralsol, Eucalyptus

[P1.130]

Do soil macrofauna promote soil organic mater sequestration?

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This contribution summaries effect of soil macrofauna on leaf litter decomposition on several spatiotemporal scales.

Fauna significantly increased microbial respiration in very fresh excrements, but this respiration decrease rapidly and in older excrements respiration is typically lover than respiration of litter. Long term comparison of litter and excrements of showed that excrement decomposed more slowly than litter.

Microbial respiration of macrofauna excrements is also less responsive to freezing and thawing, drying rewetting or addition of easy available organic matter. When added to soil, macrofauna excrements cause lower priming effect compare to litter.

When we introduced soil fauna (namely Earthworms) in soil which was not worked by soil fauna before and litter was repeatedly added the Earthworm treatment promote higher microbial respiration in comparison with mixing litter into soil (to mimic tillage) after firs litter addition. However when litter was added repeatedly after being removed from soil surface by earthworm, after two years earthworm treatment show significantly lower respiration than imitated tillage. This suggests that long term fauna activity tend to promote stabilization of organic matter by soil macrofauna. This was supported by field microcosms that contain litter and mineral layer which were either accessible for soil fauna or not. Access of soil macrofauna increased litter removal from soil surface and promote organic matter storage in mineral soil.

In soil profile of developing post mining soils feces of soil macrofauna increased its proportion in soil volume over time, namely in comparison with litter and litter fragments. We also found positive correlation between amount of carbon stored in soil and proportion of soil volume occupied by earthworm casts.

This indicates that soil macrofauna can accelerate microbial activity but also promote soil organic matter stabilization. In long term stabilization mechanisms become more pronounced.

Keywords: macrofauna, carbon sequestration, mechanisms, invertebrate microbial interactions

[P1.131]

Metabarcoding of soil eukaryotes - multiple applications for biodiversity assessment to applied ecological research

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High-throughput sequencing metabarcoding (HTS-M) is a powerful approach to study the biodiversity of environmental samples. This approach now makes it possible to analyze the nearly entire taxonomic composition by retrieving up to millions of sequences, overcoming also cultural biases and morphological misidentifications.

Our focus is on soil micro-eukaryotes using the V9 region of the 18S ribosomal RNA gene. This genetic marker is short yet taxonomically informative, common to all eukaryotes and thus well adapted to HTS-M.

We use two methods to assign the V9 sequences to meaningful taxonomy: 1) Database dependent assignment of sequences (supervised method) and 2). Independent clustering of sequences (unsupervised method) and subsequent taxonomical assignment of clusters.

We will illustrate this approach with several on-going ecological studies conducted in peatlands, floodplains and forensic experiments and covering either all eukaryotic diversity or specific taxa (i.e. euglyphid testate amoebae).

Keywords: Metabarcoding, 18s rRNA gene V9 region, environmental DNA

[P1.132]

The phytopathogenic seedbank of agricultural soil

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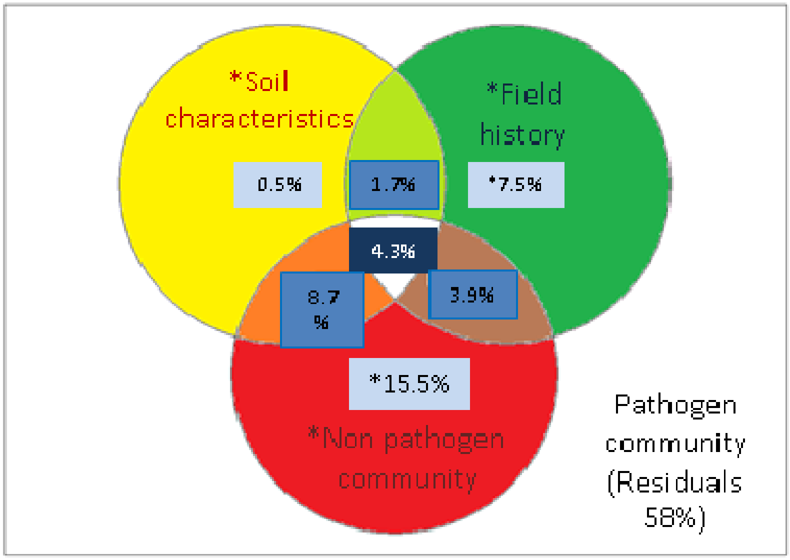
Plant pathogens form a constant threat for production of crops in agriculture. This has strong consequences for global food security as well economic impact on the agro-food industry. Most soils harbor a reservoir of pathogens that persist in the soil environment as part of the microbial community, forming the phytopathogenic seedbank and the future potential infection source. An important factor determining the infection risk is the inoculum potential: combining the inoculum density and its pathogenic capacity. Both are affected by a spectrum of factors, including biotic and abiotic soil characteristics, field management and crop history. However, insight in the relationship with these factors is still limited, hampering predictions on outbreaks of diseases. Therefore it is important to get insight in the composition and abundance of the pathogenic pool and as well as in the factors influencing it.

Our study was designed to assess the contribution of a spectrum of parameters to the presence of pathogenic fungi and oomycetes. 50 agricultural sites covering a broad range of soil types, crop histories and agricultural management were selected. In this set of soils we measured physical-chemical soil characteristics, respiration, and organic matter fractions. Furthermore the field history of the selected sites was documented. Full microbial community profiling (bacteria, fungi and oomycetes) by 454 pyrosequencing and a downstream in-depth analysis was performed to assess the diversity and function of the pathogenic and non-pathogenic community



Our results show a significant contribution by each set of the measured soil parameters. The main drivers of pathogen presence or absence are pH and clay content. Furthermore the crop history shapes the pathogenic pool. Last but not least the diversity and function of the non-pathogenic microbial community is highly influencing the presence and survival of pathogens in the soil

Keywords: soil-borne pathogens, agriculture, biotic and abiotic diversity, management practises

[P1.133]

Water stress-induced biofilm formation by inoculated Azorhizobium caulinodans ORS 571 on rice roots

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Azorhizobium caulinodans is a bacterium having biologically significant characters such as oxygen tolerance (3% v/v), non-legume root colonization and nitrogen fixing ability in free living status. Here, we assess survival and extent of colonization of roots of rice variety BG 352 by inoculated *A. caulinodans* under water stress condition.

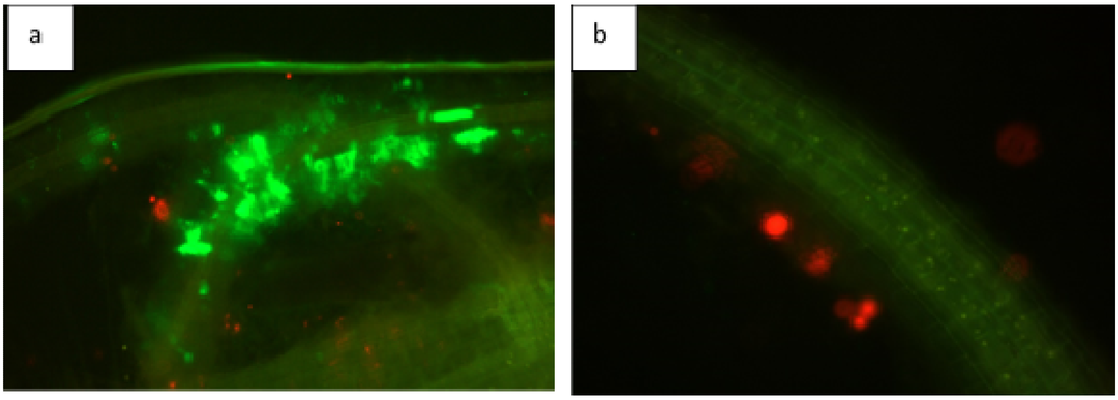
A. caulinodans cells were tagged with Green Fluorescent Protein (GFP) by inserting the gfp gene containing plasmid pBBR5-hem-gfp5-S65T in to *A. caulinodans* ORS 571, by tri-parental mating for reliable detection *invivo.* Labelled bacterium was inoculated on to pre-germinated rice seedlings grown in nitrogen free vermiculite-perlite medium.

Test plants were subjected to a water stress by sprinkling 1/10th of the volume required for flooding every other day while the control was maintained flooded. The plants were allowed to grow for 15 days. Then, the roots were analysed for Azorhizobial colonization using an epifluorescent microscope and the intensity of fluorescence was measured.

Clumps of bacteria formed in to biofilms were visible on the rice root surface after 15 days. Roots were heavily colonized in the root hair zone of the plants subjected to the water stress, whereas the colonization was significantly low in the control (plate 1). Under water stress, bacteria had developed in to biofilms encapsulated with extracellular polymeric substances (EPS) (Chang and Halverson, 2003). Here, resource channelling to produce more EPS is suggested for *A. caulinodans*, as was evident in *Psedudomonas* (Roberson and Firestone, 1992) in response to water stress, leading to hydrated micro environment and survival under water stress.

[illegible] ots,

Plate 1: a. *A.caulinodans* ORS 571 biofilms formed during a water stress on rice roots X40 b. Control plant roots X40 (Under epifluorescent microscope)



[P1.134]

Functional diversity of carbon degrading enzymes through sequence capture in agricultural soils

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Soil microorganisms play an important role in the health of the vegetation through nutrient mineralization and maintaining soil structure. They are known to be most diverse and complex, as there could be a billion microbes living in just gram of soil. This leads to poor understanding of the relation between microbial and functional diversity and also their influence over different ecosystem processes. Functional diversity of key microbial enzymes is important to understand complex ecosystem processes such as carbon cycling. Although NGS advancements have assisted us in understanding ecosystem processes by large extent, deducing enzyme diversity from metagenomes could still be tricky due to low coverage. We present a targeted metagenomics approach primarily designed for metagenomics of functional enzymes in large-scale based on “sequence capture”. As a proof of concept in metagenomics, we have investigated enzymes in large-scale related to carbon degradation in agricultural wheat soil and a grassland soil. This particular large-scale implementation of sequence capture in metagenomics is reported for the first time. We targeted around 400,000 enzymatic sequences by creating probes primarily from their conserved regions. The fraction of targeted enzymatic sequences obtained from the datasets were about 40% compared to 1.3% and 5.3% from untargeted and intensively sequenced publicly available soil metagenomes. This sequence capture method will be implemented on five pairs of agricultural and grassland soils from five different sites to analyse the distribution of functional enzymes. The conventional ribosomal (16S and ITS) sequencing will also be compared to understand the link between the microbial and functional diversity and also their influence on different agricultural managements. Their activities will also be measured using the same technique later on. Implementations of such inter-disciplinary techniques to ecosystem samples are key to their understanding and sustainability.

Keywords: Sequence Capture, Next Generation Sequencing, Targeted Metagenomics, Agricultural Management

[P1.135]

High bacterial diversity of a chlor-alkali and Hg-enriched tailing pond

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In the present work, we examined natural microbial rhizospheric communities that have developed on the pond of a chlor-alkali industry in comparison to a nearby natural site. Bacterial 16S rRNAs were amplified and sequenced using Ion Torrent technology. Diversity indices revealed that bacterial richness was higher in the tailing pond and 16S copy number/ng DNA (bacteria specific primer) increased in the tailing pond . Within emergent bacteria genera in tailing pond, all were only minor genera, representing individually less that 2 % of total sequences. A noticeable exception concerned *Pseudomonas* species, from which 17.0 % of sequences isolated from tailing pond derived, whereas only 0.9 % of the sequences were derived from *Pseudomonas* species in natural soil. We further used a qPCR method to confirm the large colonization of the tailing pond by *Pseudomonas* species. It showed an average molecular biomass of 26818 copy/ng DNA as compared to 1820 copy/ng DNA in the nearby natural soil, which confirmed sequencing data. We further characterized isolated *Pseudomonas* colonies using MALDI-TOF identification and found around 50 isolates, among which 10 colonies from the tailing pond corresponded to *Pseudomonas putida*. We also PCR-amplified *merA* gene coding for a Hg reductase, both from DNA soil samples and from isolated *Pseudomonas* colonies. *MerA* was highly present on the tailing pond, however surprisingly only a single *Pseudomonas* species exhibited this marker gene. Studies using the repetitive element PCR fingerprinting technique revealed distinctive DNA fingerprints from *Pseudomonas* and showed that various isolates were present on both tailing pond and natural soil. Capacity of *Pseudomonas* not only to survive but also to predominate in derelict conditions suggests potential application for bioremediation and enhancement of survival and growth of plants for phytoremediation of contaminated soils, especially where they were recovered.

Keywords: Bacteria diversity, Pseudomonas, Tailing pond, Mercury

[P1.136]

How do ectomycorrhizal fungi respond to changes in forest management?

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Ectomycorrhizal (ECM) fungi form a root symbiosis with trees of boreal and temperate forests. With colonizing the tips of the fine roots, these mutualists increase the extended hyphae surface and thereby the nutrient acquisition. Several other benefits, like enhanced resistance against drought and protection against root pathogens are described. In exchange the plant delivers carbohydrates to the fungus.

Changes in the community composition of ECM fungi have been shown to be influenced by plant community composition at different spatial scales. However, little is understood about the relationship between ECM fungi and forest management practices or geographical distances between forest sites.

We are currently studying soil fungal communities in three forest ecosystems to fill this gap of knowledge. Our study covers a total of 48 forest experimental plots within three large-scale and long-term research sites across Germany. Those sites were established by a large interdisciplinary consortium funded by the German Science Foundation – DFG called the German Biodiversity Exploratories. Furthermore a defined range of management types varying from young over old to unmanaged beech forest in contrast to coniferous forest complete the design of the presented study. We assessed fungal community structures and diversity in each of the 48 forest plots using high-throughput amplicon pyrosequencing, targeting the ITS region of the fungal rDNA as marker.

Our results show that communities of the ECM fungi are affected by biotic and abiotic factors, such as management types and soil characteristics. Distinct communities of ectomycorrhizal fungi under different management regimes were found. Furthermore we are able to display that each geographic location got its own set of prominent ECM genera.

Keywords: Ectomycorrhiza, Forest management, 454 pyrosequencing

[P1.137]

Modelling *in situ* activities of enzymes as a tool to predict seasonal variation of soil respiration from agro-ecosystems

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Understanding *in situ* enzyme activities could help clarify the fate of soil organic carbon (SOC), one of the largest uncertainties in predicting future climate. Here, we explored the role of soil temperature and moisture on SOM decomposition by using, for the first time, modelled *in situ* enzyme activities as a proxy to explain seasonal variation in soil respiration. We measured temperature sensitivities (Q_{10}) of three enzymes (β-glucosidase, xylanase and phenoloxidase) and moisture sensitivity of β-glucosidase from agricultural soils in southwest Germany. Significant seasonal variation was found in potential activities of β-glucosidase, xylanase and phenoloxidase and in Q_{10} for β-glucosidase and phenoloxidase activities but not for xylanase. We measured moisture sensitivity of β-glucosidase activity at four moisture levels (12% to 32%), and fitted a Michaelis-Menten function reflecting increasing substrate limitation due to limited substrate diffusion at low water contents. The moisture response function of β-glucosidase activity remained stable throughout the year. Sensitivity of enzymes to temperature and moisture remains one of the greatest uncertainties in C models. We therefore used the response functions to model temperature-based and temperature and moisture-based *in situ* enzyme activities to characterize seasonal variation in SOC decomposition. We found temperature to be the main factor controlling *in situ* enzyme activities. To prove the relevance of our modelling approach, we compared the modelled *in situ* enzyme activities with soil respiration data measured weekly. Temperature-based *in situ* enzyme activities explained seasonal variability in soil respiration well, with model efficiencies between 0.29 and 0.78. Fitting an exponential response function to *in situ* soil temperature explained soil respiration to a lesser extent than our enzyme-based approach. Adding soil moisture as a co-factor improved model efficiencies only partly. Our results demonstrate the potential of this new approach to explain seasonal variation of enzyme related processes.

Keywords: temperature sensitivity, moisture sensitivity, Q10, in situ activity

[P1.138]

Impact of phytomanagement practices on microbial communities as revealed by next-generation sequencing technology

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The goal of phytoremediation is to use plants to immobilize, extract or degrade organic and inorganic pollutants. A detailed understanding of the effect plants may have on the activities of rhizosphere microorganisms could help optimizing phytoremediation systems and enhance their use. In this study, poplars were grown on an experimental field located in Pierrelaye, in the northwest suburban area of Paris (France) where raw wastewaters have been spread from 1899 to 2002 leading to significant accumulation of trace elements (TE). Poplars were planted in April 2007 at a density of 1000 (short rotation coppice or SRC) or 10,000 (very short rotation coppice or VSRC) stems.ha^{-1}. Fourteen poplar genotypes were chosen according to the local climate conditions, their bio-concentration factors and to cover poplar genetic diversity within the limits imposed by French regulation for poplar culture. Rhizospheric soils were collected from the Skado poplar plots (SRC and VSRC) and compared to nearby control soils (soil naturally recolonized by endogenous flora, or soil from a maize plot). 16s rRNA bacterial and fungal ITS were amplified and sequenced using next-generation sequencing technology (Ion Torrent). In total 222 622 and 317 256 bacterial and fungal sequences, respectively, were obtained and analysed using two approaches, namely an OTU-based and a phylotype-based (direct taxonomic assignment) approaches. Sequence distributions were compared and showed only slight difference at the class or division taxonomic ranks, whereas differences were found at the genus level. Bacterial communities showed only little changes between the different soil samples. In contrast, analyses showed significant changes in the structure and composition of fungal communities, with i.e. the *Hebeloma* genus that appeared to dominate the poplar SRC soil. Data are further discussed, particularly in terms of phytomanagement practices for contaminated soils.

Keywords: phytomanagement, bacterial and fungal community, OTU-based and phylotype-based approaches

[P1.139]

Soil fauna love truffles as humans? A biodiversity study in natural brûlés of *Tuber aestivum* Vittad.

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Tuber aestivum Vittad. is an ectomycorrhizal fungi that produce around the trunk of its host an area, called brûlés, where the growth of other plants is inhibited. Actually not much is known about the effects that truffle induces on soil fauna. The major aim of this study is to evaluate the influence of truffle fructification on soil animals comparing soil fauna community inside and outside the brûlés.

The study is carried out in 9 spontaneous brûlés of *T. aestivum* Vittad. located near the Piacenza province (northern Italy). The project started in June 2013 and the sampling was repeated every first week of the following 12 months till May 2014. Soil samples were collected inside and outside the brûlés for: chemical-physical analysis (9 samples for pH, total organic carbon, organic matter content and moisture), microarthropods community (9 samples of 10x10x10 cm) and nematode extraction (8 small soil cores of 500 ml in volume). Microarthropods extraction was performed using Berlese-Tüllgren funnel. Nematodes were extracted with modified Baermann funnel and fixed with hot formalin (5%). Soil biological quality indices (QBS-arthropods, QBS-collembola and Acari/Collembola ratio) and biodiversity indices (Shannon-Weiner and Pielou’s indexes) were applied. Maturity Index was applied. We report the preliminary results.

Results showed some differences between inside and outside the brûlés. Truffle creates a more alkaline environment with lower levels of organic matter and total organic carbon. Taxa abundances showed higher values outside the brûlés, except for a family of collembolan, Isotomidae, which recorded an opposite trend. Tylenchida (Aphelenchoididae, Tylenchidae) is the most represented group of nematodes inside while Plectidaeoutside outside. Some genera, e.g. *Anaplectus* sp., have been found only outside, Nygolaimidae (*Paravulvus* sp.) and Mononchidae (*Clarkus* sp.), with high C-P value, have been found both inside and outside. Soil quality and biodiversity indices showed almost always higher values outside the brûlés.

Keywords: Truffles, Brûlés, Soil fauna, Soil quality and biodiversity indexes

[P1.140]

Ericoid mycorrhiza and Dark Septate Endophyte in Ericaceous shrubs in Mediterranean environment

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Ericaceous shrubs are commonly found as undestroy vegetation in boreal and mediterranean forest. The ecological plasticity of Ericaceae to grow in different ecosystems encouraged us to test if fungal community structure varies along among a soil and vegetation gradient in the north of Morocco and France to model a changing communities of root-associated fungi.

The colonized roots from four ericaceous plants species, *Calluna vulgaris, Erica sp, Arbutus unedo* and *Vaccinium myrtillus* were examined using morphological, cultural and molecular characteristics. Our results indicated that the isolated fungi belonged to a range of Ascomycota. Moreover, the data showed that a large diversity of potentially ericoid mycorrhizal fungal taxa associate with roots of *C. vulgaris and Erica sp.* These data suggest that ericaceous roots host diverse fungal communities, dominated by the Helotiales. However, these fungal communities are unlikely to be controlled by soil and plant host preferences.

Keywords: Diversity, soil, ericoid mycorrhiza, Dark septate endphyte

[P1.141]

The unaccounted yet abundant nitrous oxide-reducing microbial community: a potential nitrous oxide sink

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Nitrous oxide (N_2O) is a major radiative forcing and stratospheric ozone-depleting gas emitted from terrestrial and aquatic ecosystems. It can be transformed to nitrogen gas (N_2) by bacteria and archaea harboring the N_2O reductase (N_2OR), which is the only known N_2O sink in the biosphere. Despite its crucial role in mitigating N_2O emissions, knowledge of the N_2OR in the environment remains limited. Here, we report a comprehensive phylogenetic analysis of the nosZ gene coding the N_2OR in genomes retrieved from public databases. The resulting phylogeny revealed two distinct clades of nosZ, with one unaccounted for in studies investigating N_2O-reducing communities. Examination of N_2OR structural elements not considered in the phylogeny revealed that the two clades differ in their signal peptides, indicating differences in the translocation pathway of the N_2OR across the membrane. Sequencing of environmental clones of the previously undetected nosZ lineage in various environments showed that it is widespread and diverse. Using quantitative PCR, we demonstrate that this clade was most often at least as abundant as the other, thereby more than doubling the known extent of the overall N_2O-reducing community in the environment. Furthermore, we observed that the relative abundance of nosZ from either clade varied among habitat types and environmental conditions. Our results indicate a physiological dichotomy in the diversity of N_2O-reducing microorganisms, which might be of importance for understanding the relationship between the diversity of N_2O-reducing microorganisms and N_2O reduction in different ecosystems.

Keywords: Nitrous oxide reductase, amplicon sequencing, phlyogeny, soil

[P1.142]

Evidence of indigenous rhizobia competition for nodulation in legume cover crops hairy vetch, crimson clover and Austrian winter pea

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Biological nitrogen fixation (BNF) is a major contributor of nitrogen to managed agroecosystems in the United States (U.S.), with the presence of effective rhizobia strains being essential for optimal nitrogen fixation by legume cover crops. Organic farmers have particular interest in legume cover crops for N contribution. To maximize nitrogen contribution, a better understanding of interactions between high-performing inoculant strains and established soil rhizobia is needed. Our objectives were to 1) evaluate rhizobia inoculant effectiveness with three popular legume cover crop species cover crop legume species including crimson clover (*Trifolium incarnatum* L.), hairy vetch (*Vicia villosa* Roth), and Austrian winter pea (*Pisum sativum*), and 2) evaluate genetic diversity of nodule occupants. Legumes were planted in a randomized split plot design with and without commercial seed inoculation on three organically managed farms. Legume biomass, biomass nitrogen, nodule number, and nodule dry weight were measured and a Most Probable Number assay carried out to determine soil rhizobia population sizes. A total of 576 rhizobia strains isolated from surface sterilized nodules were fingerprinted using rep-PCR and the nodulation gene *nodC* sequenced to determine origin and diversity of nodule rhizobia strains. Across both inoculated and uninoculated treatments, plant biomass nitrogen ranged from 80 to 206 kg ha^{-1}. At three field sites, inoculation did not result in an increase in plant biomass, biomass nitrogen, nodule number, or mass. A majority of rhizobia isolates belonged to 13 DNA fingerprint clusters whose occupants were over 70% similar, with similar strains not grouping by cover crop host, farm location, or inoculation treatment. As few as 8.5% of strains isolated from inoculated nodules had DNA fingerprints similar to the commercial inoculant. Rhizobia isolated from inoculated legume nodules displayed genetically distinct *nodC* sequences from inoculants, suggesting that applied inoculant strains were not present in host nodules.

Keywords: rhizobia, nitrogen fixation, organic agriculture

[P1.143]

Emissions of atmospheric N_2O by tropical soil macrofauna

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Tropical soils account for about 23% of global N_2O emissions. These soils harbor a huge biodiversity of invertebrate macrofauna dominated by termites, earthworms, scarabaeid grubs and ants. These macrofaunal groups, also termed as soil engineers, thrive on diverse substrates with different C:N ratio. This study hypothesized that (i) the gut environment or biogenic structures of these soil engineers constitute hotspots of N_2O emission, (ii) this N_2O emission will vary according to their feeding behavior, and (iii) this N_2O emission in each soil fauna will also depend on their gut nitrifier and denitrifier genes abundance and mineral N content. In-vitro N_2O emissions were determined from either live macrofauna (30 species collected from Africa, South America and Europe) or their biogenic materials or both under aerobic incubations. Gene abundance of nitrifiers (AOA and AOB) and denitrifiers (nirK, nirS, nosZ) were quantified by quantitative PCR. Soil-feeding and fungus-growing termites and scarabaeid grubs evolved consistent levels of N_2O while ants did not. While, wood- and grass-feeding termites revealed a reduction of N_2O, establishing first evidence of N_2O reduction by soil invertebrates. Biogenic structures of earthworms and ants emitted substantial amount of N_2O while those of termites did not. It is also found that the feeding behavior (total N content and C:N ratio of food material) is the main factor explaining the observed N_2O emission pattern of each macrofaunal group investigated whereas genes abundances, particularly of denitrifiers, and gut mineral N content did not appear to be the relevant proxies of N_2O emissions. Data upscaling of results suggests that soil macrofauna could contribute from 0.1–11.7% and 0.1–8.8% of the total soil N_2O emissions, respectively, from the tropical rainforest and dry savanna ecosystems. This work should contribute to a better assessment of the soil biotic compartment in simulating greenhouse gas emissions from tropical soils.

Keywords: Tropical N2O emissions, Soil macrofauna, Denitrification, N-cycle genes abundance

[P1.144]

Do reclamation speed up recovery of soil and soil biota on post mining sites along climatic gradient across

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Soil biota community (macrofauna, nematodes and microbial community studied by PLFA) was studied together with soil development in post-mining chronosequences along climatic gradient in the USA, covering hardwood forest (TN, IN), tallgrass prairie (IL), or shortgrass prairie (WY). Post mining sites reclaimed according recent regulation which includes topsoil application and vegetation establishment were compared to local climax.

Both young and old restoration sites were much closer to the climax condition in shortgrass prairie than in the other sites. The shortgrass prairie soil community contained abundant root-feeding organisms, which may establish quicker than the saprophagous fauna that was abundant at the other sites. Absence of saprophagous groups, and especially earthworms, resulted in the absence of bioturbation in shortgrass prairie sites while in chronosequences other than the one in shortgrass prairie, bioturbation played an important role in topsoil formation resulting in more complex soil profile development compare to shortgrass prairie. This may contribute to faster recovery communities in shortgrass prairie in comparison with tallgrass prairie and forest as

At the same time sites that were reclaimed according recent regulation (topsoil application and vegetation establishment) were compare to unreclaimed sites both about 30 years old in TN IL and WY. It TN soil and soil biota seems to approach fasted to climax in unreclaimed than reclaimed sites. In IL this differences between reclaimed and unreclaimed sites was not so clear. While in WY reclaimed sites seems to approach to climax community fasted than unreclaimed one. This suggests that effect of reclamation vary along climatic gradient. In drier sites, formation of soil matrix from parent material is probably much slower and topsoil application speed up soil community recovery substantially while this effect is less pronounces in more wet sites, where soil compaction due to restoration may in some cases even slow recovery.

Keywords: restoration, post minning site, soil microflora, soil fauna

[P1.145]

phoD Alkaline Phosphatase Gene Is Affected More by pH than by P Status in a Permanent Grassland

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The soil microbial community is complex, dynamic and strongly shaped by soil properties such as pH and phosphorus (P) availability. Microorganisms play a major role in the P cycle by mediating biological processes such as organic P mineralization, which contributes to replenishing the available P pool. Microorganisms secrete a range of phosphatases, such as the alkaline phosphatases encoded by *phoA, phoD* and *phoX* genes. The *phoD* alkaline phosphatase is especially common in soil ecosystems. However, little is known about *phoD* genetic diversity in soils, or about the identity of bacteria that express *phoD*, due to the lack of suitable genetic tools.

We designed new primers targeting *phoD* gene and applied them to DNA and RNA extracted from a long-term grassland fertilization trial characterized by a pH gradient near Zurich (Switzerland). Our aims were to identify bacteria that express *phoD* and to study the effect of pH and P fertilization on the *phoD* diversity and composition using 454-sequencing. In addition, active and total archaeal, bacterial and fungal community structures were characterized by T-RFLP.

Our results showed that the newly designed primers were suitable to study *phoD* diversity and composition. Between 150 and 200 *phoD* OTUs were identified in the active community. The key bacteria that express *phoD* in all samples were associated with the Actinomycetales, Rhizobiales, and Pseudomonadales taxa. Furthermore, soil pH significantly affected the structure of all communities and also the composition of *phoD* at both RNA and DNA level. P fertilization influenced archaeal and fungal community structures only.

In our study, Actinomycetales, Rhizobiales and Pseudomonadales represented the key players in *phoD* gene expression. Soil pH was the main soil property influencing community composition. We are currently identifying bacteria that carry *phoD* and *phoX* genes in different soils in order to verify the results obtained in this study.

Keywords: phoD Alkaline Phosphatase, pH, Phosphorus Fertilization, Grassland

[P1.146]

Restoration groundwork: testing large-scale soil transplantation to facilitate rapid vegetation development on former arable fields

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The restoration of former arable fields to semi-natural grasslands is an important method for counteracting the loss of species rich grasslands. Restoration of these areas is a long process that may take decades or even centuries. High nutrient availability as well as lack of an appropriate seedbank are well-known bottlenecks for restoration. However, recent fundamental research into plant-soil interactions has demonstrated that the soil community also plays a crucial role in driving the secondary succession on ex-arable fields. Yet an explicit belowground perspective in nature restoration has so far not been applied in practice.

Here we report the first field experiment transplanting soil communities from well-developed natural sites to a new restoration area performed at a spatial scale relevant for restoration practice. In 2006, transplantation of both soil from a species-rich grassland and a heathland were carried out in four replicate areas (2.5-5 ha) on an ex-arable field. To compare with conventional restoration measures hay was spread over similar areas and these treatments were executed both on the original soil as well as on areas where the top-soil had been removed. After six years the restoration success was evaluated by quantifying vegetation structure and composition. Furthermore, fungal, bacterial, nematode and microarthropod abundance and composition, as well as edaphic factors were measured. We show that the transplantations, particularly using heathland soil, has increased plant diversity and altered the plant community composition which became more like the target community. Furthermore, transplantation led to a more abundant, relatively more fungal-dominated, microbial community. Our results show, for the first time on a scale relevant for practitioners, that soil transplantation can be an effective measure to jump-start the restoration of species-rich vegetation on former arable fields by means of co-introduction of both seed material as well as the appropriate soil community.

Keywords: Nature restoration, Soil transplantation, Succession, Soil mediated vegetation change

[P1.147]

Litter decomposition and home-field advantage during plant range shifts

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The current rapid climate warming enables many native plants to expand ranges to higher altitudes and latitudes. This phenomenon has been observed worldwide in mountain systems and across the continents. Plants develop in close interaction with soil organisms in a direct (e.g. via pathogenesis) and indirect way (e.g. via the detritus food web). During range shifts, however, these interactions might become temporally disrupted since soil organisms have limited dispersal capacity. Range-expanding plants might benefit from the release of soil-borne pathogens. However, they might also lose positive interactions with specialized decomposer organisms.

“The home-field advantage (HFA) hypothesis” predicts that litter decomposes faster in the vicinity of the plant from which it originates than away from that plant due to the presence of specialized decomposer communities. Recent research provides supporting evidence that plants have species-specific associations with decomposer communities. If decomposer microbes are indeed under selection of their host plants, range expanding plants would possess different microbial decomposer communities than closely related native plants. How introduction of range expanding plant species in the new ranges will affect local decomposers and native plant communities is, however, an unanswered question.

The present research aims to study local specialization by decomposers and HFA of plant species that shift range along latitudinal gradients. We test the hypothesis that HFA is lost during latitudinal range expansion, but that it may increase when time since arrival of the expander increases. Furthermore, we aim to investigate plant-decomposer interactions and legacy effects though litter decomposition of range expanders on native plant communities.

Keywords: home-field advantage, litter decomposition, plant range shifts

[P1.148]

Microbial regulation of biogeochemical cycles – Probing with salt stress

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Soil microorganisms are important regulators of carbon (C) and nutrient cycling. The microbial C budget is characterized by the C use efficiency (CUE), i.e. the partitioning of substrate into biomass production and respiration. Environmental factors that influence CUE will shape the role of the soil as a net C-source or sink. Salinity remains understudied in soil, despite its growing relevance. To assess how soil salinization affects the C sequestration ability and fertility of soil the responses of microbial processes to salinity need to be understood.

First, we conducted a comparative analysis of the sensitivity of different microbial processes to salt exposure. Second, we used samples from natural salinity gradients to assess if a legacy of salt exposure can influence the microbial response to changing salt exposure. If salt had an ecologically significant effect in shaping these communities, microbes sensitive to salt exposure would have been disfavoured; meaning that exposure should have induced increased tolerance. Third, we investigated how microbial salt tolerance responded over time if salt concentrations were increased or decreased from points along the salinity gradients.

The sensitivity of microbial processes to salt was investigated by establishing dose-response curves to estimate tolerance. Bacterial and fungal growth responses together with immobilisation of NH_4^+ and NO_3^-, as well as catabolic processes such as respiration and nitrogen mineralisation were interrelated. Results suggested that bacteria were more sensitive than fungi, and that growth-related measures were more sensitive to salt than catabolic processes. Communities with a legacy of salt exposure were less sensitive to high salt concentrations than previously un-exposed communities. We hypothesize that dynamics of community tolerance responses are faster when non-saline soils are exposed to increased salinity than vice versa.

Keywords: carbon cycle, salinity, nitrogen cycle

[P1.149]

Independent effects of soil organisms and plant cultivar diversity in legume-grass communities

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Different groups of soil organisms and plant diversity have been shown to influence the performance of plants and their associated aboveground organisms; however, little is known about their interactions and combined effects. Furthermore, while plant species richness has received a lot of attention, plant cultivar diversity has only recently come into the focus of community ecology as one expression of intraspecific diversity. The objective of this study was to determine in a semi-natural field experiment using in legume-grass mixtures whether the addition of beneficial soil organisms (arbuscular mycorrhizal fungi (AMF) and earthworms) and different levels of plant cultivar diversity interactively influence ecosystem functioning, including plant productivity, weed establishment, leaf damage by herbivores and pathogens, and the diversity of aboveground herbivores. Pesticides were purposely not used as a control for the soil biota treatments because of their potential negative effects on non-target organisms. The addition of AMF increased aboveground plant productivity and decreased the diversity of aboveground herbivores. Earthworm addition reduced AMF root colonization where AMF were added, but had no effect on plant productivity or herbivore diversity. Weed biomass was lower in plant communities with high cultivar diversity compared to low cultivar diversity. We did not find any interactive effects of the two soil organism groups and cultivar diversity. Our results indicate independent roles and additive positive effects of AMF and plant cultivar diversity on ecosystem functions such as productivity and resistance against weeds. We suggest that AMF and plant cultivar diversity manipulations may be applied more frequently in agricultural management programs that aim for sustainable yield enhancement and biocontrol of herbivores and weeds.

Keywords: Arbuscular mycorrhizal fungi, Earthworms, Cultivar diversity, Ecosystem services

[P1.150]

Experimental evidences on the contribution of entire free-living soil nematode communities to nutrient cycling and plant uptake

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Nematodes are the most abundant and functionally diverse soil metazoa that significantly contribute to several ecosystem processes and services such as nutrient cycling. Despite their abundance and diversity, experimental evidences on their direct and indirect contributions are mainly based on a few selected species of nematodes and microbes, often with simple organic amendments and without plants. These findings are less accurate and may not be representative of the actual field conditions where several multi-trophic interactions are present.

To understand the influences of nematodes on nutrient cycling and plant uptake under realistic conditions, we set up an incubation experiment which involved multi-trophic interactions between several species of nematodes, native microbes and plants for the first time. The entire free living soil nematode communities were extracted and reinoculated into fresh grass-clover amended soils that had been defaunated by gamma irradiation and planted with Italian rye grass. Two treatments: with (plusNems) and without (minusNems) nematodes were compared for soil nitrogen, phosphorus, sulfur mineralization, plant uptake, microbial biomass carbon (C_{mic}) and Phospholipid fatty acid (PLFA) signatures after 7th, 24th, 47th, 67th, 105th days of incubation. Nematodes communities were analysed to family/genus level at each sampling date.

Nematode reinoculation was successful in establishing comparable abundance and diversity to the field condition. The presence of nematodes showed no significant effects ($p>0.05$) on C_{mic} and on sulfur uptake, however, significantly increased ($p<0.01$) nitrogen uptake, phosphorus uptake and total grass dry biomass during most of the incubation period (Fig 1).

We provided realistic experimental evidences showing the significant contributions of the entire free-living nematode communities to N and P uptake and dry biomass yield. The collective action of these functionally diverse nematodes can be quantified by such an experimental setup, and may advance our understanding of their influences on nutrient cycling and plant growth.

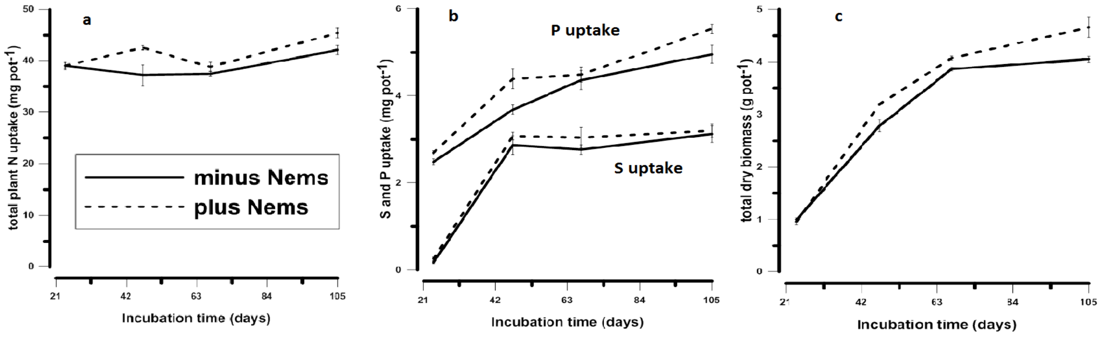

Fig 1. N uptake (a), S and P uptake (b), rye grass dry biomass (c) as significnatly increased in the presence of the entire free-living nematode communities in grass-clover amended agricultural soil

Keywords: nematodes, plant uptake, nutrient cycling, gamma irradiation

[P1.151]

Above-belowground biodiversity in extreme environment: the case of serpentine soils

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Serpentine rocks and the associated soils represent an example of extreme environments, due to the high concentration of heavy metals (Ni and Cr in particular), and to the anomalous ratio between Ca and Mg cations.

In this work we analysed vascular plants, soil microrganisms and microarthropods in two sub-sites MP1 and MP3 within an area characterized by serpentine outcrops and serpentine soils, correlating above and belowground biodiversity. MP1 site (GPS 44.65138°N – 10.08330°E) is a grassy clearing within sub-montane vegetation dominated by white oaks (*Quercus pubescens*), turkey oak (*Quercus cerris*) and hop-hornbeam (*Ostrya carpinifolia*) while MP3 site **(**GPS 44.64282°N – 10.07951°E) was a serpentinite scree rich in specialized flora as rare hyperccumulator plant species (*Asplenium cuneifolium*, *Sedum dasyphyllum*, *Alyssum bertolonii*, *Noccaea caerulescens*) among other. Above ground biodiversity (vascular plant diversity) was analysed using floristic relevés. Belowground biodiversity was characterized in terms of bacterial and microarthropods diversity. In particular Automated Ribosomal Intergenic Spacer Analysis (ARISA) targeted to the 16S-23S rDNA region, allows to estimate bacterial diversity and community composition within the rizhosphere of the Ni hyperaccumulator *Noccaea carulescens* present in the two sub-sites.

Microarthropod communities were characterized by extraction and identification of soil organisms. Abundances, Acari/Collembola ratio, biodiversity indices and the QBS-ar index were calculated.

The two sites differs in terms of soil evolution (soil depth, organic matter content and profile differentiation), and this is clearly reflected on plant communities on both vegetation cover and diversity. Belowground diversity was positively correlated with vegetation cover and soil organic carbon content, while inversely related to aboveground biodiversity.

Keywords: Serpentine soils, Above ground biodiversity, Below ground biodiversity, QBS

[P1.152]

Global diversity of arbuscular mycorrhizal fungi - everything is almost everywhere

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Compared with the global diversity patterns described for animals and plants, the biogeography of microorganisms is poorly understood. Nonetheless, microbes play critical roles in ecosystems, meaning that their distribution and function has far reaching consequences for agriculture and ecosystem management. Arbuscular mycorrhizal fungi (AMF) form a symbiotic relationship with ~80% of land plants, and the nature of these associations strongly influences the performance of plant individuals and species and shapes entire vegetation communities. However, information about the large-scale distribution of the fungal symbionts is largely unknown. Here we use extensive high-throughput sequencing of environmental samples to survey AMF diversity in natural ecosystems worldwide. We show that continent-level turnover of AMF taxa is very low, with 93% of taxa recorded on multiple continents and 33% found on all six continents surveyed. Nonetheless, the abundance of taxa varied importantly at finer spatial scales and in response to environmental and host plant variables. This pattern echoes Baas-Becking's early prediction that in the world of microbes everything is everywhere but the environment selects However, it contrasts strikingly with the continent-scale diversity patterns of other fungal taxa, and with the global biogeography of plants, which exhibit levels of endemism that are an order of magnitude higher. The cosmopolitan nature of AMF taxa probably reflects the group's ancient origin and low taxonomic diversity. Nonetheless, the influence of fine-scale spatial variables on AMF richness and abundance suggests that symbiont limitation is likely for plants in fragmented landscapes.

Keywords: biogeography, high-throughput sequencing, variance partitioning

[P1.153]

Global distribution patterns of Glomeromycota - the role of databases for sequence based classification, identification and recording of these fungi

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Arbuscular mycorrhizal fungi (AMF, Phylum Glomeromycota) are soil and root-dwelling, obligate plant root symbiotic organisms present in most terrestrial environments. Their occurrence and diversity have important roles in ecosystem functioning. Therefore, understanding the taxonomic and functional diversity of AMF is a topic of increasing importance.

Diversity of AMF is commonly measured using DNA sequences of nuclear ribosomal operon markers, most frequently the SSU rRNA gene. Total AMF molecular operational taxonomic unit (MOTU) richness of SSU rRNA gene sequences suggests at least twice as high number of species present as is currently known on the basis of morphotaxonomy. These MOTUs have been classified into “virtual taxa” (VT) in a public database Maarj*AM* (http://maarjam.botany.ut.ee). VT are delimited as phylogenetically related clades of sequences. The Maarj*AM* database collects sequences and meta-data from published ecological and taxonomic works. VT system allows synonymisation of original MOTU designations by providing a stable name. The stability of VT nomenclature is created via type sequences. VT nomenclature permits easy comparability among data and consistent communication among scientists. In addition to SSU rRNA gene, the Maarj*AM* database contains data of fungal barcoding marker ITS, LSU rRNA gene and others.

Application of the VT nomenclature has allowed consistent description of AMF diversity patterns from global to local scales. The current challenges in DNA sequence-based classification and identification of AMF include limited knowledge about intra- vs interspecific variation of the marker gene sequences, and related to this, need for more solid theoretical basis for sequence-based AMF species delimitation. More focus is also needed regarding the consistency of meta-data submissions, as this has lasting impact on the usability of data in databases and further analyses such as biodiversity mapping and cross-kingdom comparisons.

Keywords: database, DNA-based identification, biogeography, arbuscular mycorrhizal fungi

[P1.154]

Do microbial communities matter for litter mineralization along a land-use gradient?

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Whether or not a shift in microbial community structure translates into measurable differences in ecosystem functions is currently an open question. To gauge the importance of initial litter quality and microbial community structure on litter mineralization, we tested in a microcosms experiment three hypotheses using soil (grassland, plantation, culture, forest) and litter (grass, black locust, wheat, beech) originating from a land-use gradient: (i) Litter traits are the predominant control of the rate of decomposition (Litter quality); (ii) Decomposer communities from recalcitrant litter environments have a wider functional capacity to decompose a huge range of substrates (Functional Breadth Hypothesis); (iii) Litter decompose faster in an area dominated by the plant species from which it derived than in an area dominated by another plant species (Home-Field Advantage). During a 202 days incubation, we measured regularly carbon (C) mineralization, changes in substrate quality, enzyme activities and microbial community structure (PLFAs). Overall, C mineralization strongly increased with the most simple and easily degradable litters, confirming that litter quality is the main driver of the decomposition process across various ecosystems. However, FBH and HFA are two mechanisms that together generate functional differences among decomposer communities. Forest microbial community showed the highest ability to degrade litters that vary widely in their chemical properties while the match between soil and litter from grassland and plantation indicated that microorganisms are pre-adapted to their own environment. Such mechanisms may be related to the relative proportion of bacteria and fungi and the synthesis of various enzymes required for obtaining the most limiting resources. In particular, we found that the fungi:bacteria ratio was positively related to the N:P ratio of enzymes. We conclude that the utilization of different C substrates varies among distinct microbial communities and that the role of biodiversity in ecosystem functioning is probably more important than usually acknowledged

Keywords: home field advantage, functional breadth hypothesis, functional significance of microbial communities, ecosystem functioning

[P1.155]

Linking litter quality to microbial community structure and functioning in an agricultural soil

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Anthropogenic pressures on agricultural soils are known to alter their biodiversity, which may affect the capacity of ecosystems to deliver functions and services according to the insurance hypothesis on diversity – function relationship. Cropping systems is fuelling belowground biota through the quality of litter supplied, which varies in quality from year to year. Therefore we hypothesized that soil biota structure and functioning strongly respond to crop residues quality. Aerial and underground parts of maize plants were used as labile and recalcitrant litter, respectively. A dynamic experiment was performed using soil columns filled with a silty loam agricultural soil (Estrées-Mons, Northern France) in which we incorporated in the 0-5cm layer either maize leaves or maize roots (and a control treatment without litter). We measured regularly soil respiration, litter quality, enzyme activities, microbial biomass, bacterial and fungal community structure (using 16S and 18S pyrosequencing) during the incubation period.

Litter quality strongly influenced degradation rates of litter soluble fraction and polysaccharides, leading to faster C mineralization of maize leaves compared to roots. Enzyme efficiency was higher in the recalcitrant litter demonstrating different microbial strategies. After 15 days of decomposition, leaves stimulated the relative proportion of Proteobacteria and Bacteroidetes (classified as copiotrophic bacteria by Fierer et al. 2007). Similarly in the fungal community, Tremellomycetes and Sordariomycetes exhibited the most copiotrophic behavior. General functions such as soluble compounds mineralization rates were better correlated with microbial biomass ($R^2=0.65$) than with community structure. Nevertheless, more specific functions such as complex C forms degradation were related to bacterial community structure. We concluded that the decomposition of complex C forms, having a high energetic cost for microorganisms, strongly impacts the community structure. Thus, ecosystem functioning depends on biota community structure linked to the resources provided to them.

Keywords: Litter quality, Microbial communities, Enzymatic activities, pyrosequencing

[P1.156]

Soil food web structure and faunal diversity in organic farming versus conventional farming

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The present study focuses on the structure of soil food webs and taxonomic species richness of soil micro-arthropods in organic versus conventional farming in Iceland and Austria. Organic farming differs from conventional fields in that no artificial fertilizers or pesticides are applied.

We measured presence and abundance of bacteria, fungi, protozoa, nematodes and micro-arthropods, and within the group of micro-arthropods we measured the taxa richness and diversity.

We found that the structure of the soil food web did not differ significantly between organic and conventional fields, but within the trophic groups we did find a consistently higher micro-arthropod taxa richness and diversity in the organic fields compared to conventional fields. This difference was found across countries, farm-, crop- and soil-types. These results indicate that the trophic structure and functioning of the soil food webs was not very sensitive to management system, but the taxonomic diversity was.

Our results confirm those reported by Parisi et al. (AEE, 2005, 105: 323-333) for arable land and grasslands in Italy, and therefore emphasize that micro-arthropod diversity can be a sensitive and consistent indicator for soil quality under different land use regimes. At present, determining microarthropod diversity is a relative intensive activity, but when the current progress in methodology lead to faster and cheaper analyses, such as barcoding extracted microarthropods, soil microarthropod diversity will become more cost-effective and an even more valuable indicator for soil quality.

Keywords: microarthropod diversity, soil food web, organic vs. conventional farming, soil quality

[P1.157]

Mineral versus organo-mineral P fertilization: effects on soil microbial communities and nutrients allocation in plants

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When mineral phosphorous fertilizers are used, the majority of P is rapidly fixed to the soil, where it becomes poorly available to plants. In this study, mineral nutrient allocation in *Lolium perenne*, and the diversity and structure of soil microbial community in a short-term experiment based on contrasting fertilization plans (mineral vs organo-mineral P fertilization) were evaluated.

The experiment was conducted in open air containers filled with 80 Kg of low- (S1) and high (S2) available P soils. Two kinds of fertilizers were applied, mineral as triple superphosphate (M), and organo-mineral Perfoss® (OM) (NP 3:11) at 110 Kg/ha. Aboveground plant biomass and soil samples for chemical and molecular analysis were collected during a 5-months experiment. Quantitative qPCR and T-RFLP of soil bacteria, archaea and P-solubilising bacteria were performed. Variable pressure scanning electron microscopy (VP-SEM) and electronic dispersion spectroscopy (EDS) were used to evaluate morphological and compositional differences in plant and soil.

In our experiment, an increase in plant N, P and yield as well as *phoD* gene copy numbers in both soils was observed in OM treatments. Compared to control, the uptake of P in plants of *Lolium* was correlated at different extent to that of other trace nutrients, depending on mineral or organo-mineral fertilization. In the OM fertilization, assimilation of phosphorus and calcium was not related, while a higher fixation of sulphur, iron and silicon in the leaves compared to M fertilization was recorded.

The application of organic P to soil increased crop yield and fertilizer use efficiency with respect to mineral fertilization. The mobilisation of insoluble soil P appeared correlated to an increase of P-solubilising bacteria activity. An extension of the root surface area and possible different mechanisms in elements mobilisation and uptake were also hypothesised.

Keywords: phosphorous fertilizers, P-solubilising bacteria, microbial community structure, nutrients allocation

[P1.158]

Composition and function of the *Trifolium* root microbiome

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Soils are the most microbially diverse biomes on the planet, with the activity of bacteria and fungi often enhanced in areas surrounding the roots of plants (rhizosphere). Although the functions of some of these bacteria and fungi are well understood (e.g., rhizobia, AMF), the ecological roles of most groups of rhizosphere microbes remain a “black box”. Our goal is to advance the ecological understanding of these microbes, which seem symptomless at first glance. We combine culture dependent and independent methods for characterizing both composition and ecological function of the root-associated microbiota of *Trifolium pratense*. We have isolated individual strains from 25 genera of bacteria and 35 of fungi from the roots of this important agricultural plant species. Using state-of-the-art DNA sequencing, we have generated community profiles of root-associated bacteria and fungi with the aim of quantifying their abundance on the plant roots and defining a ‘core’ set of potentially ecologically relevant microbes. This information is used to conduct experiments in sterile microcosms that manipulate the abundances and diversities of these root microbes. We will then assess the impact of these root microbes on important ecosystem functions such as plant biomass production, litter decomposition, and nutrient cycling.

Keywords: rhizosphere, DNA sequencing, bacteria, fungi

[P1.159]

Soil ecosystem development in a glacial chronosequence in Iceland

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Soil is considered as important non-renewable resource for life on earth. Soil organisms play an active role in soil formation, which can be studied using soil chronosequences. The proglacial area of the retreating Skaftafellsjökull (Iceland), an outlet glacier extending from the Vatnajökull ice cap, provides an unique undisturbed system, creating a chronosequence in soil formation encompassing a period of >500 years.

We analysed soils of approximately 10, 30, 65 and 120 years old, expecting that this period encompasses the most principle soil community assemblies. We compared our data with those obtained from two reference sites with natural climax vegetation of 500 years old. We measured presence and abundance of soil microbes (bacteria, fungi) and soil microfauna (protozoa, nematodes), representing the dominant taxonomic groups and trophic levels in the soil food web. We also measured soil organic carbon, nitrogen, and vegetation diversity.

Soil populations, carbon, and nitrogen increased with soil age. The soil food web structure developed from a simple system (5 trophic groups) to a more complex web (12 trophic groups), with maximum food chain length increasing from 4 to 6 groups. Fungi were absent at the youngest site and increased in biomass through time thereafter, along with amoebae and flagellates, whereas bacterial biomass stayed constant. Nematodes occurred most abundantly at intermediate sites. Vegetation composition developed from sparsely vegetated by pioneer species to a dense shrubland dominated by Ericaceae.

A cluster analysis based on soil food web structure showed that the 120 year old soil was already quite similar to the 500 year old reference soils, whereas clustering based on vegetation diversity showed a slower development. The faster development of the soil food web indicates that soil food web formation is the driving force in soil ecosystem development, in contrast to the notion that the vegetation development drives soil formation.

Keywords: soil food web assembly, ecosystem development, glacial chronosequence

[P1.160]

Local variation of natural occurring biocontrol of the slug Deroceras reticulatum depending on soil tillage and chemical management

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Slugs are significant pests of numerous crops and because no efficient and environment-friendly treatments exist, they represent a major threat under alternative agricultures, which tend to reduce tillage and pesticides use. Yet, except for beetle banks and the single available biopesticide (Nemaslug), very little interest has been paid to the study of their biocontrol. So far, no combined study on slug pressure, generalist predation and natural abundance of slug parasitic nematodes (SPN) under various farming systems has ever been led.

In South-Western France, fifty wheat fields, organic or not, under normal-, reduced- or no-tillage are monitored for slug populations and two aspects of their biocontrol: generalist predation and nematode parasitism. The study is to be carried out from September 2014 to September 2016. Innovative simple assessments are used: attractive bran bait, egg-predation card and mimicking bait-traps (with decaying slugs). Half of all fields are completely untreated while the other is managed as usual, to estimate potential (untreated half) and residual ('as usual' half) biocontrol of slugs.

In preliminary samplings, more SPN were found in conventionally-tilled farming systems than in both conservation and organic managed fields. Nematodes seem to be more active in host seeking in conventional farming systems or to follow the population of *Deroceras reticulatum*, the main pest slugs in crops. Indeed, preliminary observations from fields under no-tillage, no-pesticides management and conventional management showed equivalent to slightly higher slugs abundance under no-tillage and organic management, with enhanced diversity. In proportion, fewer Deroceras reticulatum were found and rarer species, as *Lehmannia valentiana*, appeared. Higher predation is also expected in no-tillage and organic farming in relation to higher abundances of spiders, carabids and rove beetles.

These conclusions tend to support the hypothesis that nematodes are poorly efficient natural enemies of slugs.

Keywords:

[P1.161]

Microbial communities along glacier moraines of Iztaccíhuatl volcano, Mexico

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Glacial retreat areas are not only of interest in the context with climate change but they also offer an excellent opportunity for microbial ecologists to study ecological theories and concepts. The glaciers of Iztaccíhuatl volcano in México (19.02°N, 98.62°W) are retreating at accelerating speed. Since 1956 a continuous retreat rather than fluctuations has been observed (Delgado Granados et al., 2005). This made it possible to obtain samples along a continuum rather than only sampling distinct moraines.

Sampling has been carried out at 15 different places along the retreat area. Some of the sites have been sampled twice, in 2008 and 2009. Plant species at the sampling points have been recorded for each sampling location. Soil samples (200 g each) were frozen, and air-shipped to the laboratory.

Basic soil analyses included organic C and N, ammonia and nitrate contents, and DNA contents as a measure for microbial biomass. Structural diversity of the soil microbial community was analyzed by the ester-linked phospholipid fatty acids (PLFA) composition (Hannam et al., 2006) and by PCR-DGGE (with various primer sets targeting 16S rDNA).

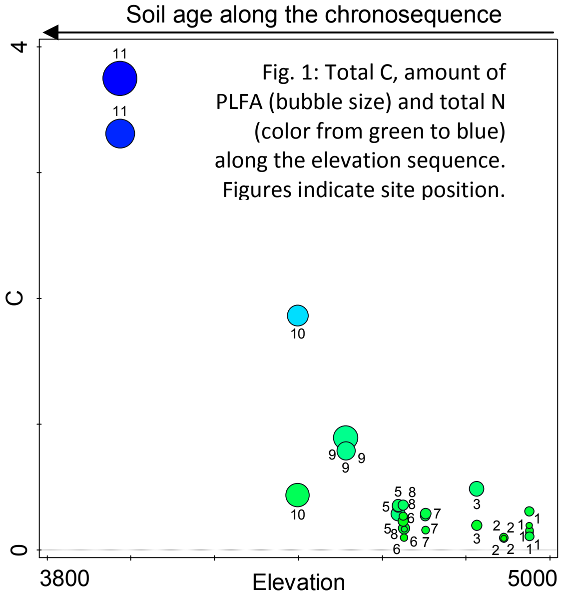

Fig. 1: Total C, amount of PLFA (bubble size) and total N (color from green to blue) along the elevation sequence. Figures indicate site position.

From the youngest sites to the oldest ones the pH increased from 2.5 to 5.1. Electrical conductivity, an indicator of salt content, decreased from the youngest to the oldest sites. We found a classical increase of C and N along the chronosequence, and also an increase in microbial biomass as inferred from total PLFA (Fig.1). The C-to-N-ratio increased from around 4 at 5000 m sea level to 14 at 3800 m, indicating soil maturation. According to PLFA analysis the microbial community showed a clear shift with soil development, and from PCR-DGGE profiles it may be inferred that the diversity of the microbial community increased with time.

Results confirm earlier studies on microbial succession along soil chronosequences (and elevation gradients) in the Alps, North American Rocky Mountains and the Andes (e.g. Insam and Haselwandter, 1989; Nemergut et al., 2007; Nicol et al., 2006).

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Keywords: chronosequence, glacier retreat, PLFA, DGGE

[P1.162]

Disentangling mechanisms that mediate the balance between stochastic and deterministic processes in microbial primary succession

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Despite growing recognition that deterministic and stochastic factors simultaneously influence bacterial communities, little is known about mechanisms shifting their relative influences. Here we aim to better understand mechanisms that drive shifts in the balance between stochastic and deterministic factors during bacterial primary succession. Synthesizing previous work, we develop a conceptual model linking ecosystem development to shifts in the stochastic/deterministic balance. We empirically tested the conceptual model by coupling spatiotemporal data on soil bacterial communities with environmental conditions in a salt marsh chronosequence spanning over 105 years of ecosystem development. Null model analysis at local scale (within but not between successional stages) revealed a progression from stochastic to strong determinism with increasing ecosystem age, supporting one main element of our conceptual model. Statistical model selection indicated that the increasing role of deterministic ecological factors was associated with an increasingly stringent environmental filter imposed by accumulative sodium concentrations. Analysis at regional scale (within and between successional stages) revealed the relative influences of stochasticity and type of deterministic ecological selection to be governed by the magnitude of change in soil organic matter (SOM). Small changes-between pairs of communities-in the concentration of SOM were associated with a consistent ecological selective pressure that caused high similarity in community composition; large changes in SOM were associated with large shifts in ecological selective pressures that caused divergence in community composition; modest changes in SOM were associated with stochasticity due to the lack of strong consistency or clear distinction in ecological selective pressures. Ecological simulation results strongly support these inferences and suggest that high stochasticity arises because two modestly different environments are separated by a ‘fitness valley’ that is shallow enough that community differences are effectively ecologically neutral. Looking forward, we collate our results within an expanded conceptual model that integrates primary and secondary succession in microbial systems.

Keywords: community assembly, neutral theory, niche theory, evolutionary niche conservatism

[P1.163]

Drivers of soil thermal sensitivity along vegetation diversity gradient in temperate forest

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Temperature is one of the most important factors affecting both biomass production and decomposition in terrestrial ecosystems. The possible loss of soil organic matter (SOM) due to climate warming may increase the concentration of atmospheric CO_2 and result in a positive feedback effect. Vast interests is concentrated now on soil significance in global carbon cycling. The aim of work was to assess effects of biological and physicochemical factors on soil thermal sensitivity, that is factors modifying temperature effect on soil organic matter decomposition processes. One of the most important is though vegetation and microbial community diversity.

The samples of O and A horizons were taken under 10 pine forest stands (*Cladonio-Pinetum* and *Vaccinio-Pinetum*), 10 beech forest stands (*Fagetum*) and 15 mixed deciduous forest stands (*Potentillo albae-Quercetum, Galio-Carpinetum, Fraxino-Alnetum*) located through Poland. Detailed floristic analyses *in situ* on vegetation covering resulted in H' plant diversity index. Soil thermal sensitivity was assessed based on soil respiration measurements in the range of temperatures (from 4°C to 28°C) and calculated as Q_{10} index. The total community level physiological profiles (CLPPs) were measured with MicroResp$^{\text{TM}}$ system using 22 different C substrates and for bacteria with Biolog$^{\circledR}$ EcoPlates using 31 C substrates (neutral sugars, amino acids, amines, carboxylic acids, polymers and others). Chemical and physical soil analyses included determination of organic C (C_{org}), total N (N_t), macro-and microelements, pH, dissolved organic C (DOC), maximum water holding capacity and texture. The three groups of forest differed significantly in plant species number ($p<0.0001$) and H' vegetation diversity ($p<0.0001$) with mixed deciduous forest stands being the most diverse. Both forest type ($p<0.001$) and soil horizon ($p<0.0001$) affected respiration rate and significant interaction between them indicated diversification in respiration rates between soil horizons only for beech and mixed forest ($p<0.0001$). However, Q_{10} did not differed nor for forest type and soil horizon. There were significant differences in CLPPs measured with MicroResp$^{\text{TM}}$ between the three forest types in both horizons. The largest contributions to dissimilarity were from carboxylic acids carboxylic acids (D-malic, oxalic, L-ascorbic and α-ketoglutaric acid). The CLPPs measured with Biolog$^{\circledR}$ differed between the three forest types only in the O horizon. The largest contributions to dissimilarity were from D-Cellobiose, β-Methyl-D-Glucoside, D-Galacturonic Acid and N-Acetyl-D-Glucosamine. Relationships between plant diversity and microbial functional diversity was positive and there were numerous significant relations with soil chemistry. Multiple regression for respiration rate with soil chemical and physical characteristics as independent factors showed significant positive relationships with C:N ratio ($p<0.04$). Plant diversity and bacterial functional diversity did not affected soil respiration rate, however we found a simple negative relationship between Q_{10} soil thermal sensitivity and H' plants for A horizon ($p<0.05$). The study was conducted on soils collected in relatively untouched forest sites including protected areas, but risk of increase of CO_2 evolution and SOM loss with temperature increase when vegetation diversity decrease is alarming and need further evaluation. This study was supported by a grant from the National Science Centre of Poland (no 00421/NZ8/2012/29).

Keywords: soil thermal sensitivity, soil functional diversity, forest soil, MicroResp and Biolog system

[P1.164]

Effects of spatial and environmental factors depend on the dispersal ability of Mediterranean soil fauna

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Soil fauna community structure within a landscape mosaic is determined by a multi-scale effect of ecological processes. Yet, the relative role of spatial and environmental factors, operating across scales, may vary between functional groups with different home range and dispersal ability.

We analyzed the changes in community structure of soil fauna differing in life-form and active dispersal power, from edaphic fauna (Collembola) to epigeous beetles (Carabidae), in a typical Mediterranean landscape. We tested the effects of spatial distances among cork-oak habitats enclosed in an agro-forest mosaic, and the environmental factors at different spatial scales, from plot habitat conditions, to patch management and metrics of landscape configuration, on collembolan and carabid beetles.

The sampling sites were four landscape units, selected along a gradient of land-use, from an unmanaged woodland to areas subjected to traditional management practices, namely forestry and pastures. We used ANOSIM to test differences in community similarities among landscape units and variance partitioning methods to disentangle the relative effects of spatial variables (MEMs) and environmental variables across spatial scales (habitat, patch management and landscape).

The relative effects of environmental and spatial factors at different scales varied between Collembola and carabid beetles. The effect of the environmental component, after removing the effect of the space component, was only significant for carabid beetles and explained a higher percentage of their community variance in relation to collembolan communities. The pure effects of the spatial component were generally higher than the environmental component for both groups of soil fauna. Carabid communities responded to landscape features related to patch connectivity of open areas as well as the shape of cork-oak habitat patches integrating the agro-forest mosaic.

We conclude that community patterns of epigeous soil fauna may be predicted by some features of the landscape, while edaphic communities require ecological assessments at finer spatial scales.

Keywords: Soil fauna, Dispersal ability, Community structure, Cork-oak landscape

[P1.165]

Historical Rotation ABC: microbial community structure and diversity over 100 years of wheat production

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The Lethbridge Rotation ABC Historical Plots were established in 1910 to evaluate the effect of fallow frequency on wheat yields. Beginning in 1967 plots were split to include nitrogen (N) and phosphorus (P) fertilizer treatments, providing a rare opportunity to examine soils which have undergone decades of adaptation to different management practices.

Variation in fallow frequency (C input) and N fertilization revealed distinct microbial dynamics after 100 years of wheat production (Table 1). Total biomass and functional group abundance in N-fertilized, continuously cropped soils were approximately twice that of soils which were fallowed every 3 years. Relative abundance of bacterial (AOB) and archaeal (AOA) ammonia oxidizers depended on the interaction of cropping frequency with N addition; abundance of AOB exceeded AOA in some cases. Denitrification functional genes *nir*K and *nos*Z varied with cropping frequency but not by N application. Further, high-throughput sequencing of bacteria (Fig. 1), archaea, and fungi revealed diverse and distinct communities in the plant-associated bulk, rhizosphere, and endophytic communities among N and P fertilizer treatments under continuous wheat.

To gain insight into potential changes in diversity over the past century, we extracted DNA from archived soils. DNA recovery was variable (8.2 – 28.4 ug g^{-1} soil; Fig. 2), but was not linearly related to sample age. Nitrifier and denitrifier gene copy numbers and bacterial diversity changed over time and with management. Soil organic matter analysis using pyrolysis field-ionization mass spectrometry and x-ray absorption near edge structure spectroscopy showed changes in organic N and C composition linking management, microbial dynamics and soil quality.

The legacy of the Historical Rotation ABC experiment provides a unique opportunity to examine the long-term adaptation of microbial communities to management, lending insight into the effects of agronomic practices on agroecosystem sustainability.

Table 1. Total, bacterial and fungal (phospholipid fatty acid analysis; PLFA) and ammonia oxidizer abundance (quantitative PCR) in Rotation ABC soils (post-harvest 2012).

Rotation (R)	Fertilizer (F)	Total	Bacteria	Fungi	*amo*A (AOB)	*amo*A (AOA)	*nir*K	*nos*Z
		nmol PLFA g^{-1} soil			LOG$_{10}$ (copy # g^{-1} soil)			
Continuous wheat	+N	36.1	16.6	2.1	8.40	7.78	7.90	9.96
Wheat-<u>wheat</u>-fallow	+N	17.2	8.5	1.1	7.59	8.05	7.54	9.77
Continuous wheat	-N	12.9	6.6	0.5	7.46	8.13	7.79	9.91
Wheat-<u>wheat</u>-fallow	-N	12.5	2.4	0.3	7.91	7.57	7.35	9.40
ANOVA	Rotation	$p<0.$	$p<0.05$	$p<0.$	$p<0.0$	$p<0.1$	$p<0.00$	$p<0.$

(R)	02		22	7	4	1	02
Fallow (F)	p<0.02	p<0.01	p<0.02	p<0.01	p<0.52	p<0.10	p<0.14
RxF	p<0.02	p<0.07	p<0.36	p<0.001	p<0.001	p<0.67	p<0.26

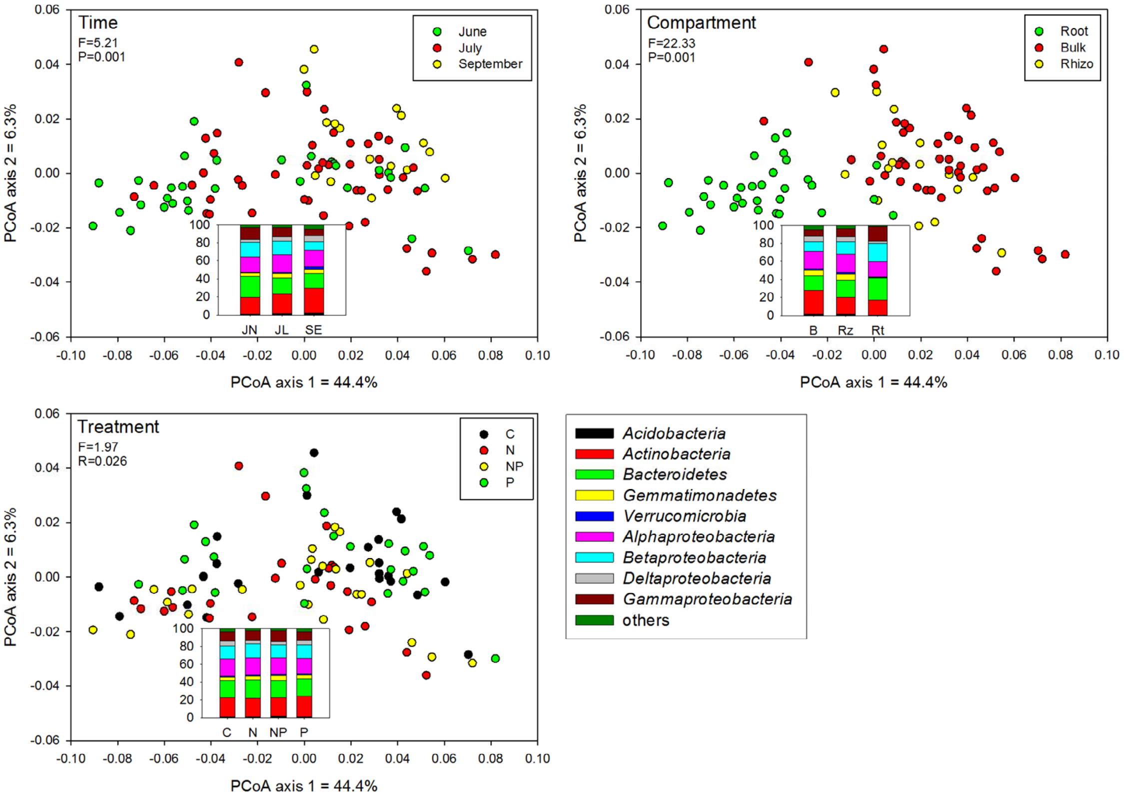

Fig. 1. Temporal dynamics of bulk soil, rhizosphere and root-associated bacterial communities in different fertilizer treatments in Rotation A continuous wheat (based on Illumina MiSeq 16S rDNA profiles).

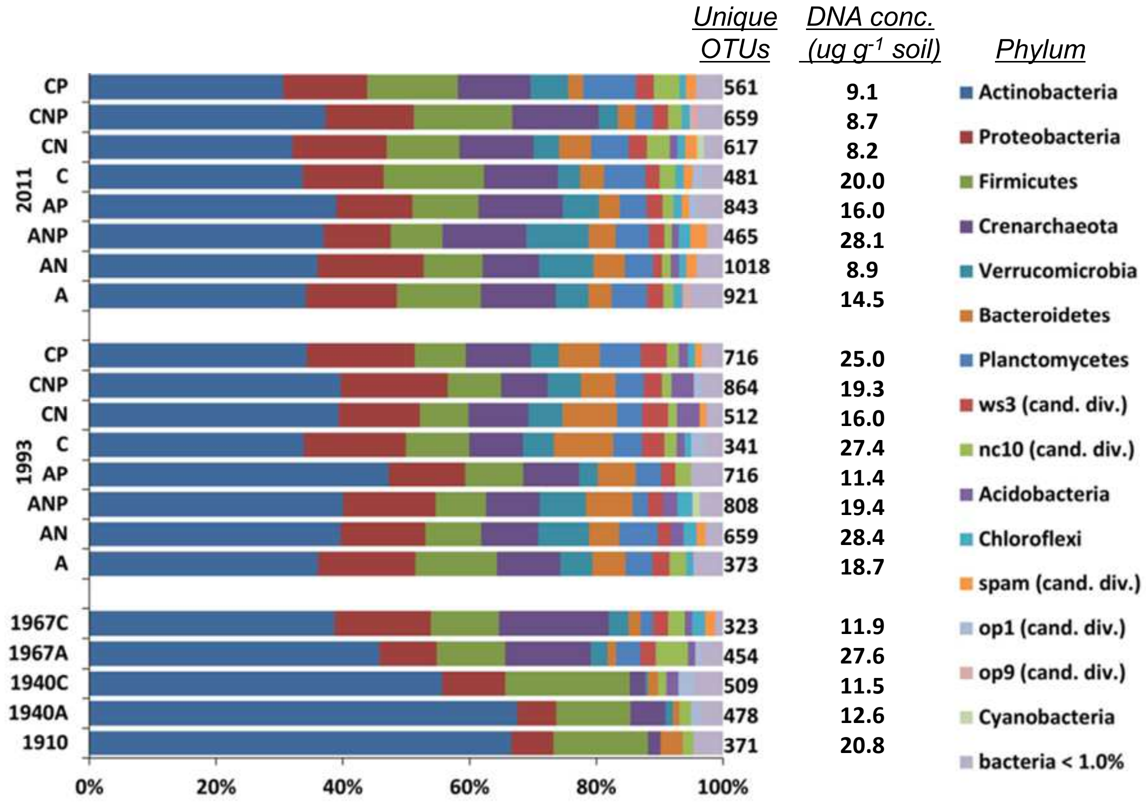

Fig 2. DNA concentration and relative abundance of different bacterial Phyla in DNA extracts from archived soils revealed by pyrosequencing of 16S rDNA.

Keywords: agroecosystem sustainability, carbon and nitrogen cycling, archived soil

[P1.166]

Effects of land-use intensification and host identity on arbuscular mycorrhizal fungal communities in Mediterranean peaty soils

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Arbuscular mycorrhizal fungi (AMF) are ubiquitous plant root symbionts and have beneficial effects on soil fertility, plant growth and nutrition, but all these benefits are declining upon agricultural intensification. Therefore it is important to gain better understanding about the impact of agricultural intensification on AMF diversity. In this study we performed a field experiment with four land-use types with different intensity: a cultivated peaty soil (CU); a one-year-old energy crop plantation (BM); a one-year-old managed grassland (GR) and an agricultural peaty soil abandoned for 15 years (UNC). To evaluate the effect of the land use intensification on AMF diversity, a common and co-occurring plant species was sampled (*Calystegia sepium*). In addition, six plant species were sampled across these land-use types to test the plant host effect: *Arundo donax, Bromus tectorum, C. sepium*, *Poa pratensis*, *Phragmites australis* and *Ranunculus acris*. AMF were identified by 454-sequencing of the SSU rRNA gene. With regard to the land-use intensification, AMF community structure in the roots of *C. sepium* was different among land-use types. Furthermore, AMF richness was significantly lower in CU compared to UNC and BM. Host plant identity had also a significant effect on AMF richness and community composition. Differences were mainly driven by a member of Acaulosporaceae and a member of Glomeraceae, which were preferentially associated with *R. acris*/*A. donax* and *Poa* sp., respectively.

Our data suggest that higher AMF diversity is present in less intensively managed peaty soils and that these key microbes can be used as indicators of soil quality taking into account the effect of the host plant specificity of AMF.

Keywords: arbuscular mycorrhizal fungal diversity, 454-sequencing, host preference, land-use change

[P1.167]

Compounded perturbation increases variability of functional gene abundances in Dutch agricultural soils

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It is widely accepted that biodiversity loss may lead to reductions in function, stability, resilience, and adaptive capacity in ecosystems; however this paradigm is not applied to the soil microbiota, where outstanding levels of biodiversity and corresponding functional redundancy are believed to act as strong buffers to environmental change. Here, we treated identical soil microcosms with none, one, or two equal, severe disturbances, and studied the abundance of microbial functional genes during a one-month recovery period following each treatment. As expected, the abundance of functional genes decreased after the first disturbance: more common, or redundant genes (i.e. 16S rRNA, ITS) were less sensitive than those connected to narrow ecological functions, such as ammonia oxidation. The second disturbance caused further reductions in functional gene abundances as well as a notable increase in between-replicate variability, which followed the treatment and continued to increase over time as replicate microcosms diverged. For the double-perturbation treatment some replicates exhibited recovery while in others gene abundance continued to decrease over time. This phenomenon was observed for all genes studied, but was more apparent in the narrower ones. We suspect that these microcosms underwent "catastrophic shifts", where a switch in internal feedbacks caused a suppression of recovery in economically important genes. Our results support the notion that repeated perturbation increases unpredictability. Even in soils, where outstanding diversity is expected to overcome the effects of stressors, repeated perturbation may lead to functional loss.

Keywords: Disturbance, Resilience, Stability, Soil

[P1.168]

Tea anyone? Engaging citizen scientists in an open distributed experimental network in urban soil ecology

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Soil science is a declining discipline in our institutions of higher learning, even while soils are being recognized as an important component of urban ecosystems and the services they provide. Urban soils have also been recognized as *in situ* laboratories for students and residents (e.g., citizen scientists) to learn about the importance of biodiversity and ecological systems. Moreover, citizen science is increasingly being recognized as a strategy to conduct widespread comparisons across different locations. Unfortunately, citizen science programs have rarely been devoted to learning about soil communities and the ecosystem services they provide.

In an effort to both engage citizen scientists and to study urban soil ecological systems, we have recently initiated a "proof of concept" for a Global Urban Soil Ecological Education Network (GLUSEEN), which when fully implemented will be a worldwide multi-city comparison investigating the effects of urban environments on decomposition and soil community structure. GLUSEEN is a "distributed" network that builds upon a worldwide set of decomposition experiments in which the substrate is kept constant in several habitat types associated with urban landscapes. The set of experiments varies in complexity, cost, and applicability to citizen science from simple comparisons of weight loss of nylon tea bags over time, to the chemical changes of the substrate as it decays, to the inclusion of measurements of environmental factors and soil biota. These experiments address the following questions: 1) What is the response of soil biodiversity and decay rate in urban soils at local, regional and global scales? 2) Do differences in soil biodiversity among urban soil ecosystems relate to functional changes in the decomposer subsystem? We report on the overall study design of the network and preliminary results of soil measurements (pH, percentage organic matter) and our most simple protocol using commercially available nylon mesh teabags as standardized "litter bags."

Keywords: urban soil, decomposition, network, citizen science

[P1.169]

Spatial and temporal variation in the nifH gene richness in three microhabitats at a Mexican semiarid region

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Plants in arid and semiarid ecosystems modify microclimate and soil properties generating different microhabitats, which alter soil microbial communities including diazotrophs. Diazotrophs are key organisms in these ecosystems because they increase soil fertility through N inputs and participate in soil food webs. The purpose of this study was to evaluate the spatial and temporal variation in the composition of soil diazotrophs in three microhabitats: 1) beneath Prosopis laevigata, 2) beneath Parkinsonia praecox, and 3) bare soil in a semiarid region at Zapotitlán Salinas, Puebla, Mexico. Soils samples were taken every 10 cm, from 0 to 50 cm depth in the dry and rainy seasons. Soil parameters such as percentage of sand, silt, clay, moisture, water holding capacity, electrical conductivity, pH, organic matter, and orthophosphates were measured for each sample. Diazotroph composition was determined by analyzing nifH gene richness through PCR-DGGE fingerprint approach. The nifH gene richness significantly varied between microhabitats (Figure 1). During the rainy season, gene richness beneath P. laevigata and in bare soil decreased with depth, whereas it remained constant beneath P. praecox (Figure 2). The relationship between gene richness and soil properties varied depending on season. Gene richness was correlated with water holding capacity ($\chi2$ = 7.44, df = 1, p = 0.006) and organic matter content ($\chi2$ = 12.47, df = 1, p = 0.0004) during the dry season. There were no correlation between gene richness and soil properties ($\chi2$ = 13.97, df = 9, p = 0.12) during the rainy season. We conclude that nifH gene richness spatially and temporally varied depending on microhabitat. Therefore, plant species differentially affect the composition of diazotrophic communities in this Mexican semiarid region.

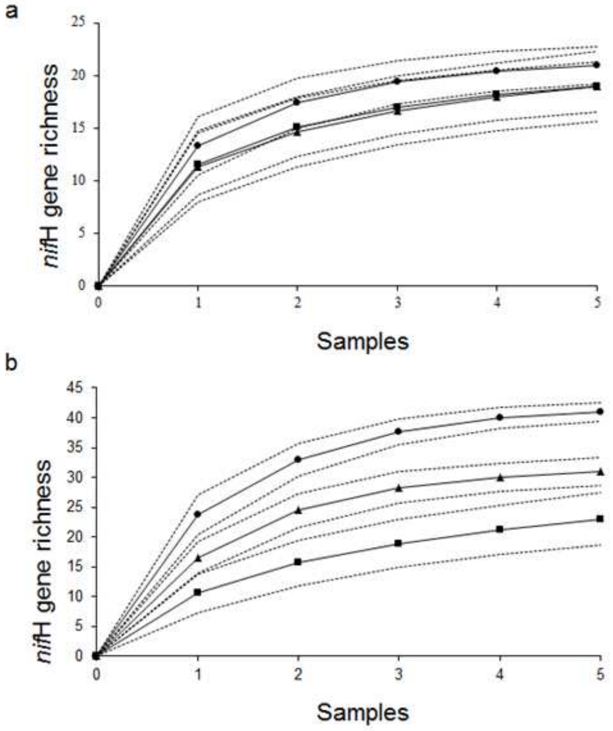

Figure 1. Richness of nifH genes in three microhabitats, beneath *Prosopis laevigata* (circles), *Parkinsonia praecox* (squares), and bare soil (triangles) during dry (a) and rainy (b) seasons in Zapotitlán Salinas, Puebla, Mexico.

Keywords: diazothops, legumes, Zapotitlán Salinas, seasonal variation

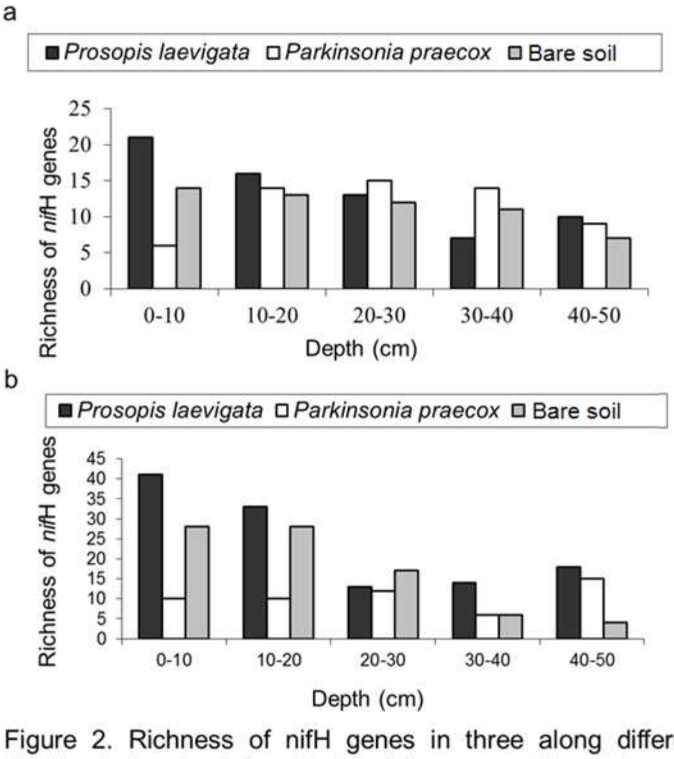

Figure 2. Richness of nifH genes in three along different depths during dry (a) and rainy (b) seasons. The data were analyzed with the Estimate S program, to evaluate the differences between the microhabitat by the confidence interval (95 %).

[P1.170]

Distribution of testate amoebae associated to biological soil crust along an altitudinal gradient at an intertropical Mexican desert

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In desert ecosystems, the biological soil crust (BSC) occupies a large surface of desert soils, and creates microenvironments enabling establishment of rich microbial communities. Mosses and lichens of BSC can be important habitats to testate amoebae communities in to the soil system of desert zones. The objective of this study was to determine the distribution of testate amoebae associated to BSC along an altitudinal gradient in an intertropical desert on the Manrubio Hill of San Antonio, Texcala, Puebla, Mexico. The sampling was carried out at the beginning of the rainy season (May, 2014) and covered a total of 10 altitudinal steps from 2032 to 2358 m. a. s. l. Samples of BSC were taken by triplicates at each step, as well as samples of the underlying soil (5cm), a 20 cm deep calcareous phaeozem, for texture, pH and moisture measuring. We found that BSC changed along with the altitudinal gradient and, in response, soil properties and testate amoebae communities changed in parallel. Soil moisture was lowest at the bottom and the top of the gradient (37.9 and 34.7 % respectively; Table 1). Other hand, texture did not change drastically (Table 1) Quadrulella and Nebela (Figure 1) were the most abundant genera at the base of the altitudinal gradient (2032 to 2200 m. a. s. l.); all species disappeared at the top of the gradient (from 2300 m. a. s. l. the top), coinciding with a decrease of BSC observed at higher elevations (2300 m. a. s. l.).

Table 1. Variation in soil properties along altitudinal gradient in Manrubio Hill of San Antonio Texcala, Puebla, Mexico

Altitudinal gradient (m. a. s. l.)	Moisture (%)	Ph range	Sand (%)	Silt (%)	Clay (%)
			Mean ± Standard deviation		
2360	37.91 ± 5.65	7.47 ± 0.05	35.73 ± 5.14	42.4 ± 4.33	21.87 ± 1.01
2329	56.12 ± 3.89	7.42 ± 0.28	38.8 ± 6.16	33.07 ± 15.13	28.13 ± 9.45
2304	46.87 ± 6.57	6.98 ± 0.86	47.6 ± 32.92	32.53 ± 25.08	19.87 ± 8.1
2252	59.39 ± 17.74	7.35 ± 0.01	45.2 ± 15.03	29.33 ± 13.18	25.47 ± 2.31
2226	63.33 ± 9.23	7.45 ± 0.27	48.13 ± 13.02	27.33 ± 9.42	24.53 ± 3.61
2200	55.84 ± 5.9	7.46 ± 0.14	60.8 ± 20.66	20.87 ± 15.89	18.33 ± 6.22
2148	58.65 ± 2.44	7.49 ± 0.08	48 ± 3.49	28.53 ± 7.26	23.47 ± 4.62
2121	47.51 ± 7.76	7.5 ± 0.32	46.93 ± 20.41	26.93 ± 16.99	26.13 ± 8.08
2078	62.43 ± 16.48	7.51 ± 0.15	54.93 ± 18.9	22.27 ± 16.77	22.8 ± 3.46
2031	34.69 ± 7.03	7.62 ± 0.09	60.8 ± 20.28	23.2 ± 17	16 ± 8.17

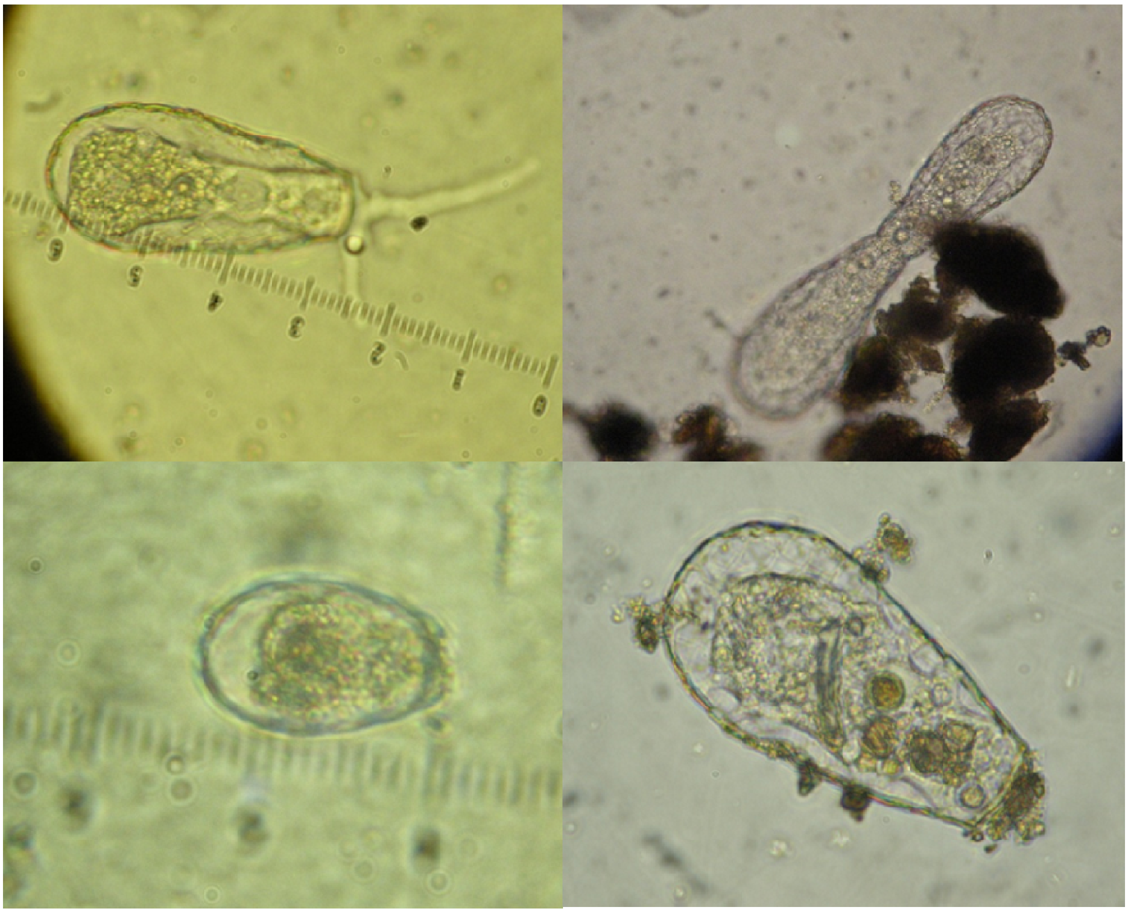

Figure 1. Light micrographs of testate amoebae (40 X): A. *Nebella penardia-minor*, B. *N. gracilis*, C. *Nebella sp.* D. *Quadrullela symmetrica*

Keywords: Nebella, Quadrullela, soil propeties, desert zones

[P1.171]

Functional vs taxa affiliation: which is better indicator of agricultural practices? The case of Rubber plantations in N.E. Thailand

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Perennial crop plantations expend quickly in South-East Asia, stimulated by a rising demand on their deriving resources. Rubber plantations lead to an important land use changes over ecologically fragile areas in the North-Eastern part of Thailand. In this context, the sustainability of these tree plantations is questionable. In this study, we hypothesized that soil organisms constitute a reliable indicator of sustainability of these perennial plantations. We measured the occurrence of three major groups of soil organisms: macrofauna, nematofauna and microorganisms, submitted to a gradient of intensity of land management practices. These 3 groups are considered as bio-indicators of physical or chemical perturbations induced by agricultural practices. Sampling was made on 12 representative plots in Khon-Kaen region, that have shown similar pedo-climatic statements, within (i) two practice intensity levels, high and low, and (ii) two age-levels of the plantations (immature <6 years old, mature > 6 years old). Macrofauna and nematofauna taxa richness or evenness indices did not show any differences between plantations' management and age. However, soil macrofauna structure and nematofauna's trophic groups varied significantly as a function of the age of the plantation, while high intensity of practices tends to homogenize macrofauna community. Main soil engineers' density (termites, earthworms) together with fungivore nematodes abundance represent a good indicator of low practices' intensity in mature plantations. On the contrary, *Diplopoda* and *Blattidae*, together with bacterivore nematodes aligned with high intensity of agricultural practices. Low intensity managed plantations revealed also significantly more macrofauna activity (earthworm casts, skeletonized litter). Community-level physiological profiles showed significantly more microbial biomass in low intensity mature plantations, than in high immature. These first results suggest that in rubber plantations, functional roles and activity assumed by soil macrofauna, nematofauna and microorganisms, are better indicators of soil perturbation rather than taxa affiliation.

Keywords: biodiversity, bioindication, South-East Asia, perennial crop plantations

[P1.172]

Effect of long-term crop management on rhizobia population size and genetic diversity in North Carolina, USA

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The nitrogen-fixing symbiosis between rhizobia soil bacteria and leguminous crops is considered important for nitrogen nutrition of plants. Whereas diversity and composition of rhizobia populations in natural ecosystems have been extensively studied, the effect of crop management on rhizobia population and diversity are poorly understood. The aim of this study was to determine the effect of long-term crop management on rhizobia population size and community diversity. We investigated soils from five different land uses that were part of long-term cropping system experiment, including a successional ecosystem (SUCC), crop animal pasture (CAP), organic production, conventional no-tillage (CNV No Till) and conventional tillage (CNV Till) in North Carolina, USA. Using crimson clover as a host plant, rhizobia were trapped from each system type in growth pouches. Nodules collected from crimson clover plants grown in soil from CAP were higher in number than other systems. Shoot dry mass from both CAP and the organic system was greater than all other systems. The diversity of 90 rhizobia strains isolated from nodules of crimson clover was examined by BOX PCR fingerprinting. Based on preliminary cluster analysis, the results showed great diversity among all collected strains, and further analysis is pending. Sequencing of the gene involved in nodulation process, *nodD*, in is currently underway to examine if crop management practices influence the diversity of rhizobia diversity at the functional level.

Keywords: rhizobia, long-term crop management, leguminous crops, community diversity

[P1.173]

Methods to evaluate soil functional biodiversity to estimate agroecosystem sustainability

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Biodiversity is fundamental to preserve soil ecosystem services (ES). In 2012-2013 in five organic and five conventional horticultural fields in Venice and Treviso provinces (North Italy), several bioindicators have been chosen providing basic ES. 1. *earthworms*, soil structure promoters, responsible for air and water soil circulation and for organic matter decomposition; 2. *mesofauna* which includes detritivores and small predators; 3. Soil *bacteria* and *fungi*, protagonists in organic matter decomposition and in nutrient cycles. The methodologies to sample biodiversity of these bioindicators have been: hand sorting with irritant mustard powder water solution for earthworms; Berlese- Tullgren extraction for mesofauna; Automated Ribosomal Intergenic Spacer Analysis technique for overall communities of bacteria and fungi, PCR with specific primers for Arbuscular Mycorrhizal Fungi (AMF). After sampling with the aim to know the biodiversity guilds, we proceeded using other innovative techniques useful to measure soil quality. Regarding the component of mesofauna, we applied the index QBS-ar, to evaluate the status of soil alteration but not applicable by a taxonomically unexperienced farmer. In order to analyse earthworms, the new index QBS-e based on earthworm ecological categories, similar to QBS-ar but easier to use also by non-experts, was successfully applied. To measure microbiological activity, soil respiration rate and Fluorescein Diacetate hydrolysis were carried out along with Fertimeters (International patent PCT N. WO2012 140523 A1, Squartini, Concheri, Tiozzo, Padova University), a simple device made of silk and cotton yarns working as reporters of organic matter degradation. Organic farms soils appear to have less disequilibrium in macronutrients, an higher respiration rate, to maintain a well conserved soil structure, to create a more comfortable environment for AMF stabilization and to host a more diverse soil fauna, that indicates a less disturbed environment with more efficient ES: according to these analyses, organically managed soil seems to be more environmentally sustainable.

Keywords: Functional biodiversity, Ecosystem services, QBS-e, Fertimeter

[P1.174]

Drivers of soil microbial abundance and functioning in grassland soils

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The identification of the factors that control the spatial distribution, abundance and functioning of soil microorganisms at local and regional scale is necessary in order to understand and predict nutrient cycling in agroecosystems. This study evaluated the influences of regional variation, land-use intensity and physico-chemical soil properties on the abundance and geographical distribution of microbes and on the enzyme activities involved in C-, N- and P-cycling.

A spatially explicit sampling regime was used to sample topsoils from 18 grassland sites in two regions of the Biodiversity Exploratories in Germany, differing in soil type and climatic conditions: the Hainich National Park and the Swabian Alb. In each region three land-use intensity (LUI) classes were sampled: unfertilized pastures (low LUI), moderately fertilized and mowed pastures (intermediate LUI) and highly fertilized and mown meadows (high LUI).

Enzyme activities associated with the C- and N-cycles, organic carbon (C_{org}), total nitrogen (N_t), extractable organic carbon, and mineral nitrogen (N_{min}) were higher in the Swabian Alb (Leptosols) than in the Hainich National Park (primarily Stagnosols). High bulk density had a negative effect on soil properties such as microbial biomass (C_{mic}, N_{mic}), urease, C_{org}, and N_t. Variance component analysis revealed a ranking of impact on the investigated soil properties by regional > inter-site > intra-site > LUI variations. LUI only showed a strong influence on nitrate and pH – properties which are directly affected by short term human management techniques like fertilization. Geostatistical analyses showed that enzyme activities were related to local abiotic soil properties but showed little spatial correlations. Physical and chemical properties showed more spatial pattern than did microbiological variables.

We conclude that microbial abundance and functioning in grassland soils were mainly driven by regional variation and the abiotic soil properties of the individual sites, while LUI of grasslands only had a minor influence.

Keywords: Biogeography, Nutrient cycles, Enzyme activities, Physico-chemical soil properties

[P1.175]

The diversity of soil fauna under impact of enhanced radioactivity (Komi republic, Vodny)

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Data about diversity of soil invertebrate fauna on the area with high levels of radionuclides and metals were obtained. The accounting of soil invertebrates was spent in the pine forests (1,2 – polluted sites, 3, 4 – background sites) and on the meadows (5, 6, 7 – polluted sites, 8, 9, 10 – background sites). As result of researches in the pine forests, about 15-21 genera of Nematoda were noted on the polluted sites. Index of Shannon diversity in these assemblages of Nematoda was 1.32 – 1.40. The diversity of Nematoda did not essentially change on the background sites: about 15-17 genera of Nematoda were registered, Index of Shannon diversity was 1.57 – 1.60. On the polluted sites Collembola were presented by 4-5 species, and Protaphorura boedvarsoni has high abundance. On the background sites number of Collembola species increased in three times, about 13-14 species were noted on these area, and Isotomiella minor, Folsomia quadrioculata dominated. We did not reveal essential difference in the composition of macroinvertebrates. About 8-11 taxonomic groups were registered on the polluted and background area. But oh the polluted area abundance of Thysanoptera was high, on the background area abundance of larvae of Elateridae (wireworms), Cantharidae and Diptera was high. As result of researches on the meadows, about 19-33 genera of Nematoda from 18 families were noted on the polluted sites. On the meadows 23 Collembola species were registered, from which two species (Protaphorura subuliginata, P. tundricola) were recorded in first in Komi Republic. The taxomomic diversity of large invertebrates higher on the meadows than in the pine forests. About 8-12 taxonomic groups were noted on the polluted meadows, about 10-13 groups – on the background meadows. Thysanoptera and Diptera (larvae) were abundant groups on the polluted meadows. On the background meadows Lumbricidae dominated and their share was 45-60 % from total number of macrofauna. In sum, oppression of soil invertebrate fauna in pine forests and meadows with high levels of radionuclides and metals was revealed. It composed on reliable decrease of number and density of different taxonomic groups of invertebrates, reduction of diversity and spectrum of trophic groups and vital forms on the area with high content of radionuclides in soil.

The research were supported by the government of Komi Republic and Russian Fond of Basic Researche (13-04-98847), STProjects-060 «Long-term consequences of enhanced radioactivity and conventional chemical pollutants for biota at the scale of individuals, populations and communities».

Keywords: radioactivity, collembola, nematoda, soil macrofauna

[P1.176]

The Centre for Soil Ecology (CSE)

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The Centre for Soil Ecology (CSE) is a virtual cooperation between Wageningen University and Research centre (WUR) and the Netherlands Institute of Ecology (NIOO-KNAW). In total fifteen research groups participate in the centre. CSE stimulates interactions between scientists of WUR and NIOO-KNAW to bring their soil ecological science to an even higher level, and promotes research opportunities for young and talented researchers in soil ecology. CSE organizes a number of activities, including annual meetings, seminars, discussion groups, BSc, MSc, PhD, and Post-doctoral courses, dissemination meetings, and members of CSE participate in joint externally funded projects. Some examples are presented in the present poster.

Keywords: virtual cooperation, soil ecologists

[P1.177]

Can mulching boost ecological connectivity between different management options in a disturbed environment?

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Today, rare are unfragmented habitats. The landscapes are transformed by human activities and species are threatened: isolation, downsizing, reduced trade between populations... The former coal mining area of Northern France is not an exception: urbanization, industry, intensive agriculture and metal pollution are the main causes of land fragmentation and disturbance. It is important to look for ways to reconnect these isolated and degraded areas. The present study aimed at evaluating the attractivity of different kind of mulches and their efficiency to promote recolonization of isolated and degrades areas.

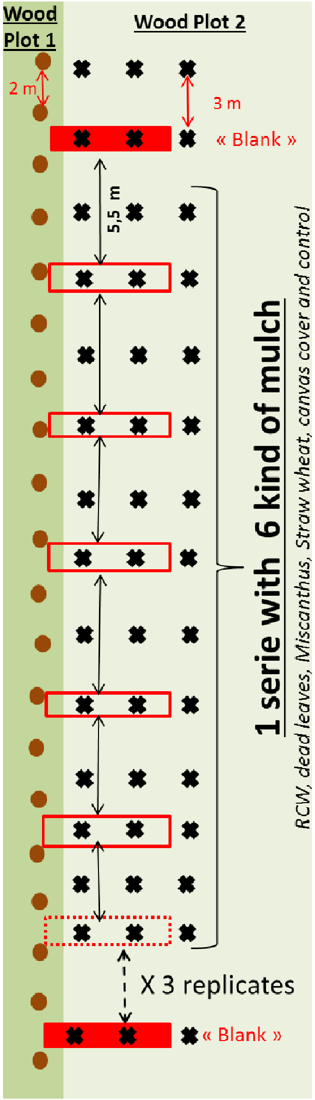
Since March 2013, 18 experimental rows (6m long x 0.5 m width) of mulch were installed between two wood plots (pluri and monospecific plantations) on a surface area which stretch on 4400 m². Five kind of mulch (Ramial Chipped Wood (RCW), dead leaves, chopped miscanthus, chopped wheat straw and canvas cover) and a control (bare soil) were tested (3 replicates each). The control consisted in 3 replicated of bare soil.

Each mulch was characterized by the loss of biomass with litter bag technique, metal concentrations, temporal monitoring of enzymatic activities and organic matter, etc.

The attendance of these mulches by pedofauna was followed using both interception and emergence traps. The formers are wet pitfall traps revealing the activity intensity of aboveground fauna. The latter track imagos of soil insects. The trapping of pedofauna was carried out from April to July 2014 using 90 pitfall traps and 78 soil emergence traps (no trap on canvas cover).

A general inventory of pedofauna trapped was made, focusing on two groups models: groundbeetles (Carabidae) and woodlice (Isopoda), which belong to two different trophic groups, predators and saprophageous.

First results show that mulches welcome more organisms than bare soil. Leaves and RCW are the modalities with the highest abundances. More detailed results will be presented and discussed.



Keywords: pedofauna, metal pollution, connection, litter rows

[P1.178]

The use of indicators to characterize the functioning of soils strongly affected by metallurgical activities.

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The former coal mining field of northern France has been heavily disturbed due to human activities (urbanization, industry and intensive agriculture). This is particularly the case around a lead smelter (Metaleurop Nord) that emitted into the atmosphere until 2003 considerable quantities of metals. In order to restore this degraded area and to help reducing the environmental hazard, the most contaminated sites were afforested started in 1997. Thus, 85 ha were planted around this former industrial plant creating a "green ring". Different tree species and different management options were established, but no study has been conducted on the effects of different tree species and managements on soil quality and functionality.

The main aim of this study was to assess soil functionality of several parcels, differing by vegetation cover (species of trees, planting density, etc.), using soil physico-chemical and biological indicators. Results would allow proposing a management for the restoration of these degraded environments.

The study site consists of 12 plots: nine wooded plots (plantations of ash, poplar, maple or mixed plantations, with or without soil amendment) and three reference soils (agricultural, **hedgerow**, forest). **The general status of** trees and the truck **diameters measurements were made. In addition,** the topsoil was characterized by texture, bulk density, pH, CEC, trace metal concentrations, etc. Several soil biological indicators belonging to different functional and trophic groups were selected: microbial activity, ergosterol quantification (as estimation of fungal biomass), enzyme activities (laccase and urease) and several groups of pedofauna. Indeed, **the** imagos **emergence** of **soil insects was monitoring. It was conducted from mid-April to July 2014 using three** soil **emergence traps per plot.**

First results will be presented and discussed.

Keywords: soil functionality, microbial activity, pedofauna, metal pollution

[P1.179]

Impact of drought intensification on vegetation-soil organism interactions in a French Mediterranean matorral

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Understanding the linkage between above and below ground communities in a changing world represents a growing concern. In the Mediterranean ecosystem, already characterized by an extended dry period, drought periods are predicted to become longer as a consequence of climate changes (IPCC, 2007). Current prediction of global warming opens a scenario of shifts in the feedbacks and equilibrium within the plant-soil system. Several studies have observed a strong interdependence between changes in plant communities and changes in soil properties in Mediterranean ecosystems (Serdans and Penuelas, 2013). Despite the visible change in the vegetation cover, the mechanisms behind the changes in soil ecosystems are not fully understood. This work aims at assessing the linkage existing between soil collembolan communities and plant diversity in a context of drought stress, in a Mediterranean garrigue.

The experimental site is located in the Massif de l'Etoile near Marseille, France (43° 22' N; 5° 25' E). Current vegetation is a shrubland dominated by *Cistus albidus*, *Quercus coccifera*, *Ulex parviflorus* and *Rosmarinus officinalis*. Plots including the 4 shrub species in all possible combinations of diversity were equipped. For each of the 15 combinations, 3 plots were installed. To simulate an experimental drought, 90 devices, overcome gutters, were installed on the site. To analyze collembolan community, in May/ 2013 1soil sample (0-5 cm) per plot was collected after 6 months of rainfall exclusion. Species and functional trait community composition were analysed.

Collembolan density strongly varies among different vegetation composition, and the effect of rainfall exclusion is evident only under some combination of vegetation cover. Richness was weakly affected both by plant diversity and drought. Functional trait community composition is affected by different combination of plant species. Body size, body shape and motion strategy are impacted by six months of rainfall exclusion.

This study was financed by the CLIMED project supported by the ANR (Agence Nationale de la Recherche)

Keywords: Climate, Collemnola, soil functioning, Mediterranean

[P1.180]

Linking litter characteristics and microbial activities in early stages of decompositionin a metal polluted environment

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Litter represents one of the prominent nutrient inputs in terrestrial ecosystems. Its decomposition is mainly ensured by fungi and bacteria that critically contribute to the regulation of atmospheric composition through carbon and nitrogen cycles. Litter quality and microbial community are influencing each other. Litter chemical and morphological characteristics affect microbial colonization and select specific groups of microorganisms. These, with their activities, modify litter composition, influencing organism litter colonization for the further stages of decomposition. However, other characteristics, such as soil properties and anthropic activities can directly and indirectly impact on organic matter decomposition process. Metal pollution, for example, selectively damages microbial community, altering the ecological equilibrium between litter resource and organisms. Several studies have observed strong shifts in microbial community mainly during early stages of decomposition. However, many studies focused on single species litter, and little is known about how microbial communities change when mixtures of leaf litter are decomposed in situ. In addition, the causal links between substrate input characteristics and microbial community composition remain not fully understood. The present study aimed at evaluating functional changes in the microbial community during initial stages of single and mixed litter decomposition, in soils with different characteristics.

The study site is located in the former coal mining region of northern France and comprises different kinds of tree Ten plots showing various physico-chemical soil parameters, metal concentrations and different vegetation covers (ash, poplar, maple or mixed species) will be studied. In September 2014 litters will be monitored along 3 months. Each 15 days analyses of microbial activity, functional metabolic fingerprint analysis and enzymatic activities will be performed. Simultaneously, litters will be characterized for the content of C, N and P, lignin, cellulose, surface area, leaf thickness and content of metals.

Microbial activities showed different trend among the different plots and among the different decomposition stages. Detailed results will be presented and discussed.

Keywords: metal pollution, microbial activity, organic matter, soil functionality

[P1.181]

Changes in rhizosphere microbial community association with different parental types of Arabidospsis thaliana MAGIC lines

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Plants interact with microbes through changes in the composition and concentration of their root exudates. The composition of bacterial communities in the rhizosphere and within roots therefore differs from the one in bulk soil. In addition it varies between different plant species and even ecotypes, but also according to the developmental stages. Recent studies on microbial communities in the rhizosphere of *A. thaliana* are mostly focusing on bacteria and disregard fungi, although these are another major group of soil microorganisms.

This study is part of the joint project “Chemical Communication in the Rhizosphere”, in which 19 parental lines of the model plant species *A. thaliana* were cultivated in pots with two different soils under controlled phytochamber conditions. When the plants had reached an early flowering stage, rhizosphere soil, bulk soil and roots were collected for DNA extraction. The genomic DNA of the rhizosphere of 6 of the 19 parental lines was analyzed to determine the diversity and species composition of the bacterial and fungal communities by paired end Illumina 16S rDNA and fungal ITS2 sequencing.

We found that the main driver of the rhizosphere bacterial communities was the soil origin. Furthermore the presence of plants on the soil as well as the accession type had an influence on the rhizosphere bacterial community due to differential release of root exudates. Those differences were significant for both relative abundance and richness. In addition we identified a dominance of the Alphaproteobacteria in the rhizosphere among all parental lines. Ongoing similar analyses concerning the fungal part of the communities will be presented, where we await a selection effect of *A. thaliana* accessions on fungal taxa.

Keywords: Arabidopsis thaliana, rhizosphere, microbial community, paired end Illumina

[P1.182]

Climosequence approach to monitor the effects of exposure and altitude on physical, chemical and microbial properties of alpine soils

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To monitor the microclimate effects on soil microbial properties, it is of paramount importance to link two of the principal indicators of soil quality and functionality, i.e. microbial biomass and soil enzymatic activities. Up to now little is known about the aforementioned link in Alpine areas. This study focuses on a climosequence approach to evaluate the impact of both altitude (from 1000 m to 2400 m a.s.l.) and exposure (north and south facing slopes) on soil properties in ten alpine sites in Trentino (Val di Rabbi, Val di Sole, Italy). A total of 450 samples were collected in August 2012. Three plots (5x5 m) located at 50 m from each other were set-up in each site and five sub-samples were randomly collected at three soil depths (0-5 cm, 5-10 cm, 10-15 cm). We performed a multiple-enzymatic assay to detect eight hydrolases that are representative of the principal biogeochemical cycles. Soil microbial biomass was comparatively assessed by using two different DNA extraction methods followed by Picogreen based dsDNA quantifications: extraction-purification of soil DNA with a commercial kit (MP, Biomedical) to obtain a pure DNA for fingerprinting analysis; direct extraction-quantification of *crude* soil DNA. Soil microbial biomass, assessed by the second dsDNA approach, decreased significantly with soil depth. Furthermore, this method was also capable to reveal an increasing trend in south exposure respect to north exposure, representing a thermal signal. Thus, this method provided a reliable estimator of soil microbial biomass, without an underestimation derived from the unavoidable DNA loss (-34%) obtained during DNA purification required for downstream analysis. In line, enzymatic activities decreased significantly with soil depth, whereas altitude and exposure effects were often masked by the site effect. Moreover, our results suggested a significant and positive correlation between microbial biomass and all enzyme activities studied in the Alpine soils.

Keywords: climosequence, microbial biomass, multiple enzyme activities

[P1.183]

Microbial diversity and activity in microhabitats are affected by soil organic matter

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Soil particle size fractions (PSF) typically differ in mineral composition and soil organic matter (SOM). They represent microhabitats with distinct microbial communities (Neumann *et al.*, 2013). SOM can also affect the partitioning of organic pollutants to different PSF and the microbial community members involved in their degradation (Neumann *et al.*, 2014). In this study, the impact of SOM on microbial communities from different PSF and their activity in mineralising phenol and 2,4-dichlorophenol (2,4-DCP) was analysed. SOM soil variants originated from the Askov long-term fertilization experiment. The abundance and diversity of *Bacteria*, *Archaea,* and *Fungi*, tightly connected to PSFs was analyzed by qPCR and T-RFLP of the microbial rRNA genes. Microbial abundances declined with increasing particle sizes. Highest microbial abundances were found in manured soil. The responses to microhabitats and fertilisation treatments were domain-specific: While the bacterial community structure was mainly affected by the PSF, *Archaea* were more sensitive to fertilisation and for *Fungi* both factors were equally important. Mineralisation rates of phenol correlated positively to microbial abundances, except for the sand-sized fraction, probably due to POM. During six weeks of incubation 2,4-DCP was only degraded by the clay fraction. While phenol mineralisation rates were highest in the manured soil variant, for 2,4-DCP it was highest in NPK. Our study demonstrates that SOM, accumulated under different long-term fertiliser regimes, leads to microhabitats that support structurally and functionally different soil microbial communities.

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Keywords: microbial diversity, soil organic matter, particle size fractions, rRNA genes

[P1.184]

Particle size fractionation of artificial soils reveals the importance of different minerals to contribute to the high microbial diversity in natural soils

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The importance of soil minerals for shaping microbial diversity was analysed with artificial soils (AS), inoculated with sterile manure and a microbial soil consortium. Particle size fractionation was applied for studying the impact of minerals in single microhabitats (Neumann *et al.*, 2013). AS composed of quartz supplemented with montmorillonite (MT), illite (IL), or illite + ferrihydrite (IL+FH), respectively, were compared to each other. Samples were analysed after 6 and 18 months. DNA from bulk soil and from particle size fractions (PSF) (sand: 63–2000 µm; coarse silt: 20–63 µm; fine silt plus clay: <20 µm) was obtained. The abundance and diversity of *Bacteria*, *Archaea,* and *Fungi*, tightly connected to theses fractions was determined by rRNA gene PCR amplicon analyses (qPCR and T-RFLP). For bulk soil, IL and, even more pronounced, IL+FH supported the growth of more *Bacteria*, *Archaea* and *Fungi*, than MT. The finest fraction (fine silt plus clay) followed the trend of the bulk soil, while mainly no effect was observed with sand. The structural diversity of *Fungi* responded stronger to the different mineral compositions than *Bacteria*. For *Bacteria* the PSF was more important for structuring the community. For *Archaea* it required 18 months to establish at the finest fraction a community distinct the other fractions and the community at this fraction showed no response to the different minerals. – Overall this study demonstrates that the mineral composition and the PSF have profound and specific effects on the diversity of the dominant microorganisms from all three domains and, thus, suggests that these factors contribute to niche separation and the high diversity of microbial communities typically found in natural soils.

Reference

Neumann D, Heuer A, Hemkemeyer M, Martens R, Tebbe CC. 2013. Response of microbial communities to long-term fertilization depends on their microhabitat. *FEMS Microbiol. Ecol.* 86: 71-84.

Keywords: artifical soils, soil minerals, particle size fractions, rRNA genes

[P1.185]

Effect of saline irrigation water on the diversity of wheat rhizosphere and soil microbial communities in a semi-arid ecosystem

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Soil salinization through irrigation water is a major limitation to a sustainable agriculture in semi-arid regions. By reducing the osmotic potential of the soil solution and ion toxicity, salt accumulation has adverse effects on soil fertility and consequently on plant yields, but it may also damage soils by losing functionally important members of the soil microbial community.

Scrubland soil collected near La Paz, Baja California, Mexico, was incubated in soil microcosms with (+C) or without straw as a nutrient source for 8 weeks and was irrigated weekly with non-saline (C, 0 dS m^{-1}), low saline (LS, 2 dS m^{-1}) or high saline (HS, 11 dS m^{-1}) water. After a “bare soil” sampling, wheat plants were cultivated in these soils and, after 7 weeks, the “rhizosphere soil” from these plants was collected.

The abundance of *Bacteria*, *Archaea* and *Fungi*, as determined by quantitative real-time PCR of extracted total DNA, ranged from 10^9–10^{10}, 10^7–10^8 and 10^6–10^9 rRNA gene copies g^{-1} soil, respectively. *Archaea* were generally significantly more abundant in the HS(+C) compared to the LS(+C) and C(+C) treatments, whereas *Bacteria* and *Fungi* showed at the domain-level differing results for bare and rhizosphere soil as well as with or without nutrient source, suggesting counteracting responses of lower taxonomic ranks. The structural diversity of the prokaryotic communities was therefore assessed by illumina MiSeq sequencing of rRNA gene amplicons yielding more than 20,000 quality filtered contigs per sample. All sequences clustered into 15,961 OTUs (97% similarity) with an average number of 1,524 OTUs per analyzed community. HS(+C) treatments harbored clearly distinct prokaryotic communities in comparison to LS(+C) and C(+C) treatments. Taxa responding sensitively to high salinity included e.g. *Acidobacteria*, *Ensifer* and *Sphingomonas*. Genera adapted to a saline environment and thus increasing with higher salinity levels encompassed e.g. *Bacillus*, *Streptomyces* and *Pseudomonas*.

Keywords: salinity, rhizosphere, rRNA genes, ultra-deep amplicon sequencing

[P1.186]

Fine-tuning DNA approach and multiple enzyme assay to assess soil microbial properties under different forest floors

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Even in the current era of high-throughput molecular techniques, the enormous heterogeneity of soil still renders the assessment of its microbiota as an arduous challenge. We aimed to assess and monitor the microbial properties of forest topsoils (0-15 cm depth) at a small scale (2.5 cm intervals) under different vegetation representatives (grass, branches, moss, litter) of alpine areas (1400 m a.s.l; Trentino, Italy) at south vs. north exposure. To assess the vertical distribution of soil microbiota (biomass and activity), we performed and linked the *fine-tuning DNA approach* (extracellular vs. intracellular vs. total soil DNA) and *multiple enzyme assay* (12 hydrolases covering the principal biogeochemical cycles). The *fine-tuning DNA approach* was proved to be a sensitive tool to quantitatively assess the vertical distribution of the soil microbiota, taking into account also the well-known method-result effect. Likewise, the comparative assessment of multiple enzymatic activities allowed for the accurate characterisation of the soils under different forest floors, overcoming the probable misinterpretation of single enzyme determination due to their specificity. Overall, the coupled *DNA-enzyme approach* is suggested to accurately assess soil microbiological properties as a function of soil type (humus forms, physical and chemical properties, soil depth), forest floor and exposure. Furthermore, the quantitative monitoring of extracellular DNA along the topsoils in comparison to intracellular and total soil DNA provided further evidences of possible movement of soil DNA by vertical advection with evolutionary implications in terms of genetic exchange by natural transformation.

Our results are suggested to provide information about the heterogeneous distribution of the soil microbiota and the interlinked effects of biotic and abiotic factors at a small scale, which should be considered for the data interpretation and/or the set up of an experimental design/sampling strategy in soil microbial ecology studies.

Keywords: Extracellular DNA, multiple enzyme assay, small scale heterogeneity, humus forms

[P1.187]

Microbial diversity in the rhizosphere of the genetically modified maize MON810 across Europe

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The approval of genetically modified (GM) crops for cultivation in Europe requires a comprehensive assessment of their environmental risks. The EU-funded project AMIGA - *«Assessing and Monitoring the Impacts of Genetically modified plants on Agro-ecosystems»* analyzes the importance of European biogeographical regions for environmental risk assessments. Soil fertility is one of the most important ecosystem services associated with crop production and it is largely influenced by soil microorganisms. However, the structural and functional variability of the rhizosphere microbial community between GM and non-GM comparators as affected by biogeographical regions has not yet been established.

We therefore analyzed the diversity of bacteria colonizing the rhizosphere of the GM maize MON810 producing the insecticidal *Bt*-toxin Cry1Ab. Rhizosphere samples of MON810 and non-GM parental comparators were collected in two consecutive years from field trials across Europe.

The abundance of *Bacteria*, *Archaea* and *Fungi* and of the functional genes *nirK* and *nirS,* established by qPCR, differed significantly between the biogeographical regions and in some regions also between GM and non-GM rhizospheres. The structural diversity of the prokaryotic communities assessed by illumina sequencing of 16S rRNA gene amplicons yielded 8.2 million quality filtered sequences covering 23 phyla, 595 genera and more than 50,000 OTUs (97% identity). Each region harbored distinct prokaryotic communities in both years. However, the overall community compositions were always highly similar between GM and non-GM crops. Sequencing of *nirK* and *nirS* will reveal insights into the functional diversity of the denitrifier communities.

The data should allow to distinguish structural and functional core communities of the maize rhizosphere from more locally defined communities which respond e.g. to soil properties, agricultural management practices or climatic conditions, and thus to define baselines to establish limits of concern for future evaluations of GM crops in Europe.

Keywords: microbial diversity, rhizosphere, ultra-deep amplicon sequencing, rRNA genes

[P1.188]

Evidence for shift from acidobacteria to proteobacteria dominance in soil profile of boreal acid sulphate soils

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Acid sulphate (AS) soils located along the Baltic Sea coast contain large carbon and nitrogen stocks in subsoil horizons. If these soils are drained and used for agriculture, large fluxes of carbon and nitrogen gases could therefore occur. In this study, we aimed to compare bacterial community composition of drained AS soils in 4 soil horizons in comparison to drained non-AS soil assessed by 16S-pyrosequencing. We sampled three AS soils – Patoniitty (P), Söderfjärden (S), and Ylistaro (Y) with the different cultivation history, and one non-AS, Alaniitty (A). A and P soils are located in close vicinity, on the research farm of the University of Helsinki. Four different soil horizons were studied: Ap, Bg, BC, and C horizons. AS and non-AS soils differed in the amount of organic carbon, total nitrogen, sulphur species, as well as in pH and microbial activities in the C horizons. Bacterial communities in A horizons were dominated by Acidobacteria, followed by Proteobactera (α- and β-), Planctomycetes, Gemmatimonadetes, and Chloroflexi. In deeper horizons (B and BC), the relative abundance of Proteobacteria increased at the expense of Acidobacteria. The differences in bacterial communities between AS and non-AS soils increased, being characterized by the enrichment of Gemmatimonadetes and Chloroflexi in non-AS soil; and Actinobacteria, Spirochaetes and Cyanobacteria in AS soils. The highest shifts has been observed in C horizons, where the higher abundance of Candidate division OP9, Planctomycetes, and Chloroflexi has been observed in AS soils in comparison to non-AS. As boreal AS soils have developed from sulphide-bearing sediments of Baltic Sea, it may indicate the remains of the bacterial communities, in particular Candidate division OP9 putatively associated with anaerobic methane oxidation coupled with sulphate reduction. In topsoils (both AS and non-AS), RNA-based bacterial community was dominated by genera: *Pirerulla*, *Gemmata*, *Planctomyces*, *Caldilinea*, *Phaselicystis*, *Candidatus Solibacter*, *Caenimonas*, and *Haliangium*.

Keywords: boreal acid suplhate soils, soil profile, bacterial community structure, subsoil horizons

[P1.189]

Changing summer precipitation pattern alters microbial community response to fall wet-up in a Mediterranean soil

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The large soil CO_2 efflux associated with rewetting dry soils after the dry summer period significantly contributes to the annual carbon budget of Mediterranean grasslands. Rapid reactivation of soil heterotrophic activity and a pulse of available carbon are both required to fuel the CO_2 pulse. Better understanding of the effects of altered summer precipitation on the metabolic state of indigenous microorganisms may be important in predicting future changes in carbon cycling.

Here, we investigated the effects of a controlled rewetting event on the soil CO_2 efflux pulse and on the present (DNA-based) and potentially active (rRNA-based) soil bacterial and fungal communities in intact soil cores previously subjected to three different precipitation patterns over four months (full summer dry season, extended wet season, and absent dry season). Phylogenetic marker genes for bacteria (16S) and fungi (28S) were sequenced before and after rewetting, and the abundance of these genes and transcripts was measured.

Even after having experienced markedly different antecedent water conditions, the potentially active bacterial communities showed a consistent wet-up response. Moreover, we found a significant positive relation between the extent of change in the structure of the potentially active bacterial community and the magnitude of the CO_2 pulse upon rewetting dry soils.

We suggest that the duration of severe dry conditions (predicted to change under future climate) is important in conditioning the response potential of the soil bacterial community to wet-up as well as in framing the magnitude of the associated CO_2 pulse.

Keywords: soil CO2 efflux, rRNA, rDNA, Birch effect

[P1.190]

Soil nematode communities from mofette fields: Long-term responses to high carbon dioxide concentration

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Mofette fields, i.e. geogenic, cold CO_2-exhaling gas vents occurring naturally in regions of volcanic disturbances were studied to see long-term responses of soil nematodes to increased CO_2 concentration. The upper centimeters of mofette soils present a small-scale mosaic of different gas composition: From 100% CO_2/ 0% O_2 around degassing vents to elevated CO_2 concentrations predicted from climate change scenarios to ambient soil atmosphere. Our objectives were to investigate the influence of CO_2 on nematode community structure, identify threshold-CO_2 concentrations and assess effects of long-term CO_2 degassing on ecosystem functioning by evaluating the mofette food-web structure.

Canonical correspondence analyses revealed strong correlations between nematode community structure and environmental parameters, primarily soil CO_2 and pH. An increase in CO_2 was followed by a steady decline in nematode species numbers, but below an ultimate limit had no significant effect on overall nematode densities: Nematodes grew individual-rich populations at up to 62% CO_2, but above 20% CO_2 nematode communities consisted almost entirely (97%) of only four mofettophilous species that belong to three feeding types. Consequences of this considerable diversity reduction on ecosystem processes are discussed.

To find possible adaptive advantages of mofettophilous species we measured survival, activity, fertility and respiration rates at different CO_2 concentrations in the laboratory, comparing one of the mofettophilous species, *Acrobeloides* cf. *buchneri*, with a non-mofettophilous species, *Acrobeloides nanus* (present only at spots of <20% CO_2). The close relatedness of the two species was genetically confirmed in the German-Barcode-of-Life-Project. In the lab, both species survived 100% CO_2 in an inactive state, but the mofettophilous species tolerated higher CO_2 concentrations before entering inactivity and reactivated faster. We assume that this combination allows the mofettophilous species to live at CO_2 concentrations inaccessible to its non-mofettophilous sister species and to build relatively large populations at high-CO_2 spots due to the lack of competition.

Keywords: carbon dioxide, natural gas vents, preadaptation

[P1.191]

Interactive effects of altitude and exposure on soil biota in different Alpine vegetation zones

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Mountain environments harbor ecosystems that are predicted to experience a rapid warming in the future with distinct consequences for soil organic matter quality and quantity. Enchytraeids are considered a keystone group that can exhibit considerable site-specific differences, and they can be used as specific ecological indicators. However, the changes in their abundance and community structure at a species level in this type of ecosystems are still insufficiently documented. Therefore, we aimed to assess and evaluate the dominant abiotic and biotic factors shaping/regulating enchytraeid species composition and abundance along an altitudinal/climatic gradient and associated vegetation zones. Ten alpine sites were investigated in the Italian Alps (Val di Sole, Trentino). Five sites were positioned at north (N) and other five at south (S)-facing slopes. To facilitate the comparisons between soils collected on N and S slopes, the altitudes of the sites were as similar as possible (ranging from 1200 up to 2400 m a.s.l.). The vegetation cover varied from different types of forests at lower elevations to alpine grasslands at higher elevations. Three plots (5x5 m) located 50 m from each other were set-up in each of the 10 study sites and soil sub-samples were randomly taken in each plot in 5 cm depth increments

(0-5, 5-10 and 10-15 cm). Microannelid extraction was performed over 48 h by a wet-funnel technique without heating and they were identified to species level under a light microscope. Soil microbial communities (bacteria, fungi and archaea) were quantitatively assessed by real-time PCR. Soil microbial biomass was estimated as double-stranded DNA yields, and the physical and chemical soil properties were also determined; together with the humus forms, which constitute the meeting point (*proxy*) of feedback interactions and any changes in their composition and properties is expected to affect the autochthonous soil biota.

Keywords: mountain environments, enchytraeids, microbial communities, humus forms

[P1.192]

Understanding the soil C cycle: analysis of microbial community structure and function during below ground/root biomass decomposition of bioenergy crops.

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Decomposition of plant material is an important part of the global carbon cycle, mainly carried out by soil microorganisms. However, the key microbes and functional genes involved in degradation of plant material under field conditions are still unclear. We hypothesized that the roots of different biofuel crops would decompose at different rates and would have different microbial community and functional gene abundance. In this study, the decomposition of dried roots from four potential bioenergy crops (*Miscanthus* x *giganteus* (MxG), *Panicum virgatum* (PV), *Zea mays* (ZM) and native prairie (NP)) was estimated, and the composition of the microbial community and functional genes on root material were compared using T-RFLP fingerprinting and metagenomic sequencing. Dried root materials in nylon litter bags were buried 10 cm below the soil surface in November at the end of the growing season. Litter bags were recovered 4, 6 7, 8, and 12 months later. Biomass decomposition of root material differed significantly between the different crops. After 12 months of incubation, NP root decomposition was highest with 65.8% root DM loss, followed by PV, ZM and MxG with 52.1, 44.3 and 37.5% root DM loss, respectively. Analysis of T-RFLP profiles showed that the composition of the microbial community degrading different plant materials were mostly separated from each other at March sampling, but became more similar after 8 and 12 months of incubation. No significant difference was observed among the communities degrading different plant materials after 8 months of incubation. This was confirmed in analysis of microbial community composition from the metagenomic sequencing data. Analysis of functional gene composition and abundance showed relatively lower similarity after 4 months compared to 8 months of incubation among the four plant materials. Whilst decomposition rates differed significantly between crops, there was no significant difference in microbial communities or functional gene abundance.

Keywords: carbon cycle, root decompositon, metagenomics

[P1.193]

Earthworms as environmental and soil quality bioindicators: the Brazilian experience

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Soil animals such as earthworms are highly sensitive to changes in land use as well as to changes in soil physical, chemical and biological conditions, often caused by land management practices. Therefore, they have commonly been proposed and used, especially in European countries, as bioindicators of soil conditions/quality as well as the sustainability of agricultural and forestry management practices. Farmers in many countries, including Brazil, have associated high earthworm populations with higher soil quality for decades. However, at present there is still no widespread on-farm use of this concept in Brazil and there is still rather poor quantitative understanding of how earthworm abundance (e.g., numbers or biomass per m^2) is actually related to soil quality, particularly soil texture, bulk density, nutrient availability or organic matter content of soils. Therefore, a large database on earthworm abundance and soil chemical attributes (available P, K, Ca, Mg, exch. Al, pH, SOM, CEC) and soil texture (% sand, silt & clay) from over 400 sites throughout Brazil was constructed and is presently being analysed using parametric and non-parametric univariate and multivariate analyses (including RDA, PCA, multiple regressions and co-inertia analyses). Results from specific regions of Brazil have shown significant positive correlations between earthworm abundance and SOM, base contents and pH, as well as sand or clay contents. However, the relationships vary depending on the site conditions as well as on the species of earthworm chosen, revealing particular soil niche preferences and site-specific situations. This presentation will cover the results obtained of the overall and regional analysis of this database in the light of the potential usefulness of earthworms as soil quality bioindicators in Brazilian agricultural (especially no-tillage) and forestry ecosystems.

Keywords: soil quality, earthworms, soil management, conservation

[P1.194]

Interactions between earthworms and bacteria used as bio control agents of soil-borne plant diseases

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Several microorganisms have been successful as bio control agents (BCA) against several soil-borne plant diseases on crop plants. How these BCA may affect non-target soil organisms and how they interact with soil fauna is not well-known. We studied the effect of the BCA bacteria *Bacillus amyloliquefaciens* on the earthworm species *Aporrectodea longa* and *A. caliginosa*. We also studied how *A. caliginosa* and *B.amyloliquefaciens*, separately and in combination, affect *Alternaria brassicae* infection in oilseed rape plants.

Earthworms were exposed to *Bacillus amyloliquefaciens* by (1) dipping into a solution of bacteria, (2) keeping in soil amended with bacteria and (3) feeding with oilseed rape leaves amended with bacteria. Treatments were applied in isolation or in combination. Earthworm mortality, individual growth and production of egg cocoons were measured during 1-2 months while the earthworms were kept in soil mesocosms and feed with stable manure mixed into the soil.

Oilseed rape plants (*Brassica napus*) were grown in 30 L soil in containers under outdoor conditions. *B. amyloliquefaciens* was added to the plant root environment and *A. caliginosa* earthworms (corresponding to 300 ind. m^{-2}) were added, in isolation or in combination. Plants were infected with *A. brassicae*. *A. brassica* infection of plants, plant biomass, earthworms' survival, growth and reproduction, and density of *B. amyloliquefaciens* were measured as response variables.

Preliminary results show no effects on earthworms by *Bacillus amyloliquefaciens.* This important and new information indicates that the use of this BCA probably has no negative impact on earthworms. The ongoing experiments on *B. amyloliquefaciens*- and- earthworm effects on *A. brassica* infection will give information on the efficacy of this BCA in a complex environment and if the possible disease suppressing effect of *B. amyloliquefaciens* will be enforced or counteracted by earthworms, which by themselves also may suppress the disease.

Keywords: Earthworms, Microbial bio control agents, Soil-borne fungal plant diseases, Bacillus amyloliquefaciens

[P1.195]

Changes in activity and genetic diversity of microbial community during decomposition

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Decomposition of organic matter is an important process mediated mainly by soil microorganisms. Therefore, the knowledge about the performance of micro-decomposers (their abundance, diversity, efficiency in processes they carry out, etc.) is essential for better understanding of ecosystem functioning. One of the currently supported hypotheses states that microbial community composition undergoes shifts due to changing substrate quality during decomposition.

The aim of this work was to compare genetic and metabolic diversity of microbial communities in freshly fallen litter and in litter at moderate and advanced stages of decomposition.

Freshly fallen brown Scots pine (*Pinus sylvestris* L.) needles were collected and transported to the laboratory. Part of the material was stored at 4°C in darkness until analyses, and the other part was used to make litter bags which were later placed back at the site of collection. The litter bags were picked up after 92 and 242 days of incubation. In the fresh litter and in the subsequently collected bags, an overall microbial activity (respiration rate) and community level physiological profiles (Biolog™ ECO and SFN2 plates) were determined. To track the on-going changes in taxonomic composition, the metagenomic DNA was extracted and sequenced (Roche 454 Sequencing). Additionally, pH and concentrations of C, N, Ca, Cd, Fe, K, Mg, Mn, Na, Pb and Zn in litter were measured.

A considerable drop in respiration rate and an increase in microbial activity on Biolog™ plates were observed during decomposition. Also, shifts in taxonomic composition over time were noted, especially with respect to the contributions of Actinobacteria, Proteobacteria and Cyanobacteria. Among fungi, a transition from Ascomycota to Basidiomycota-dominated community was observed.

Keywords: litter decomposition, microbial diversity, community level physiological profiles, metagenomics

[P1.196]

Shifts in soil microbial communities structure in response to experimental nutrient manipulation in a tropical montane rain forest.

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Atmospheric nitrogen (N) and phosphorus (P) depositions are expected to increase in the tropics as a consequence of increasing human activities in the next coming decades, which will likely have detrimental effects on the high biodiversity of tropical ecosystems. Thus, it is crucial to understand the response of the tropical forests to increased nutrient deposition to predict the effect on the soil communities and ecosystem functioning.

We investigated the role of N and P as limiting factors of microorganisms in an Ecuadorian montane rain forest on a temporal basis. N (as CH_4N_2O), P (as NaH_2PO_4) were added to soils under a fourfold replicated randomized block design (control, +N, +P, +NP). Soils samples were collected bimonthly from experimental plots for 12 months. The response of microorganisms to experimental treatments was determined by analyzing microbial biomass, fungal and bacterial abundance (community structure) measured by a DNA-based approach (i.e., Quantitative PCR). The structure of microbial communities did not vary significantly over time, however small changes were found to be significantly correlated with soil moisture and temperature. Temporal shifts in microbial community structure under enriched nutrient conditions were less predictable and are likely a product of complex interactions between the soil environment and the diverse plant community. Our preliminary results indicate that the relative abundance of fungi in tropical montane soils is mainly determined by the N availability in an inverse relation. Furthermore, fungal communities benefit from high availability of P. After one year, no patterns were seen in bacterial communities. Temporal variability needs to be carefully assessed when comparing microbial diversity in tropical regions to face an eventual climate change scenario.

Keywords: Soil microbial communities, Ecuadorian montane rain forest, Temporal shifts, Nutrient manipulation

[P1.197]

Functional traits explain current and may predict future distribution patterns of soil fauna

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One of the Herculean tasks we face as soil ecologists is to understand and predict how climate and land use change will impact the community of functional important soil organisms, such as soil fauna. The huge diversity of soil fauna poses a real challenge to ecologists with respect to predict how changes in the environment influence community structure, not in the least because of a strong context dependency. It has been proposed that ecological generality will improve with a shift from a nomenclatural approach focusing on species number and identity to a more functional approach focusing on species' functional traits.

We selected functional traits that underpin resistance of soil fauna to an array of soil environmental stressors, such as drought, inundation, heat waves and declining habitat patch area (and increasing patch isolation). Morpho-physiological traits were measured under standard laboratory conditions, or obtained from trait databases in case of trait proxies.

Using a functional trait approach we found that interspecific differences in trait values explain species distribution patterns of various groups of soil fauna in relation to soil climate gradients, habitat fragmentation gradients and variation in habitat surface area in various biomes. Interspecific dissimilarity in functional trait values explained a large fraction of the variability in soil fauna community composition across soil environmental gradients. Also, the selected traits could be directly linked to the environmental variables that underlay environmental stress gradients.

These findings contribute to the increasing need to generate empirically tested, mechanistic predictions on the effect of global changes on functionally important organisms such as soil fauna. Identifying and quantifying the functional traits that underlie interspecific differences in tolerance to environmental stresses will enhance our ability to predict both soil fauna community responses to changing soil conditions and the consequences of the associated species shifts for key soil processes.

Keywords: Functional traits, Species distribution, Soil fauna, Global change

[P1.198]

Effect the application of tequila vinasses on carbon and nitrogen mineralization in an agricultural soil

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Tequila is produced from *Agave tequilana* Weber var. Azul mainly in the state of Jalisco, Mexico. Every liter of tequila produced generates around 10 L of vinasses, producing 1,647 million L of vinasses in 2013 (55% Alc. Vol.). The high organic matter (OM) content from vinasses has suggested that soil application may be beneficial, however, studies about soil processes (nitrification, denitrification, etc.) had not been documented. The objective of this study was to evaluate the effect of application of tequila vinasses on carbon and nitrogen mineralization process in agricultural soil. Two soil were sampled from sugarcane crop located in "El Arenal", Jalisco, Mexico, the first one was a soil where vinasses are frequently added (VS) and the second one from a site where never have added vinasses (control soil-CS). An experiment was achieved to evaluate the mineralization of C and N, where the CS or VS were placed in microcosms and adjusted to different water holding capacity (WHC) of 40, 80 and 100% with water or vinasses, and dynamics of C and N were monitored during 70 days. Addition of vinasses increased C mineralization 5.6 and 5 times more than in control soilat100% and 80% WHC respectively. In the first 28 days the highest N mineralization was found in 100% and 80% WHC. This indicated that in high moisture content conditions were aerobic microsites where nitrification can occur for a period of time (28 days). However, only 0.1% from N added from vinasses was mineralized in 100% WHC, these indicated that immobilization of N was dominant in the soil. The nitrogen mineralization was higher in the control soil with 40% WHC at 70 days, this indicated that the organic matter mineralization was maintained in the nitrification process under aerobic conditions.

Keywords:

[P1.199]

Emissions of greenhouse gases by application of tequila vinasses in an agricultural soil

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The application of tequila vinasses to soil is a common practicum in Jalisco, Mexico. Vinasses are wastewater form tequila process and every liter of tequila generates around 10 L of vinasses, producing 1,647 million L of vinasses in 2013 (55% Alc. Vol.). It is thinking that the high organic matter content from vinasses could be beneficial into the soil; however, studies about emission of greenhouse gases (GHG) by tequila vinasses applications to soil had not been documented. The objective of this study was evaluates the generation of GHG (CO_2, N_2O and CH_4). Two soil were sampled from sugarcane crop located in "El Arenal", Jalisco, Mexico, the first one was irrigated frequently with vinasses (VS) and the second one without vinasses (control soil-CS). An experiment was achieved to evaluate emissions of GHG, where the CS or VS were placed in microcosms and adjusted to 40, 80 and 100% water holding capacity (WHC) with water or vinasses, sealed and CO_2, N_2O and CH_4 content was monitored in the headspace of microcosms during 7 days. A parallel experiment was achieve added 0.1% acetylene to inhibit nitrification process and with this only to evaluate emissions by denitrification way. The highest emissions of CO_2 and N_2O by denitrification were found at 80 and 100% WHC in soils with vinasses without significant differences between WHC. The emissions of N_2O in VS soils at 100 and 80% WHC were 2.7 and 2 times higher than in CS soil, respectively. A minimal CH_4 emission was found by vinasses application with the highest emission at 3 days. Estimation with 100% WHC emissions indicated that by every m^{-3} of vinasses applied to 1 ha soil (depth 20 cm and density 1.4 kg m^{-3}) could be generating 535 ton CO_2 eq ha^{-1} $year^{-1}$ (sum of CO_2, N_2O and CH_4).

Keywords:

[P1.200]

Influence of overstory-induced acidification on the belowground ecosystem in the Gaume Forest (Belgium)

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Acidification, caused by emissions or forest management and overstory-species, alters soil properties and litter layer characteristics and potentially causes the forest ecosystem to evolve non-linearly to an alternative steady-state. This research focuses on the changes that occur when a mixed forest stand is replaced by a spruce monoculture. More specifically, it assesses if the above-gound shift is mirrored by an alteration in the soil microbial community.

The Gaume forest, a 200 ha old-growth forest in Belgium, consists of a natural deciduous forest matrix consists of uneven stands dominated by oak, beech and hornbeam. Between 1950 and 1980, patches of 2-15 ha were replanted with spruce. Soils developed on sandstone with variable lime content, creating a gradient in soil texture and buffering capacity. This setting allows the establishment of 20 twin-plots, where one was converted to spruce and the other remained under broadleaved forest, evenly spread over the lithological gradient.

For each plot, herb layer composition and forest floor properties were described. Samples were taken from the litter layer, topsoil and subsoil and analysed for pH, texture and organic matter content. Functional diversity of the microbial community was assessed using biolog multiwell ECOplates. Results indicate that conversion to spruce caused a change in understory species, significantly correlated to higher Ellenberg-values for light. As the spruce stands were relatively open, conversion to spruce surprisingly led to a higher biodiversity in the herb layer. Conversion also caused a significant drop in pH of 0.3 at 0-5 cm and a drop of 0.1 at 15-20 cm. Microbial functional diversity shifted from the topsoil to the litter layer. Changes are less pronounced in the subsoil, where functional biodiversity is lower for both types of stands. Apart from these general observations, changes in functional diversity were site-specific, with an important influence of soil texture.

Keywords: functional biodiversity, acidification, Gaume forest, Spruce

[P1.201]

Do Mycorrhizae affect Nitrogen Allocation with Biochar Additions in Poplars?

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With the addition of biochar, a carbon rich charcoal-like material, to the soil it is believed that there will be an enrichment of nutrients. Therefore, the dynamics of root activity and that of the associated mycorrhizal fungi is expected to change reflecting in terms of plant nutrient uptake. In this paper we focus on biochar effects on mycorrhizal growth and on the degree of root colonization. Six replicates of poplar cuttings were grown in pots filled with sand using two types of biochars, a solid and a liquid, with and without the presence of mycorrhizal inoculum. Biochar as it is did not seem to have an effect on mycorrhizal colonization. Instead Inoculum additions proved to enhance significantly arbuscular mycorrhizal colonization, however, without impacting the nitrogen allocated in poplar leaves.

Keywords: Mycorrhizae, Biochars, Nitrogen, Poplars

[P1.202]

Etudier la diversité fongique du sol au lycée

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Les programmes de SVT intègrent l'étude du sol et des êtres vivants qui s'y trouvent. Diversité biologique essentiellement macroscopique oubliant les acteurs majeurs du sol que sont les microorganismes.

Afin d'aborder la diversité fongique du sol en classe, un protocole de mise en culture sur milieu gélosé de différents échantillons de sol a été développé. Il prend en compte les règles de sécurité propres au milieu scolaire. Les élèves ont ensuite observé les colonies (taille, couleur, forme, aspect, contour…) dont ils ont réalisé l'inventaire (nombre de types différents de colonies, nombre de colonies pour chaque type). Une clé de détermination simplifiée leur a permis de traiter ces résultats. Cette approche microbiologique a été complétée par une approche moléculaire menée sur ordinateur et au cours de laquelle les élèves ont analysé deux séquences d'ADN (ITS d'ADNr) de microorganismes non identifiés, provenant de bases de données scientifiques (EBI, NCBI)

Les observations ont montré, selon les prélèvements, 2 à 8 types de colonies différents.

En parallèle, l'étude, par le biais du site « MABL » de l'Université de Marseille des séquences ADN choisies, révèle qu'elles sont proches de celles d'espèces connues mais néanmoins suffisamment distinctes pour considérer qu'il pourrait s'agir d'espèces nouvelles.

Certains microorganismes ne pouvant être cultivés, c'est donc en extrayant leur ADN directement à partir du sol que l'on parvient à les identifier. Etape que le scientifique peut pratiquer mais qui est difficilement réalisable au lycée. Toutefois notre participation à l'opération « Génome à l'Ecole » (partenariat Sciences à l'Ecole-INRA-Genoscope) devrait nous permettre d'évaluer la possibilité de sa mise en œuvre au Lycée.

Keywords: pedagogy, soil biodiversity, microbiological approach, molecular approach

[P1.203]

Nanofibre biomass carriers as a promising tool for genetic analysis of microbial community from highly polluted sites

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Introduction:

The applicability of nanofibre material as a carrier for indigenous microbial communities was tested at sites contaminated by chlorinated ethenes (CE). CE are the second most common soil contaminants worldwide. One of the most successful remediation methods is enhanced reductive dehalogenation (ERD), which utilises anaerobic microbial degradation. However, cis1,2-DCE and cancerous vinyl chloride can unpredictably accumulate at some polluted sites during ERD. A deeper insight into the key-factors affecting the ERD process is therefore highly desirable. The nanofibre biomass carriers can help to characterize indigenous microbes in a well-defined and controlled way. The technique includes sample stabilisation for safe transport to a laboratory, isolation DNA and PCR/qPCR amplification.

Methods:

Nanofibre carriers of a high specific surface were installed in polluted underground water for at least two months. Stabilization of biomass on carriers was done four different ways, right after sampling: i) in cooling box, ii) using RNA later solution, iii) on dry ice and iv) in liquid nitrogen. DNA concentration was measured on Qubit (Life Technologies). Isolated DNA samples were analysed using PCR/qPCR for presence of certain bacterial taxa and vinyl chloride reductases.

Results and Discussion:

Nanofibre carriers ensured stable biomass growth and thus good DNA yield. The DNA yield was comparable for all stabilization procedures. All DNA samples were of high quality and able to be amplified by PCR/qPCR without inhibition. We were able to detect microbial taxa and VC reductases. Nanofibre biomass carriers are still being tested, the main issue is carrier selectivity. It has to be proved that microbial community in the groundwater and on the carrier does not differ.

Acknowledgements:

This study was supported by Ministry of Industry and Trade of Czech Republic within the project FR-TI3/564 and by the Ministry of Education of the Czech Republic within the SGS project.

Keywords: nanofibre biomass carrier, reductive dahalogenation, molecular genetic testing

[P1.204]

Soil microbial biomass, microbial respiration activity and fungi-to-bacteria ratio in Chernozems typical of Russia

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Chernozems is an important natural resource of Russia, which is under intensive anthropogenic impact (plowing, urbanization). The research was focused on assessing soil microbial biomass carbon content (C_{mic}), basal (microbial) respiration (BR) and fungi-to-bacteria ratio (F/B) in Chernozems typical (Kursk region) along ecosystems (steppe, black fallow, urban - industrial zone) and soil profile gradients (24 samples in total). The C_{mic}, F/B were measured by SIR and SI technique, respectively, the qCO$_2$ and C_{mic}/SOC ratio were calculated.

For upper mineral 10 cm layer the C_{mic} and BR were found 84-1954 µg C g^{-1} and 0.20-1.11 µg CO$_2$-C g^{-1} soil h^{-1}, respectively. The C_{mic} of fallow and urban soils reached in average 482 and 160 µg C g^{-1}, respectively, that was by 3 and 10 times less than steppe. Along the row steppe-fallow-urban the BR was decreased (by 2-3 times). The C_{mic}/SOC was ranged 0.4-6.6%, in fallow and urban it was less by 2 and 7 times than steppe, respectively. The qCO$_2$ in urban was by 3 times higher compared to steppe and fallow. The fungal portion in steppe reached up 90%, in fallow and urban it was less (78 and 68%, respectively). The F/B in steppe, fallow and urban was found 6.0, 5.2 and 1.8, respectively, indicating fungal portion decreasing.

The C_{mic} and BR pools of fallow and urban soil profile (1.5 m) were less than steppe (by 3 and 10, 3 and 6 times, respectively). The contribution of upper 10 cm layer in C_{mic} and BR soil profile pool was amounted in average 68 and 64%, respectively.

Thus, the anthropogenic impact lead to a change in the functioning of Chernozems microbial community, which expressed a significant decreasing C_{mic}, BR, profile pool, F/B, C_{mic}/SOC, and, opposite, increasing qCO$_2$.

Keywords: Chernozems typical, microbial biomass, basal respiration, land use

[P1.205]

Impact of microbial diversity erosion on pesticide degradation

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Soil microbes possess vast phylogenetic and functional diversity and are key contributors to pesticide degradation. Functional redundancy is observed where species richness declines but ecosystem function is maintained. However, little is known about the relationship between microbial diversity and pesticide biodegradation kinetics. This study explores the sensitivity of pesticide biodegradation to microbial biodiversity reduction and aims to better understand the causes of DT50 variability in soil degradation studies.

Soil mesocosms encompassing a gradient of species richness were constructed by inoculation of soil sterilised by gamma irradiation and autoclaving with dilutions of fresh soil (dilution to extinction approach). A five month equilibration period allowed for the recovery of microbial abundance and activity. Four radiolabelled compounds covering a range of structural types and degradation behaviour (2,4-Dichlorophenoxyacetic acid, Terbuthylazine, Azoxystrobin, Bicyclopyrone) were subjected to aerobic degradation studies using soil from equilibrated mesocosms. The degradation studies followed the OECD307 design (mass-balanced systems, 20°C dark incubation, flow of moistened air) and compounds were applied at field rate equivalent to 50g aliquots of soil.

Analysis of degradation data revealed a clear effect of soil dilution on compound biodegradation kinetics. 2,4-D degradation function was robust to dilution up to 10^{-6}, but was severely disrupted in highly impoverished systems. Azoxystrobin degraded with a half-life of 74 days in undiluted soil, but half-lives in all dilutions exceeded the previously reported range of up to 226 days (35 studies), indicating a high dependency on microbial diversity. An idiosyncratic relationship between level of dilution and DT50 was observed for Terbuthylazine, suggesting a possible reliance on community structure rather than species richness.

Our findings suggest that structurally different chemicals respond differently to microbial diversity erosion. Data so far indicates that this test system is suitable for distinguishing three types of relationship (redundant, dependent, idiosyncratic) between microbial biodiversity and pesticide biodegradation function.

Keywords: mesocosms, pesticide, degradation, microbial diversity erosion

[P1.206]

Investigating the impact of ecosystem change within agriculture on the soil food web.

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The soil invertebrate food web drives nutrient cycling and decomposition. However, the food web can be affected by perturbations differently depending on plant type within an ecosystem. An experiment was set up to test the hypothesis that previous forage cropping and cultivation method would alter the soil ecosystem leading to changes in the food web, during crop rotation. Plots were grown containing monocultures of chicory (*Cichorium intybus*), red or white clover (*Trifolium pratense, T. repens*) and perennial ryegrass (*Lolium perenne*). Four replicate plots of the forages were established (12 x 7.5m) in 2009; these were split (10 x 3.75m) in spring 2013 and wheat established either after ploughing, or seeds directly drilled; with wheat harvested autumn 2013. It was hypothesised that direct drill would disturb the food web less than ploughing, whilst the plots which were previously legumes would retain a different soil faunal population, even though the crop was the same across all plots. The effect on soil faunal populations of these previous different forage crops and sowing method were assessed after wheat harvest; the soil fauna sampled included microfauna, mesofauna, and macrofauna. Overall our results have shown that for a number of soil faunal groups across the three scales of sampling, the previous forage still had a significant effect over the current soil food web, even though the ecosystem has now been standardised between the different plots. There was also a significant affect over all soil faunal populations when assessing the difference in cultivation method – plough versus direct drill. Our findings have begun to show the linkage between soil biodiversity and the effect of agriculture on the whole ecosystem and shows the potential for managing a healthy soil food web and maintaining it, within agricultural production.

Keywords: Soil food webs, Agro-ecology, Ecosystem engineers, Mesofauna

[P1.207]

Changing population patterns - when an alien pest becomes a problem at home? First recorded pest outbreak of the springtail Sminthurus viridis in Europe.

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The springtail *Sminthurus viridis* (Collembola: Sminthuridae) is classed as an alien pest of economic importance in Australasia – costing over $50 million annum^{-1} in damage and control measures to the agricultural industry. *Sminthurus viridis* has never been considered a pest in its native Europe, where it has a ubiquitous distribution in grasslands, as native predators and environmental conditions keep abundances below damaging infestations. However, during an experiment assessing different cultivation practices for lucerne (*Medicago sativa*) in the UK, an abundant outbreak of *S. viridis* was observed in an initial field assessment, with a number of individuals visible per plant. *Sminthurus viridis* numbers were immediately quantified over a 24 hour period to ascertain whether this was comparable to any other reported outbreak; as well as sequence data obtained to compare to Australasian "pest" populations of *S. viridis*. As this outbreak occurred within a statistically-robust replicated experiment, we could also assess how different cultivation techniques affected the abundance of crop pests within ecosystems.

Lucerne established by direct drilling with herbicide had the highest abundance of *S. viridis* compared to other treatments (lucerne established by direct drill or plough, with or without herbicide). The *S. viridis* population abundances were found to be ten-fold greater than populations found on a nearby site of established lucerne. Within the EU, over 60 million hectares are devoted to grassland containing clover and lucerne, the main food sources of *S. viridis*. If there were further outbreaks similar to our findings across Europe, allowing *S. viridis* to cause damage on a similar scale as Australasia (20-50% losses), it would cost millions to the European agriculture industry. Our findings highlight the need for greater monitoring of *S. viridis* within agriculture worldwide and that we need to increase awareness within the farming community of this potential future pest, to safeguard crops.

Keywords: Crop protection, Lucerne flea, Agro-ecology, Collembola

[P1.208]

Multiple heavy metal and antibiotic resistant strains of Bacillus isolated from sediments of a south Algerian salt lake

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Abstract for poster communication:

Sebkhas are dry salt lakes mainly found in North Africa and are defined as halophilic environments. They are common landscapes in Algerian Sahara and are known as polluted and heavy metal contaminated environments as they receive domestic and industrial effluents.

In this study, 3 multi metal and antibiotic resistant strains belonging to the genus *Bacillus* were isolated from sediments of Ain-Salah sebkha, in the Sahara desert (Wilaya of Tamanrasset).

The bacteria isolation was made from 1g of dried sediment sample on a nutritive broth containing lead and cadmium at a concentration of 100µg/L for each metal.

Cultures showing turbidity after 2 weeks of incubation at 30°C were subcultured into Nutritive Agar Petri dishes containing the same concentrations of heavy metals. This protocol allowed us to isolate and purify 5 different strains. A molecular identification was then carried on by 16s r RNA gene sequencing and reveled that 2 strains belonged to the genus *Pseudomonas* while the other 3 belonged to the genus *Bacillus*.

Minimum inhibitory concentrations for 8 heavy metals were determined by spot plate method and antibiotic resistance was tested by disc diffusion method towards 35 antibiotics.

The 3 *Bacillus* strains presented a high level of resistance to all of the 8 heavy metals tested and were resistant to 20 of the 35 antibiotics.

The genus *Bacillus* being known as a natural heavy metals remover (Pepi and al., 2007; Minyan and al., 2010; Verma and al., 2009), our isolates can be promising for bioremediation processes on the basis of their high level of heavy metal resistance.

Keywords: Bacillus, Multiresistance, Heavy metals, Antibiotics

[P1.209]

Tracking earthworm-microbe interactions and GHG emissions in green sugarcane production

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Many vital soil processes such as nutrient cycling, mineralization and decomposition are microbially-mediated, but can also be influenced by soil fauna. Recent advances in green sugarcane production allow us to propose the hypothesis that organic matter input (straw) and earthworms are priming forces that activate specific microbial communities involved in nutrient cycling, mineralization, decomposition and greenhouse gas (GHG) emission. Next Generation Sequencing (Illumina MiSeq) shotgun of DNA and RNA from soil samples will be correlated with environmental data (soil physical-chemical and biochemical analysis) in a factorial greenhouse experiment (began in March 2014) including a one year cycle of sugarcane installed in 24 experimental units filled with a podzolic dark red Oxisoil in the presence and absence of: 1) earthworms (*Pontoscolex corethrurus*), 2) sugarcane straw and 3) fertilizers. GHG emission (N_2O, CH_4 and CO_2) from soil are being measured throughout the experiment. We hypothesize that earthworms will impact microbial diversity and that there will be significant changes in both microbial pools and activity due to the three factors. Partial results show statistically significant differences (Tukey HSD $p<0.05$) between treatments. Straw addition increased plant height, which was also observed in straw+earthworms compared to the treatment with only fertilizers. Regarding GHG emissions, for N_2O and CO_2, straw may be the driving factor (although earthworms were also important), and the full treatment (earthworms+straw+fertilizers) had higher emissions than the three factors separately. Also the interaction between the three factors increased N_2O concentrations inside the soil compared with the other treatments. For CH_4 earthworms alone caused the highest emission rates, being significantly higher than with only fertilizer applied ($p = 0.0106303$). DNA recovered from soil samples reached an average of 36.62 ng/µl with a quality of 1.92 (NanoDrop).

Keywords: Metagenome, Metatranscriptomics, Microbial ecology, Agroecosystems

[P1.210]

Abundances of microbially-mediated nitrogen ecosystem processes within two biodiversity conservation parks in the Brazilian savannah biome

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The Brazilian savannah is the second largest biome in Brazil and presents a range of vegetation in which soil characteristics influence the microbiota taxonomic composition. These savannah soils are nitrogen-limited, the major nitrogen input being biological fixation and with high ammonia concentration and low levels of nitrate. We hypothesized that vegetation and soil parameters would influence the relative rates of different microbially-mediated nitrogen ecosystem processes because of their different water, gravimetric carbon and nitrogen contents. To assess these differences, we sampled eight areas with different vegetation cover and soil characteristics in triplicate in two natural parks for biodiversity conservation that are 500 km from each other and at different altitude. Metagenomes were obtained from these 24 native soil samples using the 454 platform. Annotated sequences in MG-RAST were analysed in STAMP and the compositions for nitrogen metabolism functional genes differed significantly between areas but not between the two parks, indicating that the diverse vegetation cover sampled within each park masked the effects of altitude and location. α-diversity was greatest in soils with high and low water content, possibly through greater evenness of species to overcome the less favorable conditions. Functional genes associated with nitrogen fixation, nitrosative stress and nitrate and nitrite reduction to ammonia differed significantly between the phytophysiognomies sampled. Across all soils, the most abundant functional gene subsystems of nitrogen cycle were those related to ammonia assimilation. Genes associated with denitrification were also annotated but functional genes associated with nitrification were not detected, possibly through limits in the depth of sequencing, as nitrifier abundance is low in these savannah soils. The results suggest that the nitrogen cycle processes differ between the areas. Future studies will investigate whether vegetation cover or other soil parameters are associated with these differences.

Keywords: soil metagenomics, brazilian savannah, nitrogen cycle, soil microbiota

[P1.211]

Responses of soil biotas to human impacts: from local to global

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Soils provide crucial ecosystem services, including supporting the majority of food production, regulating water supply and quality, along with buffering against floods and droughts. Soil fauna play a significant role in the provision of these services but, despite this, little is known about the influence of land use change on soil and leaf litter biotas and subsequent impacts on ecosystem services.

At a very local scale, a detailed study of an ash-field maple woodland partially converted to conifer plantation demonstrates the influence of environmental variables, microhabitats, and land-use on soil macrofauna. Using multivariate ordination and indicator species analysis, we found distinct species assemblages of soil and leaf litter invertebrates between microhabitats, with pronounced differences in the area converted to conifer plantation.

Such local studies can provide a wealth of detail - but additional insights can be obtained through collating and analysing pooled data from many studies to estimate the average effects of gross changes in land use and land use intensity. VJB's PhD research, supervised by Andy Purvis, Paul Eggleton and Tom Bell, aims to develop an integrated understanding of soil biodiversity in the UK. It will combine new and existing data to develop models of how soil and litter communities will respond to predicted land use and climate change and how this will impact on ecosystem services.

We are seeking to collate published studies of soil and leaf litter biotas, focusing on UK ecosystems. Those using the same sampling method to compare sites with different land use type or intensity are particularly welcome. Data will be fed into the PREDICTS database (www.predicts.org.uk), which supports global modelling of human impacts on local diversity. All contributors will be included as authors in an open-access paper on the database and acknowledged appropriately in all publications.

Keywords: Ecosystem services, Land use change, Human impacts, Soil biodiversity

[P1.212]

Does climate change affect litter decomposition and microarthropods associated in Mediterranean oak forest?

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Determining the responses of terrestrial ecosystems to climate change is a major challenge of current ecological research. Roughly 90% of global terrestrial plant production enters the dead organic matter pool making the decomposition of plant material one of the most crucial processes of ecosystems. Climate change is likely to alter decomposition process through changes in litter and soil moisture affecting directly both composition and activities of decomposer communities. Indirectly, climate change can alter decomposition through chemical changes of leaves and through potential shifts in plant species composition.

In Mediterranean ecosystems, water availability is the most important environmental constraint, due to the concomitant combination of high temperatures and low rainfall during summer. These ecosystems are therefore expected to be extremely vulnerable to climate change.

In this context, we experimentally manipulated both plant litter mixtures and precipitation regime in a Mediterranean Oak forest, by using the O_3HP experimental site equipped with a rain exclusion device reducing 30% of rainfall for increasing summer drought period. We carried out a two-year litter decomposition experiment in litterbags in order to follow litter decomposition process (litter mass loss rates, litter nutrients and phenolics releases) and microarthropods (detritivorous and predators) abundance and diversity according to litter diversity and precipitation regime.

Litter diversity positively affected litter decomposition process and both abundance and diversity of microarthropods whereas reduced precipitation negatively affected litter mass loss rates, nutrient releases and detritivorous abundance and diversity. Increasing plant diversity in litter mixtures did not counteract negative effects of reduced precipitations. Moreover, we observed a homogenization of Collembola and Acari populations for all litter mixtures and an increase of predation pressure in reduced precipitation plot.

Our data demonstrate how climate change, through shifts in precipitation regime and in plant diversity, could strongly affected microarthropod communities and consequently nutrients cycling and ecosystem functioning.

Keywords: Litter decomposition, Climate change, aboveground-belowground relationships, soil microarthopod communities

[P1.213]

Case studies in microbial biodiversity and functioning of urban soils

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Soils of urban ecosystems are often subject to heavy disturbance and contamination. The role of soil organisms, particularly microbes, in providing ecosystem services is especially critical in an environment where functioning can be altered by human activity. However, because so many disturbed and contaminated sites are unique, it can be very difficult to study urban soil biodiversity and its effects on ecosystem functioning thoroughly. Here we present two case studies in soil microbial diversity from two very different but heavily disturbed ecosystems. The first is a soil with a metal concentration gradient at Liberty State Park (LSP) in Jersey City, New Jersey where post industrial land was abandoned and natural succession has been occurring for over forty years. The second is an urban to rural riparian transect along the Toms River in New Jersey that is subject to flash flooding and heavy nutrient loading. The goal of both of these projects is to measure soil microbial biodiversity (primarily fungal) and functioning as it relates to the local plant community composition and abiotic factors. Our research at LSP has shown that fungal community composition as well as microbial community functioning as measured by free soil enzyme activities varies with soil metal contamination. In fact, we find an increase in several soil enzyme activities with increasing soil metal concentrations. Along the urban to rural transect of the Toms River, the associated above ground plant community is the most important driver of biodiversity and community composition rather than proximity to urbanization and likely sources of nutrient loading. Understanding the relationships between soil microbial diversity, plants and the altered abiotic environment is central to restoration practices, and it has become a highly relevant area of ecological research.

Keywords: urban, plant community, fungi

[P1.214]

Litter secondary metabolites as a driving force for diversity, abundance and activity of detritivorous in a Mediterranean oak forest

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Mediterranean region is considered as a hot spot of biodiversity and is also supposed to be seriously threatened by climate changes. These changes can lead to a shift in plant communities with important feedbacks for ecosystem functioning. Within this, leaf litter decomposition is a key process controlled by leaf chemistry determining diversity and activity of detritivorous (dominated by collembola). However, the way that leaf chemistry can affect these organisms is still poorly understood.

In order to explore this relationship, three complementary experimentations were carried out to test at different scales the potential impact of four different types of litter (*Quercus pubescens*, *Acer monspessulanum*, *Cotinus coggygria* and *Pinus halepensis*) on diversity, abundance and activity of soil detritivorous: (i) *in situ* litter decomposition experiment; (ii) mesocosms experiment that mimic effects of natural litter leachates on soil biodiversity; (iii) *in vitro* ecotoxicological tests on *Folsomia candida* (ubiquitous species of Collembola).

During the field experiment, *C. coggygria* litter exhibited the lowest abundance and diversity on Collembola contrary to the three other plant species. *P. halepensis* and *Q. pubescens* showed the highest diversity with a strong increase of some Collembola species associated to these litters.

In laboratory, aqueous extracts of *C. coggygria* showed inhibitory effects on survival and reproduction of *F. candida* and on Collembola abundance over the mesocosms experiment.

These results suggest that litter chemistry can drive decomposers communities and then highlight the key role of secondary metabolites in plant-decomposers interactions.

Keywords: Mediterranean forest, litter decomposition, diversity-functioning relationship, Collembola

[P1.215]

Changes induced by 2,4-dichlorophenol and 2,4,5-trichlorophenol in soil bacterial communities.

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The 2,4-dichlorophenol (2,4-DCP) and the 2,4,5-trichlorophenol (2,4,5-TCP) are toxic chlorinated organic compounds which frequently appear as soil contaminants. Previous studies indicated that one of the main factors affecting their toxicity was the soil pH, probably because of their rate of ionisation to the corresponding phenolate ions, which appear to be the toxic form to microorganisms. Since the pK_a of 2,4-DCP and 2,4,5-TCP are 7.9 and 6.9, respectively, the formation of phenolate ions will be more intense in calcareous than in acidic soils.

The aim of this study was to analyse the impact of 2,4-DCP and 2,4,5-TCP on bacterial communities present in soils with different pH. Two agricultural soils (one alkaline, pH=7.19, and one acidic, pH=5.39), were contaminated at the laboratory with 500 mg kg^{-1} of 2,4-DCP and 2,4,5-TCP. After a contact time of 72 h between the soils and the clorophenols, molecular techniques were employed to study the changes induced by the pollutants in several bacterial groups.

Soil DNA was extracted with a commercial kit and 16S rDNA fragments were amplified by (nested)PCR employing universal primers for *Eubacteria* and primers specific for *Alfaproteobacteria, Betaproteobacteria, Actinobacteria,* and *Acidobacteria*. PCR products were analysed by Denaturing Gradient Gel Electrophoresis (DGEE).

The impact of DCP and TCP was clearly noticeable in the Eubacterial and Betaprotobacterial communities, while the changes in Alfaproteobacterial and Acidobacterial communities were less evident. The changes detected were influenced by both soil and contaminant type.

Keywords: Bacterial communities, Chlorophenols, Soil pH, Soil contamination

[P1.216]

Microbial activity of biocrusts in arid zones with different levels of degradation as affected by diverse temperature and moisture conditions

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Arid and semi-arid ecosystems are prone to soil degradation, which may be aggravated by intense grazing and cropping and by climate change. Degradation of these ecosystems has important repercussions at a global level as it influences the extent to which the areas (one-third of the Earth's terrestrial surface) will act as sources or sinks of CO_2. The study was carried out at two sites included in the CARBOEUROPE and FLUXNET networks established for measuring carbon flux: Balsa Blanca (non-degraded) and Amoladeras (degraded, due to intensive grazing). The sites are located in Almeria (SE Spain) and are representative of two distinctive degradation stages in semi-arid Mediterranean zones. The vegetation at both sites is scarce alpha grassland with areas occupied by biocrusts.

Aiming to study the extent to which degradation affects soil metabolic processes, at both sites various biological (microbial biomass C, soil respiration) and biochemical properties (hydrolase and oxidoreductase activities) were measured in the upper layer (0-2.5 cm) of biocrusts dominated by *Diploschistes*.

The total C and N content, and the absolute values of all of the biological and biochemical properties were higher in Balsa Blanca than in Amoladeras. However, the values of these properties expressed in relation to total C were very similar at both sites. This suggests that the degradation processes do not greatly affect edaphic metabolism. However, under laboratory conditions the emission of CO_2 from the surface layers of the biocrusts in response to different moisture and temperature regimes was very different. Thus, at the higher temperature the emission expressed per unit of C was much higher in the biocrust of the degraded site, independently of the moisture content. This reflects a greater risk of structural collapse in the degraded soil at extreme temperatures and clearly suggests that degradation affects the microbiota, thus modifying the edaphic biodiversity.

Keywords: Biocrusts, Diploschistes, Basal respiration, Temperature and moisture

[P1.217]

An integrated assessment of soil erosion dynamics with GIS and RS (Case study: the Southwest of Iran)

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Soil erosion by water is a significant problem in arid and semi arid areas of large parts of Iran. Especially human impacts have increased the erosion susceptibility of vast areas. Water erosion is one of the major phenomena that leads to decreasing soil productivity and pollution of water resources. Especially in the Mazayjan watershed in the Southwest of Fars province gully erosion contributes to the sediment dynamics in a significant way. Consequently, the intention of this research is to identify the different types of soil erosion processes and to assess the process dynamics in an integrative way. Therefore, we applied GIS (Geographic Information System) and satellite image analysis techniques to derive input information for the numeric models. For sheet and rill erosion the Unit Stream Power-based Erosion Deposition Model (USPED) was utilized. The spatial distribution of gully erosion was assessed using stream power index (SPI) together with a flow accumulation threshold defining gully headcut conditions. The eroded gully volumes were estimated for a seven years period by fieldwork and Google Earth high resolution images. Finally the gully retreat rates were integrated into the USPED model. The majority of the study area has silt loam and sandy loam soils that show high erodibilities. Current land use was identified from Landsat Thematic Mapper (TM) image. We use a frequency ratio approach to compare the classes of soil erosion and deposition (USPED map) with the gully locations. The results show that the integration of the SPI approach to quantify gully erosion with the USPED model is a suitable method to qualitatively and quantitatively assess soil erosion processes (gully erosion and sheet/rill erosion). The application of GIS and stochastic model approaches to spatialize the USPED model input yield valuable results for the prediction of soil erosion in the Mazayjan catchment. The results of this research help to develop an appropriate management of soil and water resources in Southwestern of Iran.

Keywords: Soil erosion, Gully erosion, GIS, Stream Power Index (SPI)

[P1.218]

Microbiological and physico-chemical analyses of soil samples from experimental plots in Benin, Irrua and Igbodo (Nigeria) in relation to Fusarium wilt of tomato

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Soil samples from Benin, Irrua and Igbodo in old Mid- Western region of Nigeria were analysed microbiologically and physico-chemically to determine the microflora density and the influence of soil physico-chemical effects on their populations. Total heterotrophic bacterial, fungal propagules and selective fusarial counts were carried out using standard plating technique on nutrient, potato dextrose and Nash and Snyder agar, respectively. Physico-chemical analysis carried out on the samples include determination of pH value, texture, water holding capacity, exchangeable cations (Ca^{++}, K^+, Mg^{++} and Na^+), cation exchange capability (CEC), phosphorus, organic carbon, nitrate and trace elements concentrations using a flame photometer, Pelkin Elmer atomic absorption spectrophotometer and a Technicon autoanalyser. Incidence of Fusarium wilt in field-grown tomato in these locations was also examined. The mean total fungal count ranged from 6.15×10^4 cfu/g (Irrua) to 3.16×10^5 cfu/g (Benin) while selective fusarial count ranged from 6.51×10^3 cfu/g (Irrua) to 2.84×10^5 cfu/g (Benin). Percentage incidence of Fusarium wilt in field grown tomato was significantly high in Irrua (20.10 %) as compared to Igbodo (5.83 %) and Benin (0.42 %). The mean pH values of the three different soil samples were acidic (5.96 - 6.27). Benin soil samples had highly significantly higher ($p=0.01$) concentration of potassium (7.80 meq/100g), sodium (0.68 meq/100g) and phosphorus (11.710 mg/kg), manganese (30.13 mg/kg), copper (0.65 mg/kg) and zinc (15.93 mg/kg) compared to others; with corresponding higher cation exchange capability (12.40 meq/100g). Irrua soil had the highest concentration of iron (173.28 mg/kg) and lead (0.07 mg/kg) and lowest percentage of sand (85.40 %). Benin soil samples had significantly higher potassium, nitrogen and phophorus contents which contributed to the low incidence of Fusarium wilt disease, even though Benin had the highest total fungal count.

Keywords: microbial counts, physico-chemical analyses, Fusarium wilt, Tomato

[P1.219]

Benchmarking the interactions between soil microbes, insects and plants and the ecosystem services they drive

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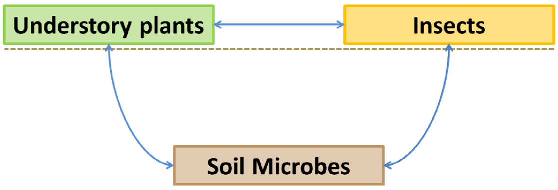
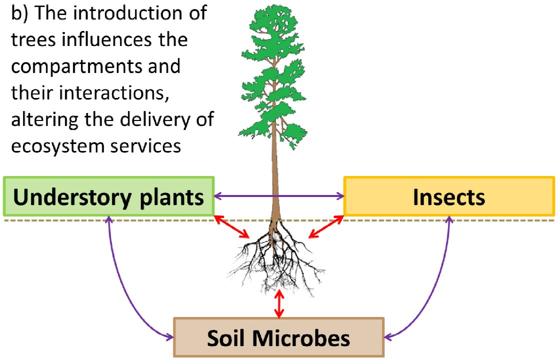
Changes in land use drive alterations in soil biodiversity. Afforestation is a common land use change that can alter the diversity of soil microbial and insect communities, plant life, and the ecosystem services they mediate, as illustrated below.

a) Biomass compartments and the interactions between compartments influence provisioning and regulatory ecosystem services

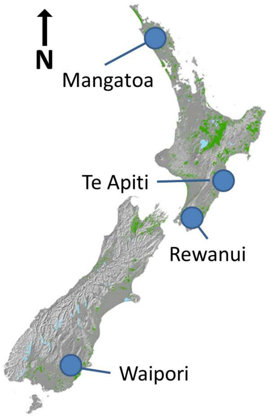


b) The introduction of trees influences the compartments and their interactions, altering the delivery of ecosystem services

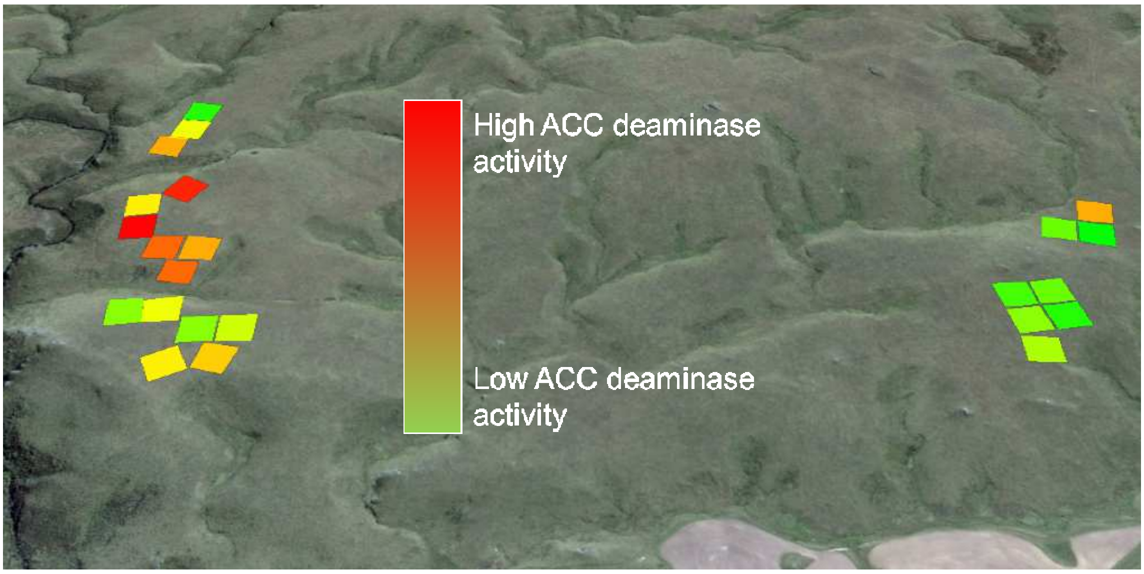


To determine how the traits of different exotic and indigenous forest species influence the delivery of ecosystem services a trial series was established at four sites in New Zealand along gradients of predicted climate change. Prior to afforestation a wide range of baseline data was collected at plot level to characterise the existing microbial, insect and plant communities across the sites.

Here we present results from the analysis of this data. We have identified several linkages between soil microbial and plant communities that are associated with ecosystem services such as biomass production, the provision of soil resources and the maintenance of biodiversity.



A key example is the correlation between the activity of 1-aminocyclopropane-1-carboxylate (ACC) deaminase produced by the soil microbial community and the diversity of the plant community at the sites. ACC deaminase attenuates plant stress responses, and can therefore influence plant diversity by enhancing the range of conditions suitable for a given plant species.



The image above illustrates the spatial variation in ACC deaminase activity over the 23 plots established at the Waipori site, and is correlated with plant diversity. Plots are 2500 m^2.

This is the start of a long-term study to understand the impact of different forest species on soil biodiversity and the delivery of provisioning and regulatory ecosystem services under a changing climate. This baseline data describes the current linkages between biodiversity and ecosystem service provision, and provides a benchmark for assessing any future changes in diversity and service provision with afforestation, while unplanted control plots allow the impact of climate change to be evaluated.

Keywords: soil - biota interactions, productivity, plant growth promotion

[P1.220]

Effect of methyl parathion in soil bacterial diversity of a chinampa from xochimilco, mexico

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Introduction: The methyl parathion pesticide is an organophosphorus compound which is used to control insect pests on crops in chinampas of Xochimilco, Mexico. When farmers apply the pesticide to the plants, it also reaches the ground. Because it is a highly toxic compound, it is important to know how it behaves on the floor. In this work we studied the effect of methyl parathion on the bacterial diversity of agricultural soil of Xochimilco chinampa. Methods: A completely randomized factorial experimental design is performed under aerobic conditions, where the experimental units are microcosms. Results: The bacteria types that are found in soil belong to five groups: α-Proteobacteria, β-Proteobacteria, γ-Proteobacteria, Bacillales and Fermicutes. Three DNA sequences that are obtained from soil bacteria of the chinampa are similar to bacteria that can degrade organophosphate pesticides and aromatic rings (*Achromobacter xylosoxidan, Brevundimonas diminuta y Ochrobactrum lupini*). Richness values are significantly reduced when any of two conditions occurs: 1) the pesticide concentration is high (equal to 280 mg/kg), or 2) the 4-nitrophenol concentration rises in the soil (from 0.76 mg/kg). Discussion: These results suggest that the bacteria which are present in soil could degrade organophosphorus pesticides as methyl parathion.

Keywords: chinampa, Mexico, methyl parathion, soil biodiversity

[P1.221]

The majority of minors: on the identity and function of rare soil bacteria

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Most bacterial taxa in soil are low abundant or rare. Usually, rare species are not expected to contribute substantially to ecosystem functioning, however, recent studies suggest that rare bacteria can play a crucial role in soil, for example by possessing distinct traits and acting as keystone species in biogeochemical cycles, by providing an insurance function under changing environmental conditions, or through interactions with other organisms such as plants and plant enemies. Our aim is to identify rare bacterial taxa in soil and investigate their contribution to ecosystem functioning.

We use a number of approaches: First we identify bacterial taxa that are constantly rare or exhibit fluctuating abundances by mining sequence databases. Cultivation-based approaches employing flow cell sorting and nutrient-poor media will be used to investigate specific characteristics of permanently rare bacteria, such as cell size and growth rate and the ability to degrade certain substrates. Then, we test their putative role in the insurance of ecosystem functions by monitoring the abundance of selected rare taxa using qPCR under disturbance regimes such as are likely to occur under human influence. Finally we will assess the effects of the loss of rare bacteria on plant biomass production and plant community evenness. Ultimately changes in the induction of systemic plant defences as the result of loss of rare bacterial taxa will be investigated as one mechanism by which rare bacteria might affect plant performance.

The combination of approaches will enable us to determine the roles of a selection of rare bacterial taxa in ecosystems. We will test which factors may be influenced by rare taxa: the possession of distinct traits, insuring ecosystem functions under environmental change or affecting plant defences. This approach will enable us to predict consequences of losing rare soil bacteria from ecosystems.

Keywords: rare bacteria, ecosystem function, insurance, plant-herbivore interactions

[P1.222]

Complex effects of habitat fragmentation on plant-soil-microbial interactions in Mediterranean Holm oak forests

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The adverse effects of habitat fragmentation on biodiversity have been widely explored; however, little research has been conducted to understand its effects on ecosystem functioning. Effects of forest fragmentation are tightly linked to the surrounding matrix in terms of nutrient inputs and spatial constraints, leading to complex edge effects. Soil ecosystem processes related to carbon cycling are particularly important since soils are the largest carbon pool in terrestrial ecosystems, and habitat fragmentation affects their sink capacity and their vulnerability to global change. Soil organic matter (SOM) decomposition is affected directly by the canopy cover. Thus, the effects of an agricultural matrix could be overridden by the direct effects of canopy rather than by habitat fragmentation itself. In order to evaluate which key factors could be driving SOM decomposition in fragmented landscapes, we analyzed potential enzymatic activities (β-glucosidase, chitinase and phosphatase acid) and field soil respiration in fragmented Mediterranean Holm oak forests. We evaluated if the impact of fragmentation on soil microbial functioning could be explained through its effect on microhabitat characteristics by using structural equation models. Variables measured included biotic (microbial biomass), abiotic (soil moisture, temperature, organic matter, pH, nutrients) and tree structural (stem diameter, canopy projection, leaf area index) characteristics. Tree effects on soil functioning (enzymatic activities) were potentiated by the influence of the agricultural matrix. As expected, trees created a microenvironment where the increment of SOM modified the pH, increasing soil moisture and decreasing temperature, rising the amount of microbial biomass and, therefore, improving the functioning of soil microbial community. Agricultural matrix influence on SOM decomposition was mainly indirect, through its positive effect on tree size. Mediterranean fragmented forests with high influence of agricultural matrix could increase SOM decomposition rates, decreasing soil carbon sink capacity.

Keywords: Habitat fragmentation, Enzymatic acitivity, Soil microorganisms, Quercus ilex

[P1.223]

Sublethal copper effects on species and their interactions, and impacts on organic matter decomposition: a microcosm approach

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The numerous applications of heavy metals render their complete eradication from everyday use highly improbable. Hence, scientists and policy makers have to establish criteria to distinguish ‘acceptable’ from ‘harmful’ levels of pollution. Earlier studies have shown that even sublethal amounts of metal pollutants, well below EC_{50} concentrations, can affect the fitness of individual bacterivorous nematode species, as well as the balance of the horizontal interactions between them. Species interactions are critical in shaping community structure and promoting ecosystem functions like organic matter decomposition - a key process that drives the flow of energy and nutrients in ecosystems.

In this paper, we exposed two bacterial feeding soil nematodes, *Plectus acuminatus* and *Acrobeloides nanus*, to different sublethal Cu concentrations in monospecific and two-species microcosms containing leaf litter of the common grass species *Urochloa mutica* for a period of 60 days. We demonstrate that chemical concentrations regarded as ‘sublethal’ not only affect the fitness of, but also the interactions between the two nematode species. We also show that sublethal Cu concentrations impair the stimulatory role of the nematodes n the decomposition of leaf litter. Specifically, our results show that a) in monocultures, *P. acuminatus* and *A. nanus* were negatively affected at Cu concentration of 4 mg L^{-1} and higher from the start and towards the end of the incubation, respectively, b) such decrease in population abundance of both nematodes slowed down the litter decomposition process, c) in combined cultures, a trend of mutual facilitation between the two nematode species was observed in both unpolluted and polluted treatments during the early phases of the experiment when food was not limiting, and that d) low Cu levels changed these interactions as well as the decomposition rates.

Keywords: bacterivorous nematodes, sublethal, decomposition, pollution

[P1.224]

Earthworm casts, is there a typology of such a key component of soil functioning?

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Earthworm have been long time recognized to be key organisms for soil functioning. They play crucial roles on the dynamics of organic matter (OM), of physical and of chemical properties. This role has been demonstrated to depend on initial soil characteristics, soil use or cropping practices. The aim of this work was to quantify and compare the effect traits of many earthworm species on aggregation, OM dynamics (microbial activities, OM mineralization) and structural stability. The hypothesis was that it is possible to establish more accurate functional groups than the ecomorphological groups.

An experimental approach was set up to expose juvenile and adults of 6 earthworm species to 4 contrasted types of soil. Three types of land use were investigated (crop, meadow and grassland). Soils were incubated in the presence or absence of earthworms. This led to ~50 conditions (species x development stage x soil type x land use). Aggregate production was assessed after 7, 14 and 21 days of incubation. Water structural stability of aggregates was measured on air-dried casts. Four extracellular enzymatic activities and basal respiration rate were measured in re-humected casts.

Result idiosyncrasy did not permit to discretize earthworm species into functional groups of effect on soil functioning. The hypothesis was thus not verified. Reality seems to be complex. Casts production depended on species, soil type and land use. Cast stability was lower than initial soil stability in sandy soils and meadow/grassland but higher in cropped soils. Casts acted as sink or as source for C, but globally tended to limit C mineralization. Earthworms promote extracellular enzymatic activities in meadows in grassland soils and contrasted effects were recorded on cropped soils. In conclusion, today our knowledge does not allow us to typologize patterns of earthworm effects on soil functioning.

Keywords: soil aggregation, soil structural stability, SOM dynamics, functional traits

[P1.225]

Functional traits distribution as causal link between environmental pressure (local climate and cropping systems) and soil invertebrate abundance

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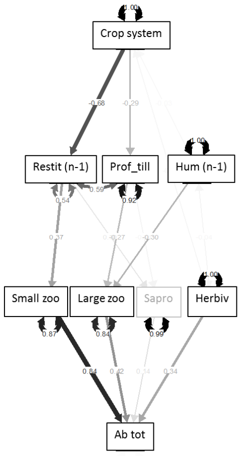
Soil invertebrates are key organisms for soil functioning and *in fine* to the provision of agroecosystem (dis)services. To be able to drive biodiversity to improve agricultural sustainability, two “hot topics” of soil invertebrates ecology need to be addressed: how can we model (i) invertebrate responses to immediate environment (induced by agricultural management)? and (ii) the effect of soil invertebrates on soil functioning and services? In the present work, we propose and test a path analysis involving a functional trait-based approach to address the first question. The conceptual model assumes that external pressures affect total abundance indirectly *via* their direct effects on functional groups.

Soil’ surface invertebrates were collected in LTER trial (SOERE ACBB) located in Picardy, France (49°52′44″N 3°00′27″E). It consisted in 24 plots (4 blocks) in which 6 cropping systems were tested. Systems differed in soil tillage, organic matter restitution level and the type of plant rotation (annual and perennial crop). Invertebrates were collected using pitfall traps, in spring, from 2011 to 2014. Dataset consisted in 120 observations (24 plots x 5 years). Functional groups derived from the BETSI database on soil invertebrate functional traits. SEMs were computed with ‘lavaan’ library for R.

Figure 1. final path model.



The initial model (Fig 1) was tested and re-specified to remove non-significant paths. The final model is shown (Fig 1b). Changes in total abundance are thus driven by changes in zoophages and herbivores, but not by saprophages. Dynamic of trophic groups distribution is mediated by agricultural practices (till deep and last year organic matter restitution) and a meteorological variable (last year mean atmospheric humidity). Path analysis therefore reveals the key role of functional groups as mediating the effects of external pressures on total abundance. Taking into account other sites will strengthen these conclusions.

Keywords: path analysis, LTER trial, agricultural sustainability

[P1.226]

SOFIA project, studying the effects of cropping systems on the temporal dynamics of relationships between soil biodiversity and ecosystem functions.

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SOFIA project aims to provide new insights on environmental stakes linked to crop system management, in the context of biodiversity conservation, climate changes and biogeochemical cycles understanding. SOFIA deals with the impact of agricultural practices on taxonomical and functional diversity of soil biota, and the functions soil biota participate to (GHG emission, C storage and nutrient availability for crop). SOFIA brings together 8 academic partners and 1 private partner, and relies on a LTER site “Agroécosystèmes, Cycles Biogéochimiques et Biodiversité” (SOERE ACBB) located at Estrées-Mons, Picardie, France (24 plots). This trial consists in series of experimental treatments varying on anthropogenic pressure according to: crop rotation, fertilisation, residue management or soil tillage. These treatments allow modulating the quantity, quality and localisation of resources (trophic or habitat) for soil biota. The effect of cropping systems on the link between soil biodiversity and soil functioning is assessed both through in-situ and ex-situ experiments.

The aim of the communication is to present the first results of the 5-year project (2010-2014). The dynamics of microorganisms (molecular approach) and micro-, meso- and macrofauna (morphological identification) will be presented and compared. Similarly, the 5-years dynamics of GHG emission, soil organic matter and crop yield will be presented with respect to the different treatments. Finally, we will present some relationships among soil functional diversity (microorganisms, micro-, meso- and macrofauna) and agroecosystem functioning. Results will allow us to assess the ecosystem services potentially provided by the different cropping systems (habitat for biodiversity, maintenance of soil physical quality and nutrient cycles).

Keywords: LTER trial, comprehensive sampling

[P1.227]

Orchard protection strategies influence both functional and taxonomic ground beetle diversity

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The functional trait-based approach provides a mechanistic description of environmental constraints on soil invertebrates to complement taxonomical approaches. Commercial orchards are precisely managed crops on which large amounts of pesticides are used. However, there has been little work on the impact of pest management strategies on the soil biota, which includes a lot of recognized beneficial animals. We aimed to provide a clear understanding of the response of the taxonomic and functional diversity of carabids to orchard management strategies over one apple-growing season.

Field sampling was carried out in the autumn of 2009 and spring and summer of 2010 in 15 commercial orchards. A total of 1073 animals were sampled using pitfall traps and 46 species were identified. The abundance of carabid communities was solely influenced by season. Their species richness was affected by orchard management, but only during the worst situation. Relative species distribution patterns are likely to be explained by environmental limitation, inter-specific competition, chance or a combination of these, mainly depending on management strategy. The differences in orchard management throughout the year acted as environmental filters by selecting individuals on the basis of their morphology and their ecological preferences.

Our results illustrate the value of the trait-based approach in depicting the effect of orchard management on the within-year dynamics of ground beetles, when combined with taxonomic approaches.

Keywords: pest management, seasonal dynamics, functional trait-based approach

[P1.228]

Do soil fungi actively decomposing plant litter respond to global climate changes?

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Plant litter degradation is a key process which controls not only the equilibrium between soil carbon storage and the CO2 release in the atmosphere, but also the release of essential soil nutrients trapped in dead plant biomass, such as organic forms of P and N. The primary degradation of lignocellulosic material in soil is believed to be carried out essentially by fungi.

Little is known about the effect of global changes, such as rainfall reduction, on the diversity of this group of soil organisms as well as on the enzymes they express. For example, in the context of global warming, the Mediterranean biome is predicted to be one of the most impacted and may experience a drastic 20% reduction in rainfall.

Metaproteomics is not thus far a high-throughput method to dissect soil processes (Schneider et al. 2012, Becher et al. 2013). Therefore, to assess the impact of drought on soil organic matter degradation, we applied a targeted-metatranscriptomic approach on soil samples from the experimental Quercus ilex forest of Puéchabon (southern France) where a long-term rain-exclusion experiment was initiated in 2003. For this study we sampled over two consecutive years (2010-11), in both spring and autumn, three rain exclusion plots (-33% water input) and their corresponding control plots. Three gene families encoding key enzymes active on the three major components of plant litter (cellulose, hemicellulose and lignin) as well as a constitutively-expressed gene (EF1-alpha) were amplified from reverse-transcribed soil RNA and subjected to high-throughput sequencing in order to assess the effects of simulated global changes on soil fungal communities actively degrading plant litter.

Keywords: climate changes, soil fungi, target metatranscriptomics, plant litter degradation

[P1.229]

Role of functional and structural biodiversity of fungi in the development of two volcanic soils

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Fungi have several key ecological functions associated with nutrients and carbon cycling processes in leaf litter and soil. Their environmental role come from their versatility in the production of a wide range of enzymes directly or indirectly involved in organic residues degradation, and from their ability to form a network of hyphae that transfer and redistribute nutrients and minerals over a wide spatial scale.

In this study we used a combination of experimental techniques to compare fungal communities developing in two leaf litter environments, characterised by the same rock substrate (volcanic soil), but with a different forest coverage (*Quercus* spp. and *Fagus sylvatica* L.). Culturable fungal strains developing on the decaying leaves of the two contrasting systems were isolated, cultured and identified by means of ITS barcoding. The functional diversity of these representative pools of fungal assemblages was analysed and compared by means of Phenotype Microarray technique.

Moreover, the decomposing leaves were examined with a variable pressure Scanning Electron Microscope instrument equipped with a detector for electron backscattered diffraction (BSD). The relationship between the potential activity showed by pure fungal isolates (*in vitro*) and their ecological role in the field was compared with the chemical-physical characteristics of the leaf litters, as investigated by means of Energy Dispersive X-ray Analysis (for elemental composition) and Thermal Analysis (for thermal degradability).

Statistically significant differences in the speed of substrate use between the compared fungal assemblages were documented. Moreover, redundancy in the degradation of N-related compounds indicated a potential interspecific competition especially at the beginning of substrates' exploitation. Elemental composition, thermal stability and some micro-morphological characteristics of the leaves' surface could have a role in fungal colonisation and decomposition processes, and thus explain some of the structural and functional differences observed between *Quercus* and *Fagus* fungal communities.

Keywords: fungi, litter, pedogenesis, function

[P1.230]

What are the effects of heavy metals on the stoichiometry of three detritivorous arthropod species?

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The emphasis in research on ecosystem functioning and services as well as on biodiversity has increased over the last years. Especially the influence of anthropogenic actions has been a major focus. In particular the input of chemicals to the environment and its effects on the ecosystem at different levels has been well studied. On the one hand, the input of chemicals can have positive effects on ecosystem services, on the other hand, the negative impacts of chemical inputs in the form of pollutants are observed. One of the most studied groups of pollutants are heavy metals. To date the negative effects assigned to the input of heavy metals comprise local declines in biodiversity of different taxa including animals and microbes, but also effects on the rate with which ecosystem processes are carried out.

The effects of pollutants on soil macro-invertebrates have to date been studied in terms of direct effects on survival, growth and reproduction with respect to concentration range of the metal. Nevertheless, data on metal mixtures and other effects such as body stoichiometry are less pronounced or even absent in literature. Therefore, in this study we investigated whether the body composition of three macro-invertebrate decomposers was altered when fed with diets differing in heavy metal concentrations. For this two isopod species and a diplopod species were exposed for 14 days to litter pellets differing in elemental composition. Animals' weight was measured every other day and faeces were collected. Afterwards, remainders of food and animals were collected, and stored dried at -20°C until analysis. In food, faeces and animals 12 elements were analysed. To assess changes in elemental concentrations between treatments we used PCA-analysis.

We hypothesized that increased metal concentrations have an effect on the uptake and elimination of not only the respective metal but also other key nutrients.

Keywords: Heavy metals, Ecological stoichiometry, Macro invertebrates, Food web

[P1.231]

Microbial community formation and resilience in plant roots.

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Though it is known that the root microbiota plays an important role for plant health and productivity, many questions still remain as to how these microbial communities are formed and what determines their composition. The questions that we set out to answer in our experiments were: What is the role of plant age on its ability to form associations in its roots? Do plants have a ‘window of opportunity’ for colonization by rhizosphere microbes? If so, when does it occur? We wanted to know whether older plants have more stable communities in their root system or if the community formed at an early age was resilient to the introduction of a new soil borne microbial community.

Our results show that plants of various ages were able to take up new microbial associations and that timing of inoculation had little effect on the composition of the root microbiota in mature plants. Instead, it was clear that the age of the plant had the strongest influence over community composition in the root microbiota. Plants harvested at the same age showed no significant differences in community composition, even if they had been inoculated at different times of their life cycles. These results suggest that it is possible to manipulate the composition of the root microbiota, even in older plants, and that plant roots are continuously responsive to changes in the soil around it.

Keywords: root microbiota, community resilience, rhizosphere

[P1.232]

Can deep-burrowing earthworms counteract the effects of extreme rainfall events on soil and plants?

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Introduction

Climate change projections by IPCC predict that some regions will experience rarer but more intense rainfall events. These may increase soil erosion and compaction, and hamper plant growth and seedling establishment. Earthworms that dig permanent vertical burrows in the soil (anecic species) often improve macroporosity and water infiltration, so they might counteract such effects. We present the first experimental test of this hypothesis.

Methods

We performed a field experiment using intact soil mesocosms sown with ryegrass, either inoculated with the widespread anecic earthworm *Lumbricus terrestris* or not. Over 8 months, we investigated whether *L. terrestris* modulated the response of soil and plants to two precipitation regimes: an ambient regime, without extreme rainfall events, and an altered regime, with longer intervals between rainfall events and two extreme events (>35 mm/h).

Results

The extreme rain events decreased aboveground plant biomass compared to the ambient rainfall regime, but only in the absence of *L. terrestris*. Soil moisture measurements with NDVI probes after the rain events and numbers of continuous macropores recorded at the end of the experiment suggest that the effect is, at least partly, due to a faster alleviation of waterlogging through burrow formation by the earthworms. More continuous burrows were found with extreme rainfall than in the ambient treatment, whereas earthworm survival did not differ, suggesting behavioural change in *L. terrestris*.

Discussion

We provide what may be the first direct experimental evidence that the presence of keystone soil organisms such as deep-burrowing earthworms has the potential to modulate the effects of extreme rainfall events on soil and plants. As some of the most dramatic effects of climate change may occur through pulse events rather than modifications in average trends, the role of earthworms and other soil fauna groups in mediating these changes should be a topic of future investigations.

Keywords: Earthworm, Climate change, Ecosystem stability, Keystone species

[P1.233]

Structural and functional microbial biodiversity along two soil profiles developed on the same bedrock but under contrasting plant covers

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Fungal and bacterial biodiversity play a key role in soil formation, but at the same time the underlying parent material and the dominant plant cover can model the structure of microbial communities. To better understand the selective pressure of either tree crown cover or parent material on soil differentiation, a Silandic Melanic Andosol and a Typic Melanudand, from a volcanic apparatus located in central Italy, were investigated using the pedologic horizons as sampling units. The two soil systems developed under oak and beech, respectively, within the same climate and pedo-environment. The main chemical parameters as well as physical structure of the two soils were compared. Moreover, diversity and abundance of the dominant groups of microorganisms were analysed through the T-RFLP and qPCR techniques. Respiration, denitrification and gross nitrification rates of the two profiles were measured by means of the Barometric Process Separation (BaPS), on undisturbed soil cores. In the soil under oak coverage a significant difference between the A1 and A2 horizons occurred with a sharp decrease of bacteria and the fast disappearance of archea along the profile going to the deeper horizons. The structure of the microbial community suggested the establishment of an efficient ecological succession, rich in guilds capable of ensuring the degradation of oak plant material that, therefore, "enter" the organic horizon (A2) already largely decomposed. In contrast, in the soil under beech, it was observed a less marked change of microbiological diversity through the profile. Interestingly the fungi to bacteria ratio increased significantly with soil depth, showing a dominance of fungi in the deeper horizons, possibly related to the plant’s roots. Microbial assemblages, functional guilds and resource quality in the organic horizons appeared differently influenced by the two opposing forces: biological (plant cover, fungi and bacteria) and chemical (the volcanic bedrock), that act downwards and upwards respectively.

Keywords: Andosols, Microbial Biodiversity, Pedodiversity, Plant-cover

[P1.234]

Management strategies to manipulate soil biodiversity in relation to the ecosystem service disease suppressiveness

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There is an urgent need to develop sustainable management strategies to increase disease suppressiveness. Ultimately this should be investigated with long-term measurements of biological and chemical parameters and their final impact on crop yield. The present study focusses on eight treatments (compost, chitin, marigold, grass-clover, biofumigation, anearobic soil disinfestation, a physical control method and a combination of marigold, compost and chitin) and two reference treatments (a chemical control with 300 L/ha Metam sodium and un untreated control). These 10 treatments were studied for their effects in conventional and organic farming systems during 8 years. The present study did demonstrate that in comparison to chemical control, additions of chitin, anaerobic soil disinfestation and marigold are excellent alternatives to improve disease suppressiveness and that some of these treatments performed better in the organic farming systems. Grass-clover, biofumigation, Cultivit and compost are not effective alternatives for chemical control yet and further development is needed. All treatments caused a yield increase in comparison with the control. The biggest increases of more than 60 % were found for the treatments with chitin. Furthermore it was demonstrated that these yield increases were probably less influenced by changes in chemical soil properties, but the consequence of changes in the soil biota. Furthermore it has been demonstrated that most of these treatments could already be implemented in arable crop rotations throughout the world.

Keywords: disease suppressiveness, soil biodiversity, management strategies

[P1.235]

AMF communities distribution in semiarid areas: influence of soil characteristics

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Arbuscular mycorrhizal fungi (AMF) are an important soil microbial group that affects multiple ecosystems functions and processes, including nutrient cycling, plant productivity and competition, and plant diversity. We carried out a study where we investigate AMF communities in the roots and the rhizosphere of *Brachypodium retusum* (pers.) Beauv., a common plant species of great ecological importance that grows in different type of soils in semiarid Mediterranean areas. We hypothesized that if both factors, host plant species and climatic conditions, cannot influence the differences in AMF communities in the roots and in the rhizosphere of *Brachypodium retusum*, variances in communities distribution, AMF richness and diversity could be due to soil characteristics. Hence we study the relationships between physical, chemical and biological soil characteristics and AMF community composition found in the roots and in the rhizospheres. We recorded forty-nine AMF operational taxonomical units (OTUs). While AMF populations in plant roots were similar, by contrast, each soil type presented a different AMF community composition and thus, can be characterized by its own AMF communities. A combination among some of the soil parameters could define the AMF species present in the roots and the rhizosphere of *B. retusum*. It was the case for some soil properties related with biological activity, such as enzyme activities, carbohydrates and aggregate stability which explained the variation in the AMF communities. In conclusion, soil characteristics can be decisive in the assembling of the AMF communities, managing the diversity and composition of these communities.

Keywords: Arbuscular mycorrhizal fungi, Diversity, Communities, Soil properties

[P1.236]

Efforts to increase crop yield on smallholder African farms are synergistic with the functional capacity of soil microbial communities

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Increases in mineral fertilizer use have helped more than double global crop yields over fifty years. Excess fertilizer use is known to cause environmental damage, but less is known about how fertilization affects the ecosystem processes that sustain agriculture, such as soil nutrient cycling. Soil microbes are key drivers of such processes, yet understanding of the effect of efforts to increase yields on microbial functioning is limited. This knowledge is especially sparse for soil processes in tropical smallholder agriculture, despite supporting 900 million of the world's poorest people. We studied the effect of an effort to increase yields in western Kenya on soil microbial communities and their potential to perform processes key to agricultural sustainability. Consistent with theory and observations in temperate systems, we found that soil bacterial diversity decreased with fertilization, with a community shift towards taxa that thrive in high-resource conditions. These taxonomic responses did not, however, correspond with changes in microbial functional capacity—measured as abundance of functional genes related to nutrient cycling and ability to catabolize carbon substrates. Functional capacity was instead highest, along with yields, when fertilizers were combined, over longer time scales, with agroforestry practices that add organic matter to soil. Our findings suggest an important synergy between increasing yields on smallholder farms and maintaining the long-term functional capacity of the soil microbiota.

Keywords: microbial diversity, agriculture, functional diversity

[P1.237]

Tree species and plantation age shape the structure, biomass, and diversity of soil microbial communities in a mining restoration site

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Soil microbial community characterization is increasingly being used to determine the responses of soils to stress and disturbance, as well as an indicator ecosystem health. However, there is little experimental evidence to indicate that predictable patterns in microbial community structure occur during ecosystem restoration. In order to determine the effect of landscape restoration on soil microbial communities, we investigated the soil microbial composition of the Kunyang phosphate mine, in Southwest China. Using PLFA analyses, we examined the changes in the soil microbial community structures, using three chronosequences (2, 23, and 30 years), for three different plantations, *viz.: Eucalyptus globulus*; *Pinus yunnanensis*; *Cupressus torulosa*. This study demonstrated that the mining process resulted in a significant decline of soil microbial diversity and biomass. However, the diversity and biomass of the soil communities improved across all restoration treatments and with time. The *Cupressus* plantations, for the first two age groups, showed the greatest improvement in soil microbial biomass, whereas, by 30 years, the biomass was similar for the different plantations. Initially, at 2 years, there were no significant differences in the soil microbial composition between plantations, but by 20 years the *Cupressus* plantation differed significantly from the other plantation types. However, after 30 years the *Eucalyptus* plantation was significantly different in soil microbial community composition to the *Cupressus* and *Pinus* plantations. Changes in soil microbial community characteristics were significantly related litter thickness, and total and available K concentrations. These findings suggest that soil microbial community dynamics respond differently to different plant species and plantation ages, and can be conceptualized as providing an integrated assessment of the mining restoration process.

Keywords: soil microbial community, restoration, chronosequence, plantation type

[P1.238]

Biodynamic management practices improve soil structural and functional diversity of vineyard soils in central Italy - Preliminary results

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In recent years, the biodynamic viticulture has received increasing attention. In addition to the common tools of organic agriculture, it makes use of specialized preparations in compost and in field sprays, which are added in very low doses to the composting organic material. Biodynamic preparations are supposed to stimulate the processes of nutrient cycling and energy flow, hasten decomposition and improve soil and crop quality, without adding nutrients.

The present study aimed to compare soil quality in biodynamically and conventionally managed vineyards. In both management systems, the cultivated varieties were: Passerina del Frusinate (*Vitis vinifera*, L.; white grapes), and Cesanese del Piglio (*Vitis vinifera*, L.; red grapes). Biodynamic vines (seven years old converted) were Demeter certified.

Soils were sampled at Piglio (FR; (41°49'0" N latitude - 13°07'60" E longitude)) on March 2013 at 0-20 cm depth in triplicate. Total organic C, total N, pH, inorganic N (NO_3 and NH_4), soluble P, microbial biomass C and N, basal respiration, eight enzyme activities, ester linked fatty acids profiles (EL-FAME), CLPP-MicroResp were determined. Shannon diversity index (H') was calculated using enzyme activities, MicroResp and EL-FAME data.

All chemical and biochemical indicators determined were significantly and positively influenced by the biodynamic treatment, some of these effects being more evident for white wine variety than for red wine variety (TOC, NH_4, H' for enzymes).

In particular, biodynamic management improved soil organic matter in terms of total C and N, reduced nitrates and soluble phosphorus, increased microbial biomass content both as bacteria and fungi. Enzyme activities, microbial basal respiration and CLPP-MicroResp were increased indicating higher metabolic activities and capabilities to use different soil C sources, even the most recalcitrant ones (phenolics). EL-FAME data reported higher content of protozoa, a decreased ratio of Gram+ to Gram- bacteria and reduced stress indices (S/M and cy/pre) which indicate equilibrium conditions for soil microorganisms under biodynamic treatment.

Keywords: stress indices, biodynamic management, soil quality, soil microorganisms

[P1.239]

Ecological response of soil macrofaunal community in a fire disturbed forest gradient

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Ecological resilience of species communities and restoration of key ecosystem functions following disturbance has been a thrust area of inquiry in ecological research in recent times. The aim of the present study is to assess the long term impact of fire on soil invertebrate community structure and maintenance of ecosystem functions of a forest detritus system exposed to recurrent fire. It also explores the linkage between forest fire, invertebrate community structure and ecosystem processes.

The study site was located in Bankura district of West Bengal, India, a Tropical Dry Deciduous forest undergoing recurrent forest fire. Forest patches at different time lag after fire were categorized in a gradient. Soil macrofauna was sampled according to the TSBF (Tropical Soil Biological and Fertility) methodology while soil chemical parameters were determined according to standard protocols.

The overall effects of fire on ecosystems are complex, ranging from the reduction or elimination of aboveground biomass to impacts on belowground physical, chemical and microbial mediated processes. The total number of orders per sample and the population density of Annelida, Chilopoda, Diplopoda, Arachnida and some Hexapoda were lower under burnt forest patches compared to the sites with highest forest history throughout the study period. Ants, termites, and spiders were most affected by the forest fire. Species richness also increased as biomass increased from rescent burned site to intermediate but it dipped at the site where maximum biomass was recorded in the oldest site.

Indicator species of each habitat type or group of habitats were determined using the Indicator Value (IndVal) method. Among the 5 species examined in Isoptera, only 1 showed IndVal ≥25% whereas among 47 species examined in Hymenoptera, 5 showed IndVal ≥25% and showed significant association with Organic Matter, pH and Phosphorous in soil.

Keywords: Macrofauna, Forest fire, Soil quality, Indicator value

[P1.240]

MidDRIFTS-based partial least square regression analysis allows predicting microbial biomass, enzyme activities and 16S rRNA gene abundance in soils of temperate grasslands

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There is an increasing demand for predictive, but reliable soil ecological data for environmental monitoring and soil quality assessment at different spatial scales. However, spatial analyses of soil ecological properties are often hampered by the necessity for large numbers of samples based on time consuming and costly analytical procedures. Spectroscopic approaches are a promising alternative to measure large sample sets requiring minimal sample preparation and can even replace conventional methods. The objective of this study was to underpin the capability of diffuse reflectance Fourier transform mid-infrared spectroscopy (midDRIFTS)-based partial least squares regression (PLSR) analyses to accurately predict soil microbiological properties across six temperate grassland ecosystems differing in their land-use intensity; three sites of low land-use intensity (low LUI) and three fertilized mown meadows (high LUI). Additionally, the potential of midDRIFTS-PLSR analyses for spatial studies between soils of contrasting grassland ecosystems was evaluated. 304 samples were subjected to midDRIFTS-PLSR-based predictions of soil microbial biomass, activities of beta-D-glucosidase, xylosidase and urease, as well as bacterial abundance based on 16S rRNA gene quantification. Accuracies of midDRIFTS-PLSR-based predictions across both LUI were, on basis of the residual prediction deviation (RPD), ‘acceptable’ for all soil microbiological properties, in particular soil microbial biomass (coefficient of determination (R^2) = 0.92; RPD = 3.55), urease (0.91; 3.42) and beta-D-glucosidase (0.89; 3.01). Predictions of ‘moderately successful’ accuracy were developed for 16S rRNA gene copies (0.88; 2.93) and xylosidase (0.84; 2.55). Spatial midDRIFTS-PLSR-based predictions between grassland ecosystems were ‘acceptable’ for soil microbial biomass, while the other studied microbiological properties revealed only ‘moderately successful’ predictions. The potential of midDRIFTS-PLSR to predict a range of soil microbiological properties including molecular data with ‘acceptable’ accuracies across the two investigated grassland ecosystems with contrasting land-use intensities was substantiated. However, the prevailing ‘moderately successful’ prediction accuracies between grassland ecosystems were probably due to the dependence on land use-specific data sets for calibration and validation. For prospective tracking and monitoring of microbial properties via midDRIFTS-PLSR-based approaches, predictions of soil microbiological properties considering particularly, but not yet ‘acceptable’ molecular data will greatly advance the understanding on abundance and functional dynamics of soil microbial communities across spatial and temporal scales of contrasting ecosystems.

Keywords: Grassland ecosystems, MidDRIFTS-PLSR analysis, Prediction of microbiological properties, Spatial predictions

[P1.241]

Are hedgerows and grassy margins of arable fields biodiversity refuges for soil fungi?

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Continuous arable cultivation has depleted important functional components of soil biodiversity and degraded soil structure, and now requires large chemical and energy inputs to sustain yields. There is increasing need to manage soils for more sustainable crop production and to meet the challenges of variable weather conditions. We hypothesised that hedgerows and grassy field margins act as biodiversity refuges for microorganisms depleted by conventional cultivation and chemical inputs, and if so, might be important in restoration of soil biodiversity and functioning under more sympathetic management.

We sampled 10 cm deep soil monoliths along transects from under hedges, in uncultivated grassy margins and 2 m into arable fields, at the University of Leeds farm, run as a commercial, intensive arable unit in England. Six fields growing winter wheat in 2012 were chosen based on similar soil type and previous year crop (winter wheat, vining peas or oil seed rape). Soil fungi were studied by pyrosequencing of the ITS1 region and multivariate statistical analyses.

Fungal communities differed strongly between fields and cropping history, the strongest pairwise difference being for fields that grew vining peas and oilseed rape in 2011. Taxa contributing most to this difference were relatives of plant pathogens like the cereal disease *Didymella exitialis* and *Verticillium* or *Fusarium* spp. Relatives of the biocontrol agent *Simplicillium lamellicola* were more abundant after vining peas were grown. Pairwise comparisons between hedge and field samples displayed a small but significant difference. Fungal species richness was highest in the field, and diversity was slightly lower under hedges, but Shannon diversity index showed no consistent differences between hedge, margin and field samples.

Contrary to our hypothesis, we found that hedgerows do not harbour higher diversity in the below ground fungal communities than the arable fields, and we detected strong legacy effects of the previous year's crop.

Keywords: fungal diversity, cropping, next generation sequencing, pathogens

[P1.242]

Internal spatial and temporal heterogeneity of soil microbial communities in spruce swamp forest (Czech Republic)

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We studied the internal heterogeneity of soil microbial communities of spruce swamp forest (SSF) in relation to soil functioning. In SSF, spruce, peat mosses, and cottongrass are responsible for peat accumulation. The patchy co-dominants, increase internal spatial variability and affect the functioning of the whole ecosystem, in particular switch from aerobic to anaerobic processes. We compared sites without vascular plants (*Sphagnum* sp., SP) with sites with co-dominating cottongrass (*Eriophorum vaginatum*, EV) and blueberry (*Vaccinium myrtillus*, VM) on three localities. Additionally, anoxic horizon of blueberry (A-VM) site has been compared to upper elevated horizon (O-VM). To cover seasonal variability, 3 seasons has been sampled (spring, summer, autumn). We employed qPCR analysis and next-generation sequencing to indicate the dynamics in microbial functional guilds, bacteria-to-fungi ratio, and microbial communities across seasons and localities. The abundance of bacteria was significantly affected by locality, plants and soil horizon, while no effect was found for season. In contrary, type II methanotrophs (MOB) dominated in spring and decreased in summer. Bacterial community was similar in all three sites, being dominated by Proteobacteria, Acidobacteria, and Verrucomicrobia. O-VM was dominated by Acidobacteria and MOB, while A-VM was enriched by δ-Proteobacteria, Clostridia, Verrucomicrobia, Methanomicrobia, and Thermoplasmata. Methanogens were also affected by plants with the highest abundance in A-VM and EV. Relative contribution of fungi was significantly higher in O-VM than in EV and SP, being the highest in autumn. Soil fungal communities were affected by co-dominant plant, soil horizon, and interaction of locality and plant. VM affected the community structure in significant way, in both horizons, while EP did not show the clear trend. In conclusion, the co-dominating vascular plant significantly affects the functioning of the ecosystem and soil microbial community composition, including the abundance of microbial functional guilds. All these effects are more pronounced in VM than in EV sites.

Keywords: spruce swamp forest, bacteria, archaea, fungi

[P1.243]

Cadaver effects on soil biodiversity- results from two field experiments

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Decomposing cadavers release considerable amounts of nutrients and water into the soil and have a clear impact on the abundance and diversity of soil organisms and on soil functions. Understanding these impacts is of interest both for general soil ecology and for forensic science as soil organisms may provide critical forensic information such as the estimation of the post-mortem interval.

We conducted two experiments using decomposing pig (*Sus scrofa*) cadavers in forests near Neuchâtel, Switzerland, in 2009/10 (experiment 1) and 2013/14 (experiment 2). We analysed soil samples taken beneath the cadavers and in control plots over time.

In the first experiment we investigated the response of testate amoebae to three decomposing pig cadavers and compared them to fake pigs (bags filled with soil) and controls. The pig treatment significantly impacted the testate amoebae community: after 22 and 33 days no living testate amoebae were found. The community then started to recover but even after 10 months the recovery was not complete.

In the second experiment we analysed nematode abundance and community structure beneath five pig cadavers placed directly on the ground and five hanging pigs (1m aboveground) and again compared them to fake pigs and controls. Nematode abundance was clearly affected by the pig cadavers and increased massively two weeks after the placing of the cadavers. From over 20 nematode families present at the beginning of the experiment the community was clearly dominated by a single one, Rhabditidae (83%) two weeks later. After five weeks first Neodiplogasteridae and then Diplogasteridae appeared in increasing abundances. Both families only occurred in the cadaver impacted samples and were absent from the controls.

These results illustrate how decomposing cadavers represent ephemeral disturbance events for the soil environment, as well as the starting point of a succession process usable for estimating the time since death.

Keywords: cadaver decomposition, temporal patterns, testate amoebae, nematodes

[P1.244]

Short-term influence of compost on soil macrofauna diversity and abundance in nutrient deficient soils of Kakamega county, Kenya (submitted to Plant and Soil Journal)

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A study was conducted over three seasons to evaluate potential of six organic biomasses (bagasse, cow manure, filtermud, maize stover, sugarcane straw and *Tithonia diversifolia*) for compost production and their influence on soil fauna diversity. Treatments comprised of the six composts, commercial fertilizer and no-input control, laid out in randomized complete block design in four replicates. Soil macrofauna were collected using soil monolith method. Data obtained were subjected to analysis of variance (ANOVA) using GenStat whereas differences were evaluated using Fisher's least significant difference (LSD). Correlation between macrofauna and soil chemical properties was done using CANOCO 3.1. The ANOVA showed significantly higher N and P on filtermud (10.0 g N kg^{-1} and 979 mg P kg^{-1}) and *T. diversifolia* (9.6 g N kg^{-1} and 614 mg P kg^{-1}) composts. Generally, amending soils with composts increased soils' C, N and P by 90%, 29% and 20%, respectively, while fertilizer treated plots recorded 42%, 4% and 110% increase in C, N and P, respectively. Control plots recorded 25% increase in C, but 15% and 50% decline in N and P, respectively. Soil macrofauna responded positively to addition of composts. Isopterans, Oligochaeta and Hymenopterans dominated the sites constituting 44%, 26% and 17%, respectively of all the macrofauna. Relationships between macrofauna and soil chemical properties were positively significant. Results of this study demonstrate the potential of composts in increasing soil biodiversity and therefore generally improving soil productivity.

Keywords: filtermud compost, soil macrofauna, soil organic carbon, soil biodiversity

[P1.245]

Pathogen invasion disrupts host rhizosphere microbiome

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Close relationships between plant rhizosphere microbiome and plant health have been widely discussed but only insufficiently evidenced. Purpose of present study is to identify commensal microbiome, illustrate commensal disruptions, specify organisms for maintaining health status, and answer the question why some plants were healthy but others were diseased in the same field. Rhizosphere soil samples were collected in time-series from healthy and diseased tomato plants grown in a prolonged monoculture field. The bacterial communities were characterized by high-throughput sequencing approach and were analyzed using statistical methods as well as network inference tool. Our data demonstrated that *R. solanacearum* outgrew the indigenous bacteria, dramatically increased its abundance, reduced microbiota diversity, disrupted the commensal microbiota, and successfully invaded host plants in diseased soils. *R. solanacearum* could behave like these in diseased soils because it was not effectively inhibited by other organisms. It stayed calm in healthy soils because it was effectively inhibited by a high-degree node belonging to *Bacteroidetes*, which in turn was thus considered as the keystone organism determining plant health status. Soil properties did not directly affect *R. solanacearum*, as the networks inferred. The importance of *Actinobacteria* in healthy soils and unclassified bacteria in diseased soils was infered but could not be specified and nor related to plant health status. This study provided evidences demonstrating close relationships between rhizosphere microbiome and plant health. The usefulness of co-occurring network inference in studying soil microbial ecology was highlighted.

Keywords: Ralstonia solanacearum, diversity, bacterial community, network

[P1.246]

The effect of native revegetation on soil microbial diversity in south-western Australia

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Many regions of Australia have been cleared of native vegetation for agriculture, contributing to ecosystem degradation. Broad-scale restoration efforts are currently underway in many areas. Given the central ecological role of soil microbes, understanding their response to such revegetation efforts is critical. As part of the Biomes of Australian Soil Environments (BASE) project, the response of soil microbial diversity to revegetation was studied within the Gondwana Link in south-western Australia. Gondwana Link is a landscape-scale conservation project that aims to reconnect fragmented ecosystems to protect, restore and maintain fundamental ecological processes that underpin these ecosystems.

Soils were collected from six sites within a 300 km^2 area. At each site, surface (0-10 cm) and subsurface (20-30 cm) soils were sampled from three adjacent plots of uncleared remnant native vegetation, agricultural land, and land that had been revegetated 5-10 years earlier. Soil edaphic properties were determined and Illumina Miseq amplicon sequencing of soil bacterial 16S rRNA, fungal ITS and eukaryotic 18S rRNA genes was performed.

Site-specific responses to agricultural land use and revegetation were observed for each studied community, which were unrelated to time since revegetation or the revegetation method. Fungal and eukaryotic communities, but not the bacterial community, were structured by land use across all sites. All communities were structured by depth in the soil profile. Soil type (clay, sandy gravel, loam) affected the structure of the bacterial but not the fungal community. Alpha diversity (Chao1 richness estimate) was unaffected by land use but changed with depth in the profile, with significantly lower diversity of bacteria, fungi and eukaryotes in subsurface versus surface soils.

Specific responses of several functional groups (e.g. rhizobia, mycorrhizae) to revegetation and drivers of the community structures will be presented, as well as potential implications for ongoing broad-scale revegetation efforts across Australia.

Keywords: revegetation, bacteria, fungi, eukaryotes

[P1.247]

Responses of soil fungal communities to different forest managements

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Soil fungi play a major role in ecological and biogeochemical processes within forest ecosystems. Fungi have developed a close relationship with plants, which provide c substrates on which the fungi survive. This C is provided through symbiotic relationships, or as labile compounds leaked form roots or via litterfall. Forest management practices relating to timber and litterfall harvesting disturb the quantity and quality of these carbon resources, thus leading to changes in the soil fungal communities. In order to evaluate these changes, we set up long-term plant manipulation experiments in an old growth, subtropical forest. We employed root-trenching techniques to simulate timber harvest and floor-mass removal, simulating litter-fall harvest. Four years after treatment, fungal communities were characterized using DNA-based profiles alongside clone sequencing methods. Though no significant difference was found in the soil characteristics, the DNA profiles of the soil fungal communities indicated that both floor-mass removal and root trenching exerted a significant control on fungal communities. In addition, both root trenching and floor-mass removal increased the fungal diversity. In the case of community analysis, ectomycorrhizal fungi were the most dominant fungi, and their relative abundance significantly decreased in both treatments. As the most important economic mushroom, the ectomycorrhizal fungi *Russula* had a loss of up to 80% of the abundance in the treatment plots. With the decline of ectomycorrhizal fungi, the floor-mass removal plots were favored by certain dominant root associated fungal species, while root trenching presented numerous, rare fungal species, belonging to saprophytic opportunists. The results suggested that forest management practices could result in negative impacts on forest ecosystem services, by lowering forest production, and nutrient cycling.

Keywords: Fungal communities, soil, Forest management, DGGE

[P1.248]

Risk assessment of insect conservation and commercialization: phorectic mites associated with dung beetles

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For the conservation of insect species, fundamental understanding of its biology and ecology is crucial to develop the program more effective. The same is true for the commercialization of insects. Among many interaction, phoresy is one of the dispersal mechanisms of wingless microarthropods such as mites. Mites associated with two scarabaed beetles, *Copris ochus* and *C. tripartitus* (Coleoptera: Scarabaelidae) were collected. from Holoce Ecosystem Conservation Research Institution, Gangwon-do. Four unrecorded species of *Eviphis hastatellus* Berlese, 1910 (Eviphididae), *Holostaspella scatophila* Takaku, 1994 (Macrochelidae), *Macrocheles japonicus* Evans & Hyatt, 1963 (Macrochelidae), *Pachylaelaps siculus* Berlese, 1921 (Pachylaelapidae) were recorded from Korea for the first time. Also, *Parasitus consanguineus* Oudemans & Voigts (Parasitidae) was originally recorded from the northern part of Korea by Oudemans and Voigts in 1904, but since then no one has recorded. This is the second observation of this species over 100 years since the first description in Korea. Description of this species is presented for comparison to the original description. Further discussion explored the relationship between the mites and dung beetles, and possible implication for the conservation of the endangered species

Keywords: conservation, phoresy, beetle, mite

[P1.249]

The effects of effluent irrigation on soil microarthropod communities in a short rotation coppice willow system

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Introduction

Disposal of by-products from wastewater treatment processes, such as sewage effluent and sludge, presents a major challenge worldwide. Commonly channelled into water bodies, environmental concerns of eutrophication has increased pressure for land disposal of municipal wastewaters. An attractive bioremediation alternative to food-crop irrigation, which carries contamination risks, is the disposal of sewage by-products within silvicultural systems such as short rotation coppice willow (SRCW). Long-term irrigation with sewage effluent is associated with changes to the chemical properties of soil, including increased concentrations of essential nutrients and heavy metals, as well as higher organic matter content and a lower pH, which in turn, are associated with changes in microarthropod communities. This study is the first to quantify the effects of sewage effluent irrigation on the soil microarthropod community within a SRCW system.

Methods

Five experimental blocks consisting of four effluent treatment plots and a control were randomly positioned within a SRCW plantation (fig.1). Microarthropods were sampled with 10cm soil cores and extracted using Tulgren funnels. Soil water content and pH where also measured.

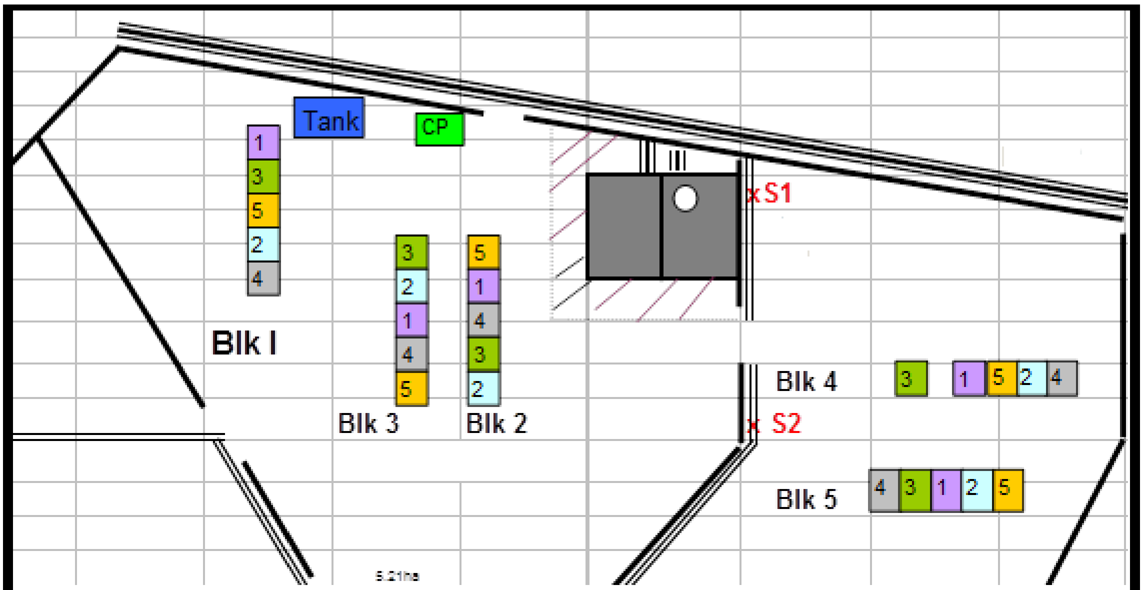

Figure 1: Schematic of experimental blocks (Blk 1, 2,3,4&5) and treatment plots, within a SRCW plantation. Treatment plots 1 and 3 received 0.8m^3 and treatment plots 2 and 4 received 1.6m^3 of effluent; control plot 5 received no treatment.

Results

The treatments had a significant effect on the micro-arthropod communities (*p*<0.001) and accounted for 20% of variation within the data after controlling for spatial effects (fig.2), water content and pH had no effect. Collembolan species *Desoria violacea* & *Sminthurinus concolor* were the most abundant microathropods and *Megalothorax minimus* and the predatory mite *Lysigamasus armatus* showed the greatest response to the treatments.

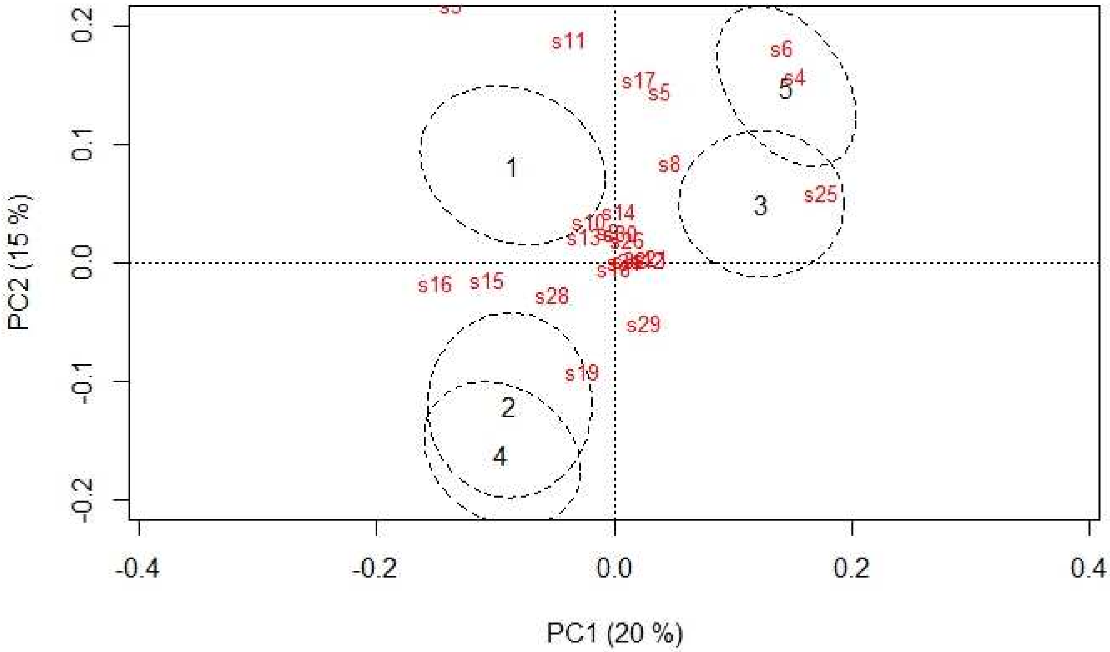

Figure 2: Ordination plot of first two axis of RDA, after the species matrix transformed to reflect Hellinger distance. Ellipsoids represent 95% confidence for treatments & species are represented by numbers.

Discussion

This study indicates that effluent irrigation in SRCW systems can cause significant changes to microarthropod communities. Soil microarthropods play important roles in the agro-ecosystem and changes to these communities could have both environmental and economic impacts. We advocate that the precautionary principal should be followed and widespread, long-term use of SRCW for effluent disposal should not be rolled out until further research is carried out.

Keywords: Willow, Agriculture, Microarthropod, Effluent

[P1.250]

Role of microbial diversity in mitigating the emissions of the greenhouse gas n2o in relation to agricultural practices

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Agriculture is the main source of terrestrial N_2O emissions. This gas is the main depleting substance of the ozone layer and contributes to about 6% of total global warming. The unique known biological process able to convert N_2O is its reduction to N_2 by organisms possessing the *nosZ* gene, which encodes the nitrous oxide reductase. A recent publication (Jones *et al.*, Nature Climate Change, in press) showed that the abundance and the diversity of a recently discovered clade of *nosZ*_carrying microorganisms are important players of soil N_2O sink capacities. Therefore, enhancing the comprehension of the role of the abundance and the diversity of microbial populations in N_2O emissions and looking for agricultural practices that could favour microbial populations able to reduce N_2O into N_2 is key in determining N_2O emissions mitigation strategies.

In this study, two experimental sites comprising nine management strategies that differ in crop rotation, tillage depth, fertilization, straw incorporation and cover crop were chosen. To characterize the activity of soil microbial communities, potential denitrification rates and N_2O/N_2O+N_2 emission ratios were measured. The abundance of the different microbial guilds involved in N-cycling was quantified by real-time PCR, and the diversity of the *nosZ* gene was determined by 454 pyrosequencing.

Our results suggest that the agricultural practices we tested were not sufficient to modify deeply the abundance and the diversity of denitrifying microbial communities related to the N_2O emissions. However, the diversity and the abundance of these guilds were strongly dependent on the experimental site and responded to soil physico-chemical parameters (e.g.: pH, loam). We also confirmed the link between the diversity of *nosZ* microorganisms and the soil N_2O sink capacity (Fig.1), which emphasize the importance of microbial diversity for ecosystem functioning.

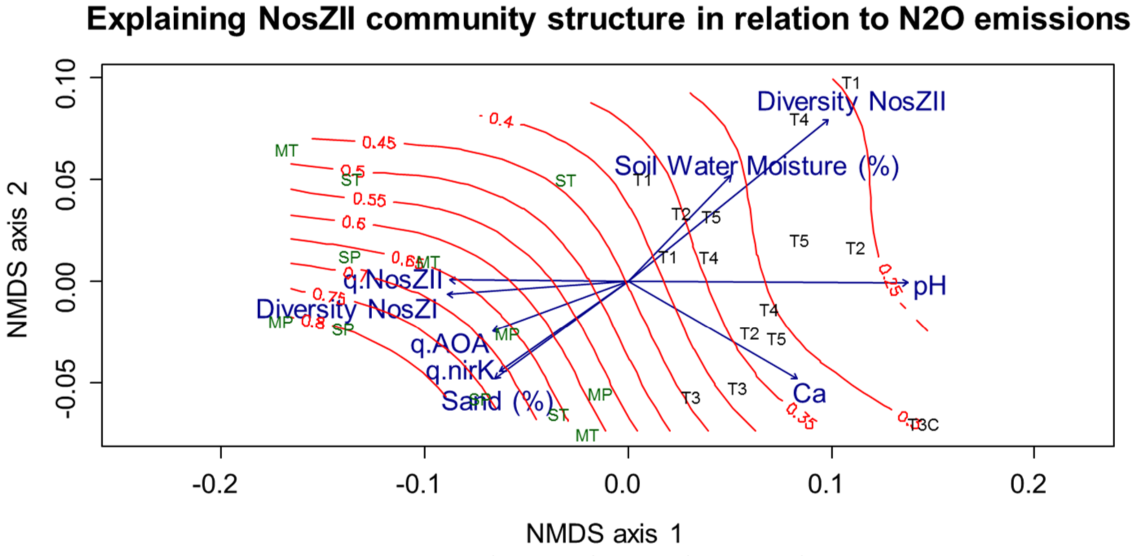
Explaining NosZII community structure in relation to N2O emissions

Fig1. NMDS ordination of weighted unifrac distance matrix (stress: 0.1094) at two sites (green and black). Red curves represent N2O emissions ratio gradient (higher ratio indicates higher N2O emissions). Significant explanatory variables represented as vectors in blue (p<0,1): diversity of NosZII (simpson diversity index for NosZII), diversity of NosZI (simpson diversity index for NosZI), Ca (calcium g/kg of soil), q.AOA, q.nirK and q.NosZII represent the quantification of ammonia oxidizing archaea, nitrite reductase bacteria nirK, and nitrous oxide reductase NosZII respectively by nbc/g soil. Sand and soil water moisture are expressed in percentage.

Keywords: N2O emissions, Denitrification, Agroecology, Functional Diversity

[P1.251]

Tree species effects on nitrogen cycling processes and functional communities in soil at a common garden experiment

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The understanding of how nitrogen (N) is cycled in forests is important for improving models of global biogeochemical cycles and potential climate change mitigation practices, as forests can serve as important sinks and sources of greenhouse gases. To determine the role of tree species identity on N cycling we used two sites within a common garden experimental forest on Vancouver Island, British Columbia, Canada. We used the ^{15}N pool dilution method to ascertain gross and net rates of N mineralization and nitrification in soils taken from pure stands of four tree species (western red cedar, western hemlock, Douglas-fir, and Sitka spruce). We also measured soil microbial biomass carbon (C) and N to determine if the microbial pool was storing the ^{15}N by the end of the pool-dilution experiment. We used qPCR to determine the abundance of functional genes associated with nitrification (AOA *amoA*, AOB *amoA*) and denitrification (*nirS*, *nirK*) in the soil communities. Tree species identity influenced soil communities among species grown on the same site for AOA *amoA* and *nirS,* but not for AOB *amoA and nirK*. These results identify that tree species foster different abundances of nitrification and denitrification functional groups, and the pools and fluxes of N those communities regulate. Site strongly influenced nitrifying bacterial communities with differences observed between the two sites and among the same tree species for AOA *amoA*, but not with AOB *amoA*. Denitrifying communities differed for *nirS* for cedar and spruce, but not for fir hemlock, where *nirK* did not differ among the tree species, or between the two sites. This is consistent with previous studies of N mineralization at our study sites, which suggested that microclimate features may be responsible for the strong differences in mineralization rates between sites.

Keywords: nitrogen cycling, common garden experiment, functional genetics, tree species effects

[P1.252]

Bacterial communities associated with natural and commercially grown rooibos (*Aspalathus linearis*) plants

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The fynbos biome in the Cape floristic region of South Africa is well known for its high floral diversity. Some of the plant species are harvested for commercial use e.g. *Aspalathus linaeris,* which is used to make an herbal tea called Rooibos. Due to increased demand large commercial farms have been established were *A. linearis* is planted in monoculture. This study aimed to characterise the bacterial diversity associated with natural and commercially grown *A. linearis*. Rhizosphere soil, root samples and bulk soil were collected from natural and commercial rooibos sites located on two different farms. Bacterial communities were characterised using a molecular approach based on the isolation of total genomic DNA and next generation sequencing technology using the Ion Torrent (PGM). The hypervariable region V4-V5 of the 16S rRNA were amplified and sequenced. Sequence reads were processed using MOTHUR software and statistical analyses were performed using R. Results indicated that the microbial communities in the bulk and rhizosphere soils were significantly different. Higher bacterial diversity was observed in the bulk soils than in the rhizosphere soils. This is mainly due to the influence of plant roots in the rhizosphere soil which selects for certain bacterial species, resulting in a less diverse but greater in size bacterial community. Taxonomic analysis indicated that bulk soils were dominated by the order Actinomycetales, whereas rhizosphere soils showed a higher abundance of root nodulating bacteria, including species from the orders Burkholderiaceae, Bradyrhizobiaceae and Actinomycetales. When comparing the rhizosphere soil of natural and commercial areas, differences were detected in the relative abundance of different root nodulating species. This is the first report of the effect of commercial farming of a native fynbos plant on soil bacterial communities.

Keywords: fynbos, rooibos, bacterial communities, Ion Torrent

[P1.253]

The role of microarthropods in determining the rate of carbon sequestration in grassland soils

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“**Micro-arthropods i.e. mites and collembolans, play an essential role in the sequestration of Carbon in soil systems**.” As agriculture is the leading source of greenhouse gas emissions in Ireland, it is vital to determine the role of the agricultural soil communities in the sequestration of carbon while also maintaining the soils economic value for agriculture. Micro-arthropods play a vital role in grassland soil systems, in decomposition, nutrient cycling, and regulation of microbial communities. The aim of this research project is to ascertain the role that these micro-arthropods play in the sequestration of Carbon in the soils of grassland systems in Ireland.

In this study we will compare micro-arthropod communities in intensively and extensively managed grasslands with three soil types in a large scale field study. The study will assess the contributions of micro-arthropods to C and N dynamics using (i) a mesocosm experiment and (ii) through the application of biomass and functional group data to food web models.

A preliminary study of the micro-arthropods in intensively and extensively managed grasslands with three soil types has been carried out using soil samples from some of the potential sampling sites. The results of this showed that there were significant differences between intensively and extensively managed systems, both in terms of population size and composition. Based on these results further sites have been selected, sampled and sorted for the food web analysis. The mesocosm experiments will be carried out on one of the soil types and will involve measuring both CO_2 and Nitrogen from soil under intensive and extensive management conditions, from which sequestered carbon can be calculated. The aim is that the food web analysis will validate the results obtained from the mesocosms and will therefore give an indication of the role micro-arthropods play in carbon sequestration.

Keywords: Micro-arthropods, Carbon, Sequestration, Grasslands

[P1.254]

Relationship between the activity of endemic earthworm Allolobophora hrabei and microbial diversity in soils of steppe fragments of central Europe

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The earthworms modify the soil by their burrowing and casting activity and thus change the intrinsic soil heterogeneity that is known to be an important factor influencing microbial abundance, diversity and activity. In central Europe, about 40% of earthworm species are endemic to this region, some of them dominating forest and grassland ecosystems and playing a keystone role in the soil foodweb. However, current knowledge about the effects of earthworms on soil microorganisms derives from studies on a few peregrine species only. Therefore, we focused on the relationship between soil microbial diversity and the activity of *Allolobophora hrabei* an endemic earthworm fragmentary distributed in the border regions of the Czech Republic, Austria, Slovakia and Hungary.

Our study was carried out in three steppe fragments, where *A. hrabei* represented a key earthworm species, in 2012-2013. Here, *A. hrabei* burrowed up to more than one metre depths and produced more than 3 kg /m^2 of casts per year. To assess the effects of *A. hrabei*, we compared bulk soil, casts and drilosphere *sensu lato* using several approaches to monitor microbial diversity at different levels. (i) The extended PLFA analyses were used to show the diversity on complex (prokaryotic and eukaryotic) community level; (ii) The DGGE analyses allowed to compare community profile of fungi, bacteria and archaea; (iii) The species determination of dominant bacterial isolates based on their 16S rDNA indicated diversity of cultivable bacterial community; (iv) Pyrosequencing analyses of soil 16S rDNA amplicons allowed to see the information about total bacterial and archaeal community.

In general, all approaches showed that (i) there was significant shift in microbial diversity from bulk soil to casts, (ii) bacteria were susceptible to the burrowing activity of *A. hrabei*, and (iii) both earthworm activity and dry steppe microclimate contributed to specific microbial composition of earthworm casts.

Keywords: Microbiota, Interactions, Earthworm, Steppe ecosystem

[P1.255]

Microbial community changes as a possible factor controlling carbon sequestration in subsoil

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To get a better idea of the mechanisms, which control carbon dynamics in subsoil, it is necessary to have a closer look at the microbial community. What is known is that microorganisms and substrate influence each other mutually. On one hand microorganisms influence carbon dynamics as decomposers, the rate of activity and the community structure being important factors, and on the other hand their residues are an important component of soil organic carbon (SOC).

Soil samples were taken at four different depths on two neighbouring farmland sites; one Kolluvisol with high SOC concentrations (8-12 g/kg) throughout the profile and one Luvisol with low SOC concentrations (3-4 g/kg) below 30 cm depth. The multi substrate induced respiration (MSIR) method was used to identify shifts in the microbial community structure of the depth profiles. Amino sugars were measured as indicators for bacterial and fungal residues and ergosterol was determined as marker for saprotrophic fungi.

The results of the discriminant analysis of the respiration values obtained from the MSIR show that the substrate use in subsoil is different from the substrate use in topsoil. The amino sugar analysis and the ratio of ergosterol to microbial biomass C indicate that the fungal dominance of the microbial community decreases with depth.

The results from this study support previous findings, which also observed decreasing fungal dominance with depth. Furthermore the MSIR approach shows clearly that not only the structure of the microbial community but also their substrate use changes with depth. Thus, a different microbial community with altered substrate requirements could be an important reason for enhanced carbon sequestration in subsoil. The fact that the MSIR was also able to differentiate between the two sites proves the assumption that resources are an important factor controlling the functional diversity of the microbial community, as abiotic factors are very similar for the two profiles, but the sites show a different depth gradient for SOC.

Keywords: functional diversity, microbial community, subsoil

[P1.256]
Diversity of the South African *Trichoderma* population from soil

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Members of the fungal genus *Trichoderma* often occur in soil environments and can be commercially employed as biological control agents, crop growth promoters and industrial enzyme producers. Despite the importance of *Trichoderma* spp., few studies have investigated the genus in South Africa and as a result we currently only have a superficial understanding of their local diversity. This presents an opportunity to survey the genus in South Africa, which serves as an ideal location for such a study as the native fungal and plant communities are known to be diverse. *Trichoderma* strains were isolated and identified through phylogenetic analyses using DNA sequence data and morphological analyses were performed to confirm species identifications. The survey resulted in the isolation of 161 *Trichoderma* strains which represented 19 different species, four of which were discovered to be new to science. Ten of these species are first reports for South Africa. In addition, strains that belong to eight *Trichoderma* species, commercially employed as biocontrol agents, were isolated and might show promise for possible future development as biological resources. The opportunistic human pathogen *T. orientalis* was found to be the most commonly isolated species during this study and also seems to be widely distributed within South Africa. This is a concerning finding in light of the number of immune compromised people living in South Africa. Previous studies that investigated *Trichoderma* species from South Africa showed little overlap in terms of the species that were reported. This suggests that continued exploration of the genus in South Africa could yield more species. The current study serves as a preliminary diversity assessment of the South African *Trichoderma* population and provides a base from which to plan and conduct similar studies in future.

Keywords: Soil diversity, Trichoderma, Survey, South Africa

[P1.257]

Succession of ectomycorrhizal fungi in mesh bags over a three year period in a fertilized and unfertilized Norway spruce forest

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Ingrowth mesh bags are commonly used to estimate ectomycorrhizal (EM) production in forest ecosystems. The bags can be viewed as an empty space in the soil that is open to fungal colonization. In this study we inserted mesh bags in fertilized or unfertilized plots in a Norway spruce forest in south-eastern Sweden. The bags were harvested annually over a three-year period in order to follow the fungal succession over time. The substrate consisted either of quartz sand or quartz sand mixed with 1% maize compost. Fertilization was done every second year to maximize forest production and mesh bags were also placed inside PVC-tubes (16 cm wide) that were forced to 30 cm depth in order to reduce the ingrowth of EM fungi. The DNA extracted from the mesh bags was sequenced (454) and fungal biomass was estimated with the ergosterol assay. Preliminary results suggest that fertilization reduced the production of fungal biomass considerably but had only minor effects on the fungal community, although the effect of fertilizer increased over time. On the contrary, sampling time had a major influence on the fungal community with yeast-like fungi (Guheomyces, Cryptococcus, Candida) dominating early in the succession (30% at start, declining to 0% at the end), while EM fungi became much more important as the succession proceeded (30% at start, 80% at the end). The most common EM genera after three years were Tylospora, Piloderma and Amphinema. Piloderma olivaceum was the most common fungus in control bags after three years (30%) but totally absent in bags collected from fertilized plots. Both maize amendment and trenching had significant effects on the fungal communities in the mesh bags and the importance of different factors for shaping EMF communities in the soil will be discussed at the conference.

Keywords: ectomycorrhizal fungi, succession, forest soil, mesh bags

[P1.258]

Recovery of bacterial and fungal communities from soil through the use of pressure cycling technology

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Current molecular methodologies, specifically DNA-based approaches, provide access to previously hidden soil biodiversity and are routinely employed in environmental studies of microbial ecology. Selection of cell lysis methodology is critical to community analyses due to the inability of any single extraction technology to recover the absolute genetic structure from environmental samples. Numerous methodologies are currently applied to interrogate soil communities, each with its own inherent bias. Improving our understanding of methodological biases will make cross comparisons more accessible. In this study, we compared the efficacy and bias of three physical cell lysis methods in conjunction with the PowerLyzer PowerSoil DNA Isolation Kit (MoBio) for direct DNA extraction from soil: bead-beating, vortex disruption, and hydrostatic pressure cycling technology (PCT). PCT lysis is novel to soil DNA extraction and was optimized for soils of two different textures prior to comparison with traditional bead-beading and vortex disruption lysis. All lysis methods successfully recovered DNA with the two traditional mechanical lysis (bead-beating and vortex) techniques yielding greater genomic, bacterial, and fungal DNA per gram soil. Lysis method had a significant impact on bacterial and fungal community fingerprints. Although the abundance of bacterial and fungal genes recovered per gram soil was significantly less with PCT versus traditional mechanical lysis methods, PCT recovered a significantly greater number of phylotypes. Results indicate the importance of diversity and quantity measures when assessing DNA extraction bias as soil DNA retrieved by PCT lysis represented populations unique from the traditional mechanical lysis methods despite significantly lower DNA yields.

Keywords: Pressure Cycling Technology (PCT), DNA Extraction, lysis method, T-RFLP

[P1.259]

Diversity of ericoid mycorrhizal fungi in bulk soils of the South African fynbos region.

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Soils of the fynbos region in South Africa are notoriously nutrient poor, but this region is a biodiversity hotspot with high levels of endemism. *Erica* plants are one of the dominant plant types in this area, with over 660 species present. These plants are able to thrive in nutrient-poor soils because of their relationship with ericoid mycorrhizal fungi. Unlike many other mycorrhizal fungi, these fungi are able to survive without a host plant, and can be found in bulk soils. As *Erica* plants are one of the dominant plant types in fynbos, it can be expected that ericoid mycorrhizal fungi will be abundant in fynbos soils.

The aim of this study was to investigate the diversity and abundance of fungi able to form ericoid mycorrhizae in bulk soils of the fynbos region. An ITS sequence database of ericoid mycorrhizal fungi was compiled by combining known ericoid mycorrhizal fungal sequences with sequences of ericoid mycorrhizal fungi found in the fynbos region. The fynbos sequences were obtained from both culture-based and molecular studies of ericoid mycorrhizae of *Erica mammosa* and *E. versicolor*. Some ericoid mycorrhizal fungi could be cultured from bulk fynbos soils, confirming their presence in soils without a host plant. To investigate the broader distribution of these fungi in the region, the ericoid mycorrhizal ITS sequence database was compared to high throughput sequence data obtained from multiple fynbos sites.

Results showed that many ericoid mycorrhizal fungi are present in bulk soils, and some, e.g. *Oidiodendron*, are dominant and widely distributed in the fynbos region. The physiology of ericoid mycorrhizal fungi has been well studied, and so this information can be used to elucidate the role of these fungi in bulk soils. This is one of the first studies to investigate the diversity and distribution of ericoid mycorrhizae in this region.

Keywords: diversity, ericoid mycorrhizae, distribution, bulk soils

[P1.260]

Phylogenetic community ecology of soil biodiversity using mitochondrial metagenomics

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Knowledge about the magnitude and distribution of biodiversity is essential to our understanding of ecosystem processes and their responses to anthropogenic disturbance, yet, we have catalogued only a fraction of the existing species diversity on Earth. Particularly, major knowledge gaps exist about species richness, distribution and phylogenetic assemblies on soil mesofauna. The development of Next Generation Sequences technologies provides unprecedented possibilities to accomplish the study of such complex communities. Here, we use high-throuput shotgun sequencing of pooled genomic DNA to study the community ecology of largely uncharacterised soil ecosystems using mitochondrial genomes. We focused on coleopteran soil communities and investigated structure and phylogenetic beta diversity patterns among three regions and soil layers in the Southern Iberian Peninsula. Our study reveals high compositional and phylogenetic turnover among sites and layers. Phylogenetic analyses of mitochondrial genomes furthermore unravelled genetic structures that suggest that limited dispersal promotes the diversification of euedaphic Coleoptera. Soil beetles of this area are an extensive representation of the main lineages within Coleoptera, and the significant number of mitochondrial genomes obtained resulted in a fundamental advance to the assembly of the global beetle Tree of Life. Our study indicates that direct sequencing of environmental samples allows biodiversity assessment of previously uncharacterised ecosystems. The method applied results in a large number of long, highly informative, mitogenome sequences, and therefore provides a cost efficient tool to estimate phylogenetic distance, and characterise hyper-diverse arthropod communities.

Keywords: Mitochondrial metagenomics, phylogenetic community structure, NGS, beta diversity

[P1.261]

Does the chemical composition of litter determine the biodiversity of decomposer communities? A case study about *Pinus halepensis* succession

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In the French Mediterranean region, since the early twentieth century, the agricultural land abandonment promotes strong reforestation with pioneer and expansionist species, such as Aleppo pine (*Pinus halepensis* Mill.). Owing to its richness in secondary metabolites, Aleppo pine may play an important role in plant succession through several processes, such as needle decomposition and allelopathic mecanisms. The decomposition of litter, a key process connecting ecosystem structure and function, is governed by the activity of soil organisms, which is regulated by different biotic and abiotic factors. Among these factors, secondary metabolites are known to affect the activity or presence of detritivorous organisms (mesofauna) and decomposers (bacteria and fungi).

In this context, we propose to study, during decomposition, dynamics of soil communities in relation to dynamics of secondary metabolites contained in Aleppo pine litter from pine forests with different stages of maturity. Our results show, during decomposition, a succession of invertebrates and microbial communities, determined by changes in the composition of litter secondary metabolites. There is an apparent shift in springtails and microbial communities when terpenoids and phenolic compounds have almost disappeared. Moreover, we observed a greater content of phenolics in the litter of young pines, especially certain compounds known to be allelopathic (e.g. gallic acid or p-coumaric). The abundance of decomposers is therefore lower in young pines litter, resulting in a slower decomposition process compared to other stages.

Keywords: Litter decomposition, Secondary metabolites, Collembola, Diversity

[P1.262]

Metatranscriptomics reveals differential expression response of paddy soil microorganisms to salt stress

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Paddy soil slurries amended with rice straw were selected as a model system to investigate the microbial community response to salt stress. The slurries were incubated anaerobically for 6 hours (short response) and 48 hours (late response) with 0, 300 and 600 mM NaCl. Increasing salt stress inhibited CH_4 production, thereby resulting in an accumulation of acetate. Illumina RNA-seq of total RNA and enriched mRNA was used for metratranscriptomic analysis. Assembled paired-end SSU ribo-tags were selected by SortMeRNA and further analyzed via QIIME and USEARCH, while functional annotation of putative mRNA sequences was made by the MG-RAST pipeline using SEED subsystems.

Taxonomic analysis of SSU ribo-tags showed widespread changes in the bacterial and archaeal community composition in late stress response. *Clostridium* and *Methanosarcina* were the most dominant groups. Relative ribo-tag abundance of *Clostridium* was greatest in 600 mM NaCl treatment, while *Methanosarcina* showed highest relative ribo-tag abundance in 300 mM NaCl treatment. The relative ribo-tag abundance of *Methanosaeta* and *Methanobacterium* significantly increased with increasing salt stress. By contrast, the relative abundance of *Symbiobacterium* and *Syntrophomonas* decreased (p<0.05).

Our experimental approach resulted in a total of 17,309,837 putative mRNA reads from enriched mRNA. As compared to the control, differential expression was more pronounced with increasing salt stress (300 vs. 600 mM) and exposure time (6 vs. 48 hrs). Changes in the gene expression profiles were related to various level 1 subsystems such as, “carbohydrates”, “nitrogen metabolism”, “dormancy and sporulation”, and “stress response”. Among level 2 subsystems, salt adaptation was reflected by overrepresentation of transcripts involved in “methanogenesis”, “ammonia assimilation”, “nitrogen fixation”, “fermentation”, “heat shock” and “osmotic stress”. By contrast, transcripts related to “clustering-based subsystems”, “flagellar motility in prokaryota”, “dormancy and sporulation”, “cell wall and capsule”, “regulation and cell signaling”, “ABC transporters” and “cell division and cell cycle” were underrepresented in the salt treatments relative to the control. Taxonomic assignment of mRNA transcripts suggests that *Clostridium* and *Methanosarcina* exhibited the greatest functional response to increasing salt stress. Upon NaCl exposure, *Clostridium* showed a strong transcriptional response related to “fermentation” and “osmotic stress”, while transcripts of *Methanosarcina* were overrepresented in the level 2 subsystems “methanogenesis”, “ammonia assimilation”, and “heat shock”. Both groups, *Clostridium* and *Methanosarcina*, showed an increased transcript abundance related to nitrogen fixation.

Collectively, this study revealed the consistency of both SSU rRNA and mRNA data sets, identifying the key functional microorganisms and transcriptional processes related to salt stress adaptation.

Keywords: metatranscriptome, salt stress, rice straw, transcriptome

[P1.263]

A three-edged sword – can the constraints of conservation policy, biodiversity assessment, and long-term biomonitoring be reconciled?

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Conservation policy should ideally be based on sound scientific evidence. This includes biodiversity inventories and assessments of conservation status (species and/or ecosystem red lists) based on long-term monitoring of biodiversity and elucidation of the functional linkages between soil organisms and ecosystem services. Developing policies is a long-term process and a major concern of policy-makers is therefore the use of standard methods and protocols for biodiversity assessment and monitoring.

However in the case of soil organisms, taxonomic knowledge is embryonic for many groups, especially microbes (including micro-eukaryotes) and mesofauna. Their true diversity is therefore unknown as well as their conservation status. Methodological developments such as high throughput sequencing now allow to assessing the full breadth of this poorly-known diversity. Yet, as these methods are constantly being improved no standard approach could realistically be proposed for a long-term monitoring program of soil biodiversity. Under those circumstances assessing long-terms changes in the diversity of soil organisms and designing effective policies is extremely challenging.

Policy-makers therefore face a true dilemma: can they accept to base policies on scientific data generated using ever-changing state of the art methods or should they favour obsolete approaches but that have the advantage of allowing comparisons over longer periods of time?

The wise solution is perhaps to design “fuzzy-adaptive” policies primarily aiming to conserve habitats, which can later be improved to take into consideration knowledge on biodiversity, its dynamics and its link to ecosystem functions.

Keywords: long-term monitoring, biodiversity assessment, changing methodological approaches, holy grail of conservation policy

[P1.264]

Optimized and standardized 192-plex solution for 16S rDNA gene sequencing on Illumina Miseq platform to assess soil biodiversity

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The growing need to survey the tremendous microbial diversity in a culture independent manner, has led to the development of molecular methods through sequence profiling of conserved genes such as 16S rDNA. Next-generation sequencing technologies are now used routinely to assess bacterial communities composition in complex environmental samples. Recently, the improvement of the Illumina MiSeq platform to a 2×300 bases paired-end version made it much more attractive for 16S rDNA amplicons sequencing enabling the analysis of a longer region thus facilitating taxonomic assignation. Additionally, the Illumina V3 chemistry enables high-throughput metagenomics analysis at the greatest coverage yet possible with a lower cost per sequence. Nevertheless, known limitations associated with the sequencing of low sequence diversity samples have hampered harnessing its true potential to sequence 16S rDNA gene amplicons. Moreover, validated Illumina 16S rDNA amplicon sequencing protocols do not support more than 96 samples per run, which underutilized the overall capacity of a sequencing run.

We therefore worked on the development of a standardized and optimized high-multiplexed metagenomic solution for the exploration of complex environments. We developed an integrated solution combining several technical and bioinformatical strategies that are (i) a custom and standardized amplification protocol for 16S rDNA library preparation to minimize as full as possible technical biases; (ii) a custom 192-index strategy within a single run; (iii) the inclusion of a nucleotide sequence variability at the first sequencing cycles; (iv) an accurate paired-end reads assembly process for full length amplicon analysis and (v) a dedicated pipeline for taxonomic affiliation of 16S rDNA sequences and microbial communities analysis.

Our solution validated within soil samples provides high sequencing accuracy and technical reproducibility with no index biases based on taxonomic distribution analysis. The association of technical and bioinformatical improvements yields substantial cost reductions and provides greater target flexibility to assess soil biodiversity as well as functions of microbial communities through carbon, phosphorus or nitrogen cycles in future developments.

Keywords: Metagenomic, next-generation sequencing, soil biodiversity

[P1.265]

SOIL VITALITY IN LONG-TERM TILLAGE AND STRAW MANAGEMENT SYSTEMS ON *CAMBISOL*

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Understanding of the soil CO_2 fluxes remains unclear because of the complexity of processes involved and different experimental conditions. The goal of this study was to evaluate the influence of soil key properties on *Cambisol* vitality – microbiological activity and soil respiration (SR) after long-term conventional (CT) and no-tillage (NT) either with or without crop residues application.

Straw incorporation under conventional tillage (CT-2) revealed higher soil vitality under dry environmental conditions, compared to vitality in CT without residues (CT-1) and in NT on both backgrounds with (NT-1) or without crop residues (NT-2). Residues improved soil agrochemical quality, water content (W) and urease activity in 0-10 cm layer, compared to residues removing. NT significantly increased accumulation of carbon and basic plant nutrients, bulk density, fungal community, and enzymes activity. Substrate utilization potential (AWCD) and microbial community (H') in NT were lower than in CT. Dehydrogenase activity, fungi population and substrate utilization potential was lower on background with residues than without them.

Increase in soil air-filled porosity accelerated AWCD and H‘. Residues input changed the balance between competition and mutualism of microorganisms, reduced ratio between air-filled porosity and W, improved availability of nutrients, and conditioned better development and respiration of plant roots. Accordingly, SR in CT-2 treatment increased, compared to SR under CT-1. SR in NT-1 was similar as in CT-1, but in NT-2, low SR emerged as result of W deficiency and its influence on reduction of soil microbial community and substrate utilization potential.

Under CT, the higher C:N ratio was registered (residues returned) the higher SR was found. While increase in C:P, C:K, N:P and K:P ratio initiated reduction of SR. In NT, the higher C:N ratio was registered (residues removed) the lower SR was documented. However the increase in C:P, N:P and K:P ratio initiated the intensification of SR.

Keywords: Soil management, Microbial diversity, Basic nutrients, Soil respiration

Poster session 2

[P2.001]

Taxonomic and functional diversities reveal the response of soil biota to managed soil systems

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It is broadly recognized that ecosystem properties are greatly influenced by the many functional characteristics of living organisms. However, recent evidence shows that the chosen degree of taxonomic resolution at which ecosystems are investigated strongly affects the ability to link community structure and ecosystem functioning. Hence a real understanding of the relationships between taxonomic diversity and functional diversity is needed to unravel the mechanisms underlying ecosystem functioning.

As a case study, we analysed how soil biota respond to different agricultural management practices by exploring relationships between soil biodiversity and community structure in the arable fields with field margins. Although the importance of field margins for supporting above-ground biodiversity (e.g., birds, pollinating insects, etc.) is accepted, much less is known about below-ground biodiversity in the margins and their contribution to the ecosystem functioning of entire agroecosystems. We measured the taxonomic and functional diversity for the total soil fauna and for each of the five major taxocenes (i.e., Nematoda, Collembola, Acarina, Enchytraeidae, Lumbricidae) in soils from arable fields and their adjacent field margins in the southwestern part of The Netherlands.

Despite an overall effect on the total soil biodiversity, our field margins had significant influence only on two (Enchytraeidae and Acarina) of the five major investigated groups. In contrast, the differences in functional diversity were strong for most taxocenes and suggested compartmentalisation and fungal-driven pathways within the detrital food webs of the field margins. When looking only at species composition, food webs of the field margins appeared more heterogeneous in comparison to food webs of the arable fields. These differences as revealed by changes in functional diversity underline the importance of considering both trait-based diversity and taxonomic diversity to assess the complex relationships between soil communities and ecosystem functioning.

Keywords: functional diversity, community structure, field margins, ecosystem functioning

[P2.002]

Water Mediated Changes of Microbial Community in the Soil

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Moisture fluctuations affect heterotrophic respiration and nutrient mineralization in the soil. In agriculture soil moisture levels are artificially manipulated by irrigation for intensive crop production. The Water framework Directive (European Commission) has identified Agriculture as one of the priority sectors which needs to reduce water consumption in order to avoid scarcity. In the UK significant amount of irrigation is used by potato growers to control common scab disease, which is caused by soil-inhabiting Streptomyces, for which irrigation is the only control method available. To explore and expand our knowledge on the mechanism of irrigation-mediated disease control method a study was carried out to investigate the effect of water on microbial communities in the soil. We wished to further our understanding of how microbial communities are influenced by water dynamics in the soil.

Glass house experiments were carried out with two different soil types, peat and sandy loam. Each soil type was maintained at high or low levels of water for 8 weeks; the level of water was calculated from the water holding capacity for the specific soil type. A metagenomic approach was used to investigate the differences in microbial community in different soil-water treatment regime (high and low) at the starting and end points of the experiment.

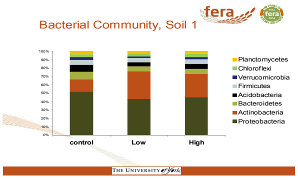

Figure 1. Relative abundances of bacterial community at high and low level of water

Proteobacteria (47%) and Actinobacteria (30%) were found to be the two most abundant phyla in the soil with Alphaproteobacteria (22%) and Actinobacteria (32%) are the most abundant classes respectively. However it was observed that relative abundances of bacterial phyla across soil samples maintained at high and low level of water were highly variable (Figure 1). This finding supports the previous observation by Beth et al (2012), who observed that soil moisture is the main driver influencing the composition of microbial communities across seven biogeoclimatic zones in western Canada.

Keywords: Agriculture, Irrigation, Common Scab, Soil Moisture

[P2.003]

An Attempt to Study Bacterial Diversity of Compost Following Traditional and Proteomics Approach

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Microbial life plays a primary role in the regulation of nutrient and organic mater fluxes in an ecosystem and mediating important interactions between biotic and abiotic component of the ecosystem. Bacteria inhabiting almost all the different environments that exist on the earth from the lining of our guts to harsh environments are to be explored. But still our knowledge about bacterial diversity in natural environments is limited, and studying the microbial diversity in nature is not an easy. Therefore linking the bacterial diversity to ecosystem functioning, it is necessary to focus on functional traits and genes of the important bacteria significantly important for biogeochemical cycling that govern nutrient cycles. Various researchers have studied a variety of environmental samples and as per estimates only 0.1 to 1 % of bacteria are cultivated on common media using cultural techniques. Several traditional methods have been used globally to study the bacterial diversity, however, these methods have not been able to provide suitable nutrients to support the growth of majority of microorganisms. Due to lower sensitivity in taxonomical assignments for metagenomics reads, much of the genome remains unmapped and minimal sequence information is available for only a limited number of genes. To address various restrictions in genome analysis, the last decade has witnessed advancement of technologies and post-genomic developments enabling the study and analysis of proteome. This unique contribution resulted in many scientific disciplines incorporating metaproteomics as one of their “omics” platforms. Studying wide array of the bacterial diversity in terms of their physiological activity in compost is a daunting task. In context of studying complex biological functions in any ecosystem, transcriptomes, proteome, or even metabolome analyses have emerged as promising techniques. These rapidly evolving technologies are attempting to understand the environmental microbiology at an extraordinary pace. Considerable efforts have been devoted to metaproteomics analyses. This method aims to deepen our fundamental understanding of the coupling between microbiology and biogeochemistry of compost and the interaction occurring within them. Inspite of constant efforts of researchers to study microbial diversity, relatively little is known about the relationship between bacterial diversity and ecosystem functioning. The present study has revealed a close symbiotic link between compost and communities residing in it. A chronometric comparison of bacterial diversity based on comparative 16S rDNA and metaproteomics analysis has been made. The result of 16S rRNA gene sequence revealed an overall dominance of *Firmicutes* (78.8 %) with the bacilliales as major order followed by *proteobacteria* (15.1 %) and *actinobacteria* (6.1 %). The phylogenetic tree showed that 16S rRNA gene sequences were clustered into two groups, separating *firmicutes-actinobacteria* from *proteobacteria* (γ, β). After comparing the number of different bacterial phyla and classes assigned by 16S rRNA gene sequence and the protein hits revealed in proteomics study, a more assorted picture in the compost was visualized regarding the phylogeny. Identified proteins were found to be related to several protein families and metabolic functions. By analyzing complex communities, 50.08 % prokaryotic, 4.01 % archaea, 2.44 % viruses and 42.58 % eukaryotic protein dwelling within the compost sample were evaluated. The majority of cultivated isolates belonged to bacterial community of diverse phylogenetic division of *proteobacteria*, and seconded by those of *acidobacteria*, *cytophaga-flexibacter-bacteroidetes* (CFB) and then *actinobacteria*. The proteome analysis of compost samples has revealed identification of twenty nine phyla compared to three phyla based on 16S rRNA gene sequence analysis. The comparison of the results on the relative percentage of bacterial classes based on 16S rDNA chronometer and the sequence assigned through metaproteomics attributed huge divergence. This vast difference makes us to comprehend to use more appropriate techniques for studying bacterial diversity of environmental samples.

Keywords: Culturable vs Unculturable, Compost metaproteomics

[P2.004]

Plant endophytes and precipitation alter belowground organisms in a primary successional sand dune system

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Soil biodiversity is known to play an important role in regulating succession, especially in primary successional systems such as sand dunes. Soil nematode communities, in particular, have been implicated for their influences on plant succession in sand dunes. However, plant-nematode interactions are not exclusive and can be influenced by other plant symbionts, such as arbuscular mycorrhizal fungi (AMF) and endophytes. In this study, we examined the effects of an aboveground endophyte found within the dominant dune builder *Ammophila breviligulata* on AMF and nematodes communities in North American Great Lakes sand dunes. In May 2010, we set up a factorial experiment in Michigan, USA to examine endophyte effects on *Ammophila* populations in the context of climate change (reduced, ambient, or augmented precipitation). We evaluated AMF root colonization and extra-radical hyphal (ERH) production in plots from 2011-2014, and conducted surveys of soil nematode functional groups (plant parasites, predators, bacterivores) in 2013-14. AMF colonization of *Ammophila* roots increased by 33% in endophyte-present plots, and was highest in ambient compared with reduced or augmented precipitation plots. ERH length was not affected by either the endophyte or climate manipulation. Endophytes caused a 40% increase in predatory nematodes and a 20% reduction in plant-parasitic nematodes under ambient precipitation, though effects disappeared under altered precipitation. A three-way interaction cascade involving endophytes, AMF, and nematodes crosses the soil boundary and could have unexpected effects on *Ammophila* populations and dune succession.

Keywords: epichloe, climate change, roots, dune building

[P2.005]

The national rhizolab facility at East Malling Research

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Direct, in situ and non-destructive, observations of plant root interactions with soil were pivotal to the understanding and development of the renowned East Malling apple rootstocks, which are now grown worldwide. In the 1930s such observations were facilitated by the construction of temporary root observation trenches, but in 1961 the first underground laboratory was built. This was replaced in 1966 with an improved version, upon which many other similar laboratories around the world have been modelled. The quality of both the design and construction methods, of what has become an iconic root laboratory, have stood the test of time and, despite falling into disuse in 1989, the root laboratory at East Malling Research (EMR) is once again being used to study the interactions between perennial root systems and soil in the field.

Funding from the Biotechnology and Biological Science Research Council enabled refurbishment of the rhizolab in 2013. In addition to new plate glass for the 48 observation windows, an above-ground preparation laboratory was constructed to replace a previous temporary structure. The rhizolab will be used to study the flow of carbon from roots to soil and the ability of managed perennial cropping and pasture systems to root in subsoil. In the summer of 2014 a high-intensity apple orchard was planted on one side and perennial grasses, including novel *Festulolium* (ryegrass spp. x fescue spp.) hybrids on the other. The site is being instrumented and methods developed to translate observations of root growth at the observation windows into models of root growth in the bulk soil.

The EMR Rhizolab is a UK national capability and offers an unparalleled opportunity for multi-disciplinary collaboration and the deployment of novel optical and analytical techniques in both short- and long-term studies of plant-soil-biota interactions, carbon sequestration and other soil processes.

Keywords: Carbon sequestration, Rhizosphere, Root observation, Soil biota

[P2.006]

Landscape scale drivers of the spatial distribution of earthworms in grasslands with implications for ecosystem services

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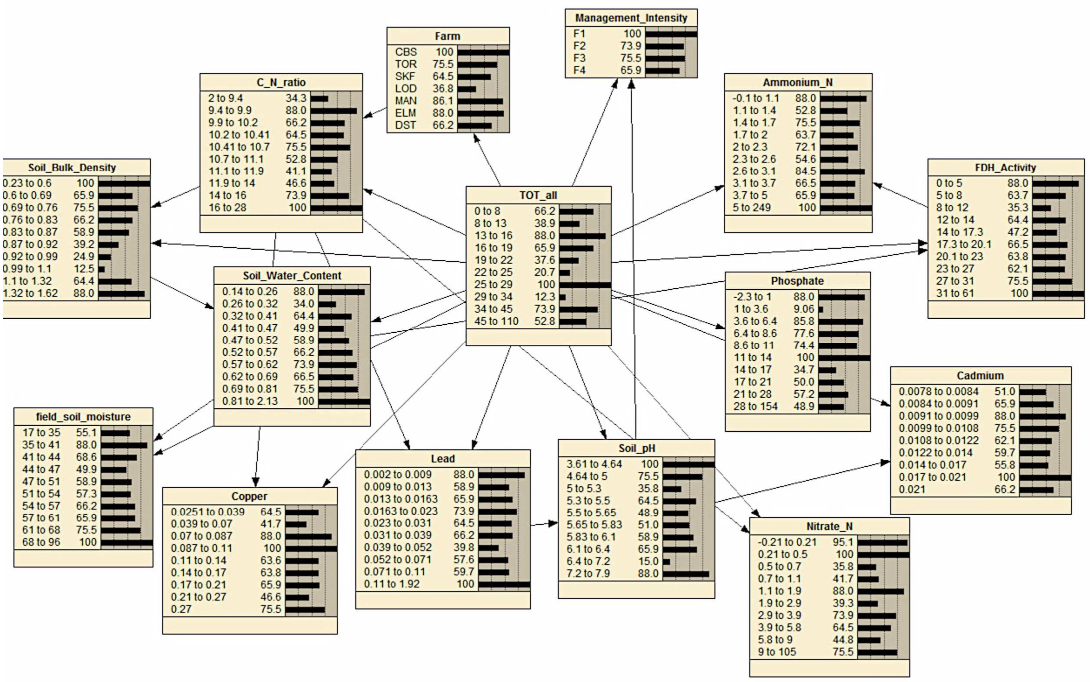
A fundamental concept within ecology is that species have an ecological niche. This asserts that the distribution of an organism across the landscape is limited by environmental factors and that organisms are adapted genetically to a limited range of environmental conditions ('environmental tolerances'). In broad terms controls on earthworm distributions are well documented in the literature e.g. Edwards and Bohlen (1996). Earthworms have a thin permeable skin and are therefore very sensitive to changes in soil condition. Important drivers of earthworm distribution are soil moisture content, pH, texture, temperature, organic matter content. However, many, if not all of the above factors vary spatially and are intercorrelated and so it is hard to separate out their effects or their relative importance in the field. No study we know of has explicitly considered this multifactorial complexity on earthworm distributions.



The important ecosystem services that semi-natural and managed grasslands provide, in particular related to food production as well as water storage and infiltration are heavily reliant on healthy earthworm populations. Here we report on a large spatial study of earthworm distribution across 28 grasslands spanning the breadth and length of the UK, over which we sampled a total of 529 soil pits for earthworm composition and associated drivers. We then developed a set of quantitative models for earthworm distributions that are capable of taking into account a number of established variables simultaneously. In this study we link network models such as Structural Equation Models and Bayesian Belief Networks (Figure) to geostatistics so providing the modelling framework with which to determine spatial controls on earthworm distribution. Through this analysis, we found that the soil nutrients nitrate and phosphate were amongst the primary controls on total earthworm distributions, with effects on the epigeics, anecics and endogeics.

Keywords: Earthworm, Spatial, Distributions, Modelling

[P2.007]

Temporal and spatial linkages between microbial diversity and soil function

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To address an overarching goal of increasing our knowledge of the relationships between soil microbial community structure and biogeochemical pools and fluxes, we established three paired sites with adjacent low-intensity pasture and remnant native woodland vegetation on the western slopes of the New South Wales tablelands, south-east Australia. This remnant woodland, dominated by *Eucalyptus microcarpa, E. melliodora* and *Acacia* spp., with an understorey comprising *Themeda triandra* and *Poa sieberiana* grasses, is of high conservation value having been mostly cleared for agricultural land use.

Within each paired site, an initial survey yielded 240 individual soil samples which were analysed for microbial community structure and soil biogeochemistry. At each of the six plots, 25 sensor nodes (n=150 total) were installed to capture high resolution spatiotemporal information on soil moisture and temperature. At each node, soil samples were collected every three months (n=150 per time point) to evaluate relationships between variation in local moisture and temperature, microbial community structure and soil biogeochemical processes.

We found that bacteria and fungi were interlinked and formed independently correlating modules with soil parameters such as C and N pools. Across the sites, there was significant localised heterogeneity in stability of soil moisture and temperature, which appeared to directly influence microbial community structure and functional diversity.

Immediately before and for four months after a natural bushfire event in January 2013 at one of the paired sites, additional microbial community and N process rate measurements were conducted to assess recovery rate in the two contrasting ecosystems. The bushfire resulted in contrasting rates of soil N function recovery between the two ecosystems, coupled with dissimilarities in bacterial and fungal communities. Work is ongoing to link periodic data from soil samples to continuous high-resolution spatiotemporal data from the environmental sensors across these sites.

Keywords: Australian ecosystems, High-resolution spatiotemporal data, Biogeochemical cycling, Fire response

[P2.008]

Soil variability in relation to tree species diversity along a latitudinal gradient in western China

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The underlying mechanisms of latitudinal gradient of plant diversity have been explored and discussed in numerous researches, from which some important theories or hypotheses emerged. However, there is no perfect answers for it and efforts can not be ceased. This study also attempted to seek the correlation between soil variability and tree species diversity. Soil samples were taken with grids method in seventeen distinct forests along a latitudinal gradient in western China, in the mean time, we investigated community composition and evaluated tree species diversity for these forests. Semi-variogram analysis soil carbon and nutrient contents was involved to indicate soil variability, and coefficients of variation as well. Not surprisingly, tree species diversity negatively correlated with latitudinal gradient. Furthermore, soil variability do exhibited significantly latitudinal gradient, which can be demonstrated by the results that the coefficient of variation of soil exchangeable Ca and Mg were significantly and negatively correlated with adjusted latitude, and that the effective ranges of spatial variation of exchangeable Ca, exchangeable Mg, and base cation were positively correlated to the mean annual temperature. Consequently, we can find significant correlation between soil variability and tree species diversity- one of facts was that the diversity of tree species in these forests were positively correlated to the heterogeneity of soil base cation. These results may imply that higher soil variability can maintain more plant species in forest ecosystems.

Table 1Correlations of plant diversity and the heterogeneity of soil properties in the seventeen forests in western China. “-” indicates that there are no significant correlations. The significance level is 0.05

Variable	Variable	Mean	Coefficient of variation	Range	Range/ mean	Effective range	Spatial dependence
Latitude adjusted	C	-	0.508			-	-
	N	-	0.546			-	-0.607
	C/N	-	0.504	0.569		-	-
	Ca	-	-0.553		-0.583	-	-
	Mg	-	-0.620		-0.654	-	0.667
	Fe	0.500					
	Base cation	-	-		-0.600	-	0.886
Mean annual temperature	N	-	-0.625			-	-
	C/N	-0.598	-			-	-
	Ca	-	0.526			0.898	-
	Mg	-0.53	0.635		0.645	-	-0.720

		1					
	K	-	-			0.905	-0.903
	Base cation	-	0.487			0.886	-
	Fe	-0.575		-0.536			
	Mn	-0.659	-			-	-
Mean annual precipitation	C/N	-0.529					
	C/P	-	-			-0.773	-
	Ca	-0.505-	-		0.563	-	-
	Mg	-0.569	-		0.538	-	-0.672
	Mn	-0.569					
	Base cation	-	-		0.572	-	-0.928

Keywords: soil variability, heterogeneity, tree species diversity, latitudinal gradient

[P2.009]

Fine and coarse arbuscular mycorrhizal fungi in *Bromus diandrus* invasion

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Invasive plants have the ability to alter the rhizosphere microbial community upon establishment and form either positive or negative feedbacks that affect their dominance. Associated native species also form either positive or negative feedback, and the direction of the feedback will affect interspecific competition. By examining root-associated fungi microscopically we broke open the soil black box to assess plant-soil feedback as a potential mechanism altering the competitive ability of native forbs in a southern California exotic annual grassland dominated by *Bromus diandrus*. In a controlled greenhouse environment, four native forb species (*Amsinckia menziesii*, *Layia platyglossa*, *Lasthenia californica*, and *Plantago erecta)* were grown with different microbial inocula in monoculture and in mixture with *Bromus*. A constant density was maintained using a substitutive design. Inoculum consisted of 20g of soil collected from the rhizosphere of native or invasive plants in a sterile soil matrix with treatments of (1) whole soil inoculum, (2) filtrate through a 20 µm sieve, and (3) arbuscular mycorrhizal fungi (AMF) spores. The soils of our recently abandoned agricultural site proved to have a high load of potential pathogenic fungi and fine AMF, often identified as *Glomus tenue*. The fine AMF was found colonizing the roots of *Bromus* and native forbs more than coarse AMF when grown with inoculum from the rhizosphere of *Bromus*. However, native plants were infected more heavily with coarse AMF when grown with native inoculum, and *Bromus* was always colonized more by fine AMF. Filtrate inoculum included fine AMF (spores < 20 µm) that appeared to cause most of the observed positive feedback effect even with the presence of pathogenic fungi in roots, suggesting fine AMF are more important to plant growth than pathogens in *Bromus diandrus* invasion. Continued work on identifying the potential root fungal pathogens is underway using high-throughput sequencing.

Keywords: plant-soil feedback, plant invasion, Glomus tenue

[P2.010]

Activity and abundance of methane-oxidizing bacteria in secondary forest and manioc plantations of Amazonian Dark Earth and adjacent soils

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The oxidation of atmospheric CH_4 in upland soils is mostly mediated by uncultivated groups of microorganisms that have been identified solely by molecular markers, such as the sequence of the *pmoA* gene encoding the β-subunit of the particulate methane monooxygenase enzyme. The objective of this work was to compare the activity and diversity of methanotrophs in Amazonian Dark Earth (ADE) and their adjacent soil. Secondly, the effect of recent land use in the form of manioc cultivation was examined by comparing secondary forest and plantation soil. CH_4 oxidation potentials were measured and the structure of the methanotroph communities was assessed by qPCR and amplicon pyrosequencing of the *pmoA* gene. The CH_4 oxidation potentials were relatively high in all the secondary forest sites of both ADE and adjacent soils. CH_4 oxidation in one of the ADE soils that was only recently (5 years) converted to a manioc plantation was also relatively high. In contrast, both the adjacent soils used for manioc cultivation and the ADE soil with a longer history of agriculture displayed minimal CH_4 uptake. Amplicon pyrosequencing of *pmoA* genes indicated that USCα, *Methylocystis* and the tropical upland soil cluster (TUSC) were the dominant groups depending on the soil type. USCα, which are believed to mediate atmospheric methane oxidation, were more abundant in all ADE soils than forested adjacent soils, and were below the qPCR detection limit in manioc plantations of adjacent soil. In contrast, *Methylocystis pmoA* genes in ADE soils were approximately 2-orders of magnitude lower than USCα and their abundance was not significantly different between ADE and adjacent soils, or between forest and plantations. The results indicate that ADE soils harbor high abundances of atmospheric CH_4 oxidizers and are potential sinks for atmospheric CH_4, but as in other upland soils this activity can be inhibited by the conversion of forest to agricultural plantations.

Keywords: Methanotrophs, Amazonian Dark Earth, Forest soils

[P2.011]

Will primary producer-release of labile carbon influence litter degradation differently in terrestrial and aquatic experimental systems?

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The quality of organic matter (OM) is highly diversified and covers a large gradient of resistance to degradation. It is possible that recalcitrant organic matter (ROM) can be 'activated' and thus involved in carbon (C) and nutrient cycling in both aquatic and terrestrial ecosystems through the priming effect (PE).

In order to understand the PE, or the increased mineralization of ROM through inputs of labile organic matter (LOM), it is of importance to investigate how OM pools of different recalcitrance are degraded by microbial communities. Most previous assessments of PE have utilised pulse additions of single substrates at high concentrations. However, to achieve an assessment of the true importance of the PE it is important to simulate a realistic delivery of LOM.

In laboratory experiments, we investigated how primary producer (PP)-release of LOM can influence litter degradation in terrestrial and aquatic experimental systems. We used soil (terrestrial) or stream water (aquatic) microbial communities to which litter was added. We monitored the successional dynamics of fungal and bacterial growth, PP activity, and respiration with and without litter under dark and light.

In aquatic ecosystems it is thought that periphytic algae release LOM (e.g. amino acids), and such excretion might stimulate the synthesis of microbial exoenzymes and thus effectively subsidise recalcitrant organic matter utilisation. Analogously, in terrestrial systems, it is hypothesized that the LOM released in plant rhizospheres stimulate the activity and growth of ROM decomposers. In both cases, the presence of LOM substrates seems to favour LOM decomposition and supply ROM decomposers with energy and extracellular enzymes that enhance ROM degradation. Thus we hypothesize that PP input of LOM will result in an elevated decomposition of ROM, and that the larger production LOM of higher quality in aquatic compared with terrestrial systems will result in a stronger effect there.

Keywords: priming effect, algae, bacteria, fungi

[P2.012]

Diversity of arbuscular mycorrhizal fungi in crop systems in Cerrado in Brazil Central

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Degradation of Cerrado soils affects arbuscular mycorrhizal fungi (AMF) diversity and may result in the selection of species with low symbiotic efficiency. Moreover, systems with greater diversity of plants can increase AMF diversity.

The AMF species survey was conducted at Federal University of Goiás, in an Oxisol in Cerrado from Central Brazil. Cropping systems evaluated were CS-1: Pasture, degraded soil, CS-2. Soybean, degraded soil, CS-3: Soybean, fertile soil, CS-4: Soybean/Corn, fertile soil, CS-5: *Panicum maximum,* fertile soil, CS-6: *Brachiaria ruziziensis*/soybean, fertile soil, CS-7: Sorghum/soybean, fertile soil, CS-8: *Stylosanthes sp.* /soybean, fertile soil.

We identified fifteen species: *Acaulospora denticulata, A. foveata, A. mellea, A. scrobiculata, A. undulata, Ambispora leptoticha, Rhizophagus clarus, Glomus sp., G. formosanum, G. macrocarpum, G. tortuosum, Gigaspora sp., Racocetra fulgida, Scutellospora scutata* e *S. pellucida*.

Some species were generalists: *G. macrocarpum, G. tortuosum, A. scrobiculata, A. undulata, Glomus sp.* and *Gigaspora sp. A. undulata*, do not occurred in degraded soils. Other species were exclusive: *A. denticulata* in CS-5; *A. foveata, R. clarus* and *S. pellucida* in CS-3, which exhibited highest species richness; *S. scutata* in CS-7.

Crops on degraded soil (CS-1 and CS-2) showed a reduced richness (3 and 5 species, respectively). CS-2 stimulated increased AMF diversity, with occurrence of genus *Acaulospora*, *Glomus*, *Gigaspora* and *Racocetra*. CS-3 showed highest species richness (10 species). CS-4 showed comparable richness of CS-1, with dominance of *G. macrocarpum* and *G. tortuosum*. CS-5, CS-7 and CS-8 presented 8 species, with occurrence of *A. scrobiculata*, *A. undulata*, *Glomus sp., G. macrocarpum*, *G. tortuosum* and *Gigaspora sp*. CS-6 had no exclusive species.

Our data indicate a decreased in AMF diversity in degraded soils. Furthermore, crop systems with different host plants affect directly species richness and AMF community structure and, together appropriate soil management, improve AMF diversity, which enhance chances of efficient combinations between fungus and host plant.

Keywords: tropical soil, crop sequence, soybean, pasture

[P2.013]

Fire recurrence differentially affects the functioning of ectomycorrhizal and soil fungal communities in mediterranean pine forests

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Fire is a major disturbance of Mediterranean forests. Predicted wildfire increase associated with global change may modify the soil environment altering microbial communities, which are of key importance in forest ecosystems.

We surveyed *Pinus pinaster* Ait. (Ppi) and *Pinus halepensis* Mill. (Pha) forests, to evaluate whether fire recurrence (low/high) affected the functioning of fungal communities. Eight enzymatic activities (EAs) involved in different nutrient cycles were measured on ectomycorrhizal root tips (EM) and soil samples.

Fire recurrence effects on EAs highly diverged depending on both, the tree species and the type of sample. In general, for soil, Ppi showed higher EAs than Pha, whereas the contrary effect was observed for EM. In the case of Ppi, high fire recurrence significantly reduced most EAs in EM tips but not in soil. Contrastingly, for Pha, EAs of EM tips were almost unaffected by fire recurrence, whereas significant higher phosphatase and chitinase activities were detected in recurrently burned soils. A significant increase of laccase activity associated with high fire recurrence was observed in EM tips of both pine species, and in the case of Pha also in soil.

Contrasting edaphic-climatic conditions and/or divergent host fungal communities could be at the origin of the observed differential fire recurrence effects on fungal functioning, which could have relevant implications on decomposition rates and nutrient availability in forest ecosystems.

Keywords: Ectomycorrhizas, Fungal communities, Enzymatic activities, Fire recurrence

[P2.014]

Communities of ephemeral habitats: Do pyrophilous organisms contribute to global soil diversity and functioning?

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The vast majority of soil biodiversity and functioning research takes place in either undisturbed ecosystems or those changed by anthropogenic activity. There are also ephemeral areas recovering from fires, floods, windfalls etc. These events are recurrent phenomena, and there are species adapted to such habitats. On an example of fire-adapted soil living organisms, I review the importance of these habitats in soil biodiversity assessment.

Fire-adapted (pyrophilous) organisms live exclusively on freshly burned areas. In Finland among polypore and corticoid fungi, 46% of species recorded post-fire were not recorded before the fire (Penttila, Kotiranta, 1996). In Australia, hundreds of species out of 11846 are considered pyrophilous (McMullan-Fisher et al., 2011). Many of them grow on burned logs creating a range of compounds and microhabitats suitable for other biota.

Among carabid beetles, the proportion of pyrophils is much lower. There are approximately 10 species out of 350 in Sweden. There were 40 species (two pyrophilous) of carabids in a wildfire area close to Stockholm. Pyrophils became dominating next spring after the autumn fire constituting up to 83% of the total carabids' catch (Gongalsky et al., 2003).

Since fires affect every forest once 50-200 years, each forest patch undergoes the stage of burned area. Pyrophils inhabiting these ecosystems for up to 5-10 years, occur in approximately 1-10% time of ecosystem cycle. Their role in ecosystem functioning is by far underestimated.

Keywords: Ephemeral habitat, Pirophilous, Carabidae, Fungi

[P2.015]

Diversity of bacteria isolated from legume nodules cultivated in soils from a tropical mountain ecosystem

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Tropical mountain ecosystems cover 25% of the Earth's surface and are known for their high degree of endemism and plant species richness. In Brazil, these ecosystems exist in different biomes, but little is known about them, especially regarding soil microorganisms and their functions and interactions.

The aim of this study was to assess the diversity of bacteria isolated from legumes nodules from different habitats that compose rupestrian fields (quartz gravel field, sandy bogs, peat bogs, rocky outcrop and cerrado), an important environment type located in tropical mountains from Serra do Cipó, Minas Gerais, Brazil. To capture legume nodulating bacteria (LNB) - two trap plants species (*Macroptilium atropurpureum* and *Mimosa tenuiflora*) were grown in a mixture of soil inoculum and sterile substrate. After 90 days, the nodules were collected, and the isolated bacteria were characterized by culturing. In total, 381 isolates were characterized, which were mostly fast-growing and culture medium 79-acidifying bacteria with colonies of up to 1 mm in diameter.

A total of 90 distinct culture groups were found, indicating high phenotypic diversity of the bacteria isolated from legumes nodules in rupestrian fields. We partially sequenced 16S rRNA from strains representing 55 culture groups. Most isolates belonged to the alpha- and beta-classes of proteobacteria, with a predominance of the *Rhizobium* and *Burkholderia* genera, respectively. The use of more than one trap plant belonging to distinct subfamilies (Faboideae and Mimosoideae) was essential for capturing greater LNB diversity. The high diversity of LNB cultures found in rupestrian fields did not correlate to a specific habitat or to the occurrence of legumes (present in the different habitats).

However, the greatest genetic and culture group diversity was found in the cerrado habitat, and there is evidence that this diversity is important in maintaining the bacterial diversity in other habitats.

Acknowledge: CNPq, FAPEMIG, CAPES

Keywords: Rupestrian fields, Burkholderia, Rhizobium, Soil biodiversity

[P2.016]

Diversity and biotechnological potential of bacteria isolated from nodules of cowpea grown in floodplain soils

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Certain nodulating nitrogen-fixing bacteria in legumes and other non-symbiotic nodule endophytes perform different plant-growth promoting processes.

The objective of this study was to evaluate 26 bacterial strains isolated from nodules of cowpea grown in floodplain soils of southwestern Piauí State, Brazil, regarding genetic diversity, performance of plant-growth promoting processes and the effect of inoculation on soybean and cowpea plants.

The following processes were evaluated: free-living biological nitrogen fixation (BNF), solubilization of calcium, aluminum and iron phosphates and production of indole-3-acetic acid (IAA). The abilities to nodulate and promote growth in soybeans and cowpea were evaluated in glass bottles and Leonard jars, respectively.

Partial sequencing of the 16S rRNA gene identified 60% of the strains as belonging to genus *Paenibacillus*. The following four genera were also identified: *Bacillus*, *Bradyrhizobium*, *Enterobacter* and *Pseudomonas*. None of the strains fixed nitrogen free-living, 80% solubilized calcium phosphate and the highest IAA concentrations (52.37, 51.52 and 51.00 μg mL^{-1}) were obtained in “79” medium with tryptophan by *Enterobacter* strains UFPI B5-7A, UFPI B5-4 and UFPI B5-6, respectively. Only UFPI B3-4 (*Bradyrhizobium* sp.) nodulated soybeans, but 50% of the strains increased production of the root dry matter. Only eight strains nodulated the cowpea, however, all increased production of the total dry matter.

The fact that the strains evaluated to act in different biological processes and in promoting plant growth indicates that these strains have potential application in agricultural crops, for promoting increased plant production and environmental sustainability.

Acknowledgments: The Technology and National Council for Scientific and Technological Developmentfor financial support (CNPq), the Brazilian Federal Agency for the Support and Evaluation of Graduate Education (Capes) the CNPq and the Minas Gerais Research Foundation (FAPEMIG*)* for granting scholarships.

Keywords: plant growth promotion, biological nitrogen fixation, phosphate solubilization, indole-3-acetic acid

[P2.017]

Characterization of Growing Bacterial Populations in McMurdo Dry Valley Soils through Stable Isotope Probing with ^{18}O-water

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Initial surveys of microbial diversity in soils of the McMurdo Dry Valleys, Antarctica using 16S rRNA gene sequencing revealed a surprising bacterial richness, including representatives from at least fourteen different phyla. However, given the low rates of microbial activity and decomposition, it is unclear whether this richness represents functioning rather than dormant members of the community. We used stable isotope probing (SIP) with ^{18}O-water to determine if microbial populations grow in McMurdo Dry Valley soils by characterizing changes in the microbial community of soils amended with $H_2{}^{18}O$ and $H_2{}^{18}O$-organic matter. We show that DNA of microbial populations was indeed labeled with ^{18}O-water, indicating these microorganisms grew in the McMurdo Dry Valley soils. Bacterial richness and diversity was not significantly different between the labeled and non-labeled DNA of all treatments, but in general, decreased in the $H_2{}^{18}O$-organic matter treatments. Significant differences existed in the community composition of the labeled and non-labled DNA fractions of the $H_2{}^{18}O$ and $H_2{}^{18}O$-organic matter amended samples. The control samples and the non-labeled DNA fraction of the $H_2{}^{18}O$ amended samples were dominated by representatives of the phyla Deinococcus-Thermus, Proteobacteria, Planctomyces, Gemmatimonadetes, Actinobacteria and Acidobacteria. Proteobacteria were more prevalent in the labeled DNA fractions from the $H_2{}^{18}O$-water and the $H_2{}^{18}O$-water-organic matter treatments than in the control treatment or the light fraction from the $H_2{}^{18}O$ water treatment. In addition, the Firmicutes were more abundant in the light DNA fraction of the $H_2{}^{18}O$-organic matter treatment . Our results indicate that SIP with $H_2{}^{18}O$ is a viable technique even in this cold, low bacterial biomass environment. This technique may offer new insights into the environmental parameters that govern growth of microbial populations in soils of the McMurdo Dry Valleys.

Keywords: Antarctica, Stable Isotope Probing, Growth

[P2.018]

Springing away? Collembola responses to different traffic and tillage farming systems

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Diversity in soil fauna communities has often been linked to ecosystem function. This is important in agricultural ecosystems where there are trade-offs between provisioning and regulating ecosystem services. Multiple studies have shown that soil fauna are negatively affected by high intensity agricultural management, such as deep cultivation (tillage) and soil compaction from agricultural traffic.

Collembola are an important component of soil mesofauna to consider in soil management. As detritivorous hexapods feeding on organic matter they have been shown to increase decomposition rates, by increasing substrate surface area for microbiota and by the transmission of microbiota across substrate via the Collembolan gut. As prey of natural enemies such as Carabid beetles and spiders, Collembola act as an important link between the macro and mesofauna communities. Collembola predominantly live in the upper soil layers and are negatively affected by high intensity agricultural management.

As part of an experiment at Harper Adams University, looking at the effect of different traffic and tillage systems on crop yield, Collembola were monitored before and after the harvest of winter barley (KWS Cassia). Soil cores of 65mm x 100 mm were taken in June and July 2014 from plots in a 3x3 replicated factorial experiment of three traffic systems: random traffic farming, low ground pressure and controlled traffic farming; and three tillage systems: deep tillage (250mm depth), shallow tillage (100mm depth) and zero tillage. Bulk density, soil moisture and organic matter were also measured to quantify structural and environmental changes in the soil habitat.

Collembola species and community responses to traffic and tillage farming systems will be explored with univariate and multivariate statistical analysis. Results will aid future soil management strategies.

Keywords: Collembola, Community, Ecosystem, Management

[P2.019]

Soil functional diversity and global warming potential in pasture under T-FACE systems.

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Recently, a novel link in methane-nitrogen cycle interactions has been discovered in the not well-known form methane-oxidizing bacteria (MOB) which are capable of denitrification into N_2 and to do the first step of aerobic methane-oxidation, catalyzed by either soluble or particulate methane monooxygenase (pMMO). Our objective was to assess the consequences of climate change on soil microbial communities. The research was conducted in a T-FACE (*temperature free-air controlled enhancement* e *carbon dioxide free-air enrichment*) facility at the University of São Paulo, Ribeirão Preto, São Paulo, Brazil, with *Stylosanthes capitata* Vogel e *Panicum maximum* Jacq. grown in consortium. We used real-time PCR to quantify the functional genes AOB, *pmo*A, *nos*Z, and higt-throughput sequencing approaches of the Illumina platform to access the denitrifying composition. The greenhouse gas emissions were mesured using the closed static chambers. In the T-FACE system plants were exposed to elevated CO_2 (eC, +50% of ambient CO_2), heated (eT, +2ºC of ambient temperature), heated+elevated CO_2 (eT+eC) and control, with four replications. The global warming potential was increased with elevated temperature by 37 to 41% in eT+eC and eT, respectively. These results suggest that the temperature rising during this experiment may favor the emission of greenhouse gases. The abundance of the gene *nos*Z and MOB with the capacity to complete denitrification to N_2 was increased after soil fertilization, a result that suggests greater sink capacity of N_2O by the soil, but without clear effects of elevated temperature and CO_2. In this study, the most representative taxonomic groups involved in soil denitrification in this study were bacteria (*Actinobacteria and Protobacteria)* and archaea (*Thaumarchaeota* and *Euryarchaeota)*. The taxonomic composition was redundant between C and eT+eC, but functional diversity was distinct and higher for eT+eC, showing clear effects of elevated temperature and CO_2 concentration, possibly associated with N_2O emissions. Financial support: FAPESP 08/58075-8

Keywords: Functional markers, microbial ecology, elevated CO2, climate change

[P2.020]

Composition of decomposers community depending on N availability and litter degradation

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Introduction

Despite numerous data on C- and N-cycling in soil, considerable uncertainties remain concerning the relationship between N availability and decomposition of organic matter. We hypothesized that reactive N from fertilizers and from depositions will change both the respiration activity and community structure of organisms decomposing woody debris (WD) with high C:N ratio. We estimated these shifts at the initial and progressive stages of WD decomposition.

Methods

We analyzed phospholipid fatty acid (PLFA) profiles of WD decomposers in the incubation experiment (samplings at 1, 3, and 6 months) with woody pine material milled to saw-dust size. There were 2 unfertilized controls: fresh undecomposed wood (C:N = 510) and woody material after 5-yr decomposition (C:N = 88) and 2 N–fertilized treatments. KNO_3 was added to adjust C:N ratio to 125 and 30 in fresh and decomposed WD, respectively.

Results and Discussion

Addition of mineral N increased the proportion of fungal PLFA from 18 to 31% in fresh WD compared to unfertilized control, while that in decomposed WD strongly decreased their percentage from 19 to 7%. Bacteria-to-fungi ratio varied insignificantly from 2.5 to 3.2 during the incubation in both unfertilized treatments. By contrast, this ratio in N-fertilized fresh WD increased from 1.5 to 6.4, while that in N-treated decomposed WD decreased from 8.5 to 4.9. Besides, N addition increased microbial respiration in fresh and inhibited CO_2 efflux from decomposed WD.

Thus, oppositely directed shifts of microbial respiration in fresh and decomposed WD caused by N fertilization were strongly related to the percentage of fungal biomass in decomposers community.

Acknowledgements

The research was supported by the Alexander von Humboldt Foundation, the Russian Foundation for Basic Researches, Presidium of the Russian Academy of Sciences, and the grant NSh-6123.2014.4.

Keywords: coarse woody debris, decomposers, PLFA profiling, CO2

[P2.021]

Impact of logging-associated compaction on forest soil microbial community structure and activities

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Heavy traffic can cause drastic changes in soil porosity and structure, but we lack a fundamental understanding of how this affects the soil microbiome (Hartmann et al., 2014). The optimal soil water content for aerobic microbial activity depends significantly on soil bulk density among others soil parameters (Schjønning et al., 2003). Thus, alterations in soil porosity after compaction may strongly affect microbial community structure and activities. Here, we assessed those parameters after 7 years of soil compaction following heavy traffic. The site studied is located in a state-owned forest in northeast France (Azerailles, Meurthe et Moselle). The soil is a Luvisol developed on a silt loam layer approximately 50 cm thick laying on a clayey layer; this strong textural discontinuity causing limited temporary water logging (Goutal et al. 2012). In May 2007, a 8-wheel drive forwarder (25T) drove for an equivalent of one pass back and forth. In March 2014, soil samples were collected in the trafficked and undisturbed plots and gas emissions were measured in the field. The quantification and diversity of different microbial groups were studied by combining q-PCR and terminal restriction fragment length polymorphism (TRFLP), respectively targeting 16S rDNA and ITS genes for bacterial, fungal and archae communities (Osborn et al., 2000; Fierer et al., 2005). Microbial functions were monitored by measuring enzymatic activities, catabolic profiling using MicroResp^{TM} technique (Campbell et al. 2003) and gas measurements. Field measurements first showed significant changes in soil processes, resulting in reduced CO_2, and increased CH_4 and N_2O emissions from compacted soils. Compactions significantly reduced abundance of microorganisms and to a less extend microbial activities. It also persistently altered the structure of the microbiota This study demonstrates that physical soil disturbance induces profound and long-lasting changes in the soil microbiome and associated soil functions.

Keywords: Soil Microbial Communities, Soil Compaction, Forest, Resilience

[P2.022]

Influence of food availability and placement on earthworm communities after introducing lumbricus terrestris in arable fields

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Agricultural practices differentially affect earthworm species, due to species-dependent response traits. Intensively managed arable fields are largely dominated by endogeic species. Epigeic and anecic species, while often absent in these systems, may potentially provide many ecosystem services, such as crop residue decomposition (epigeic and anecic) and water infiltration through their large burrows (anecic species). Many factors can hamper the establishment of these functional groups, e.g. food availability, tillage, and competition, but the extent to which these play a role is not understood. We studied the response of i) the local earthworm community to different food quantities and placements; ii) the local community to the introduction of an anecic species (*Lumbricus terrestris*), which was previously absent from our study site; and iii) the response of the introduced *L. terrestris* to different food quantities and placements. We aim at tackling these issues in terms of community response traits.

Two parallel field experiments were established in the Fall of 2013, in two adjacent arable fields: one is mouldboard-ploughed (CT) yearly and the other is under non-inversion tillage (NIT). Both experiments consist of a split-plot design, where the main-plot is introduction of *L. terrestris (*presence or absence) and the sub-plot is food availability (quantity in NIT and placement in CT). Earthworm sampling occurred during Spring 2014, and is planned for the Fall of 2014 and 2015. Forthcoming results will illustrate the effects of our treatments in the local and manipulated earthworm communities. The underlying mechanisms are further studied in a parallel greenhouse experiment, where single- and multi-species mesocosms are subjected to different food placements in the soil profile. The acquired understanding will improve our knowledge on species interactions within earthworm communities, strengthen the use of trait-based approaches in earthworm ecology, and therefore help with predicting earthworm community in arable landscapes.

Keywords:

[P2.023]

Driving Factors for Communities of Nine Groups of Soil Organisms in Eastern Brazilian Amazon

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Brazilian Amazon is a huge reservoir of biodiversity, including below-ground organisms that mediate key process for the functioning of ecosystems. Determining the driving factors that shape the community structure of these organisms, including anthropogenic factors, is an important step toward understanding and managing sustainably these ecosystems. The diversity of nine groups of soil organisms (Culturable and unculturable Bacteria, microfungi, arbuscular micorrhizal fungi, nematodes, mesofauna, macrofauna, ants, termites and beetles) were studied in 98 sampling points which comprised six land uses: Primary Forest, Old Secondary Forest, Young Secondary Forest, Agroforestry, Agriculture, and Pasture. These sampling points were located in Benjamin Constant Municipality (Amazonas State, Brazil), Upper Solimões river, on the triple frontier of Brazil, Colombia and Peru and included the indigenous communities of Guanabara II (Ticunas) and Nova Aliança (Cocamos) and the town of Benjamin Constant. Here, we perform a variance partitioning for these nine groups of soil organisms into four matrices of explanatory variables: spatial structures, vegetation, edaphic conditions, land use, and the interrelationships among them. We also calculate the indicator value index for six of these groups of soil organisms. We found that land use change, either alone or with its associated changes in soil conditions and/or vegetation, explains significant proportions of the total community variation for seven of these groups. Despite the predominance of actively dispersed organisms in these groups, evidences of dispersal limitations were found in 55% of them. Many species in all land use systems were good indicators. However, beetles in Primary Forest and Agriculture as well as arbuscular mycorrhizal fungi and termites in Pastures had species with highest IndVal (>0.60). Thus, the communities studied for all nine groups of soil organisms are significantly associated with environmental conditions, and that, for five groups, spatial dynamics is also an important driving factor for community structure.

Keywords: microorganisms, microfauna, mesofauna, macrofauna

[P2.024]

Effects of aboveground herbivores of different body size on soil mesofauna communities in subalpine meadows

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Introduction

Most grasslands harbor diverse assemblages of aboveground herbivores, including ungulates, rodents and invertebrates, as well as a diverse and functionally important soil mesofauna community. Impacts of herbivores on these soil communities are mostly known from studies on ungulates in agroecosystems. However, recent microcosm studies on aboveground-belowground interactions are revealing that smaller herbivores can also exert important effects on soil fauna populations. Our aim was to investigate how aboveground herbivores of different body size affect soil mesofauna in a natural system.

Methods

We used size-selective fences to progressively exclude large (deer and chamois), medium (marmots and hares) and small (mice) vertebrate as well as invertebrate herbivores in subalpine meadows in the Swiss National Park. Exclosures were erected in two vegetation types: short- and tall-grass vegetation, resulting from a long-term difference in ungulate grazing pressure. We studied how soil microarthropod and nematode communities responded to vegetation type and herbivore exclusion treatments.

Results

Nematode abundance was higher and nematode community composition different when all or all but invertebrate herbivores were excluded. Effects of the herbivore exclusion treatments on soil microarthropod communities were limited to a reduction in springtail richness when all herbivore groups were excluded.

Tall-grass vegetation had higher springtail richness and mesostigmatid mite abundance, a lower bacterivorous nematode richness and a different oribatid mite community structure compared to short-grass vegetation. We explored mechanisms behind these changes using analysis of covariance and structural equation modeling.

Conclusion

Excluding herbivores of different body size elicited changes in soil communities even after only a few growing seasons, and small herbivores generally had a larger effect than ungulates. The strong differences between the two vegetation types, moreover, indicate that over centuries, ungulates can indirectly alter soil communities through changes in vegetation. Our results show that differently sized herbivores can have specific effects on grassland communities.

Keywords: aboveground-belowground interactions, grazing, nematodes, microarthropods

[P2.025]

Diazotrophic communities respond less to fertilizer regime than soil depth and seasonal variation

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N_2 fixation by diazotrophic communities is a considerable source of nitrogen input to soil. As we know, lots of microorganisms inhabit in the deeper soils, nevertheless, little information is available for the diazotrophic communities in these oligotrophic and anaerobic living conditions. In present studies, soil vertical profile samples across nine rice-wheat rotations growing seasons from 12-Oct to 13-Oct with four different fertilizer regimes were collected. Quantitative PCR were used to determine the nifH gene and total bacterial 16SrDNA gene abundance. Abundant of nifH (>10^6 copies per gram dry soil) and 16SrDNA (>10^8 copies per gram dry soil) genes were found in the deepest soil layers, and both of them were apparently stratified and decreased by soil depth. Besides, the nifH gene abundance were significantly positively correlated to the bacterial abundance in subsoil layers, but not necessary in the topsoil. Furthermore, we used the terminal restriction fragment length polymorphism (T-RFLP) to describe the diazotrophic structures. The T-RFLP profiles showed that the diazotrophic structures were different among soil layers, with further analyses of multivariate regression tree (MRT) and variance partitioning analysis (VPA), it is definite that soil depth instead of sampling time or fertilizer regime was the decisive factor influencing the diazotrophic structures. Overall, our results indicate that soil depth is the strongest factor influencing the diazotrophic size and structure, the effect of fertilizer regime is secondary to sampling time.

Keywords: diazotrophic communities, soil vertical profile, seasonal variation, fertilizer regime

[P2.026]

The Global Atlas of Soil Biodiversity

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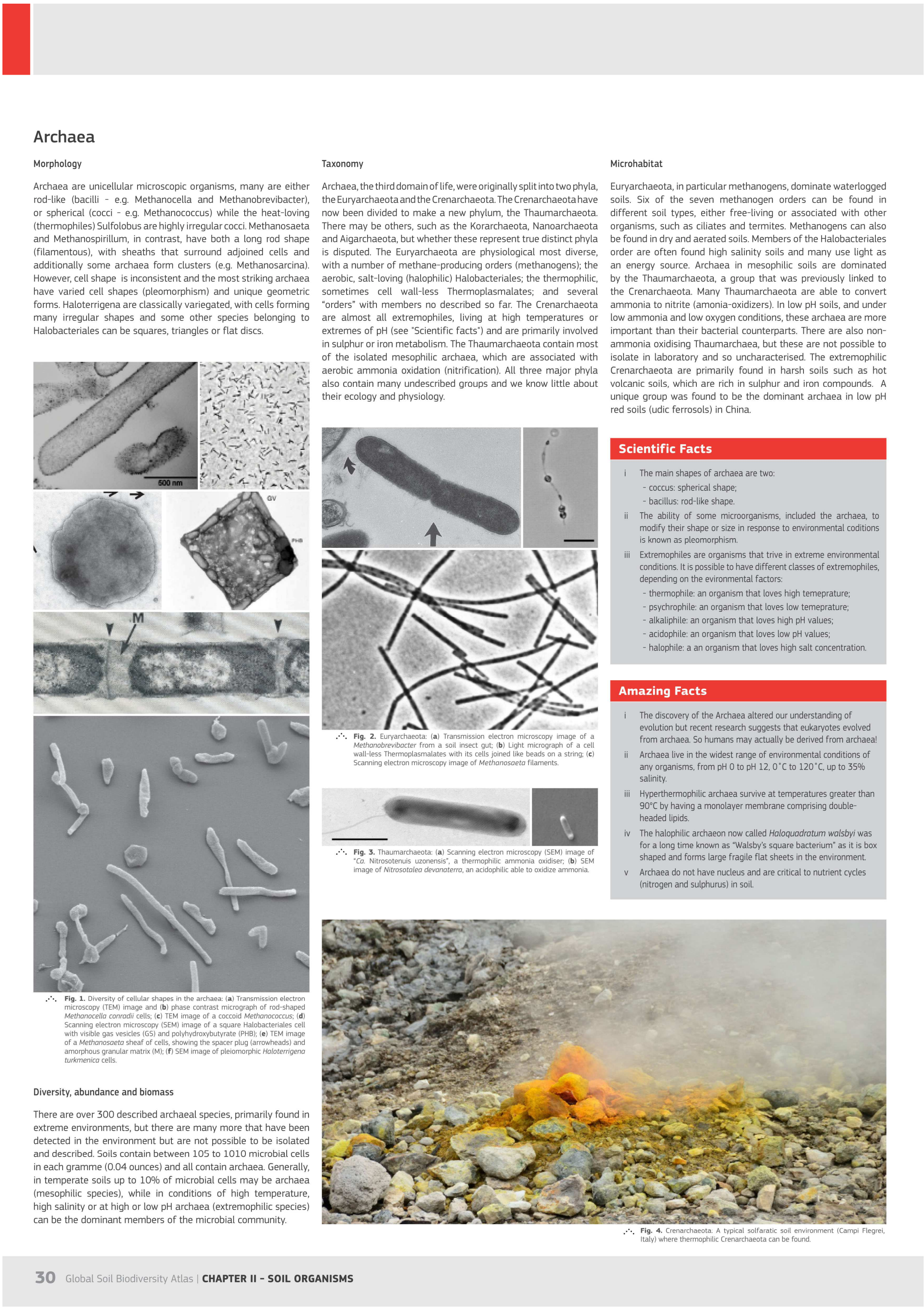
Soils provide numerous ecosystem services. Most people do not know that the key drivers of soil ecosystems are the living organisms within the soil. Soils may be home to over one fourth of all living species on Earth, with a significant part not yet characterized.

The first Global Soil Biodiversity Atlas is a product of the Global Soil Biodiversity Initiative. It aims at raising awareness of the importance and beauty of soil biodiverity among the general public and policy makers. Furthermore, it highlights the need to increase efforts to develop a global assessment of soil biodiversity. Data on distribution of soil-dwelling organisms are often difficult to combine. The atlas represents an attempt to create a unique network among soil biodiversity scientists. Such an effort may help in reaching the level of attention that research on soil biodiversity deserves. With contributions from over 80 experts in soil biodiversity from all over the world, and over 170 pages, the atlas will also display distribution maps of the main soil organisms. Furthermore, an exceptionally high number of images will allow non-specialists to get in touch with this fascinating and mysterious world.

Everybody can contribute toward developing the Atlas thanks to the call for photos open until the end of 2014. Details are available at the First Global Soil Biodiversity Conference.



Archaea

Morphology

Archaea are unicellular microscopic organisms, many are either rod-like (bacilli - e.g. Methanocella and Methanobrevibacter), or spherical (cocci - e.g. Methanococcus) while the heat-loving (thermophiles) Sulfolobus are highly irregular cocci. Methanosaeta and Methanospirillum, in contrast, have both a long rod shape (filamentous), with sheaths that surround adjoined cells and additionally some archaea form clusters (e.g. Methanosarcina). However, cell shape is inconsistent and the most striking archaea have varied cell shapes (pleomorphism) and unique geometric forms. Haloterrigena are classically variegated, with cells forming many irregular shapes and some other species belonging to Halobacteriales can be squares, triangles or flat discs.

Fig. 1. Diversity of cellular shapes in the archaea: (**a**) Transmission electron microscopy (TEM) image and (**b**) phase contrast micrograph of rod-shaped *Methanocella conradii* cells; (**c**) TEM image of a coccoid *Methanococcus*; (**d**) Scanning electron microscopy (SEM) image of a square Halobacteriales cell with visible gas vesicles (GS) and polyhydroxybutyrate (PHB); (**e**) TEM image of a *Methanosaeta* sheaf of cells, showing the spacer plug (arrowheads) and amorphous granular matrix (M); (**f**) SEM image of pleiomorphic *Haloterrigena turkmenica* cells.

Diversity, abundance and biomass

There are over 300 described archaeal species, primarily found in extreme environments, but there are many more that have been detected in the environment but are not possible to be isolated and described. Soils contain between 105 to 1010 microbial cells in each gramme (0.04 ounces) and all contain archaea. Generally, in temperate soils up to 10% of microbial cells may be archaea (mesophilic species), while in conditions of high temperature, high salinity or at high or low pH archaea (extremophilic species) can be the dominant members of the microbial community.

Taxonomy

Archaea, the third domain of life, were originally split into two phyla, the Euryarchaeota and the Crenarchaeota. The Crenarchaeota have now been divided to make a new phylum, the Thaumarchaeota. There may be others, such as the Korarchaeota, Nanoarchaeota and Aigarchaeota, but whether these represent true distinct phyla is disputed. The Euryarchaeota are physiological most diverse, with a number of methane-producing orders (methanogens); the aerobic, salt-loving (halophilic) Halobacteriales; the thermophilic, sometimes cell wall-less Thermoplasmalates; and several "orders" with members no described so far. The Crenarchaeota are almost all extremophiles, living at high temperatures or extremes of pH (see "Scientific facts") and are primarily involved in sulphur or iron metabolism. The Thaumarchaeota contain most of the isolated mesophilic archaea, which are associated with aerobic ammonia oxidation (nitrification). All three major phyla also contain many undescribed groups and we know little about their ecology and physiology.

Fig. 2. Euryarchaeota: (**a**) Transmission electron microscopy image of a *Methanobrevibacter* from a soil insect gut; (**b**) Light micrograph of a cell wall-less Thermoplasmalates with its cells joined like beads on a string; (**c**) Scanning electron microscopy image of *Methanosaeta* filaments.

Fig. 3. Thaumarchaeota: (**a**) Scanning electron microscopy (SEM) image of "*Ca.* Nitrosotenuis uzonensis", a thermophilic ammonia oxidiser; (**b**) SEM image of *Nitrosotalea devanaterra*, an acidophilic able to oxidize ammonia.

Microhabitat

Euryarchaeota, in particular methanogens, dominate waterlogged soils. Six of the seven methanogen orders can be found in different soil types, either free-living or associated with other organisms, such as ciliates and termites. Methanogens can also be found in dry and aerated soils. Members of the Halobacteriales order are often found high salinity soils and many use light as an energy source. Archaea in mesophilic soils are dominated by the Thaumarchaeota, a group that was previously linked to the Crenarchaeota. Many Thaumarchaeota are able to convert ammonia to nitrite (amonia-oxidizers). In low pH soils, and under low ammonia and low oxygen conditions, these archaea are more important than their bacterial counterparts. There are also non-ammonia oxidising Thaumarchaea, but these are not possible to isolate in laboratory and so uncharacterised. The extremophilic Crenarchaeota are primarily found in harsh soils such as hot volcanic soils, which are rich in sulphur and iron compounds. A unique group was found to be the dominant archaea in low pH red soils (udic ferrosols) in China.

Scientific Facts

i The main shapes of archaea are two:
  - coccus: spherical shape;
  - bacillus: rod-like shape.

ii The ability of some microorganisms, included the archaea, to modify their shape or size in response to environmental coditions is known as pleomorphism.

iii Extremophiles are organisms that trive in extreme environmental conditions. It is possible to have different classes of extremophiles, depending on the evironmental factors:
  - thermophile: an organism that loves high temeprature;
  - psychrophile: an organism that loves low temeprature;
  - alkaliphile: an organism that loves high pH values;
  - acidophile: an organism that loves low pH values;
  - halophile: a an organism that loves high salt concentration.

Amazing Facts

i The discovery of the Archaea altered our understanding of evolution but recent research suggests that eukaryotes evolved from archaea. So humans may actually be derived from archaea!

ii Archaea live in the widest range of environmental conditions of any organisms, from pH 0 to pH 12, 0˚C to 120˚C, up to 35% salinity.

iii Hyperthermophilic archaea survive at temperatures greater than 90°C by having a monolayer membrane comprising double-headed lipids.

iv The halophilic archaeon now called *Haloquadratum walsbyi* was for a long time known as "Walsby's square bacterium" as it is box shaped and forms large fragile flat sheets in the environment.

v Archaea do not have nucleus and are critical to nutrient cycles (nitrogen and sulphurus) in soil.

Fig. 4. Crenarchaeota: A typical solfaratic soil environment (Campi Flegrei, Italy) where thermophilic Crenarchaeota can be found.

A page of the Global Soil Biodiversity Atlas.

Keywords: soil biodiversity, atlas, awareness, global soil biodiversity initiative

[P2.027]

Diazotrophic communities respond less to fertilizer regime than soil depth and seasonal variation

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N_2 fixation by diazotrophic communities is a considerable source of nitrogen input to soil. As we know, lots of microorganisms inhabit in the deeper soils, nevertheless, little information is available for the diazotrophic communities in these oligotrophic and anaerobic living conditions. In present studies, soil vertical profile samples across nine rice-wheat rotations growing seasons from 12-Oct to 13-Oct with four different fertilizer regimes were collected. Quantitative PCR were used to determine the nifH gene and total bacterial 16SrDNA gene abundance. Abundant nifH ($>10^6$ copies per gram dry soil) and 16SrDNA ($>10^8$ copies per gram dry soil) genes were found in the deepest soil layers, and both of them were apparently stratified and decreased by soil depth. Besides, the nifH gene abundance were significantly positively correlated to the bacterial abundance in subsoil layers, but not necessary in the topsoil. Furthermore, we used the terminal restriction fragment length polymorphism (T-RFLP) to describe the diazotrophic structures. The T-RFLP profiles showed that the diazotrophic structures were different among soil layers, with further analyses of multivariate regression tree (MRT) and variance partitioning analysis (VPA), it is definite that soil depth instead of sampling time or fertilizer regime was the decisive factor influencing the diazotrophic structures. Overall, our results indicate that soil depth is the strongest factor influencing the diazotrophic size and structure, the effect of fertilizer regime is secondary to sampling time.

Keywords: diazotrophic communities, soil vertical profile, seasonal variation, fertilizer regime

[P2.028]

Soil photosynthetic microbial communities as bioindicators for pesticide stress assessment

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Standardized soil microbial indicators, used to assess the impacts of agricultural practices and/or contaminations, lack of sensitivity and genericity against pesticide stresses, especially for herbicides. Soil photosynthetic microorganisms, mainly represented by micro-algae (chlorophyceae, xanthophyceae and diatoms) and cyanobacteria, can growth in soil surface (grassland, cereal crops and rice fields). So, they could be an original microbiological model for herbicides risk assessment in agricultural soils. Nevertheless, the knowledge of their structural and functional biodiversity and of environmental factors influencing their dynamics is still largely unknown. Improving our understanding of this microorganisms require 1) developing biochemical and molecular methods to characterize activities and genetic diversity of photosynthetic microorganisms and 2) analysing their responses to contaminants.

Several methodologies commonly used for aquatic systems were adapted to soil. Cultural approaches are still helpful to isolate edaphic species for further ecotoxicological tests and barcoding approaches. Photosynthetic pigments can provide biomass (chlorophyll-*a*) or structural (pigment diversity) indicators. Several genetic markers from aquatic studies were successfully applied on soils samples. A major limit remains the lack of specific databases of genetic markers for photosynthetic microorganisms.

Throughout field and microcosm approaches, micro-algal and cyanobacterial communities showed a higher sensitivity, compared to commonly bacterial and fungal community endpoints. Several studies showed toxic effects or tolerance acquisition towards various herbicides, applied at agronomical doses. Comparison of responses of photosynthetic microbial communities, between different cropping systems (organic vs. conventional), highlighted tolerance acquisition towards a new herbicidal stress, in relation with the intensity of pesticide treatments. Genetic diversity characterization of micro-algal and cyanobacterial communities in these cropping systems, provides further results to identify taxa relating to tolerance or sensitivity.

These innovative investigations demonstrate the suitable issues of soil photosynthetic microorganisms as indicators reporting herbicide non-target impacts on soil biodiversity. Prospects for monitoring remediation of polluted soils (heavy metals, HAP) should be considered.

Keywords: soil microalgae, herbicide, cyanobacteria, bioindicator

[P2.029]

Biochem-Env, a platform of environmental biochemistry for research in ecology and ecotoxicology

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The consortium ANAEE France (http://www.anaee-s.fr) aims at understanding and predicting the biodiversity and ecosystems dynamics in a context of global change. It will allow improving the understanding of biotic processes/environment interactions, mobilizing experimental and modelling platforms devoted to the biology of continental ecosystems, both terrestrial and aquatic.

In this context, the objectives of the platform Biochem-Env (http://www.biochemenv.fr) are to provide skills and innovative tools for biochemical characterizations of soils, sediments, and living micro-macroorganisms. These approaches are related to the assessment of ecosystems functioning.

The scope of the platform Biochem-Env includes:

- the technology intelligence and the development of tools used for the biochemical characterization of solid environmental matrices and macrofauna,
- the development of an Environmental Information System (referential for functional biodiversity) for managing the traceability of samples and data, and improve our ability to characterize the biological status of environmental matrices.

Available as a scientific partner in the frame of collaborative research projects, the platform's abilities ranges from advice providing (sampling, protocols and data analysis), to technical training, including analysis and experimentation in regional, national and international research programs.

The tools of the platform have been deployed in programs targeted at assessing the sensitivity and restrictions of biological indicators of soil quality, subjected to various constraints (waste landfilling, farming practices, contaminated sites and soils…).

For example, long-term experimental sites provide opportunities to assess the effects of pressures and threats on soils and their functioning. In a context of soil contamination, we can conclude using global soil enzymatic activities that soil functioning is enhanced in biological farming comparatively to conventional practices.

Keywords: Environmental biochemistry, microbial, macrofauna, enzymes

[P2.030]

Soil biotic legacy effects on the drought response of microbial communities and carbon cycling.

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Interactions between aboveground and belowground biota have the potential to modify ecosystem responses to climate change. While there is growing evidence that drought affects plant growth and soil microbial communities, little is known about the effect of drought on the direction and strength of plant-soil feedbacks, and the consequences for processes of carbon cycling. Recent studies suggest that legacy effects of dominant plant species and drought on soil microbial communities could both influence future responses of plants to drought, in terms of growth and nutrient uptake, but the mechanisms involved are poorly understood. We set up a glasshouse experiment to test the hypotheses that plant growth is less affected by drought in soil conditioned by conspecific species (i.e. by the same species) and when soil has previously experienced drought conditions, and that these changes are related to shifts in the soil microbial community composition. Two plant species were grown in soils with four different histories (conspecific or not, undergone previously drought or not), in monoculture or in competition, and were then exposed to a drought. Plant community responses were examined by measuring growth, phenotypic plant traits and biomass resource allocation traits. Soil microbial community responses were characterised, and CO_2 fluxes were quantified. We found that conditioning changed soil microbial community composition. The response of soil microbial communities to drought depended on soil history, and also plant identity and competitive interactions. Associated effects on soil processes occurred as soil respiration and net ecosystem exchange are modified. Finally, plant resistance and resilience to drought have changed, with consequences for nutrient uptake by plants, as evidenced by changes in the C/N ratio of plant biomass. Our findings suggest that recurrent droughts have long lasting effects on belowground communities with consequences for feedbacks to aboveground communities and for carbon cycling.

Keywords: Drought, plant-soil interaction, C and N cycling, Legacy

[P2.031]

Ten years of QBS-ar index application: state of the art

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During the last century, soils have been over-exploited by humans through agriculture and industrial development. These activities have caused dramatic consequences not only for the human health but also for the environment and soil biodiversity. The need to assess different aspects of soil degradation has become a priority in the soil protection management.

Combined with the physico-chemical methods, biological monitoring is important to assess soil degradation correctly. For this reason the use of bioindicators represents a needful tool to evaluate soil health. The complex relations that link soil fauna with their ecological niches, their limited mobility and their inability to leave the soil in negative conditions, make some taxa (e.g. Collembola, Protura, Pauropoda) particularly vulnerable to soil changes and good “tools” for soil bioindication. Usually, soil invertebrate-based indices consider the consistency and richness of populations. The difficulties to identify soil fauna at species level are well known; in addition, this level of identification asks long time that makes this approach not suitable for monitoring systems.

QBS-ar index, a biological method that joins the biodiversity of soil microarthropods community with the degree of soil animals vulnerability, can be a valid tool in the monitoring actions. This index has been proposed by Italian researchers (Parma University) more than ten years ago and it has been applied in several ecosystems, agricultural lands, grasslands, urban soils, woods at different level of naturality, and degraded soils, by Italian and European specialists. Several published papers reported the results of the QBS-ar application. We would make a critical evaluation of the results obtained in these ten years of QBS-ar application.

Keywords: Bioindicators, Soil microarthropods, QBS-ar, Soil quality

[P2.032]

Measurement of soil functional diversity: do CLPPs and enzymes target the same microbial processes?

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Microbial functional diversity represents the sum of the ecological processes developed by the organisms of a community and it can be expressed through species or important groups to maintain several functions in the soil, while the genetic one represents gene and genotype variations. Distinct from the genetic diversity of the soil microbial biomass which assess potential diversity, functional diversity is related to the actual activities resulting from that potential so that "functional rather than taxonomic diversity may provide greater insight to microbial roles in ecosystems". In the current literature, functional diversity of soil microbial communities is determined alternatively either through enzyme activities or by means of community level physiological profile (CLPP) techniques, such as Biolog™ and/or MicroResp™. In very few studies both approaches are used and thus it is discussed whether the same results were obtained.

We measured microbial functional diversity, using both methodological approaches, in four case-studies differing in pedogenetic substrates, plant cover and land use.

In all cases the diversity indexes calculated using enzyme activities and CLPP gave opposite results suggesting that we are probably pointing to different components of microbial functional diversity. We thus hypothesize that measuring microbial functional diversity by means of enzymes or CLPP methods provides information on sequential processes occurring in soil: firstly the exemplification of complex organic substrates obtained after enzymatic hydrolysis and secondly the direct utilization of simple substrates, derived from the previous step, by microorganisms (CLPPs). An promising research field could be the search for a synthetic index that takes into account and integrates different components of microbial functional diversity.

Keywords: Microbial functional diversity, CLPP, Enzymes

[P2.033]

The influence of slash and burn clearing on bacterial community diversity in Fynbos soil

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Soil microbes are important role-players in the functioning of ecosystems. Disturbances such as fire are of particular interest in microbial ecology due to the dramatic effect on the diversity and structure of soil bacterial communities. Species such as Acasia saligna, are extremely invasive and is now a prevalent in the fynbos habitat . Acacias often form monocultures in the oligotrophic soils of the Fynbos and in certain areas have completely displace native vegetation. Clearing of invasive Acacias are done in an attempt to restore the natural vegetation. Slashed trees are often burned to remove unwanted plant biomass. This study aimed to determine the effect of an Acacias slash and burn clearing method on the soil bacterial community. The experimental sites consisted of plots, which were slashed and followed by a controlled burn treatment. Soil samples were taken from natural Fynbos reference sites, invaded control sites and from experimental sites before and after slashing and burning of invasive trees. Sampling was repeated every two weeks for three months, and once a month thereafter. Targeted amplicon sequencing of the 16S variable region V4-V5 was done using the Ion Torrent PGM platform. The chemical properties of the soil samples were determined and using multivariate analysis the link between Acacia invasion, soil properties and the bacterial community composition was investigated. The results revealed significant differences in the community structure between Acacia stands and natural Fynbos sites. Bacterial community structure from burnt sites showed high variability. The effect of fire had a short-term effect on the available nitrogen and this correlated with changes in the bacterial community structure. The impact of fire on the bacteria community is, however, still evident one year after the burn treatment and can be seen in the long-term changes to the soil environment.

Keywords: Soil bacteria, Fire, Invasion

[P2.034]

Primary decomposer channel depend on plant species but elevated CO2 increase flow through fungal channel

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As plants of different life-forms generate different soil communities, assessment of climate change impacts on soil communities and soil services must consider how these impacts are conditioned by the vegetation above.

We investigated how soil communities under different plant species in the same ecosystem respond to global change. In a heathland FACE-experiment, we modelled projected global changes in the field i.a. by increasing CO_2 and temperature. We assessed trophic composition of nematode communities and abundance of bacteria and fungi (by qPCR) in rhizospheres of the two dominant plant species *Calluna vulgaris* (dwarf shrub) and *Deschampsia flexuosa* (grass).

Fungivores dominated nematode communities under *C. vulgaris*, whereas relative abundances of bacterivores, herbivores, and omnivores were all significantly higher under *D. flexuosa*. Elevated CO_2 stimulated fungivores and increased their abundance relative to bacterivores under both plant species. The pattern was similar for microorganisms; fungal abundance generally increased relative to bacterial under elevated CO_2.This corresponds with the hypothesis that when CO_2 available for photosynthesis increases without a corresponding increase of nitrogen, more carbon will flow through fungal rather than bacterial channels.

For both plant species warming increased abundance of the dominant microbivore under elevated CO_2 (fungivores under *C. vulgaris*, bacterivores under *D. flexuosa*), perhaps due to greater activity in their respective microbial food source. Further, elevated CO_2 increased relative abundance of omnivores in accordance with an increased carbon input to the decomposer food web. This increase did not subsist, however, when CO_2 and warming were combined to model future climate.

Together, these results indicate that decomposition at future CO_2 levels may to a greater extent be mediated by fungi. With the corresponding increase in temperature, however, this effect will depend on plant species. Also, the CO_2-induced increase in relative abundance of omnivores and the increasing length of food chains that follows may not occur.

Keywords: Nematode communities, Global Change, Heathland, FACE experiment

[P2.035]

How the edaphic microarthropod community reacts to the biochar application in soils

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The use of biochar, a carbon rich residue of thermal treatment of biomass, as soil conditioner is proposed as a promising strategy to climate change mitigation associated to improvement of soil physical-chemical and biological properties and agricultural productivity. Unfortunately, the effects of biochar application on edaphic biota are still poorly investigated, particularly considering the potential toxic consequences of heavy metals and polycyclic aromatic hydrocarbons.

Different tests have been performed, both in laboratory and in field conditions, to detect the effects of biochar applications in soil on survival, reproduction and composition structure of microarthropods. Laboratory tests were performed on four biochars, obtained by a fixed-bed gasifier and derived from different originating materials (conifer, grape marc, poplar, wheat straw) at different percentages (from 0.5 to 50%). Ecotoxicological effects on the survival and reproduction and the behavioural avoidance of the springtail *Folsomia candida* were tested, according to the standard protocols ISO 11267-1999 and ISO 17512-2:2011. The field experiment was achieved in a poplar short rotation forest: four plots with biochar (produced with a fixed-bed gasifier from maize residues) at the rate of 30 t/ha, were compared to control plots. Soil microarthropods communities were characterized by taking a topsoil core (10x10x10 cm) from each plot; the specimens extracted were identified and counted and soil biological quality index (QBS-ar) was calculated.

The results of the laboratory tests underlined some effects on *F. candida* adults survival at higher percentages, while reproduction was significantly affected also at intermediate rates. At lower percentages, *F. candida* showed to tolerate biochar and didn’t tend to avoid it. The results of field experiment showed differences in microarthropod community and some soil parameters induced by the biochar application.

Keywords: Biochar, Soil fauna, Ecotoxicology, QBS-ar

[P2.036]

The effect of maize cultivation on soil invertebrate communities

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Maize (*Zea mais*) is an important crop in the UK with over 175000 ha grown annually. It is valuable as a forage crop, usually ensiled, but is becoming increasingly important as a feed for biogas generation. There are, however, a number of negative environmental and ecological impacts associated with maize cultivation including soil erosion, sediment loss and reduced biodiversity. This is due to maize being a poor competitor and therefore, intensive soil preparation and high application rates of biocides are required to reduce early competition from non-crop species. Few investigation have been undertaken to understand the impact of this on soil invertebrate diversity. In this study we assessed the impact on the soil fauna of growing maize in five different cultivation systems; i) conventional, ii) strip tillage with ryegrass understory, iii) strip tillage with biodiverse understory, iv) plastic mulch or v) minimum tillage. We have utilised the difference in the stable isotope signatures from the maize (C4 metabolism) and other plants (C3 metabolism) to determine feeding preferences and trophic position of the soil meso- and macro-fauna. Our results show that the different maize cultivation techniques impact on invertebrate soil biodiversity. We found that an increase in non-crop vegetation richness and abundance drives the respective increases in richness or abundance of the soil invertebrate community. We have also identified that in maize systems the herbivore and decomposer food chains are separate and acquire carbon from different primary resources.

Keywords: Maize cultivation, Food webs, Stable isotopes, Soil fauna

[P2.037]

Soil microbial activity in a chronosequence formed due to the retreat of the Breiðamerkurjökull glacier in Iceland

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Increasing glaciers retreat in association with climate change promotes the emergence of large amounts of land that become gradually exposed, giving us the opportunity to study *in situ* evolution in time since retreat of plant succession, soil microbial functioning and their interactions. We used a chronosequence (0-110 years of exposition), formed due to the retreat of the Breiðamerkurjökull glacier (Iceland), to study the evolution in time since glacier retreat of vegetation colonization (vegetal cover), potential microbial activity (microbial respiration, N mineralization and greenhouse gasses emission) and greenhouse gas (GHG) emissions mediated by microorganisms. To get a better understanding of the effect of projected climate change scenarios on these systems, we investigated how microbial activity responded to different moisture and temperature levels. We show that, as time passes after exposure, primary succession occurs through colonization by lichens, then by bryophytes and ultimately by vascular communities (shrubs) in the last stages of the chronosequence (100 years). Parallel to this succession, we observed a significant drop in soil pH and a significant increase in the size of both the soil organic matter (SOM) and the organic and mineral N pools. Rates of microbial respiration and N mineralization also significantly increased with time of exposure after glacier retreat, while no changes were observed for rates of microbial-mediated CH_4 and N_2O production. Moisture and temperature manipulations further indicated differential sensitivity to climate change of different microbial functions, e.g. N mineralization as well as CH_4 and N_2O production appeared to be more sensitive to changes in soil moisture while optimal temperatures of microbial respiration were more sensitive to time since exposure after retreat. Our results, therefore, shows a tight and complex relation between plant successional evolution after glacier retreat and climate that may strongly affect microbial functioning and rates and patterns of GHG emissions.

Keywords: Glacier retreat, ecological succesion, green house gass, microbial functioning

[P2.038]

Determinants of the distribution and composition of bacterial communities at the landscape scale in the sub-saharan tropics

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Soil bacteria are important drivers for biogeochemical cycles in terrestrial ecosystems. Nevertheless, little information is available regarding the landscape-scale distribution and composition of bacterial communities and its environmental determinants in the sub-saharan tropics.

We used a pyrosequencing-based analysis of the V2-V3 16S rRNA gene region to characterize the bacterial community distribution and composition along landscapes characterized by contrasted land use and tree cover trends as well as an average annual rainfall gradient ranging from the arid zone of northern Mali (400 mm), to the semi-arid zone southern Burkina-Faso (900 mm) and the sub-humid deciduous forest of middle Ghana (1200 mm). Soil samples were retrieved from sentinel sites of 100 km^2 (10 km x 10 km) each as part of a long-term observatory network on soil information.

Results indicated that correlations between bacterial community distribution and diversity with soil properties are specific to each agro-ecological zone. Soil pH appeared to be the best predictor of bacterial community distribution and diversity in the arid landscapes, whereas the C:N ratio and total N were the main drivers in the semi-arid and the sub-humid deciduous forest landscapes, respectively. Significant variations in relative abundances of the dominant taxonomic groups were observed accross environments, with the arid landscapes being dominated by *Acidobacteria* (22% of total sequences), the semi-arid by *Actinobacteria* (36%), while the *Firmicutes* (37%) were dominant in the sub-humid deciduous forest landscape. These differences were strongly related to soil properties especially soil pH, total N, and C:N ratio which are specific to each agro-ecological zone.

This study identified different soil parameters as the main determinants driving the distribution and composition of bacterial communities at the landscape scale within the sub-saharan tropics and showed that they varied according to the agro-ecological zone.

Keywords: bacterial diversity, soil properties, pyrosequencage, sub-saharan tropics

[P2.039]

Impact of long-term fertilization on activity and composition of bacterial, fungal and arbuscular mycorrhizal communities in one of the oldest agricultural experiments in the world

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Nowadays, intensive agricultural practices often take place worldwide without considering how these management strategies influence ecosystem biodiversity. However, studies in agricultural long-term experiments allow to enlighten the effects of different land management on the ability of cropping systems to ensure productivity but equally maintain soil quality and biodiversity. The static fertilization experiment Bad Lauchstädt, established in 1902, is one of the oldest field experiments in the world. Its aim is to provide a comprehensive understanding on the effects of different fertilization regimes on crop yields and quality as well as on soil fertility. In our study we used soil samples from the ploughed layer of four different fertilization regimes (no fertilization, mineral fertilization, organic fertilization, and combined mineral and organic fertilization) to address the question on how long-term organic and mineral fertilization and its accompanying nutrient inputs influenced the microbial community structure and the corresponding hydrolytic enzymatic activities in the soil. As expected we found huge differences in the nutrient availability among the different fertilization regimes. Analysis and comparison of the bacterial and fungal diversity were carried out using high-throughput amplicon pyrosequencing. Significant differences were observed in the structural diversity of soil microorganisms, as well as in the activity of microbial exoenzymes. Furthermore, in order to evaluate the temporal dynamics of these distinct, long-term-shaped microbial communities, microcosm and pot experiments were carried out for three month. The results suggested that the dynamics and stability of the microbial community was strongly influenced by the nutrient input. Our results reveal that land management, in particular the fertilization regime, is one of the main driving forces on dynamics of soil nutrients and biodiversity.

Keywords: soil microbial diversity, community dynamics, long-tem fertilization, enzyme activities

[P2.040]

Unravelling the biogeography of UK soil biodiversity

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Biodiversity underpins the ecosystem services delivered by soils. However, relatively little is known about the biogeographically-based governors of species, genera or trophic groups and their distribution at national scales. We characterised the genotypic, phenotypic and functional profiles of soil communities at 101 locations across the UK mainland, selected as a subset of the British Countryside Survey with the assumption that there had been no major land-use change in the previous 40 years and sites were representative of the dominant land-use/habitat types across the latitude and geography of the country. The soil biodiversity characteristics were quantified on all samples by TRFLP (bacteria, archaea, fungi), microbial phenotypic community profiling (PLFA), classical taxonomic identification (nematodes and microarthropods), multiple enzyme and multiple substrate-induced respiration (MSIR) profiling.

Partial redundancy analysis with variance partitioning was used to explore the relative influence of soil and habitat on this range of soil biodiversity characteristics. The data revealed that the combination of soil physico-chemical and habitat factors explained between 22-51% of the total variance in the structure of the individual soil biodiversity characteristics: the greatest variance was expressed via PLFA and MSIR profiles and the lowest via bacterial community structure. When a range of functional gene profiles were also analysed on a representative subset of 50 samples, the range of variance then accounted for was 22-77%, with functional gene profiles always accounting for more than 50%, and ammonia oxidiser (AmoA) maximal. The influence of soils alone ranged from 9-44%, and habitat alone 21-89%, whilst the overlap between soil and habitat ranged from 1-25%.

These results have profound implications for understanding national-scale patterns of soil biodiversity in that the extent to which soil and land-use factors govern community structure is variable and highly context-dependent. In addition, there appears to be deep intrinsic coupling between the influence of these factors.

Keywords: Soil community structure, National scale patterns, Biogeography

[P2.041]

The linkage between the microbial diversity and mineral weathering in soil

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Soil microorganisms play an important role in mineral weathering and biogeochemical cycling of iron. In soil, microorganisms can synthesize siderophores with high affinities for metals as a strategy to promote the mineral dissolution and obtain the elemental nutrition. The present study aims to 1) investigate the microbial diversity in a podzol soil profile, and 2) correlate between the diversity of the siderophore producing microorganisms in the soil and their ability of hydroxamate siderophore production.

Soil samples were collected from O- (organic), E- (eluvial), B- (upper illuvial), and C- (parent material) horizons of a podzol profile in central Sweden. Total DNA was extracted, and 16S and 18S genes were sequenced by MiSeq, Illumina. Siderophore producing bacteria and fungi were isolated from the whole profile and were genetically identified. Siderophores were extracted from the microbial cultures and hydroxamate type siderophores i.e. ferrioxamines, ferrichromes, fusigen and coprogens were detected and quantitated by HPLC-ESI-MS.

Our findings indicated that there was a high diversity of different bacterial and fungal classes within the soil profile. The maximum taxa were present in E-horizon, whereas the minimum taxa were found in C-horizon. The siderophore producing bacteria and fungi were highly distributed throughout the soil profile. For example, *Streptomyces* spp. was the most common taxa throughout the profile, however, *Penicillium* spp. was only found in the O- and E-horizons. Furthermore, the siderophore producing bacteria showed different abilities in the production of ferrioxamines (E, B, G and D). However, the siderophore producing fungi showed a high variety in the production of ferrichromes, coprogens and fusarinines. In conclusion, our findings reflected that the characteristics of each soil horizon in the podzol profile could not only affect the diversity of the soil microbial communities, but also enhance the genes involved in siderophore biosynthesis, therefore regulate the microbial ability in soil mineral weathering.

Keywords: Microorganisms, Podzol, Siderophores

[P2.042]

Impacts of spruce budworm (Choristoneura fumiferana) on soil communities and their functioning

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Spruce budworm (SBW) is an ecologically and economically important conifer defoliator in northeastern North America that outbreaks approximately every 35 years. Feeding by high densities of larvae can strip entire forests of most foliage resulting in extensive tree mortality and growth loss with associated impacts on local economies and ecosystem functioning. While SBW population and community ecology has been well studied, it remains uncertain how these outbreaks might drive large-scale environmental change through their influence on interactions with below-ground trophic communities. For instance, frass and needle deposition associated with larval feeding may dramatically alter nutrient availability in the soil with cascading effects through the ecosystem by shifting carbon and nutrient flow from fungal to bacterial decomposition pathways or vice versa. Root herbivore load may also be affected by reduced photosynthate production caused by SBW feeding and in turn may influence resistance/resilience or susceptibility of forest stands to SBW outbreaks as a control on nutrient uptake by trees. We will present some preliminary results of our ongoing work investigating how SBW outbreaks influence soil community structuring and ecosystem functions (e.g., nutrient cycling dynamics).

During our first year of examining these potential above-below ground interactions, we sampled mite and nematode communities in eastern Canada in the soils of spruce-fir stands of different age classes (young, intermediate, mature) and SBW outbreak intensities (low, moderate/high). Ongoing work will correspond to SBW population rise through decline to capture changes in ecosystem dynamics associated with the outbreak. Mites will be sorted to suborder and nematodes are being sorted to trophic group to assess changes in trophic structuring and ecosystem functioning.

Preliminary analyses revealed no differences in nematode communities due to forest age class; effects of outbreak intensity are currently being determined and will be presented along with mite data.

Keywords: above- belowground interactions, trophic ecology, nematodes, mites

[P2.044]

Management of soil microbiome for plant health in intensified cropping land of China

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Exploring soil microbiome is a promising strategy for sustainable soil utilization, this report provided our efforts to manage the soil microbiome for plant health in intensified land of China. Efficient root colonization is a prerequisite for rhizosphere beneficial microbes to perform their function. *Bacillus amyloliquefaciens* SQR9 isolated from the cucumber rhizosphere suppresses the growth of *Fusarium oxysporum*. We found that lipopeptide bacillomycin D, the global transcription regulator AbrB and the phosphorylation level of DegU regulate the root colonization activities of SQR9.

Rhizosphere beneficial microbes are important to maintain plant health, but in natural condition, it is the whole soil microbiome and their interactions finally decided the plant health and productivity. Banana *Fusarium* wilt disease, which is caused by *Fusarium oxysporum* f. sp. cubense race 4 (FOC) is the most limiting factor in banana production worldwide, application of bio-organic fertilizer (BIO) to a banana monoculture orchard with serious *Fusarium* wilt disease effectively decreased the number of soil *Fusarium* sp. and controlled the soilborne disease. Deep sequencing revealed BIO-treated soil has higher abundances of Gemmatimonadetes and Acidobacteria, while Bacteroidetes were found in lower abundance. Correlation and redundancy analysis showed that the abundance of Gemmatimonas and Sphingomonas and the soil total nitrogen and ammonium nitrogen content were higher after BIO application, and they were all positively correlated with disease suppression. Application of the BIO also suppressed the cucumber wilt disease by 83% compared with the application of common compost (OF). Analysis of microbial communities in rhizosphere soils by high-throughput pyrosequencing showed that more complex community structures were present in BIO than in OF treated soils. Abundance of beneficial bacteria or fungi, such as *Trichoderma*, *Hypoxylon*, *Tritirachium*, *Paenibacillus*, *Bacillus*, *Haliangium* and *Streptomyces*, increased compared to the OF treatment, whereas the soil-borne pathogen, *Fusarium*, was markedly decreased.

Keywords: Soil microbiome, Plant health, Intensified cropping land

[P2.045]

Maintaining soil macrofauna diversity in agricultural landscapes: is habitat heterogeneity the key?

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Soil macrofauna communities were sampled in the smallholder ‘Quesungual’ agroforestry system from upland western Honduras. Maize, beans and sorghum are the major food and fodder outputs. This agroforestry system incorporates practices that should increase soil organic carbon input and provide soil fauna habitat, such as not using fire or tillage to prepare fields, selective pruning of existing trees and application of tree biomass as mulch, and situation within a dynamic, mosaic landscape.

Transect-based sampling was undertaken in sites representing forests and fields of different ages that constitute the Quesungual agroforestry land use cycle. All categories of land use harboured diverse, abundant, highly variable soil macrofauna populations. In the dry season, total density of soil macrofauna ranged from 1265±308 individuals m^{-2} in forest to 1924±436 individuals m^{-2} in fields recently converted to cropping. In the wet season, total density ranged from 907±294 individuals m^{-2} to 1637±358 individuals m^{-2}. Biomass ranged between 4.3±1.1 g m^{-2} to 24.8±8.2 g m^{-2} in the dry season and 13.1±3.0 g m^{-2} to 41.9±11.1 g m^{-2} in the wet season. Community composition at a functional group level was similar across all land uses.

Detailed spatial sampling within fields, together with interviews and participatory mapping with farmers, were employed to better understand the high temporal and spatial variability of soil fauna populations. Our results suggest that high habitat heterogeneity within fields, due to varied topography, dispersed trees and shrubs, and differences in soil types, is related to patterns of soil macrofauna distribution.

The Quesungual agroforestry system has expanded beyond its area of origin into Nicaragua, El Salvador and Colombia, aided by a funded research program and farmer-farmer knowledge transfer. Greater uptake of agricultural management practices that foster habitat heterogeneity could contribute to broader strategies to conserve soil biodiversity *in situ* and maintain ecosystem services provided by these organisms.

Keywords: soil macrofauna, agroforestry, Central America, spatial variability

[P2.046]

Microbes, soil and light: what drives testate amoeba communities in Sphagnum?

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Testate amoebae are free-living protists abundant soils and mosses and especially in peatlands. They and very sensitive to mire surface wetness and are commonly used as indicators of present and past water table depth in *Sphagnum* peatlands. However, studies of seasonal patterns of testate amoebae communities in relation to hydrology, micro-environmental conditions (topography, climate, light intensity) are very rare. We monitored the changes of *Sphagnum*-inhabiting testate amoebae in a peatland in northern Poland (Linje mire) in relation to microsite and climate. We established 25 sampling plots over the surface of the peatland, around 5 piezometers and 5 meteo micro-stations. During the growing season of 2012 we monitored depth to water table (DWT), pH, conductivity, dissolved oxygen, air temperature, relative humidity, precipitation and photosynthetically active radiation (PAR) and calculated vapour pressure deficit (VPD). *Sphagnum* was sampled for testate amoeba analyses five times over the year (May, June, September, October, November). We observed temporal changes in testate amoeba community composition and density and community-environment correlations varied among seasons. Testate amoeba densities were highest in late summer, at the end of the vegetation season (September). Plots with the highest water table had low diversity due to strong dominance of two mixotrophic taxa possessing zoochlorella *Hyalosphenia papilio* and *Archerella flavum* and of *Hyalosphenia elegans*. Communities in dry plots were more diverse and species rich. Overall testate amoeba communities were most strongly correlated to PAR, VPD, conductivity and DWT. The abundance of mixotrophic testate amoeba taxa was correlated to PAR to open (tree-less) habitats.

This research was supported by the Ministry of Science and Higher Education, Republic of Poland, grant No. NN306060940. We acknowledge support from grant PSPB-013/2010 from Switzerland through the Swiss Contribution to the enlarged European Union.

Keywords: peatlands, testate amoebae, soil, monitoring

[P2.047]

Substrate use, survival and development of fungal plant pathogens on infested residues of maize under field conditions in winter - A soil warming experiment

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Soil-borne fungal pathogens cause several diseases in crops leading to high yield losses. Crop residues on the soil surface, in particular large amounts of maize debris, serve as substrate for pertotrophic pathogenic fungi; they represent a major source of inoculum for crop plant infection. Knowledge on the effects of changing winter climate temperatures on infection and colonization of crop residues and the subsequent development of fungal pathogens is important for assessing their disease potential. A soil warming experiment was performed to examine the effects of rising winter soil temperatures on inoculum load and disease potential of fungal plant pathogens (*Fusarium culmorum*, *Fusarium graminearum*, *Rhizoctonia solani*) under field conditions.

Using heating cables, arable soil was subjected to temperature treatments simulating medium (up to 2050) and long-term (up to 2100) climate warming scenarios. Mesh bags filled with pathogen inoculated and non-inoculated maize leaf litter were placed on top of the soil. After 152 days, changes in soil microbial biomass, maize residue decomposition as well as microbial amino sugars and pathogen DNA were measured.

Soil warming increased mean temperatures at 5 cm depth and decreased days of soil frost. Rising soil temperatures increased decomposition of pathogen infested maize residues, without correlation to the degree of fungal colonization. *F. culmorum* produced the largest amount of biomass but showed no significant response to increased soil temperatures. In contrast, *F. graminearum* showed a considerably lower ability to colonize the maize leaf litter but was able to significantly increase the biomass with rising soil temperatures. Mycelia and sclerotia of *R. solani* were stronlgy decomposed, no growth was observed.

An increased decomposition of maize residues does not significantly reduce the pathogen load. A high *F. culmorum* biomass and the increased inoculum of *F. graminearum* point to an increased infection risk with future climate warming.

Keywords: Soil-borne fungal pathogens, Winter climate change, Soil warming, Decomposition

[P2.048]

Exploring the biodegradation potential of potato cultivated soils for the carbamate nematicide oxamyl: The role of pH and cehA gene

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Introduction: Oxamyl is a soil nematicide used in potatoes. We studied its degradation in soils from a potato monoculture area in Greece, the Lasithi Plateau, Crete aiming to identify the factors, abiotic and biotic, controlling its soil degradation.

Methods: Degradation was studied in sterilized vs non sterilized soil samples, collected from 16 field sites in the Plateau area, in order to clarify the biotic nature of oxamyl decay and identify interactions with pH. The dynamics of known carbamates catabolic genes (*cehA, mcd*, *cahA*) were determined via qPCR and statistical correlations between oxamyl degradation, pH and catabolic genes were determined.

Results: Sterilization retarded oxamyl degradation in most soils indicating the significant contribution of soil microbiota to oxamyl degradation. Hydrolysis of oxamyl was pH-dependent, with longer persistence observed in acidic soils, sterilized or not. qPCR analysis resulted in the detection of all three genes. *CehA* and *cahA* were detected in most soils, in contrast to *mcd* which was rarely found. Correlation analysis showed that soil pH ($r = -0.845$) and *cehA* abundance ($r = - 0.787$) was negatively correlated ($p<0.001$) with oxamyl's DT50s.

Discussion: Degradation of oxamyl in soil is controlled by both abiotic (pH) and biotic factors which interact. The clear correlation between rapid biodegradation of oxamyl and *cehA* gene in potato cultivated soils provides first evidence for its widespread distribution in potato monoculture areas where oxamyl is regularly used and its involvement in the biodegradation of oxamyl. This is in accordance with the recent isolation of *cehA*-carrying oxamyl-degrading bacteria in our lab from a banana plantation in Crete. The reasons for the co-detection of *cahA* and *mcd* genes in the soils from the Lasithi Plateau (since those genes did not contribute to oxamyl biodegradation) should be investigated in relation to the use of alternative carbamates in the region.

Keywords: oxamyl, biodegradation, abiotic degradation, cehA gene

[P2.049]

Arbuscular mycorrhizal fungi diversity and glomalin production along an altitudinal gradient of a cloud forest in Brazil

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Arbuscular mycorrhizal fungi (AMF) form a diverse group, as much in number of species as in function. However, studies on AMF diversity have been limited to some vegetable or ecosystems formations and little is known regarding to mycorrhizal state of vegetation which compounds cloud forests of tropical mountains in the world.

In this work an initial drive was made about occurrence of species and abundance of AMF spores as much as glomalin production by these fungi in altitudinal gradient of a cloud forest in Brazil. AMF diversity was accessed from soil sample spores collected close to the root of 18 more frequent vegetable species, in permanent parcels and established in the study field in heights of 1500, 1700, 1900 and 2100 meters.

Our result reveals the presence of 15 AMF species, with predominance of genus *Acaulospora*. In 1500m altitude, occurred greater richness and abundance of spores. Amounts of total glomalin (BRSP) and easily extractable (EE-BRSP) were greater in altitudes of 1900 and 2100m. For this later altitude, amounts of BRSP and EE-BRSP, among several ecosystems evaluated, were the greatest registered until this moment in Brazil.

Chemical and physical attributes do not show relation with abundance of AMF spores. Altitude influenced in composition and distribution of AMF species, along the altitudinal gradient and also in glomalin production.

Acknowledge: CNPq, FAPEMIG, CAPES

Keywords: Tropical mountain, Glomeromycota, Glomalin, Richness species

[P2.050]

Impacts of elevated ozone and temperature on wheat rhizosphere microbial communities

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Ozone (O_3) has increased significantly in recent decades as the result of anthropogenic activities (Naja et al., 2003). This gas is responsible for reductions in crop yields and plant biomass production of forest and grassland ecosystems. O_3 pollution, like other environmental stresses, can generate an oxidative stress into the plant affecting photosynthesis and plasma membrane (Mitter, 2002). Rhizosphere microorganisms are in close relation with plant roots and feed on sloughed-off plant cells and organic compounds released by roots and, as a feed-back, they are involved in improvement of plant fitness (Lynch, 1990). Little is known on the impact of elevated O_3 on rhizosphere microbial communities. Our objectives were to access O_3 and temperature impacts on wheat physiology, soil parameters and rhizosphere microbial communities' structure and activities. The experiment consisted on a 3 week fumigation with or without O_3 (70ppb) of two different varieties of wheat (Premio and Soissons, O_3-tolerant and O_3-sensitive, respectively) at two temperatures (20°C and 30°C). Samples without plant were used as controls. The effect of O_3 was measured on plant physiological parameters (biomass, CO_2 assimilation…), on soil parameters (pH and DOC). Microbial communities' structure (bacteria, archaea and fungi) was evaluated by T-RFLP and qPCR. Functional diversity has been estimated by using catabolic profiling (MicroResp^{TM}). The results show a significant effect of ozone on plants (in particular by reducing their root biomass) in interaction with temperature (Premio was less resistant to O_3 at 30°C). Shifts in the microbial communities' structure were also observed under elevated ozone conditions, with a reduction of bacteria and increase of fungi. These changes were largely shaped by plant physiology and soil properties including pH and DOC. This study provides new insight into our understanding of the influence of O_3 and temperature on the interaction between plants and soil microbial communities.

Keywords: Soil Microbial Communities, Ozone, Temperature, Rhizosphere

[P2.051]

Changes in mycorrhizal colonization due to management and fertilization applied in a mountain grassland ecosystem

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At world level climate evolution tends to produce disturbances increasingly stronger over the grasslands, amplifying the effects of applied management in these ecosystems. In Romania, due to actual socio-economic conditions, the areas occupied by grasslands are either abandoned, either subjected to a process of intensification, issues that lead to the decrease of biodiversity.

Due to concomitant evolution with higher plants, mycorrhizal symbiotic fungi represents a component capable to interconnect root systems with soil particles, while having a much faster response even at low perturbations levels due to changes in applied management, compared to plants.

The aim the study is to assess the response of vesicular-arbuscular mycorrhizal fungi, developed on roots of dominant plants from a mountain grassland ecosystem, caused by modification of management types and levels of fertilization, and to obtain projections in a short period of time about the potential disequilibrium that may arise in a long time in the entire ecosystem. For *Poaceae* family was selected *Festuca rubra* species, and for *Fabaceae* - species *Trifolium repens*, the overall coverage achieved by these species being more than 50% of the vegetation in the ecosystem.

The use of complex fertilizers with micronutrients in addition to the standard content of nitrogen, phosphorus and potassium or supplementation of manure with chemical fertilizers may represent viable solutions for increasing the colonization degree in roots and maintaining nutrient transfer efficiency.

The inclusion of substances with zinc sulphate or fungicides in fertilization recipes may represent a coherent alternative to a management by mowing or mulching, for the preservation of nutrition space of dominant species in the ecosystem and avoiding biodiversity loss over a long period of time.

Keywords: mycorrhizal colonization, grassland disturbances, management, fertilization

[P2.052]

Evaluation of arbuscular mycorrhizal fungi of an irrigated maize system with winter cover crops

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Replacing the traditional fall-winter fallow with cover crops in irrigated cropping systems might enhance soil quality properties, like the development of arbuscular mycorrhizal fungi (AMF). Increasing AMF is often associated to improvements of soil structure, water retention, nutrient absorption and crop productivity. This work studied the effect of two winter cover crops on different parameters related to AMF measured during cultivation of irrigated maize in Aranjuez (Madrid, Spain) under semi-arid Mediterranean climate. Twelve plots were randomly distributed in four replications of three treatments: barley (*Hordeum vulgare* L.) and vetch (*Vicia villosa* L.) as cover crops during the fall-winter period and bare soil as control. Samples of the root system and soil from the rhizosphere were collected at 54 and 69 days after sowing maize. The direct variables measured in the samples were mycorrhizal colonization, hyphae length of extra-radical mycelium and number of AM fungal spores. Also, easily extractable glomalin related soil proteins (EE-GRSP) and β-Glucosaminidase activity were determined as indirect variables.

Compared with bare soil, the use of cover crops improved the development of AMF. Cover crop treatments showed higher values than the bare soil in the variables directly related to fungi activity (mycorrhizal colonization, extraradical mycelium and abundance of spores), as well as in the indirect variables (EE-GRSP and β-glucosaminidase activity). Compared to the Vetch treatment, the Barley improved further the AMF development. The treatment effect on the measured variables depended on the the sampling date. Therefore, the sampling date should be selected on the basis of the studied variable or to find a compromise in the case of several variables. The positive relationships found among most variables, especially between direct and indirect measurements, suggest the possibility of using the indirect measurements as indicators of AMF with the advantage of easy determination.

Keywords: Arbuscular mycorrhizae fungi, β-Glucosaminidase, Glomalin related soil proteins, Cover crops

[P2.053]

Large earthworms affect soil chemical and physical properties

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Brazil is home to more than 300 earthworm species, of which over 60 are very large earthworms, with length surpassing 25 cm and width of approx. 1cm. These earthworms, commonly called minhocuçus in Brazil, are very popular as fish bait, and approximately 10 species are widely used and commercialized locally and regionally. However, the ecology and biology of most species is still unknown, and only three species have been partially studied thus far: *Glossoscolex paulistus* (from São Paulo), *Chibui bari* (from Acre) and *Rhinodrilus alatus* (from Minas Gerais). Furthermore, almost nothing is known of their effects on soil properties and processes, since up to now, only one species has been studied (*C. bari*). Therefore, the present study was undertaken to evaluate cast production rates and the physical, chemical and biological properties of casts of five large Brazilian earthworms kept under laboratory conditions: *Glossoscolex* sp.nov. (a new species), *Glossoscolex uliginosus*, *G. paulistus*, *Rhinodrilus duseni* and *R. alatus*. In this presentation, we focus on the chemical and physical properties of two species: *G. paulistus* and *R. alatus*, two earthworms widely used and commercialized as fish bait and occurring in pastures and forest fragments in the regions surrounding Rio Claro (*G. paulistus*) and Paraopeba (*R. alatus*). The earthworms weighed approximately 14 g (*G. paulistus*) and 56 g (*R. alatus*) wet weights, respectively. Both produced large castings on the surface and within the soil, and *G. paulistus* deposited on average 5 g/individual/day (dry weight). The air dried casts were analysed for soil texture, exchangeable cations (Ca, Na, K, Mg, Al), CEC, Mehlich-1 extractable P, exchangeable acidity, pH, total C and N, as well as using near infra-red spectroscopy (NIRS). Soil analyses are presently underway, and this poster will focus on the differences between physical, spectroscopic and chemical characteristics of uningested soil and earthworm castings, and explore some of the possible reasons for these differences.

Keywords: Oligochaeta, soil fertility, NIRS, soil function

[P2.054]

Shifts in functional diversities of soil microbiomes in response to no-tillage practice and bagasse mulching in a sugarcane plantation

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Sugarcane is cultivated primarily in tropical and sub-tropical regions and recently growing areas have been extended because of an increase in the demand for food and biofuel. However, soil fertility is degrading under conventional sugarcane monocropping. Conservation tillage practice is one of the objectives of the field management for increasing and maintaining soil fertility. In addition, the application of sugarcane bagasse (sugarcane fibers from which the juice has been extracted) to the soil has been found to increase soil organic matter content. The functions of soil microbial communities are important mechanism for productive soil. However, the effect of no-tillage systems and bagasse mulching on the structure and functions of soil microbial communities remains unclear, and our understanding of microbial communities in cropped areas of tropical Southeast Asia is still poor. In this study, a metagenomic approach was adopted to assess the phylogenetic and functional diversities of soil microbiomes in an Alisol under four agricultural managements; conventional tillage (CT), CT with bagasse mulching (CTM), no-tillage (NT), and NT with bagasse mulching (NTM) in a sugarcane plantation in Lampung Province, Sumatra, Indonesia. After four years since introducing no-tillage and bagasse application (80 Mg/ha/yr), soil carbon contents increased in NT and NTM managements, and there was significant increase in earthworm biomass in CTM and NTM management. More than 1 million sequence reads per treatment revealed very high levels of microbial diversity. About 30% of total sequences contained predicted proteins with known functions and about 50% of total sequences contained predicted proteins with unknown function. The majority of the taxonomic domains were Bacteria (98%), followed by Eukaryota (1.2%) and Archaea (0.8%), respectively. Further analyses will examine the differences among four agricultural managements and discuss how such results are link to soil biochemical properties.

Keywords: Soil microbial diversity, Soil functional diversity, Soil metagenomics, No-tillage

[P2.055]

Structuring forces of oribatid mite community diversity across Europe

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Finding trends, reasons and mechanisms which are responsible for the existing spatial heterogeneity of soil fauna distribution may be one of the most appealing current challenges. This issues becomes even more important due to the ongoing processes of Global change and increasing stress associated with the growing human population. On the example of oribatid mites (Acari: Oribatida) at different levels of spatial coverage in European forests I analyze key factors which support or prevent migration and survival of sustainable populations of single species and whole communities. The work is based on the own and literature material collected in over 100 locations across Europe for which information about oribatid mite taxonomic diversity and representation of functional groups is known. I mainly focused on pristine and disturbed forest habitats, which are subject to different types of natural and anthropogenic impacts. Results enabled to build a three-dimensional matrix of factors classifying driving forces of oribatid taxonomic diversity in space: (1) spatial and ecological “corridors”, which facilitate oribatid mite migration as well as barriers and borders of theoretical distribution of certain species; (2) resource availability in soil; (3) biotic and abiotic parameters which result in certain species extinction. Co-action of these factors with the initial potential species pool leads to the actual species and hence diversity distribution of oribatid mites in space as well as structure ratios of individuals with different ecological traits within a given habitat or physical-geographical area. Simultaneously action of factors limiting distribution may temporary increase entropy (in a broader sense) for oribatid communities. In opposite presence of the unlimited amount of resources and favorable conditions may lead to its increase. For example in heavily polluted soils or in conditions of soil degradation the average probability density to meet more tolerant generalist oribatid species is higher than those with high specialization. However, in the result of the ongoing adaptation of species to the changing conditions and colonization of new areas oribatid communities may rather quickly adapt to the new environmental situation in-situ increasing thus diversity and entropy at the local level. The research was supported by the grant of the Russian Science Foundation grant No 14-14-00894 “Zonal differentiation of soil biota ecosystem services in forests after fires”.

Keywords: Oribatida, Spatial distribution, Europe, driving forces

[P2.056]

Colonization of a constructed Technosol by soil macro-invertebrates

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In the context of industrial abandonment, constructed Technosols made of anthropogenic materials can be used intentionally to reclaim brownfield ecosystems. To assess the sustainability of such a pedologic engineering process, the ecological fate of a Technosol constructed with green-waste compost, mixture of treated industrial soil and paper-mill sludge, implemented in 2007 on a derelict brownfield in the Lorraine Region (France) has been in situ studied. The macro-invertebrates hosted in the soil play important functional roles and are involved in the provision of several ecosystem services.

To answer the question if the described Technosol can host soil biota and, if any, what are the early (6.5 years) steps of colonization by the macro-invertebrates, a two-fold sampling methodology has been set up: (i) for soil and litter dwelling organisms, hand sorting in soil monolith (N=24) was done each spring from 2008 to 2011; (ii) for active invertebrates at the soil surface, pitfall traps were left for one week (N=24) in spring from 2008 to 2011 and in 2014.

The results showed an increase of the total density and the species richness of macro-invertebrates with an average from 0 to 851 soil and litter organisms.m2 for the 2008-2011 period and from 0 to 48 active individuals per trap from 2008 to 2011 and 123 organisms per trap in 2014. The density of crane fly larvae, earthworms, and woodlice (detritivores groups) continuously increased in the soil and litter, and densities of spiders and ground beetles (zoophages) increased at the soil surface. The ants and millipedes especially colonized the Technosol between 2011 and 2014.

According the observation of the constructed Technosol colonization by soil engineers (earthworms, ants) and the increase of detritivores macro-organisms density during the 6.5 years study, we might expect to recover a functional system similar to natural soils in the near future.

Keywords: brownfield ecosystem, reclamation, early colonization, trophic groups

[P2.057]

Soil enzyme activities in a *Tuber aestivum* truffle orchard: spatial relationships with soil, symbionts and truffle colonization

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Tuber spp. (*Ascomycota, Tuberaceae*) are symbiotic ectomycorrhizal fungi that produce subterranean edible ascocarps renowned as truffles. Some of them act against grass species, thus originating a bare area around the symbiont – called *brulé* – that can be considered a surface marker of the area of fungal colonization. Knowledge about soil type-*Tuber* colonization-biochemical activity relationships is important for understanding ecosystem functioning. Since no information is available about the effect of the *brulé* on enzyme activities in soil, we did a detailed investigation in a truffle plantation where the *brulé*-producing species *T. aestivum* was present. In a rectangular area of 70m x 120m we collected 180 geo-referenced soil samples that were analysed for five enzyme activities. The screening of enzyme activities was performed using a fluorescent-based, high throughput procedure involving soil extracts and fluorogenic substrates in microplates. Alkaline phosphatase displayed the highest values in the *brulé* areas where truffles were collected in the last decade, but the spatial pattern was also related to variations in soil type. By contrast, distribution of β-glucosidase was closely related to plant cover and in particular with the presence of grasses. Arylsulphatase displayed a pattern distribution comparable to β-glucosidase but with a more patchy distribution. Leucine aminopeptidase and Chitinase displayed a random distribution with no noticeable pattern. Therefore, a relationship between spatial variability of enzyme activity on one side and soil variability, plant cover and *T. aestivum* colonization on the other has been established.

Keywords: truffle, enzyme activity, spatial variability

[P2.058]

Preparation of a standard operating procedure for a functional method: the bait lamina test

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Introduction:

It is an important goal of the EcoFINDERS project to specify and validate indicators of soil functions in a way that these methods can be standardized by the International Organization for Standardization (ISO). One example of a functional method is the bait lamina test (BLT). It was developed for measuring the feeding activity of soil invertebrates (e.g. earthworms, Collembola, Diplopoda, Enchytraeidae) and, to a lesser extent, microbes.

Methods:

The test consists of small plastic sticks with holes, in which bait material is filled in. The loss of bait material is assessed by counting the empty apertures after a certain exposure time. The number of empty apertures as well as their vertical distribution are used as assessment endpoints. As environmental conditions such as climate or soil moisture may influence the results, the test should preferably be applied for comparing the biological activity between closely situated plots. Within the EcoFINDERS project, tests were performed at five indicator sites twice in 2012 and 2013. At each site 3 control and 3 treatment (e.g. fertilized or tilled) sites were compared. In the standard operating procedure (SOP) prepared for this project, test set-up, sampling and evaluation of the feeding activity of soil organisms were described in detail. It formed the basis of a standard guideline describing the performance of the BLT according to ISO rules.

Results:

The application of the SOP worked well in the tests performed within the EcoFINDERS project. Test results differed at the five study sites but were well interpretable and statistically evaluable. Effects of the agricultural treatments as well as climate on feeding activity and its depth distribution were observed.

Discussion:

The BLT is recommended as a functional method for soil quality assessment. Based on EcoFINDERS (and other) experience the BLT will be become an ISO standard (no. 18311) soon.

Keywords: standardization, feeding activity, soil invertebrates, soil function

[P2.059]

Impact of biochar on short-term biochemical soil activity

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Soil application of biochar has been proposed as an effective management to maintain and enhance soil ecosystem services which are directly linked to microbial activity. Both stimulation of microbial activity, due to a favourable environment for soil microorganisms, and inhibition effects, due to adsorption of a range of substrates, have been reported. The aim of this study was to assess the effect of contrasting biochars and their interactions with fertilizers on key soil enzyme activities (EA).

Six biochars proceeding from different feed-stocks (oak wood, municipal solid waste, anaerobic digestate, green wastes, greenhouse wastes) and different pyrolysis conditions were added (0.5% w/w) to a silty clay loam soil either separately or in combination with a rapeseed meal or an organo-mineral fertilizer (rate 340 kg N ha^{-1}). EA linked with C, N, P and S cycles (□-glucosidase, leucine aminopeptidase, alkaline phosphatase and arylsulphatase) was quantified after 2, 7 and 28 days of incubation applying a fluorometric, high throughput, microplate-based, soil enzyme assay.

Separate addition of biochar and organo-mineral fertiliser did not significantly affect EA, while addition of rapes meal caused a relevant increase in the hydrolytic capacity of the soil.

Simultaneous addition of biochar and rapeseed meal caused a further increase in soil EA that was particularly relevant after 1 week of incubation. The synergic effect on EA of biochar and rapeseed meal tended to level off at the end of incubation. Such results are in agreement with previous works suggesting that there is an initial stimulating effect of biochar on soil biological activities that decreases over time.

On a whole results of the present work showed that biochar has no negative effects on EA in soil. Instead, it may also have a stimulating effect under specific conditions, such as in the case of simultaneous addition with organic amendments.

Keywords: biochar, biochemical activity

[P2.060]

A spatial Upscaling Strategy to Assess Soil Microbial Community Assembly and the Impact of Land-Use

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Soil microorganisms are one of the most abundant and diverse living organisms on earth. The environmental filters shaping soil microbial community abundance and assembly were studied through spatial approaches at different scales during the last decade without a consensus: similar environmental filters were involved in shaping microbial community at different spatial scales but also particular filters prevailed at particular spatial scales. In this context, it is now crucial to investigate multiple spatial scales simultaneously to determine with genericity: i) which filter(s) for which scale(s); and ii) the relative influence of environment *vs* human activities on soil microbial diversity across scales.

We characterised soil microbial diversity and abundance (pyrosequencing and DNA yield) at different spatial scales: microscale (µm²), plot scale (m²), landscape scale (km²), regional scale (hundreds of km^2) and territory scale (>100,000 km²). The sampling strategy involved multiple systematic sampling grids sharing sampling sites representing several tens, hundreds and thousands of soils samples for plot to territory scales, respectively. Samples from the plot scale were fractionated for their micro- and macroaggregates to investigate the microscale. Soil physico-chemical, land-use and climatic characteristics were described and used in a variance partitioning approach. In parallel, taxa-area relationship (TAR) was calculated for each scale to better evaluate the microbial community diversity turnover and the processes involved.

Significant TAR were observed at every spatial scale, highlighting the heterogeneous distribution of soil bacterial communities. At each scale, environmental selection was the main process shaping soil bacterial communities, essentially by means of pH, SOC, C:N and land-use, but habitat size and soil texture were strongly involved at particular spatial scales. Interestingly, land-use (human activities) was more important than soil characteristics in shaping soil microbial communities at the landscape scale, highlighting that land-use changes are a leverage to manage these communities at this scale.

Keywords: upscaling strategy, soil microbial community, biogeography, pyrosequencing

[P2.061]

Metacommunity analysis of protists in grassland soils

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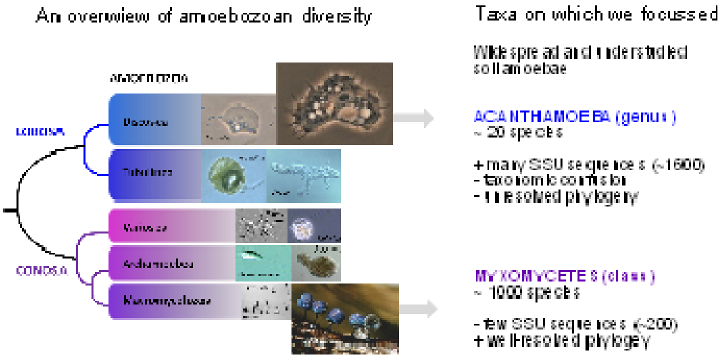
To contribute to the current understanding of free-living protists, we examined the diversity of two widespread and common groups of soil amoebae, the genus *Acanthamoeba* and the Myxomycetes (plasmodial slime-moulds). We focused on these two taxa of Amoebozoa because of the converging evidence of their prevalence in soils and because they are overlooked by both traditional and molecular sampling methodologies.



Soil samples (150) were collected in the grassland Biodiversity Exploratories located in Northeast, Southwest and Central Germany. We developed specific primers to target the variable region V2 of the first part of the small subunit of the ribosomal RNA gene, using Roche GS FLX+ high-throughput sequencing. We applied very stringent filtering and clustering parameters to avoid overestimation of the diversity, obtaining 273 acanthamoeban and 338 myxomycetes operational taxonomic units (OTUs, 96% similarity treshold) from ca. 1 million reads.

Only very few OTUs were identical to already known sequences, showing both a hidden diversity and the need to complete the exisiting reference databases. Intra- and infra-site diversities were high, showing biogeographical patterns and possible correlations with biotic and abiotic soil constituents. This study reveals the distribution across a gradient of land use intensities in grasslands of two major groups of soil amoebae, *Acanthamoeba* and Myxomycetes, that are rarely, if ever, recovered in molecular environmental studies.

Keywords: Metagenomics, Protistan soil diversity, High-throughput sequencing, Molecular ecology

[P2.062]

Soil biology in the swiss soil monitoring network NABO

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The Swiss Soil Monitoring Network NABO has been initiated in 1984 to focus primarily on heavy metal contamination of soils. Since then, environmental and political issues have considerably changed and new aspects have arisen, e.g. climate change or loss of biodiversity. Microorganisms in soils are essential for many soil functions – such as nutrient cycling and storage as well as degradation of pollutants. Therefore, soil functions and changes in biodiversity and general information on soil biological properties are crucial for soil monitoring networks. In this context, NABO has initiated monitoring of soil biological parameters for a sub-set of its long-term observation sites. Since 2012, every spring soil samples (0-20 cm) are collected at 30 NABO-sites (10 arable, 10 grassland and 10 forest sites) (Fig.1). They are analysed for soil microbial biomass with substrate-induced respiration (BM-SIR) and chloroform fumigation-extraction (BM-FE), basal respiration (BA) and DNA-quantity. Soil properties such as pH, C:N-ratio and bulk density are also measured. First results show that in general, arable soils contain less biomass than grassland and forest soils and that the different biomass measurements (BM-SIR, BM-FE and DNA-quantity) show a good positive correlation of 0.6 – 0.8 (Spearman).

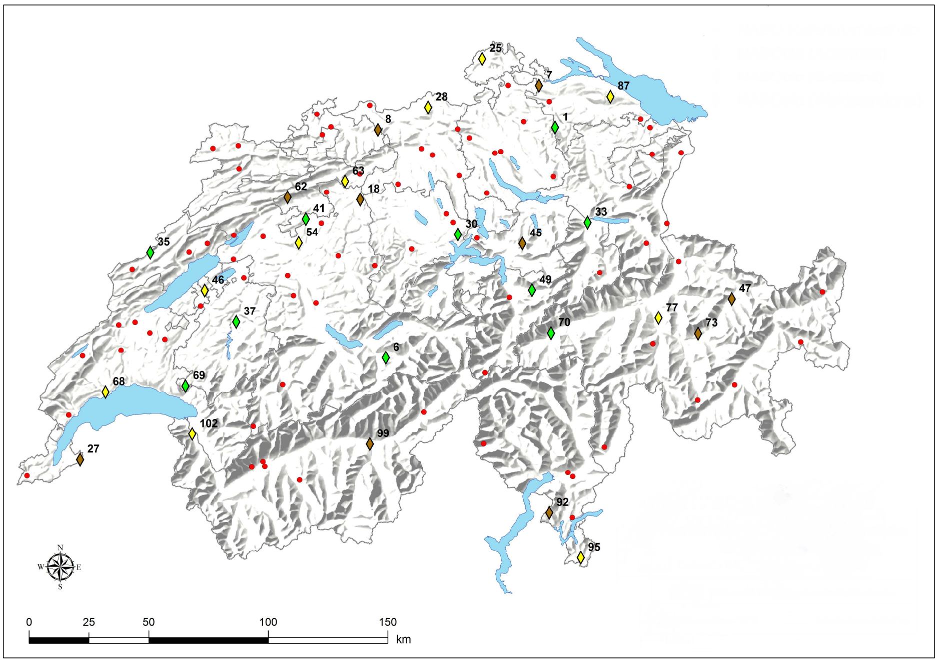

Fig.1: The 102 long-term monitoring sites of NABO spread over Switzerland (red points and rhombuses). In terms of vegetation, land use, air quality and soil type, the sites are representative of conditions typically found in Switzerland. Rhombuses: sub-set of 30 sites for the soil biological survey. Green: grassland, yellow: arable land, brown: forest. Numbers: site identification.

The comparison of the results of 2012 and 2013 also show that the BA-, BM-FE- and BM-SIR-contents in grassland and arable soils are in good agreement. In 2013, BA was 92 %, BM-SIR 103 % and BM-FE 98 % of the contents of 2012. Forest soils differed more between the two years, e.g. at one site BM-FE-content in 2013 was 50% lower than the contents in 2012. This could be partly explained by the more heterogeneous forest soils (mixture of soil horizons) compared to the other soils. In addition, DNA-quantities differed between the two years. DNA quantities in grassland and arable soils of 2013 were lower than those of 2012 (61% lower in average). DNA quantities in forest soils were more variable which could be explained by the different forest types that were included in the survey. In general, the results of the forest soils exhibit a higher variability within the same year as well as between the years

In spring 2014, the sites have been sampled for the third time. This will allow to better determine the natural base lines of each site and to interpret the results in greater detail. In medium term, NABO also wants to approach questions concerning the soil biological diversity. Extracted soil DNA offers the option to apply latest sequencing technologies for assessing the diversity of soil microorganisms and their role in ecosystem functioning. Furthermore, NABO started this spring to assess the entomopathogenic nematodes (EPN) at the same sites. This offers the possibility to learn more about EPN diversity in different habitats, such as arable soils, grassland and forest, and, if possible, to link these new data to the other biological measurements or metadata to build a more comprehensive understanding of soil biodiversity in Swiss soils.

Keywords: soil biological monitoring, microbial biomass, molecular methods, soil biodiversity

[P2.063]

How do crop fertilization affect the soil microbiome on a long-term basis?

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Understanding the role of soil microorganisms in the nutrient cycles is of great importance in agro-ecosystem as they can directly impact crop plant growth and productivity. In a previous study, microbial eukaryotic community was observed to significantly change due to long term farmyard manure fertilization, while mineral fertilization did not seems to impact their diversity and community composition (Lentendu et al. 2014). In order to describe more deeply the process governing microbial assemblages and their reaction to variable nutrient contents, soil archaeal, bacterial, fungal and arbuscular mycorrhizal fungal (AMF) community composition were assessed by high-throughput pyrosequencing alongside with total and available soil nutrients in the long term fertilization gradient of the Bad Lauchstädt static experiment (Germany). Bacterial community composition significantly responded to mineral fertilization, while fungal community composition significantly changed due to farmyard manure fertilization. The detection of AMF was greatly reduce in mineral fertilized soil suggesting important reduction of mycorrhizal formation on crop plant roots in those soils. Multivariate and network approaches will further be applied to test the correlation between AMF and rhizobia relative abundances in relation to mineral fertilization to assess crop plant nitrogen uptake strategy along the fertilization gradient.

Reference:

Lentendu G., Wubet T., Chatzinotas A. et al. (2014) Effects of long-term differential fertilization on eukaryotic microbial communities in an arable soil: a multiple barcoding approach. Molecular Ecology, **23**, 3341–3355.

Keywords: fertilization, crop microbiome, nitrogen cycle, network

[P2.064]

Effects of plant species on springtail diversity and species composition in remnant renosterveld patches of the Fynbos biome, South Africa

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The diversity patterns of soil organisms in Africa are poorly known (Thibaud 2013). One component of biodiversity that is especially poorly understood is spatial variation in the abundance and richness of soil arthropods (Janion et al. 2011). In this study we address this gap in knowledge by studying springtail (Collembola) diversity and the effects of landscape transformation on diversity patterns.

We examined springtail species composition, diversity and temporal dynamics in two remnant renosterveld patches in the Fynbos biome, Western Cape, South Africa, which has a Mediterranean climate (winter rainfall). In an experimental design we studied the effects of three different plant species differing in litter quality (C/N-ratio; Bengtsson et al. 2011) using litter traps placed in the field and sampled three times over 6 months during the wet season of 2007.

Approximately 15 species of springtails were found, of which several species appear to be undescribed. Taxonomic descriptions and barcoding is underway. Mean richness per trap was 4.5 (range 0-10). It was higher at the 2nd and 3rd sampling than at the first, but did not vary much with litter quality or shrub species. However, total springtail abundance varied both with litter type and over time. Many species showed a time effect, often with highest abundance at the 2nd sampling in mid-winter. The responses of single species and total abundances were likely partly driven by high abundances of a non-native species (*Hypogastrura manubrialis*) in the high quality litter (Leinaas et al. MS).

Litter traps were useful to sample springtails in this biome where soils are often difficult to sample by other methods. Our results suggest that many common Collembola species in South Africa’s fynbos biome are undescribed. This study provided baseline data for further investigations of springtail richness and abundance in other vegetation types of the Fynbos Biome.

Keywords: Springtail, Litter quality, Fynbos biome, Community composition

[P2.065]

Using community trait distributions to assess relationships between structure and function of soil bacterial communities

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Large scale microbial biogeography is now possible. An important next step is to extend assessments of microbial community composition to functional consequences. A way forward may be a trait-based approach. Classically the trait distribution of a community is estimated as the sum of the traits of individual populations within that community. A different approach is to directly determine the trait variation of the entire community, without specifically determine species composition. The community trait distribution of the soil bacterial community can be estimated by measuring the intrinsic bacterial growth at a range of trait conditions. This approach has been used to estimate bacterial community trait distributions to temperature, and tolerance to heavy metals and pH.

In reciprocal translocation experiments with sterilised soil microcosms, we compared the influence of inoculum (community) and environmental conditions (soil pH) for functioning (respiration, microbial productivity) and trait (bacterial community pH-tolerance) of the microbial community in soils with different pH. An inoculum from a soil with matching pH resulted in an optimal pH-trait distribution, with optimal functioning. This optimal trait-distribution was modified by an inoculum from soils with different pH, resulting in communities functioning less well compared to well-adapted communities. This mismatch, both in trait distribution, function and community composition developed very rapidly, but then remained for months, suggesting possible “legacy” effects.

The pH tolerance and function will be compared with other community traits, like heavy metal tolerance and temperature sensitivity, highlighting situations when the trait distribution will or will not be import for functioning of the soil bacterial community.

Keywords: Trait distribution, Bacterial community, pH

[P2.066]

Development and optimization of a high throughput method for soil enzyme activity screening

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Soil enzyme activity is a useful and widely used tool for assessing soil functionality and for evaluating the impact of different factors on soil biota both in laboratory and in field.

At field- and landscape level, the availability of a simple, rapid, sensitive and very high throughput method would be very helpful due to the need to process large numbers (hundreds) of samples.

We set up a microplate-based enzyme assay where several enzyme activities are assayed using a soil extract, thus avoiding the problems connected to the use of soil suspension. The feasibility of such procedure relies on an efficient desorption of soil enzymes from soil matrix while minimizing extraction of potentially assay-interfering substances such as humic substances. Use of a protein acting as a heteromolecular exchanger coupled to efficient soil aggregate disruption could potentially allow the achievement of such a goal.

We investigated the relationship between amount of lysozyme as desorbing protein and 9 enzyme activities recovered in extracts by performing desorption curves in 14 different soils using bead-beating as aggregate disrupting procedure.

Results showed that: i-desorption is very fast (mostly less than one minute); ii-Increasing the amount of lysozyme increased the enzyme activity in the extract but no indefinitely; iii-the shape of desorption curve is both soil- and enzyme-dependent; iv-extracts are generally colourless or pale yellow. Comparison of total enzyme activity (determined using soil suspension) vs extracted one (4 enzyme activities in 5 soils) showed that extractability can be as high as 30%.

Under optimized conditions the method allowed determination of 12 enzyme activites in 180 soil samples in just one day. This throughput is about 50 times when compared to classical procedure involving determination of a single enzyme at a time using test tubes. Therefore our method can meet the need for a simple, sensitive and high throughput soil enzyme survey.

Keywords: enzymes, high-throughput, survey

[P2.067]

Short term effect of no-tillage and bagasse mulching on soil carbon through modification of water stable aggregate under sugarcane field in Lampung Province, Sumatra, Indonesia

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Soil carbon (C) is crucial for maintaining soil functions, and it increases under no-tillage management compared to conventional management due to decreasing human-induced soil disturbance and the improvement of soil structure through ecosystem engineers. Soil aggregate includes soil organic matter that affects soil C dynamics. The objective of this study was to investigate the effect of agricultural management of no-tillage and bagasse mulch on soil C through change of water stable aggregate (WSA) size fraction. Our study site was set on in July 2010 in a sugarcane plantation in Lampung Province, Sumatra, Indonesia. We collected soil sample on in July 2013, and measured bulk soil C concentration and abundance, size distribution of water stable aggregate (WSA), each WSA size of soil C concentration. Bulk soil C concentration and abundance increased under no-tillage treatment compared to tillage treatment at soil depth of 0-5 cm and 0-25 cm, respectively. WSA and soil C concentration of WSA were affected by tillage and bagasse mulch at soil depth of 0-5 cm. Macroaggregate size fraction of $WSA_{>2\ mm}$ and $WSA_{0.25\text{-}1\ mm}$ increased by under mulch and no-tillage. Macroaggregate size (>0.25 mm) fraction was modified by agricultural management and this changed bulk soil C abundance. Agricultural management affected soil C concentration between WSA size fractions. Our results indicated that the effect of decreasing soil disturbance and application of organic matter on soil C can change macroaggregate size fraction in relative short time. Further studies are needed to clarify the effects of biological factors such as earthworms, microorganism and root on soil aggregation to fully evaluate ecosystem functioning in agricultural fields.

Keywords: soil aggregate, soil carbon sequestration, agricultural management, size fraction

[P2.068]

Effects of biochar application to soil on the biodiversity of a North European grassland

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Biochar application to soil is advocated as a means of concurrently sequestering carbon while maintaining or enhancing the provision of ecosystem services and crop productivity. However, the majority of published studies consist of either microcosm studies or field experiments in agricultural systems. Little work has been published on the effects of biochar application in relatively high diversity systems such as grasslands. Furthermore, few studies have monitored the effects on soil biodiversity across scales from microbiota to meso- and macrofauna. Here we report on the effects of biochar application to soil on aboveground and belowground biodiversity in a three year field experiment from a North European grassland. Plant community composition was significantly affected in the first year with legumes being three times as abundant in plots that received biochar compared to the control treatment with no addition. Biomass of individual legume plants increased four-fold and amount of N biologically fixed increased fourfold in the presence of biochar. Separate greenhouse experiments suggest that potassium (k) was the main driver for this effect. Belowground community structure, ranging from microbial (community level physiological profiles) through to meso and macrofauna did not show significant effects of biochar application at the rate used (10 t ha-1) over the three seasons of investigation used in this experiment. These results suggest that biochar application to grasslands can be an effective means of sequestering carbon with minimal effects on belowground food webs. Further, biochar represents a potential means of enhancing soil nutrients, in particular nitrogen when applied in the presence of legumes. It is possible that these nutrient and plant community effects may cascade up to other trophic groups over longer time frames and as such this study highlights the need for more long-term studies in grassland to ensure that biochar science is sufficiently robust to effectively guide policy.

Keywords: biochar, grassland, biodiversity

[P2.069]

Evaluating the effect of arbuscular mycorrhizal fungi on plant range expansion

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Recent rapid climate warming has brought about range shifts of many plant species. As a result of this range expansion, the interactions between plants and their biotic environment are also expected to change but information about this is sparse. Arbuscular mycorrhizal (AM) fungi (phylum Glomeromycota) form an important part of biotic environment by living in association with majority of plant species and delivering several benefits to plants in exchange of plant assimilated carbon. Although AM fungi are expected to be rather general in choosing their host, some preference exists between the partners. Here we present a combination of experiments to disentangle the dynamics and the effect of AM fungal communities associated to range expanding plants. Plant material collected from natural habitats in different ranges with the use of next generation sequencing enables to find out whether the association between plants and AM fungal taxa change during range expansion. The use of soil inoculum from different ranges in controlled glasshouse experiment enables to find out how beneficial AM fungal communities from different ranges are for plant growth. Answers to those questions will enable us to predict changes in plant and AM fungal communities, occurring in response of current climate warming.

Keywords: Arbuscular mycorrhizal fungi, Ecology, Climate change, Range shift

[P2.070]

Effect of leguminous position in rotation crop on soil microbial community and nitrogen availability

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Grain legumes, including Faba bean, play an important role in crop rotation, essentially as previous crop and are considered as an important protein source for food and feed. They offer many ecosystem services such as improving soil physical conditions, decreasing the amount of chemical fertilizer used and renewable inputs of nitrogen (N) into soil thanks to biological N_2 fixation. This study investigates the effects of presence and position of legumes in rotation crop under conventional-and-reduced tillage practices on soil microbial community and N availability. For this aim, Three rotation systems were examined (located in north western France, Normandy) with different position of leguminous: previous crop (N-1), faba bean sown in 2011 (N-3) and Control (without faba bean in rotation). five wheat fields were selected for each terms and sampled on April 2014. Soil microbial biomass C, Phospholipid Fatty Acids (PLFA) and four soil enzymatic activities involved in C cycle [b-glucosidase and Cellulase activites] and N cycle [N-acétyl glucosaminidase and Arylamidase activites] were measured to assess their effects on the abundance, composition and the activity of microbial community. Several soil physical and chemical indicators were estimated within conventional (CT) and reduced (RT) tillage.

Agricultural soils showed significant differences in some of physical–chemical properties (total C and N, pH, texture) between all the studied sites. Rotation with previous faba bean and reduced tillage showed the highest enzymatique activities and a significant yield increase in the following cereal compared to all modalities studied. Abundance of bacteria and fungi community is correlated with soil pH and varied with faba bean position in rotation. In addition, their structure, described by PLFA, showed a significant variation between CT and RT and are different in tested modalities.

Keywords: leguminous, nitrogen availability, Phospholipid Fatty Acids, soil enzymatic activities

[P2.071]

The effects of siderophore DFOB on antioxidant enzyme and heavy metal distribution in tomato seedlings under Cd&Pb stress

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It is shown that siderophore secreted by rhizobacteria play an important role in plant growth under heavy metal stress and may influence the assimilation and distribution of heavy metals. However, key mechanisms of siderophore-elicited tolerance are still unclear, in which their influence to heavy metal distribution may be significant.

In this research, 3 heavy metal gradients of both Cd and Pb were set and exogenous siderophore DFOB (Deferoxamine B) was added to treat the tomato seedlings in a hydroponic experiment. After 14 days of treatment, 3 kinds of antioxidative system enzyme activity were measured. The heavy metal distribution was also observed through examining heavy metal concentration in different parts of plant and the SEM-EDS technology.

The results showed that DFOB increased SOD (superoxide dismutase) but decreased CAT (catalase) and POD (peroxidase). Dosing with DFOB enhanced Cd and Pb precipitation to the root cell wall, as well as Pb precipitation to both stem and leaf cell walls. SEM-EDS results showed that DFOB hindered the transmembrane transport of Cd and Pb in the root.

Apart from ferrum, siderophore can form stable complex with other metal ions. In rhizosphere, siderophore increase the bioavailability of different metal elements by chelating them into soluble complexes and thus help plant roots assimilate them. However, the various affinity of DFOB to different metals and the different transmembrane transportation ability of DFOB-metal complexes determine whether DFOB will promote the metal concentration in the cell or not. Binding with DFOB, Cd and Pb are blocked outside of the cytoplasm, which decrease stress intensity and CAT and POD activity. This research also found that the Mn concentration in upper ground parts in DFOB treatment is higher than that without DFOB. As Mn is a cofactor of SOD, probably that is an explanation to the elevated SOD activity in DFOB treatment.

Keywords: Heavy metal stress, Tomato, Siderophore, Antioxidant enzyme

[P2.072]

Predictive models of abundance and diversity of soil microbial communities

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Soil over-exploitation for the development of intensive agriculture and industrialization has led to a significant erosion of biodiversity. Given the importance of soil biota for the delivery of many of the ecosystemic services, it becomes crucial to provide indicators and standards to soil users allowing them assessing soil biological quality and quantifying the impact of human activities. Among soil organisms, microorganisms (bacteria and fungi) are the most important in terms of density (10^6-10^9 individuals/g soil), diversity (10^3-10^6 species/g soil), and involvement in soil functioning. Consequently, the biological status of the soil depends closely on the properties of the indigenous microbial communities. Microbial indicators (density, diversity, activity) have been developed and standardized from the research conducted in environmental microbiology and they must now be transferred and made operational. To date, one missing step to develop soil biological diagnostic is the establishment of the standards needed for the robust interpretation of these bioindicators.

With this goal, we developed a mathematical strategy to provide the standards for the interpretation of microbial abundance (i.e. molecular microbial biomass) and diversity (i.e. richness and evenness), which are two of the most recognized indicators of soil quality. For this, we exploited the thousands microbial and environmental data obtained from the French Soil Quality Monitoring Network (RMQS), which covers the whole environmental variability of French territory to develop a predictive model of microbial bioindicators according to soil pedo-climatic conditions.

Technically, we developed statistical polynomial models to predict the natural range of variations of soil molecular microbial biomass and diversity. These models are innovative tools providing optimal value of microbial biomass and diversity for a given pedoclimatic condition, which must be compared with measured data to allow a robust diagnostic of soil quality. On the other hand, these models may provide more cognitive insights by their ability to evaluate the response of microbial community to pedoclimatic variations.

Keywords: Soil microbial communities abundance, Soil microbial diversity, Predictive models, Natural ranges of variation

[P2.073]

Exploiting positive plant legacies by understanding specific plant-soil feedback

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Plant-microbe interactions in the rhizosphere play a central role in plant-soil feedback. This reciprocal process of plant and soil influencing each other is mediated by the functional composition of the microbial community. Soil microbiota can promote or suppress the growth of a succeeding plant depending on the successor's sensitivity to pathogens and mutualists accumulated by the proceeding plant.

Here, we evaluate if a plant's inheritance can be exploited by managing specific plant successions. We hypothesise that plant biotic legacy effects in soil are more positive for a succeeding plant with increasing taxonomic distance to its predecessor. The same we expect to hold true for crop species combinations. However, crop successions are hypothesized to develop less positive legacy effects compared to their analogue (congener) predecessor-successor combination of wild species, because crops are selected for nutrient-rich conditions, which may trade off with faster accumulation of pathogens.

Specific plant legacy effects via soil biota were tested for crop species (7x7 combinations) and congeneric species (6x6) from a natural grassland; covering 5 plant families (Alliaceae, Poaceae, Fabaceae, Asteraceae, Brassicaceae). In the greenhouse, plants grew on sterilized soil from an agricultural field inoculated with living soil from either the same site (unconditioned), or from a previous growth phase in the greenhouse (conditioned by an individual of each of the agricultural or wild species). All treatments were replicated eight times. After 10 weeks, the plants were harvested and for each of the plant species their productivity compared between each of the specific conditioned soil treatments and unconditioned soil.

Presumably, results will range from growth suppression to growth stimulation with a major role for relatedness between conditioning and response plant species. We anticipate that plant productivity also depends on specific soil-biotic legacies and are amenable by agronomic practice.

Keywords: soil-biotic legacy, agro-ecosystem, natural grassland, taxonomic distance

[P2.074]

More bacteria, more activity? Explaining hotspots of amylase and acid phosphatase activities in the rhizosphere and drilosphere

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Hotspots of microbial activity are well known to occur in soils, especially as a result of plant and earthworm activities. The rhizosphere, the zone of soil influenced by plant roots, and drilosphere, the area of soil influenced by earthworm activity, are themselves heterogeneous with plant and earthworm activity creating very localized chemical changes including those to pH and to substrate quantity. Local hotspots may also have greater numbers of microorganisms and greater nutrient cycling activity. But do more microorganisms mean greater activity for specific processes? We used rhizoboxes with 2D access to the soil profile to try to understand hotspots and the relationship between microbes, substrate, and *in situ* enzyme activity at the fine-scale (millimetric to centrimetric). We mapped the spatial distribution of acid phosphatase and amylase activities *in situ* in intercropped chickpea and durum wheat, in the presence and absence of earthworms over 5 weeks, from small plants to post seed set. We also monitored pH at the very fine scale several times a week using optodes to understand fluctuations as well as development of pH shifts in the soil over time and with plant passage. Greater acid phosphatase activity was frequently observed near chickpea roots, root apices, nodules, and earthworm casts. We also observed heterogeneity of hotspots of microbial activity within the soil and investigated the size and frequency of these hotspots using geostatistics. We combine these results with data on pH, substrate quantity, and the soil bacteria to try to understand how bacteria may contribute to rhizosphere and drilosphere processes, ultimately impacting local nutrient availability.

Keywords: in situ, enzymes, phosphorus, soil profile

[P2.075]

Genetic diversity of Bradyrhizobium strains that nodulate soybeans from soils at different Brazilian regions

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The symbiotic N_2-fixing genus *Bradyrhizobium* includes 23 species distributed throughout different geographic regions. Only one species has recently been described based on isolates from tropical soils, although tropical region is considered to be the origin of legume rhizobia symbiosis. Besides, some authors suggested that *Bradyrhizobium* was introduced in Brazil with first soybeans inoculants from USA.

The present study aimed to analyze 46 *Bradyrhizobium* strains were isolated from soils collected in different regions of Brazil (Midwest, Northeast, Southeast, and South), using soybean as a trap plant. These strains were characterized genetically by analyzing the 16S rRNA gene and five housekeeping genes (*atpD, gyrB, dnaK, recA*, and *rpoB*). They were also characterized in terms of their symbiotic efficiency with soybean plants grown under axenic conditions in Leonard jars.

The phylogenetic analysis of housekeeping genes revealed the possible presence of novel species in the Northeast and Southeast soils, some of which exhibited high symbiotic efficiency with soybean plants. These results emphasize the great diversity among native strains belonging to *Bradyrhizobium* genus in Brazilian soils as well as potential ones to be used as inoculants.

Acknowledgments: The Technology and National Council for Scientific and Technological Development for financial support (MCT/CNPq/Ct-AGRO, Process: 559120/2009-5 Public Notice: 69/2009), the Brazilian Federal Agency for the Support and Evaluation of Graduate Education (Capes) the CNPq and the Minas Gerais Research Foundation (FAPEMIG) for granting scholarchips.

Keywords: Biological nitrogen fixation, Glycine max, housekeeping genes, phylogeny

[P2.076]

Effect of repeated organic residue applications on soil microorganisms involved in N cycle and their activities at the plot scale: consequences on ecosystem services

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Introduction

Soils are complex environments and constitute reservoirs of biodiversity. One gram of soil can contain up to 10^{10} micro-organisms belonging to about a thousand different species. Microbial activities play a major role in soil functioning, including nitrogen (N) biogeochemical cycle which is the focus of this work. Organic waste products (OWP) from agricultural (manure), industrial and urban (sludge, municipal waste composts, green waste composts) origins may be applied on cultivated soils to enhance N availability for plants. Although many studies have highlighted the effect of farming practices on microbial diversity in soil (e.g. [1], [2]), little information is available about the long term effects of repeated OWP applications in field conditions on soil microorganisms. The functioning of N biogeochemical cycle impacts ecosystems through nutrient cycling [3]. Several other ecosystem services like climate regulation, water quality, and air quality might also be impacted. The aim of the study was to decipher short and long-term effects of repeated OWP applications on soil microbial functioning in cultivated soils. Furthermore, the consequences of these applications on the N biogeochemical cycle and related ecosystem services were discussed.

Material and Methods

The Qualiagro field experiment located in Ile de France (Veolia Environment and INRA collaboration), has been started in 1998 to study the effect of 3 urban composts (municipal solid waste compost, MSW; biowaste compost, BIO; co-compost of sewage sludge and green waste, GWS) and a farmyard manure (FYM) as reference amendment on soil compared to a control treatment (CONT) without organic residue application nor mineral fertilizer and a control treatment with mineral fertilizer (CONT+N). The field is cultivated with a maize-wheat succession. All treatments are present in four replicates. The organic amendments are applied every 2 years, in September, at doses equivalent to 4 t C/ha. Two samplings have been realised: 3 weeks before (01-09-2011, assessment of the cumulated residual effect: RE) and 3 weeks after (14-10-2011, assessment of the short term effect: STE) the 8th spreading on September 23th 2011. We analysed organic N mineralization, the total microbial biomass and fungal biomass as well as specific (nitrifying and denitrifying microorganisms) microbial communities in all soil samples. Additionally, N_2O emission was measured in laboratory mesocosms (cylinders containing soil-OWP mixtures at rates equivalent to 4 t C/ha) over a period of 72 days.

Results

The average OWP's compositions are summarized in **Table 1**.

Table 1. Average Organic Waste products characteristics applied on Qualiagro experimental site between 1998 and 2011. With orgC=organic carbon, Ntot=Nitrogen total, Nmin=Mineral nitrogen, orgN=organic nitrogen, DM=Dry matter.

		GWS	BIO	MSW	FYM
orgC	$g.kg^{-1}$	265 ± 44	208 ± 47	308 ± 45	320 ± 67
Ntot	$g.kg^{-1}$	23.5 ± 2.7	17.4 ± 4.5	17.6 ± 2.0	21.9 ± 3.1
Nmin	$g.kg^{-1}$	2.6 ± 0.9	0.5 ± 0.3	0.4 ± 0.2	0.7 ± 3.0
orgN	$g.kg^{-1}$	20.9 ± 2.5	16.9 ± 4.2	17.2 ± 1.9	21.2 ± 3.0
orgC/Ntot	-	11.4 ± 2.1	12.1 ± 8.5	17.8 ± 4.0	14.7 ± 2.8

DM	%	63.3 ± 8.2	70.1 ±8.5	67.8 ± 12.0	39.6 ± 9.1
Quantity applied	t MS.ha^{-1}	16.4 ± 2.7	19.1 ± 4.2	12.0 ± 3.2	13.2 ± 2.0
Hemicellulose	%OM	5.6 ± 2.1	4.3 ± 2.3	6.8 ± 2.5	12.1 ± 3.1
Cellulose	%OM	21.1 ± 8.1	21.5 ± 2.8	33.7 ± 9.0	27.0 ± 7.1
Lignine	%OM	27.8 ± 9.6	29.3 ± 7.7	18.1 ± 8.3	21.8 ± 3.4

A significant increase in total organic carbon and nitrogen was observed in GWS, BIO and FYM plots compared to control 3 weeks after OWP application (14-10-2011, STE, **Table 2**) and this effect persisted with time after repeated applications (01-09-2011, RE, **Table 2**).

Repeated application of OWP significantly increased the total microbial biomass (01-09-2011, RE). A recent application increased even more the microbial biomass in the amended plots compared to control treatments (14-10-2011, STE). The most important short term increase was observed in the MSW treatment, 3 weeks after the application (**Table 2**).

A short term increase of fungal biomass was observed only in the MSW plot (twice more than CONT) but this stimulation disappeared with time (no residual effect), (**Table 2**).

Table 2. Microbial biomass (mgC.kg soil^{-1}), fungal biomass (µg ergosterol.kg soil^{-1}), total organic carbon and nitrogen (g C or N.kg soil^{-1}) in soils of the different treatments at the 2 sampling dates: 3 weeks before the 8th application 01-09-2011 and 3 weeks after the 8th application 14-10-2011. The same letter means no significant difference; comparisons were performed between treatments for each sampling date.

(Test de Kruskall-Wallis, $p<0.05$ for fungal biomass, organic carbon and total nitrogen and ANOVA, $p<0.05$ for microbial biomass).

	Sampling	CONT	CONT+N	MSW	GWS	BIO	FYM
Microbial biomass	01-09-2014	199±22 *b*	205±7 *b*	287±16 *a*	289±32 *a*	286±12 *a*	281±12 *a*
mgC.kg soil^{-1}	14-10-2014	213±14 *B*	237±9 *B*	404±14 *A*	324±42 *AB*	335±36 A*B*	258±42 *AB*
Fungal biomass	01-09-2014	0,77±0,12 *a*	0,97±0,10 *a*	0,81±0,12 *a*	0,93±0,06 *a*	1,06±0,24 *a*	0,91±0,13 *a*
µg ergosterol.kg soil^{-1}	14-10-2014	0,96±0,28 *A*	1,32±0,17 *A*	2,00±0,22 *B*	1,33±0,12 *A*	1,45±0,28 *A*	1,48±0,26 *A*
Organic carbon	01-09-2014	9,3±0,6 *a*	10,4±0,3 *ab*	12,5±0,8 *ab*	15,3±0,6 *b*	15,2±0,7 *b*	14,4±1 *b*
gC.kg soil^{-1}	14-10-2014	9,3±0,5 *A*	10,4±0,1 *AB*	13,7±0,9 *AB*	17±0,8 *B*	16,5±0,3 *B*	14,8±1,4 *B*
Total nitrogen	01-09-2014	0,89±0,08 *a*	0,96±0,02 *a*	1,14±0,08 *a*	1,47±0,08 *b*	1,42±0,09 *b*	1,29±0,08 *b*
gN.kg soil^{-1}	14-10-2014	0,88±0,05 *A*	0,97±0,02 *A*	1,27±0,07 *A*	1,68±0,07 *B*	1,54±0,03 *B*	1,33±0,01 *B*

The total mineral N potentially available during a year after the 8th amendment has been estimated taking into account the residual mineral N from the 7 previous amendments and measured in the sampling before the 8th application (RE: first line of **Table 3**), the increase of organic N mineralized in the amended treatments compared to the control treatment (RE: second line of **Table 3**), the increase in mineral N in soil during the 3 weeks after the 8th amendment resulting from mineral N applied with the amendments and short term N mineralization of the OWP (STE: third line of **Table 3**) and the increase in potential organic N mineralization in soils sampled before and after the 8th OWP application (STE: fourth line of **Table 3**). Results showed that 8 amendments may potentially provide 64, 146, 279 and 302 kg of mineral N.ha^{-1} in the FYM, MSW, BIO and GWS treatments, respectively (cumulated residual and short term effects in **Table 3**). On long term, the most stable GWS compost enhanced available N (**Table 3**). The BIO compost also increased the available N.

Table 3. Improvement of soil fertility expressed through extra mineral N available after 8 amendments for FYM, MSW, BIO and GWS plots.

Expressed in kg N.ha^{-1}	FYM	MSW	BIO	GWS
Residual mineral N available from the repeated amendments (RE)	14	13	15	23
Increase in potential mineralization of organic N resulting from the cumulated effects of the 7 first application of OWP (RE)	80	58	106	93
Cumulated mineral N provided by the last application and organic N rapidly mineralized after the last application of OWP (STE)	30	3	31	180
Increase in potential organic N mineralization resulting from the last application of OWP (STE)	-60	72	126	5
Total in kg.ha^{-1} mineral N potentially available after 8 amendments	**64**	**146**	**279**	**302**

Nitrifying bacterial populations increased in GWS plot 3 weeks after the 8th application (**Figure 1**), probably because the GWS compost initially contained high proportions of N-NH_4^+ directly available for nitrifying bacteria (**Table 1**). No significant differences were found for the denitrifying populations (data not shown) in STE and RE for all treatments.

The fluxes of N_2O emissions were very low: 0.02 to 0.3 % of N applied after 72 days and were larger for MSW and BIO than GWS and FYM similar to the mineral N treatment (**Figure 2).**

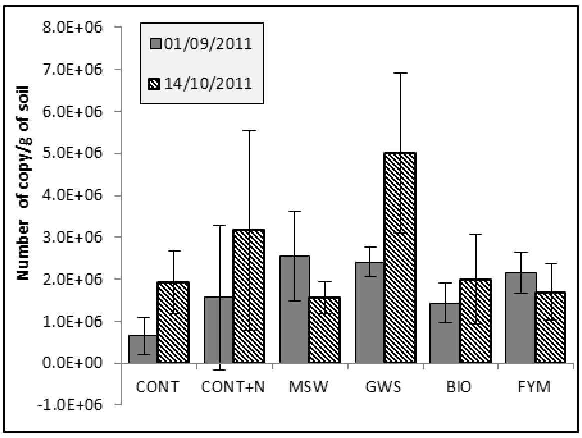

Figure 1. Abundance of nitrifying bacteria (*amoA* gene) for CONT, CONT+N, MSW, GWS, BIO and FYM plots before (01-09-2011) and after (14-10-2011) the 8th application of OWP

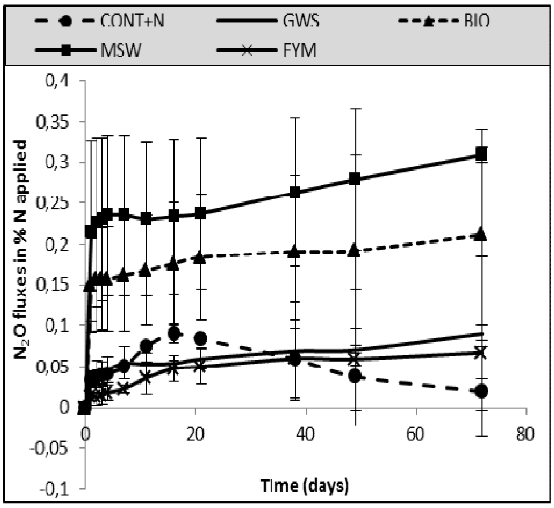

Figure 2. N_2O emission expressed in % N applied for CONT+N, GWS, BIO, MSW and FYM soil mixtures measured during 72 days.

Conclusion and perspectives

Repeated applications of organic amendments to soils have led to an increase of nitrogen contents in soils but these effects and their consequences on soil fertility and air quality vary with the type of organic amendments. The addition of organic amendments stimulated the growth and activities of total and specific microbial communities but the intensity and the duration of these effects depended on the quantity and the quality of the organic matter contained in the OWP. Finally, OWP easily biodegradable have additional short term effects on the growth of microorganisms and the emissions of N_2O after application; more stable OWP (such as GWS) have longer lasting effect.

Repeated applications of OWP play an important role in ecosystem services like nutrient availability or air quality. Further work (under laboratory conditions) will address the potential volatilization of NH_3 following OWP application. Complementary data on other N fluxes in amended soils are also needed in order to complete the environmental balance of this practice.

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Keywords: Organic waste product, Nitrogen cycle, Soil microorganisms, short and long term effect

[P2.077]

Stimulation of soil biota through organic waste recycling for sustainable oil palm cultivation

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Sixteen million hectares of oil palm has been planted within the last few decades with dramatic changes in land-use. Despite this, soil biodiversity in plantations has been little investigated.

This study aims to assess the effect of organic waste recycling on soil biodiversity in a mature plantation in order to develop sustainable practices.

Observations were made in plantations located in Sumatra, Indonesia. Plots received 60 $t.ha^{-1}$ EFB (empty fruit bunches, an organic mill by-product) every two years, on the palm inter-row, parallel to the harvest path. Based on the standard spatial organisation and practices in plantations, four main zones were defined 1)EFB application band, 2)harvesting path, 3)weeded tree circle, and 4)windrow (regular biomass recycling – pruned leaves). We assessed soil macrofauna, nematofauna and bacteria, together with soil physical-chemical characteristics. Temporal variability was assessed based on a time-sequence with observations undertaken 1, 3, 6, 12, 18, and 24 months after EFB application.

Zones treated with EFB showed higher earthworm density and “maturity index” of nematodes communities. Bacterial diversity (number of genera) was higher under EFB, in the harvesting path and in the circle than in the windrow. Three successive periods were identified: a disturbance period (0-6 months), with reduced density of earthworms, diplopods and nematodes, but a higher density of ants; a resilience period (6-18 months); and a final period (24 months, i.e. just before new EFB application) characterized by the highest density of earthworms, dermapterans, diplopods, and nematodes.

Our results demonstrate spatial and temporal variation in biodiversity and density of soil organisms in oil palm plantations, and a significant impact of EFB application. This research is the first stage towards evaluating current practices and developing new strategies for maintaining and enhancing soil biodiversity and related services for sustainable oil palm cultivation.

Keywords: agricultural practices, sustainable agriculture, soil biodiversity conservation

[P2.078]

New metrics for quantifying biological soil resilience

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Previous studies—as well as theoretical considerations—have suggested that the resilience of microbiologically-mediated soil functions to perturbation is related to the biodiversity of the associated microbial communities, but in complex ways. In such studies, a 'resilience index' is often calculated to quantify the recovery of a soil function compared to an unperturbed control at a specific time. However, such indices are generally based upon few time points, and thus provide low resolution characterisation of resilience phenomena. We propose a soil resilience model based on an analogy with a mechanical spring-damper system that characterises the entire functional response, and hence resilience, using a few model parameters. In the analogy, the properties of a conceptual 'spring' and 'damper' determine how a perturbed system returns to its equilibrium state. For example, one parameter (the 'natural frequency') describes the shape of the peak in the functional response. A large value of this shape parameter indicates a narrow peak with quick recovery from a perturbation (i.e. high resilience); a smaller value indicates a sustained period of disturbance before recovery. We fitted this model, using published data, to simulate the respiration response of several soils subjected to perturbations. Model results showed that, following a persistent stress (dosing soils with a soluble copper compound), the cumulative respiration (the area under the modelled respiration response) was of greater magnitude for agricultural soils than for grass and woodland soils, suggesting lower resilience of agricultural soils to copper stress. After a temporary stress (exposure to 40°C heat for 18 hours), larger values of the peak shape parameter (i.e. more resilient responses) were observed for soils with higher organic carbon content. This approach provides effective metrics of resilience that, alongside analysis of soil microbial community structure, should aid future study of the relationships between biodiversity and soil functional resilience.

Keywords: Soil resilience, Modelling, Respiration

[P2.079]

Soil biological quality: monitoring project in the Emilia-Romagna Region (Italy)

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In the last decades the increase of industrial activities and the intensive exploitation of soil in agriculture have enhanced the risk of soil fertility reduction and contamination by pollutants, especially in the alluvial plains such as the Emilia-Romagna Region. Biodiversity is the force that governs the main ecosystem services performed by soil (EC, DG ENV 2010) but soil degradation processes lead to loss of biodiversity (COM 231 (2006). For this reason, it is important to start up projects that aim to obtain indications about soil biodiversity at regional scale.

In the Emilia- Romagna Region (North-Eastern Italy), soil fauna biodiversity and soil biological quality have been evaluated applying the QBS-ar index, an index based on soil microarthropods community and applied in different countries (EC DG ENV, 2010).

Using data collected in several sites and based on the QBS-ar application, it was possible to carry out a preliminary assessment, in qualitative terms, of the potential level of soil biodiversity and soil biological quality of the Emilia-Romagna region and relate these data to the use and management of soil. The result of this approach is the “Map of potential soil biodiversity “on the basis of which it will be possible to develop monitoring projects in the Emilia-Romagna region.

The project, as a priority, will take into account areas characterized by agricultural management with different degrees of intensity in order to obtain relevant information to the evaluation of the Rural Development Policy 2014-2020.

Keywords: monitoring, microarthropod, map of soil biodiversity, agricultural management

[P2.080]

The response of root-associated bacterial community to the grafting of watermelon

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Several studies have reported that different genotypes, even within species, can develop distinct rhizospheric microbiomes, which show important roles in the maintenance of plant health and productivity. However, the way in which grafting affects the root-associated microbiome of watermelon and the linkage between the microbiome and the resistance of soil-borne disease remain unknown. This study addressed the variation in the microbial activity and bacterial community in the rhizosphere of own-root bottle gourd (rootstock), own-root watermelon and grafted-root watermelon under field condition. Seven types of soil enzyme activities, which were used as an indicator of microbial activity, were tested by microplate fluorometric assay, and the root-associated bacterial community was compared using 454 pyrosequencing. Our results showed a clear distinction in microbial activity and taxonomic level between treatments. Relative to the watermelon (regardless of grafted or ungrafted roots), the own-root bottle gourd rhizosphere displayed the highest acid phosphomonoesterase activity and the lowest β-glucosidase activity and was strongly enriched in Sphingobacteriia but less so in Actinobacteria. Compared with own-root watermelon and grafted-root watermelon, ungrafted watermelon recruited significantly higher beneficial bacterial genera in the rhizosphere, such as Bacillus spp. and Paenibacillus spp., suggesting that the grafted watermelon root did not have the ability to harbor highly beneficial bacteria to exert soil-borne disease resistance. Regardless, a significantly higher Shannon-Wiener index at any reads level was found in the rhizosphere of grafted watermelon compared with ungrafted watermelon, indicating that the root-associated bacteria of grafted watermelon possess a broader niche overlap to exclude the pathogen challenge. We concluded that the assemblies of the bacterial community in the rhizospheres of own-root bottle gourd (rootstock), own-root watermelon and grafted-root watermelon were different and that the grafted watermelon could exert soil-borne disease resistance by maximizing the niche occupancy of the rhizosphere rather than by recruiting more beneficial bacteria. These results will help to better clarify the disease resistance mechanisms of grafted-root watermelon based on plant-microbe communication.

Keywords: Grafting, Watermelon, Soil enzyme, Bacterial community

[P2.081]

Local extinction of earthworm diversity in Eastern Amazon threatens soil ecosystem services

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The Belém Endemism Center (CEB), the oldest frontier of Brazilian Amazon, is highly deforested (76%). Forests are fragmented (patches <1,000 ha) within a matrix dominated by degraded pastures and young fallows. Soil macro-invertebrates of the region are largely unknown despite their crucial role in soil ecosystem services provision. This study focused on the effects of soil degradation on earthworm species composition and diversity in the CEB and São Luís island. Climate is tropical humid with a marked dry season and dominant soils are Ultisols. Earthworms were collected from 2007 to 2011 at the end of the rainy season through the TSBF methodology. Four sites were collected in the CEB and one in the São Luís island. At each site young (3-7y) medium (11-15y) and old (20-40y) fallows were sampled, along with forest remnants when present. In addition, other locally relevant soil uses were sampled: pastures (2 sites), agroforestry systems with palm oil (1 site) and chop-and-mulch prepared manioc crop (1 site). A total of 12 genus and 26 morfo-species were identified with an average 7.4 (+/-5.6) species per site. Between-class Principal Component Analysis (BCA) revealed that sites were very contrasted in composition and diversity, site effect accounting for 21% of worm composition and 50% of diversity (P=0.0001). Past soil use explained 11% of worm composition and 32% of diversity (P=0.0001) while present soil use explained 9.5% of composition and 21% of diversity (P=0.0001). Most species were collected in only one site, only *Pontoscolex corethrurus* was present at all sites and *Urobenus sp*. at four sites. In the Tomé-Açu site (Pará State), only *P. corethrurus* was present. The high Beta diversity revealed for earthworms in the CEB reinforces the need for more protected areas while local extinction of native species and *P. corethrurus* invasion threatens the soil ecosystem services provision.

Keywords: Beta diversity, Pontoscolex corethrurus, Tropical Forest

[P2.082]

Contribution of legume tree residues and macrofauna to the improvement of abiotic soil properties in the eastern Amazon

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The potential advantages of positive interactions between the functional group components of the macrofauna and soil residue cover may increase the sustainability and efficiency of tropical agrosystems. The objective of this study was to link the ecological requirements of soil macrofauna with their impacts on the principal chemical and physical attributes of a cohesive soil from a humid tropical region. The soil of a no-tillage system covered with legumes tree residues was subjected to the following treatments: *Leucaena* + *Clitoria* (L+C); *Leucaena* + *Gliricidia* (L+G); *Leucaena* + *Acacia* (L+A); *Gliricidia* + *Clitoria* (G+C); *Gliricidia* + *Acacia* (G+A); and a control with bare soil (BS) and no legumes. The application of leguminous tree residue with a high C/N ratio (G+A) extended essential ecosystem functions in the no-tillage agrosystem through higher macrofauna abundance, including soil ecosystem engineers, predators and litter transformers. Litter transformers are associated with mulching effects that enhance multiple soil attributes, such as water infiltration, porosity, density, the litter carbon stock, the free light fraction (FLF) and total organic C. However, the use of fast-growing leguminous trees can increase soil acidity and decrease macrofauna diversity but, careful choice of legumes combination may avoid detrimental effects on soil macrofauna.

Keywords: Soil ecosystem services, Agroecology, Isoptera

[P2.083]

Available tools for the assessment of multi-scale spatial relationships of soil invertebrate assemblages and soil environmental variability

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Studying the drivers and determinants of species, population and community spatial patterns is central to ecology. The observed structure of community assemblages is the result of deterministic abiotic (environmental constraints) and biotic factors (positive and negative species interactions), as well as stochastic colonization events (historical contingency). The spatial patterning of soil organisms is shown to be generally clumped, with alternation of high- and low density population patches that are stable during several years. Disentangling the spatial scales at which species assemblages are structured, and if these coincide with those expressed by soil environment is of utmost importance. The combination of null-model analysis, niche overlap calculations with multivariate analysis and spatial statistics tools like cross-correlogram and Moran's Eigenvector Map (MEM) and variation partitioning analysis constitutes a powerful package of techniques to assess the determinants of spatial distribution in soil organisms. The results of several studies conducted in savannas and gallery forest of Neotropical areas showed that competitors were spatially excluded in more homogeneous environments while they coexisted in ecosystems with more patchily distributed soil resources. The spatial organization of earthworm assemblages and soil environmental variables showed explicitly multi-spatial relationships at different intensities according to species and assemblages (identified from the first axes extracted in the correspondence analysis). Soil environmental variables explained (<1% to 48% of total variance) nested population structures across multi-spatial scales for species and assemblages at very fine (<10 m), to fine (10-20 m) and medium scales (> 30 m). The effect of soil environmental heterogeneity on litter-feeding species but also the impact of endogeic species onto soil physical properties was unveiled. For some species, a large proportion of the spatial variation was not dependent on soil environmental variability what might indicate the influence of stochastic factors, contagious biotic interactions, or unmeasured soil variables.

Keywords: community ecology, soil fauna, spatial distribution, multi-scale relationships

[P2.084]

An unexpected richness in sesquiterpene production of A. alternata: Challenging our view on possible volatile mediated interactions?

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Alternaria alternata and its relatives are abundant global soil and plant pathogenic fungi. Its impact on human life – from agricultural spoilage to allergenicity – especially made *A. alternata* one of the most extensive studied fungi so far.

A. alternata and other species of the genus emit volatile organic compounds (VOC), shown so far as composed mainly of (branched or unsaturated) C3 to C8 alcohols. Only recently, hints on sesquiterpene production (C15 terpenes) were reported (Schuchardt and Kruse, 2009).

Here, we qualitatively and quantitatively analyzed the VOC headspace originated in plate culturing of *A. alternata* alone and in confrontation with *Fusarium oxysporum*, under high and low nutrients, by a method based on stir bar sorptive extraction and GC-MS. We show that both fungi release terpenes, but *A. alternata* was an unexpected strong sesquiterpenes emitter.

Compared to other studies, we were able to characterize a much larger odour profile with more than 20 sesquiterpenes dominating the blend of VOC. Production only slowly declined with the cultures' aging (4 weeks). Some compounds were unreported in fungi so far, though well-known to be emitted by plants, in which they play important ecological roles as info-chemicals for environmental interactions.

Our study indicates that changing the detection system may lead to finding an unexpected richness in compounds even for well-known fungi. Hence, it is plausible that our current picture of fungi emitting a much lesser terpenoid diversity than bacteria and plants must be redrawn in future, promoting our sparse knowledge on belowground volatile-mediated interaction.

Keywords: volatile, fungi, interaction, VOC

[P2.085]

Effects of winter climate change on the Collembola community of cryoturbated non-sorted-circle tundra

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Non-sorted circles (NSC) are a common type of cryoturbated (frost-disturbed) soil in the arctic and store large amounts of soil organic carbon (SOC) by the burial of organic matter. They appear as sparsely vegetated areas surrounded by denser tundra vegetation, creating patterned ground. Snowfall in the arctic is expected to increase, which will modify freezing intensity and freeze-thaw cycles in soils, thereby impacting on SOC dynamics. Vegetation, soil fauna and microorganisms, important drivers of carbon turnover, may benefit directly from the altered winter conditions and the resulting reduction in cryoturbation, but may also impact each other through trophic cascading.

We investigated how Collembola, important decomposers in (sub)arctic ecosystems, are affected by increased winter insulation and vegetation cover. We subjected NSC in North-Swedish subarctic alpine tundra to two years of increased thermal insulation (snow fences or fiber cloth) in winter and spring, increasing soil temperatures and strongly reducing freeze-thaw frequency. From these NSC we sampled the Collembola community in: (i) the non-vegetated center, (ii) sparsely vegetated parts in the center and (iii) the vegetated domain surrounding NSC. To link changes in Collembola density and community composition to SOC dynamics, we included measurements of decomposer activity, dissolved organic carbon and total extractable nitrogen.

We expect the presence of vegetation (and SOM) to determine Collembola community composition, density and activity. Overall, we expect increased winter insulation to increase Collembola density, diversity and activity. Moreover, we hypothesize its effects to be most pronounced in the sparsely vegetated center parts of NSC, as here increased winter insulation, reduced cryoturbation and trophic cascading all act on Collembola.

Eventually, the extent to which vegetation will expand into the non-vegetated parts of NSC, and the new balance between plant productivity, SOC burial and decomposer activity in these soils will determine the fate of this large carbon pool.

Keywords: soil invertebrates, climate change, permafrost, soil organic carbon

[P2.086]

Near infrared spectroscopy and morphology analysis of earthworm-engineered soil in subalpine pastures of Central Pyrenees

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Near-infrared reflectance spectroscopy (NIRS) is a rapid and non-destructive analytical technique for the assessment of the organic matter that involves diffuse-reflectance measurement in the near infrared region (1,000 – 2,500 nm). In this study we used NIRS to identify the origin of biogenic aggregates produced by several earthworm species from the subalpine pastures of the Central Pyrenees. NIR spectral signatures of biogenic aggregates, root-aggregates, and non-aggregated soil separated in soil blocks of 10x10 cm and 10 cm depth were established in order to compare the signals with the temporal reference signatures of biogenic structures obtained in the lab. The species <u>Aporrectodea rosea</u>, *A. caliginosa*, <u>Lumbricus friendi</u> and *Prosellodrilus pyrenaicus* were collected in the field and reared in the lab with soil of the same area, air dried and sieved at <2 mm to prepare the microcosms. Individuals were kept in microcosms for one day and retrieved after they had deposited casts in the soil volume. Soil and casts were then incubated during 0, 1, 3, 7, 15, 31, and 63 days, after which all casts were retrieved, and 200 µm sieved for NIR spectral values and C and N content determinations. Samples (non-ingested soil and casts) were packed in a quartzglass container and placed in a spectrophotometer (QualitySpec®). The spectral values were obtained for 10 nm intervals and further transformed to second derivative with the Unscrambler software to reduce the number of variables processed. PCA and PLS regressions were used to compare signals of samples and significance testing of their groupings. The NIR spectra of casts clearly differed for species and time elapsed since cast production, and spectral values of field data were projected onto the PCA axes extracted with lab experimentation data to identify species responsible for the production of biogenic aggregates in the soil matrix.

Keywords: Earthworms, NIRS, Soil organic matter, Biogenic aggregates

[P2.087]

Climate change and soil invertebrates: State of knowledge, lessons learned and opportunities

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The impact of projected climate change (CC) on soil invertebrate communities across ecosystems is limited by uncertainties in predicting the interactions of ecosystem carbon (C) cycle with global warming which are determined by our incomplete knowledge of below-ground processes. Complex and non-linear responses are expected on the interactions between soil invertebrates, plants and above-ground invertebrates. Soil invertebrate assemblages may change and hence soil processes like decomposition rates will also change. Decomposition rates in forest soils have been demonstrated not to be temperature dependent, meaning that global warming may not necessarily accelerate soil C losses.

More studies are needed on the combined effects of changes in CC-related drivers in the context of soil invertebrate diversity and function, even though there appears to be logistical constraints to the empirical approaches that would be needed in order to examine all possible interactions. In addition, new methods are requested to improve the reliability of predictions of responses to elevated atmospheric CO_2 concentrations, warming temperatures and atmospheric N_2 deposition. The role of soil invertebrates in the C cycle needs to be understood to generate more comprehensive predictive models on the effect of CC on soil invertebrates and on the processes they intervene. It is likely expected that CC will profoundly affect soil-organism performance, with either enhancement or reduction of the functions they provide, resulting in positive or negative feedbacks relevant to CC. Regarding agriculture, evidence suggests that CC will likely disrupt the role and use of invertebrates in sustainable agriculture to varying degrees, even though the precise nature of the disruptions is not yet known. These disruptions will cause production losses without rationale interventions, and the extent of these losses will justify intervention to facilitate adaptations of the invertebrates, even though the methods and policies to facilitate this intervention are not yet in place.

Keywords: Climate change, Invertebrates, Adaptation, Agriculture

[P2.088]

Shift in the microbial community after long-term application of organic fertilizers indicated by fungal and bacterial residues

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Amino sugars are the most important markers for microbial residues in soils and useful to investigate medium- to long-term effects of land-use changes on the soil microbial community. The residues of fungi and bacteria, the two largest functional microbial subgroups in soil, can be specifically quantified by analyzing glucosamine (GlcN) and muramic acid (MurN). In the presented study, we evaluated 27 years of fertilization with mineral fertilizer (MIN), farmyard manure (FM), and farmyard manure with biodynamic preparations (FMBD) on an experimental field of high pH heterogeneity on the soil microbial community. Therefore, MurN, mannosamine (ManN), galactosamine (GalN), and GlcN were analysed by HPLC analysis. Fungal C and bacterial C, respectively, were calculated based on fungal GlcN and MurN. Ergosterol was analyzed as a marker for saprotrophic fungal biomass. Organic fertilization (FM, FMBD) led to a higher accumulation of bacterial C, but had no effect on the amounts of fungal C. Bacteria were promoted by increasing pH as indicated by a significant positive relationship ($r = 0.52$; $P < 0.01$). ManN, GalN, and GlcN did not differ significantly between the treatments. A fungal C to bacterial C ratio of 3.5, 2.1, and 2.2 in MIN, FM, and FMBD, respectively, indicated the dominance of fungi in all treatments. A shift within the fungal community to more arbuscular mycorrhizal fungi at the expense of saprotrophic fungi in FM and FMBD in comparison with MIN was indicated by a significantly lower ergosterol to fungal C ratio. In conclusion, long-term fertilization of farmyard manure increased microbial residue C and caused shifts towards more bacteria and arbuscular mycorrhizal fungi.

Keywords: Amino sugars, Farmyard manure, Microbial residues, Soil pH heterogeneity

[P2.089]

Collembolan assembly processes in different types of habitats as indicated by community phylogenetics

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Species assembly in local communities depends on selection processes that filter species from the regional species pool. Collembola are a diverse soil mesofauna group, reaching high densities in various habitats including arable fields, grasslands and forests. Processes driving the assembly of collembolan communities in these habitats are little understood. The community phylogeny approach offers an alternative way to compare the relative strength of habitat filtering and niche partitioning on community assembly by comparing phylogenetic relatedness and trait similarities of species coexisting in local communities. We constructed a phylogenetic tree of collembolan communities of an arable field, grassland and forest, using sequence data of 18S, 28S rDNA and Histone H3. Both phylogenetic and trait relatedness were calculated for Collembola communities of the three habitats. We also compared the structuring forces on surface-living collembolans with soil-dwelling species. Our analyses showed that the Collembola community in the arable field is predominantly determined by environmental filtering, while in forest it is driven predominantly by selection on specific traits that are convergent in the phylogenetic tree. Further, our analyses indicated that structuring forces on surface-living collembolans differ from soil-dwelling species. In arable field and grassland, surface-living collembolans are more phylogenetically related, suggesting environmental filtering, while soil-dwelling species are more randomly assembled with regard to phylogeny. In forest the surface-living species are significantly phylogenetically related but showing trait disparity, while soil-dwelling species are phylogenetically over-dispersed but with trait similarity, suggesting different selection mechanisms working in different soil layers. We discuss discrepancies between phylogenetic relatedness and trait similarity and potential mechanisms acting on conserved and/or convergent traits in different habitats.

Keywords: Collembola, community phylogeny, environmental filtering, disturbance

[P2.090]

Species diversity of free-living nematodes in tropical soils of Vietnam, exemplified in the order Dorylaimida

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The soil nematode fauna in twelve localities of tropical forests in Huu Lien Nature Reserves in Vietnam was investigated. Nematodes in the order Dorylaimida were identified to species level in order to get an estimate on the numbers and diversity of known and undescribed taxa. More than three hundred specimens of 30 species, 20 genera and 9 families have been examined and characterized. The dorylaimid fauna of this area consisted of a few (8%) cosmopolitan species (*Aporcelaimellus obtusicaudatus, Tylencholaimus teres* and *Mesodorylaimus clavicaudatus*), some (8%) Paleotropical forms (*Longidorella xenura, Proleptonchus aestivus* and *Tyleptus projectus*), a series (50,7%) of species which presumably belong to the Oriental realm/region (*Axonchium thoubalicum, Belondira murtazai, Labronema glandosum, L. neopacificum, Oriverutus parvus, Oxybelondira paraperplexa* and *Thornedia opisthodelphis*), and a good number (33,3%) of forms belonging to non-described species of the genera *Allodorylaimus, Oriverutus* and *Sectonema*. It is especially remarkable that more than one-third of the species examined certainly represent unknown taxa, a proof of the much understudied nematode diversity existing in the poorly explored natural areas from Southeast Asia.

Keywords: Dorylaimida, free-living nematodes, species diversity, Vietnam

[P2.091]

Effects of land-use intensity on nematode communities of tropical soils in Vietnam

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Increasing land-use intensity has likely strong impacts on soil biodiversity and fertility in the tropics. Nematodes are known to respond rapidly to soil disturbance and changing resources. Therefore the functional composition of the nematode community offers a reliable measure for the biological assessment of the quality and functioning of tropical soils. In Northern Vietnam we investigated the diversity of soil nematode communities of three spatially separated karst mountain systems. The island-like character of the karst mountain systems enables biogeography comparisons between regions. To investigate how local land management interferes with species richness, we took soil samples on each location along gradients of increasing land-use intensity: i) primary forest, ii) secondary forest, iii) slash and burn agriculture, iv) intensive agriculture, to investigate changes in nematode community composition, soil carbon storage and nutrient cycling.

Nematode community composition differed between regions, but land-use intensity had general and distinct impacts on the functional composition and food web structure of nematodes. Indicators of these changes, such as the Maturity Index, Channel Index or Plant Parasitic Index will be correlated to and discussed in relation to changes in soil carbon and nutrient levels.

Keywords: Effects, land-use intensity, nematode communities, Vietnam

[P2.092]

Impact of biochar on short-term biochemical soil activity

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Soil application of biochar has been proposed as an effective management to maintain and enhance soil ecosystem services which are directly linked to microbial activity. Both stimulation of microbial activity, due to a favourable environment for soil microorganisms, and inhibition effects, due to adsorption of a range of substrates, have been reported. The aim of this study was to assess the effect of contrasting biochars and their interactions with fertilizers on key soil enzyme activities (EA).

Six biochars proceeding from different feed-stocks (oak wood, municipal solid waste, anaerobic digestate, green wastes, greenhouse wastes) and different pyrolysis conditions were added (0.5% w/w) to a silty clay loam soil either separately or in combination with a rapeseed meal or an organo-mineral fertilizer (rate 340 kg N ha^{-1}). EA linked with C, N, P and S cycles (□-glucosidase, leucine aminopeptidase, alkaline phosphatase and arylsulphatase) was quantified after 2, 7 and 28 days of incubation applying a fluorometric, high throughput, microplate-based, soil enzyme assay.

Separate addition of biochar and organo-mineral fertiliser did not significantly affect EA, while addition of rapes meal caused a relevant increase in the hydrolytic capacity of the soil.

Simultaneous addition of biochar and rapeseed meal caused a further increase in soil EA that was particularly relevant after 1 week of incubation. The synergic effect on EA of biochar and rapeseed meal tended to level off at the end of incubation. Such results are in agreement with previous works suggesting that there is an initial stimulating effect of biochar on soil biological activities that decreases over time.

On a whole results of the present work showed that biochar has no negative effects on EA in soil. Instead, it may also have a stimulating effect under specific conditions, such as in the case of simultaneous addition with organic amendments.

Keywords: biochar, biochemical activity

[P2.093]

Simultaneously driven microbial N immobilization and denitrification in temperate paddy soils

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In temperate paddy soils nitrogen (N) dynamics are driven by different biotic and abiotic processes including soil immobilization and losses to waters and atmosphere. This may significantly affect nutrient bioavailability during the rice cropping season, as well as environment quality. In this study we evaluated the changes in the distribution of fertilizer ^{15}N among available, immobilized and lost pools, with special emphasis to specific microbial communities simultaneously performing immobilization and denitrification processes.

A typical temperate paddy topsoil (Ap horizon) was incubated under different redox conditions, with or without rice straw incorporation, and fertilized with ^{15}N enriched and natural abundance ammonium sulphate. The ^{15}N tracer was followed by in difference chemical and physical N pools and by means of molecular fingerprinting and stable isotope probing techniques. To evaluate the importance of abiotic factors, a parallel experiment under sterile conditions was also carried out. Results suggested that abiotic processes were responsible for fast N immobilization (45-53% of applied N), under both oxic and anoxic conditions. However, with time, biotic processes seemed to prevail on abiotic ones. Addition of rice straw enhanced biotic N immobilization, particularly under flooded conditions, limiting N losses up to 25% with respect to 60% in the absence of straw. These losses were corroborated with the response of archaeal community harbouring *nosZ* gene, which encodes N_2O reductase and leads to complete denitrification. In addition, N assimilation and the subsequent immobilization appeared to be the precursor of this response, driven by the different availability of organic and inorganic C and N resources.

The results highlighted the predominant role of microbial communities in driving N cycling, with particular attention to the ecological implications of archaea on controlling N immobilization and losses in temperate paddy soils.

Keywords: N availability, biotic immobilization, assimilatory denitrification, archaea nosZ

[P2.094]

Distribution of nitrogen functional communities in soil aggregates from contrasting land uses

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Soil aggregates are known to directly influence the abundance, activity and diversity of the overall microbial communities (i.e. bacteria and fungi) in soil. However, little is known about the functions of the microbial communities in soil aggregates. Thus, the objective of this study was to determine the distribution of nitrogen functional communities in soil aggregates. Six sizes of soil aggregates were obtained by dry-sieving (0-0.25, 0.25-0.5,0.5-1.0, 1-2, 2-5, 5-10 mm), from 4 different sites with contrasting land uses (i.e. grassland, cropland, young forest and forest). Quantitative-PCR (Q-PCR) was used to investigate the abundance of functional guilds involved in N-fixation (*nifH* gene), nitrification (bacterial and arhaeal *amoA* gene), and denitrification (*narG*, *nirS*, and *nosZ* genes).

The Q-PCR results showed that different land uses had significantly different abundances for all the genes, with the cropland site showing the lowest abundance for all the genes except *amoA* bacteria. The young forest site showed the highest gene abundance for *nifH*, *narG* and *nirS,* while forest site showed the highest gene abundance for *amoA* bacteria and archaea, and grassland site for *nosZ* gene. Variation in genes abundance between the sizes of soil aggregates were found, but the variations were gene and land use specific, with no constant trend across land uses. For example, *nifH* gene abundance was high in soil aggregates 5-10, 1-2 and 0.5-1 mm at young forest site but not differences were found for cropland and grassland between sizes of soil aggregates, while for forest slightly higher abundance was found for 0.5-1 and 0.25-0.5 mm soil aggregates. This study show that land use is a dominant driver of the distribution of N functional communities, and that the effect soil aggregates occurred at local scale except in ecosystems highly affected by anthropogenic activities such as cropland.

Keywords: Soil aggregates, Land use, Nitrogen cycle, microbial distribution

[P2.095]

Linking plant and microbial community composition to soil function in the context of short and long-term CNP storage and turnover in physically complex, species-rich sub-alpine grasslands.

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Species richness and the role of functional plant types in the stock and mineralisation of energy and nutrients in grasslands has been the focus of a degree of research in mountain grasslands. Plant richness and microbial community composition have been shown to relate to the stocks of C and N in soils, yet the complexity of mountain grasslands from a physical perspective, and how this might direct energy flow and microbial community composition is less well understood. Additionally, measures of C and N in soils are only rarely linked with comprehensive functional metrics, and have scarcely been considered on a range of time scales relevant to ecosystem C turnover. Here, we explore how the physical complexity of mountain grasslands leads to variation in the community composition and its functional traits, and to what extent these relate to ecological processes constraining CNP cycling, and ultimately, their relation to decadal-millennial scale turnover. We find that trait response varies amongst three functional plant types, and soil functions associated with turnover differ markedly in their relationship to complexity in the physical environment. Our work adds to the diversity-function debate, and through integrating novel approaches, provides insight into multi-scale processes links in mountain systems.

Keywords: Macronutrient, Turnover, Soil-plant, Function

[P2.096]

Soil bioindicators: how soil properties influence their responses and how to select them in function of the site issues?

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Context - Despite no directive exists for soil protection, this key component of ecosystem needs to be protected. To fill the lack of tools to monitor the soil threats and to assess the impact of soil management, biological indicators have been developed in the French program Bioindicators 2 (ADEME). On the 47 plots of 13 sites (agricultural, industrial and forest), the influence of soil characteristics and soil use on the response of 80 biological parameters (fauna, flora and microorganisms) have been assessed by using linear multivariate regressions.

Results - The soil texture and the organic carbon rate has been identified as the main soil characteristic influencing the biological responses, even if each bioindicator is influenced by its own pool of soil parameters. It underlines the necessity to use battery of bioindicators for an integrative assessment of soil quality. An influence of soil contaminants (organic or metallic) have been highlighted for 86% of the bioindicators showing the necessity to consider their bioavailability for suitable soil management. To disseminate the use of bioindicators, a web interface has been implemented (http://ecobiosoil.univ-rennes1.fr/ADEME-Bioindicateur/). It presents all the biological methods developed in the program and allows consultation of the variation range of each bioindicator considering site contexts and soil physico-chemical characteristics of soils thus leading to provide a first benchmark. It also provides tools to the end-users to select the bioindicator(s) which best fit(s) with their own site problematic (agricultural practices, bioavailability of contaminants, soil monitoring...) and to communicate (technical sheets...).

Conclusion – For the first time, the soil properties influence on the response of 80 bioindicators was characterized under similar environmental conditions. As each bioindicator is influenced by a specific pool of soil parameter, chemical measures cannot be used as a surrogate of biological measures. This program has provided usable tools for a biologically-based site management.

Keywords: bioindicators, soil quality, soil properties, web interface

[P2.097]

Prokaryotic gene abundances driving mitigation of greenhouse gas emission in temperate paddy soil

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Submerged rice is planted in half of the world's rice fields and produces about 75% of the world's rice supply. Paradoxically, rice ecosystems are also characterised as CH_4 and N_2O source, due to microbially mediated carbon (C) and nitrogen (N) based greenhouse gas emissions. One important challenge in terms of climate change debates aims at understanding how the management practices adopted in rice agro-ecosystems influence soil prokaryotic communities which control organic matter mineralization and soil N inputs and outputs. Therefore, it is crucial to understand the microbial regulation of greenhouse gas fluxes as a function of crop residue incorporation and different floodwater strategies.

The research was carried out on soils sampled at different times during the cropping season from four different isolated plots within an experimental rice platform (NW Italy). The plots differed in terms of straw and water management and sampling was concentrated in correspondence of N fertilization and major changes on oxic/anoxic conditions. Methane and nitrous oxide fluxes were measured in situ by the closed-chamber technique. Chemical and molecular analyses were adopted to get new insights in the abundance and structure of microbial communities which drive CH_4 and N_2O emission.

Our results suggest a strong link between the succession of flooded - dry cycles under different management and the prokaryotic communities. Various ecological niches were created allowing the growth of phylogenetically and metabolically diverse microbial groups. A clear alteration in the abundance and structure was shown, correlated to straw addition and influenced by changes in soil redox conditions. This suggested that managing rice ecosystems to conserve or restore the activity and diversity of microbial populations could help to mitigate climate change. The different agronomic strategies distinctly influence the abundance and diversity of bacteria and archaea responsible for the consumption of two of the three major naturally-occurring greenhouse gases.

Keywords: climate change, flooded-dry cycles, rice straw, microbial control

[P2.098]

Diversity and distribution of Criconematidae nematodes in Great Smoky Mountain National Park

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The Great Smoky Mountain National Park (GSMNP) is globally recognized as an area of biodiversity unmatched elsewhere in North America. Its diversity and high endemicity were reasons for the establishment of North America's first All Taxa Biodiversity Inventory (ATBI) project within the park boundaries. The ATBI goals are to identify every species of plant and animal, their distribution, abundance, seasonal and ecological relationships within 19 one-hectare sites. The sites replicate plant communities across a gradient of disturbance. Nematode communities have yet to be surveyed in the sites. Using Criconematidae as a taxonomic unit for high resolution analysis of diversity, we have focused on two objectives: 1) analyze the diversity of Criconematidae within GSMNP, 2) determine population structure among ATBI sites. Soil cores were taken systematically within ATBI sites using Oakfield tubes inside a 40 x 40m grid. Nematodes were extracted from soil by a combination of sieving and sugar centrifugation. Individual nematodes in Criconematidae were photographed, measured, and prepared for DNA analysis. Analyzes were conducted at different levels of organization: morphospecies, haplotype lineage, and haplotype diversity. To date, 11 different morphospecies within the family have been identified from the ATBI sites. These are further subdivided into 30 haplotype groups which may represent cryptic species. Haplotype groups vary in their phylogeographic patterns. For *Criconema sphagni*, found in four ATBI sites, each site is characterized by a unique haplotype. For *Ogma octangularis* a common haplotype is spread among multiple sites, combined with site-specific haplotypes. In *Lobocriconema* five distinct haplotype groups are dispersed among the ATBI sites. Phylogeographic analysis of haplotype groups within GSMNP provides evidence of high nematode endemicity and supports an interpretation of the park as a former glacial refugium for nematodes.

Keywords: phylogeography, geographic information system, haplotype diversity, phylogeny

[P2.099]

Exploring prairie diversity: Criconematid nemtodes of North America's Central Tallgrass Prairie

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Approximately 200 years ago, North American landscapes were dominated by vast expanses of grassland. The Great Plains, an ecologically complex and diverse ecoregion, extended from Canada to the Gulf of Mexico, and from the Rocky Mountains to the border of the eastern hardwood forest in Indiana. Now the original tallgrass prairie exists in small widely dispersed remnant patches surrounded by agroecosystems. This study is an effort to characterize soil nematode diversity and population structure within those remnant patches, and to elucidate the factors that account for similarities and differences in prairie nematode diversity. The plant parasitic nematode family Criconematidae serves as our indicator for nematode diversity, due to its global distribution, high abundance, broad host range, limited dispersal capabilities, and the availability of a highly resolved COI gene tree. Twenty-five grassland sites were sampled by extracting soil cores within a 40 x 40m grid. Criconematid nematodes were screened and isolated using soil sieves and centrifugation. Nematodes were individually photographed, measured and amplified with a primer set that, after removing primers, results in 721 nucleotides of the COI mitochondrial gene. Diversity was studied at different levels, from morphospecies to haplotype lineages and haplotype diversity within lineages. Morphospecies diversity ranges from a high of eight species in prairies in northeastern Iowa and eastern Nebraska to zero in restored prairies and intensively managed pasturelands. In restored sites where plant diversity is equal to that of surrounding prairie, Criconematid diversity remains low, suggesting a legacy of disturbance detectable through nematode communities. Multiple cryptic species and genetically distinct haplotype lineages are common within all morphospecies. At the haplotype level, evidence supports phylogeographic patterns of common widespread haplotypes across the region accompanied by microendemic haplotypes confined to individual sites. Phylogenetic analysis suggests that northern haplotype lineages have ancestral roots in southern grasslands of Arkansas or Texas.

Keywords: Biogeography, Phylogeography, Grasslands, Mitochondrial DNA

[P2.100]

How grazing and fire regime influence soil biogeochemical cycling in a native grassland in central Mexico

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Fires, grazing by ungulates and variable climate have shaped the semiarid grassland biome over evolutionary time. In North America, with the introduction of livestock by Europeans, alterations in grazing and fire regimes induced changes in species composition and biogeochemical cycles in this biome. We asked the following questions: How may these changes have influenced abiotic and biotic controls of soil nitrogen cycling. In particular, how does grazing and prescribed burning modify nitrogen mineralization in the rhizosphere of grass species with contrasting forage quality. In October 2012, we set up a soil incubation experiment in sites with different grazing (continuous and no-grazing) and fire regimes (no-fire, 2-year fire legacy effect, and recent burning) in natural semiarid grassland in Jalisco, Mexico. Samples (5x10 cm depth) were taken in soils associated with desirable *Bouteloua gracilis* and undesirable *Muhlenbergia rigida* in 120 plots in four different times. We analyzed soil inorganic nitrogen (ammonium and nitrate); in addition soil temperature and humidity at 10 cm soil depth were recorded throughout the experiment. For the legacy effect, we only observed a significant increase of 27% ($P<0.02$) of ammonium in soils with prescribed fire, compared to soils with no-fire, for a period of three months. Whereas, for the recent fire treatment, we observed that grass species exhibited opposite influences on nitrate, as the concentration in soils associated to *B. gracilis* increased, while it decreased in soils associated to *M. rigida* with fire. Regarding ammonium, fire increased ammonium immediately after burning (January 2013), however, no effect of grass species was observed. Grazing only influenced nitrate concentration increasing its concentration in soils associated with fire for a period of one month. Our results suggest that elimination fire and grazing regimes influences negatively N mineralization by the key species (*B. gracilis*), while it increases when subordinated *M. rigida* is dominant.

Keywords: Prescribed fire, Grazing, biogeochemical cycling, grassland

[P2.101]

The role of biological soil crust in the contribution of soil organic carbon in semiarid grasslands of central Mexico

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Globally, semiarid grasslands are important stocks of soil organic carbon (SOC). In this biome, lichen, algae and cyanobacteria are constituents of the biological soil crust (BSC). They colonize vegetation-free interspaces between C_4 grasses, assimilate CO_2 and thus potentially contribute to carbon sequestration in grassland soils. In Mexico, overgrazing has modified BSC cover and function. The objective of this study was to quantify the contribution of cyanobacteria and different BSC lichen species to SOC considering different grazing regimes. In November 2012, we collected BSC samples in the interspaces of open semiarid grasslands in Jalisco, Mexico. In particular, we compared six different lichen species, including two species in juvenile and adult developmental stage within a moderately grazed grassland. In case of the highly abundant *Diploschistes diacapsis*, juvenile *Acarospora socialis*, and cyanobacteria, we examined how different grazing systems -intensive, moderate and no grazing systems- affected their contribution to SOC at 0 to 3.0 cm soil depth. With natural abundance of ^{13}C stable isotope information for BSC and C_4 grasses and mixing models, we quantified the contribution of soil carbon by different BSC species/types. When comparing lichen species within grazing system, *A. socialis*-adult, *A. socialis*-juvenile and *A. schleicheri* contributed with more organic carbon than *A. obpallens*-adult, *A. obpallens*-juvenile and *Disploschistes diacapsis* at all depths. However, when comparing certain BSC species across grazing systems no clear differences in carbon sequestration were observed. In general, adult lichen stages contributed with more carbon to soil than the juvenile stages. Overall, BSC contributed about 50% to total soil carbon in the top 3 cm of soil, which corresponded to about $3tCha^{-1}$. These results suggest that BSC play an important role in the spatiotemporal distribution of SOC in soils of semiarid grasslands and that BSC species richness could increase the potential of organic carbon sequestration in these ecosystems.

Keywords: Biological soil crust, grassland, grazing, organic carbon

[P2.102]

Rizosphere community composition of phosphorous mineralizing and solubilizing bacteria of native potato Solanum tuberosum group phureja

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Soils where ***Solanum tuberosum*** **group** ***phureja*** is cultivated are characterized as being highly soil phosphate binders. Therefore, to meet the nutritional demands of the crop, high phosphorous based fertilizers are applied, which increase production costs, as well as undesirable environmental effects. As a result of that, some farmers apply organic amendments as an alternative to ameliorate such negative effects. However, the effects of such practices, as well as the soil type on ***S. tuberosum*** **group** ***phureja*** P-related microbial communities are still unknown. The aim of this study was to analyze the edaphic communities related to phosphorous metabolism in spatially independent rhizosphere soil samples from ***S. tuberosum*** **group** ***phureja*** crops, contrasting in terms of soil structure and fertilization strategy. Such analysis was done through a polyphasic approach, which includes physical-chemical soil analyses, phosphatase activity quantifications, and culture-dependent and independent microbial communities composition analysis, in order to identify the factors that regulate de P cycling in this ecosystem. Statistical significative differences were found in microbial counts, community composition an phosphatase activities in the four soil samples, but it did not showed a common pattern that allow us to identify the effect of soil type or fertilization strategy on P-related microbial communities. However, the diversity indices, alkaline phosphatase activities and the results of a biological P-related variables cluster analysis, showed similar patterns between farms, which allowed us to conclude that through our polyphasic approach the functionality and composition of the microbial community associated with this particular functional group, could be the result of complex interactions strongly related with soil physical-chemical variables such as organic matter content, moisture and total nitrogen (organic plus inorganic). However, deeper studies are needed to identify the specific factors that determine these differences.

Keywords: diversity indices, pyrosequencing, Phosphate cycle, organic amendments

[P2.103]

Oribatid mites' community from the root zone of two legume bushes growing in degraded drylands

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Soil biomass productivity depends on food webs for replenishment of limiting nutrients. In this process, chewing organisms start nutrient recycling of plant material by exposing more surfaces and cell contents to microbial degradation. This activity falls mainly on Arthropods, and particularly on Oribatid mites, in soils devoid of Oligochaeta, as is the case of the alluvial terraces at the shadow rain Desert of Tehuacan, Mexico. Several terraces are under natural degradation process, shows dominance of *Prosopis laevigata* with a scattered presence of *Parkinsonia praecox* (both phreatophytic legume bushes). We wonder how similar the Oribatrid mites' community could be between a bushes keeping its leaves longer (*P laevigata*) and another littering at once (*P praecox*). We aim to elucidate how similar the Oribatid community is between both bushes at the end of the rainy season in the 0 – 15 cm soil layer. Samples were taken by triplicate under 3 individuals of both bushes and interspace soil. Mites were isolated by the Berlesse-Tullgren method and kept in 70% alcohol for morphological identification. We found 15 families of Oribatid mites under *P laevigata*, 13 under *P praecox* and only 6 families under interspace soil. Trophic groups under *P laevigata* and *P praecox* showed almost the same proportion of obligated microphytophagus, facultative predator and microphytophagous species, while insterspace soil showed only the first two trophic groups. Diversity index was very similar between bushes (H = 0.907 and H= 0.905) and lower for interspace soil (H = 0.766) Simpson index yielded a similar pattern (D= 2.47, D=2.23 and D= 1.55). Communities under *P laevigata* and *P praecox* are almost identical (Sørensen analysis yielded around 99% likeliness) and were very different from the interspace soil. We concluded the plant effect is more important for Oribatid mite's rather than the identity of the legume bushes.

Keywords: Oribatid Mites, community ecology, drylands, soil degradation

[P2.104]

Soil enzyme activities in a Tuber aestivum truffle orchard: spatial relationships with soil,symbionts and truffle colonization

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Tuber spp. (*Ascomycota, Tuberaceae*) are symbiotic ectomycorrhizal fungi that produce subterranean edible ascocarps renowned as truffles. Some of them act against grass species, thus originating a bare area around the symbiont – called *brulé* – that can be considered a surface marker of the area of fungal colonization. Knowledge about soil type-*Tuber* colonization-biochemical activity relationships is important for understanding ecosystem functioning.

Since no information is available about the effect of the *brulé* on enzyme activities in soil, we did a detailed investigation in a truffle plantation where the *brulé*-producing species *T. aestivum* was present. In a rectangular area of 70m x 120m we collected 180 geo-referenced soil samples that were analysed for five enzyme activities. The screening of enzyme activities was performed using a fluorescent-based, high throughput procedure involving soil extracts and fluorogenic substrates in microplates.

Alkaline phosphatase displayed the highest values in the *brulé* areas where truffles were collected in the last decade, but the spatial pattern was also related to variations in soil type. By contrast, distribution of β-glucosidase was closely related to plant cover and in particular with the presence of grasses. Arylsulphatase displayed a pattern distribution comparable to β-glucosidase but with a more patchy distribution. Leucine aminopeptidase and Chitinase displayed a random distribution with no noticeable pattern.

Therefore, a relationship between spatial variability of enzyme activity on one side and soil variability, plant cover and *T. aestivum* colonization on the other has been established.

Keywords: truffle, enzyme activity, spatial variability

[P2.105]

Eco-evolutionary meta-community dynamics in soil food webs: understanding the maintenance of biodiversity in extremely rich ecosystems

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Soil food webs may be extremely diverse and the stability of these ecological networks may be critical to ensure adequate ecosystem processes, such as nutrient cycling (decomposition). However, recent findings may change the angle from which we attack the problem of food web stability. First, we now know that organic evolution may occur at ecological time scales, and second that trait genetic variability within each of the embedded populations in the food web may strongly contribute to shape its structure and dynamics. Therefore, food web stability may depend on an eco-evolutionary feedback (ecology –network structure- shapes evolution, and evolution –genetic variability- shapes ecology). If in addition we add the fact that soil spatial heterogeneity is usually very high, and want to explicitly study the eco-evolutionary community dynamics of these multi-trophic communities across space (meta-community context) the challenge is enormous. We may go even further by considering that genetic variability is often multidimensional; i.e., when the genes that affect one functional trait (e.g., predator voracity) are independent of the genes that affect another (e.g., predator mobility). While collecting empirical data to understanding this enormous complexity is currently out of reach, computer simulations using sets of realistic parameters may be very helpful, especially in light of the recent advances in supercomputing. Here, we introduce Weaver, an individual-based modelling (IBM) platform to simulate eco-evolutionary meta-community dynamics in soil food webs of variable complexity. We studied the drivers of food web persistence (and thus the maintenance of soil biodiversity) and showed that persistence: increased with 1) trait genetic variability and contemporary micro-evolution, and 2) food web connectance; and is maximum at 3) intermediate water micro-island (soil water pockets) distances. Therefore, the present framework may serve to increase our understanding on the maintenance of soil biodiversity and its associated ecosystem processes, such as nutrient cycling.

Keywords: SOIL FOOD WEBS, ECO-EVOLUTIONARY DYNAMICS, META-COMMUNITY DYNAMICS, ECOSYSTEM FUNCTIONING

[P2.106]

Soil surface matters: Interactions between microbial communities, the architecture of the soil surface and hydrological processes at the soil:atmosphere interface.

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The soil surface is a crucial interface which connects the atmosphere to the pedosphere, and the nature and properties of this zone play important roles in governing many aspects of soil function, including hydrological processes, propensity to erosion, gas exchange, seedling emergence, and biotic interactions. Many susceptible soils have a distinct but thin layer at their extreme surface, referred to as a crust, that can be generated by different mechanisms. A 'physical' soil crust often develops raindrops impacting the soil surface, resulting in aggregate breakdown and particle re-organisation to form a surface layer that is less porous and more compact than the underlying soil. In addition, the biology of the extreme surface is also very distinct from that beneath it, principally with respect to the presence of microbial photoautotrophs. It is well recognised that 'biological soil crusts' are of ecological significance in many natural habitats, but relatively little is known about the nature, properties and functional significance of the soil surface biota in arable and horticultural systems, and less still about the interactions between soil structure and biology in this zone. We conducted a laboratory study to investigate the relationships between microbial community structure, soil architecture and hydrological properties in a sandy loam and silt loam used in horticultural production. Communities were manipulated by controlling light and via prokaryotic- and eukaryotic-selective inhibitors. The ultra-fine-scale spatial and temporal dynamics of structural seal formation was attained via X-ray micro computed tomography. Significant variations in porosity between different types of crusts were found, and volume of surface-connected pores varied significantly between the soil types, being consistently higher in the soil with the higher clay content. Fungal- and photoautotroph-dominated systems showed increased porosity, but reduced hydraulic connection, penetrative resistance and structural resilience, than bacterially-dominated systems. Greater hydrophobicity was manifest in the photoautotroph-dominated systems.

Keywords: Soil structure, Hydrological processes, Hydrophobicity

[P2.107]

Mangrove community assemblage and relationships with soil features in a Neotropical stand

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Brachyuran crabs constitute an important functional group that plays important roles in sediment features, vegetation structure and primary production. However, studies in the Neotropics investigating crab assemblage and other ecological variables in structuring mangrove community at young forests, are restricted. In a mangrove in northeast Brazil (Pacoti River, Ceará State), we investigated the relationships between soil physicochemical features, brachyuran fauna and tree composition and development. For this, we compared forest patches with different tree composition, i.e., areas dominated by *Rhizophora mangle* (R), Avicennia *germinans* (A), *Laguncularia racemosa* (L), areas with two species (RL and AL), one with all the three species (RLA) and a control area without vegetation (C). Data were ordinated through a Principal Component Analysis (PCA). Axis 1 explained 34.1 % of the variation and represented tree density, number of crabs *Uca* spp. and *Goniopsis cruentata* and crab richness. C and A were clearly separated from the other areas and associated with snail diversity, which varied inversely to most other parameters, such as M/J rate, organic matter, tree dominance, penetrability, *Uca* spp. burrows, crab richness, number of *G. cruentata*, seedling and tree density and diversity. R was closer to the first four parameters cited, L and RL closer to the following three like RLA, which was more related to tree diversity. Axis 2 explained 23,81% of the variation, and had a positive loading of M/J rate, organic matter and tree dominance associated to R and L, with negative loadings of tree diversity and density. Tree and seed density and tree diversity were negatively correlated to M/J rate, organic matter, tree dominance and penetrability. LA appeared close to biplot center, showing lower association with measured parameters. Evidences indicate that the crab assemblage may be resilient to support changes at forest composition determined by changes on sedimentary patterns at littoral areas.

Keywords: soil properties, mangrove crabs, Neotropical mangrove, community structure

[P2.108]

Establishing a soil biodiversity monitoring program in Portuguese forests

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Soil fauna plays an important role in soil biological processes underlying the provision of key ecosystem services. Monitoring soil biodiversity is therefore crucial to detect trends in soil quality status. Aiming to implement a monitoring program for biodiversity in Portuguese forests, the “Forest biodiversity and ecosystem services” project was set with the major aim to launch an extensive monitoring program in Portuguese forest stands to determine the Normal Operating Range for soil fauna richness in this type of ecosystem. The project covers 100 ICP Forests’ Level I sites across Portugal, comprising both autochthonous and invasive tree species, enabling the study of soil fauna diversity patterns in different forests with different levels of human intervention.

Sampling of soil meso and macrofauna began in Spring 2012 and is still undergoing, using high-gradient cylinder extractor and pitfall traps respectively; mesofauna collected is classified according to morphotypes and macrofauna sorted to order (afterwards identified to species/morphospecies). Land-use and environmental variables have been registered and soil parameters assessed. Approximately half of the sites have been sampled so far, mainly the ones located in Southern Portugal (*Quercus suber* L. and *Quercus rotundifolia* Lam. areas).

Early results on mesofauna abundance and diversity haven’t revealed significant differences on richness and diversity between stands of the two oak forests. This could be related to the similarity in habitat configuration among them and to the low intensity management adopted in most of the stands. Positive correlations arose between mesofauna abundance and diversity with vegetation cover, and more are likely to be found when a full set of explanatory variables is incorporated into the analysis. Similar results have been obtained for macrofauna.

The work developed should allow estimating the NOR for some meso and macrofauna groups and thus contribute to establish a soil biodiversity monitoring program for Portuguese forests.

Keywords:

[P2.109]

Distribution biogeographic of plant-associated nematode communities in Algerian vegetable farming systems

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This study aims to develop better knowledge of composition and structure of plant parasite in vegetable farming systems in the Algerian context. Samples were collected in 143 vegetable stations in five biogeographic areas (Numidian, Algiers, Oranes, High uplands and Saharan sector. Rhizospheric soil samples were collected in the upper rhizomes at 30–40 cm depth. The nematodes were extracted using the flotation and sedimentation procedure. The inventory revealed the presence of 21 genera, belonging to 13 families. The most abundant nematodes on vegetable crops are represented by *Pratylenchus, Ditylenchus, Tylenchorhynchus, Rotylenchulus, Meloidogyne, Paratylenchus, Globodera, Paratrichodorus, Amplimerlinus, Scutellonema and Pratylenchoides.* While, *Hoplolaimus*, *Helicotylenchus*, *Trophorus* and *Xiphinema* are observed rarely and in small numbers. The distribution of global nematode abundance varies according biogeography areas. Saharan sector is the most heavily populated compared to the north areas (Numidia, Algiers, Oranes and High uplands). The study showed that 25% of genera are common to all biogeographic sectors and 45% are specific to Numidia or Saharan area. Genus richness varies along East-West gradient; the highest is reported in the Numidia (16), amounts decreases moving towards the central sector, Algiers (11) and the west sector Oranes (8). The various ecological indices: Shannon Index (H') and Equitability index (E) shows that these vary significantly according biogeographic area. The change in community structure seems to depend on several factors, climatic conditions, agricultural practice and soil type. It is noteworthy that in the northern sectors, including Algiers and Numidian there is favorable climatic (humid and sub humid climate) promotes nematodes proliferation. But Oranes sector and high uplands with a semi-arid to arid climate is not the best living conditions due to the habitat degradation and climate constraints. Knowledge about plant-associated nematode community structures in vegetable farming systems would helps develop sustainable management strategy for nematode populations and environmental conservation

Keywords: vegetables crop, Biogeographic sectors, Plant-associated nematodes, diversity

[P2.110]

Soil mesofauna under different technologies for tropical forest restoration

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The edaphic fauna is sensitive to interferences in the ecosystems and can be used as bioindicators in environmental monitoring programs. The goals of this study were to compare areas under different technologies for restoration of forest degraded areas in relation to soil mesofauna composition and diversity.

The technologies evaluated were: passive restoration; high diversity tree plantations; and nucleation. The experiments were implanted in 54 x 40 m permanent plots, with four replications in randomized block design at the Federal Technological University of Paraná, Southern Brazil. Sampling of mesofauna occurred in June 2013, and in each block six samples were collected, totaling 24 samples per treatment. The mesofauna was extracted by Berlese-Tullgren funnel method. The principal component analysis (PCA) was performed using Canoco statistical program.

In total eighteen different groups of arthropods were found (Acari, Araneae, Collembola, Chilopoda, Coleoptera, Dermaptera, Diplopoda, Diplura, Diptera, Gastropoda, Hemiptera, Hymenoptera, Isoptera, Lepidoptera, Opillionida, Protura, Psocoptera and Thysanoptera), where the orders Acari, Collembola and Psocoptera represented more than 70% of the frequency of organisms in all treatments .

The first two PCA axes explained 32.4% of data variation and revealed a spatial separation between the studied restoration technologies. The passive restoration and the nucleation technology were characterized by greater abundance of organisms in comparison to the trees plantation technology.

The groups Hemiptera, Diplura, Diplopoda, Diptera and Coleoptera were more associated to passive restoration, whereas the nucleation technology presented a strong association with Araneae, Psocoptera, Protura and Isoptera. We recommend a longer term monitoring to better understand the studied technologies that are still in the initial restoration process (3 years old).

Keywords: mesofauna, Biodiversity, forest restoration

[P2.111]

Tree stumps as hot spots of biodiversity

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Due to the increasing need to replace fossil fuels with renewable energy alternatives forest products like coarse dead wood (CDW) are investigated as potential sources for bioenergy production. However, many forest-dwelling invertebrates are dependent on CDW like slash and stumps and large scale stump removal may significantly reduce the diversity of these organisms.

The present study was part of an investigation funded by the Swedish Energy Agency into the environmentally sustainable production of bioenergy through the removal and burning of tree stumps. The study examined the potential impact of stump removal on several soil invertebrate groups.

In southern and central Sweden, oribatid mite and collembolan communities on Norway spruce and Scots pine stumps were investigated, at three forest stands that differed in time since felling (5, 10, 20 years). Stump communities were compared to the surrounding soil in regard to total and relative abundance, species richness and community composition.

In particular for oribatid mites, species richness in older stumps (>5 years) was significantly higher than in the surrounding soil. Differences in community composition between both habitats were largest when stumps were 10 years old mainly due to a great proportion of species restricted to the stump habitat. It can be concluded that ‘middle-aged’ stumps in particular harbor microarthropod communities more diverse than and distinctly different from that found in the forest floor.

Keywords: tree stump removal, oribatid mites, Collembola, bioenergy

[P2.112]

Underground biodiversity of tropical soil: crisis of earthworm diversity in Sumatra

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Introduction:

Soil degradation and consequent degrease in crop yield are urgent environmental issue in many countries, and Indonesia is not an exception. Unfortunately, many studies revealed that tropical earthworm fauna had been largely modified with land use change from primary forests to the others. To compare biomass and diversity of earthworms in different land-use, we investigated earthworm fauna in Lampung province, southern Sumatra, Indonesia.

Methods:

The earthworm sampling was conducted at six localities of Lampung from July 2011 to March 2012. We selected seven representative land-use as follows: secondary grassland, sugarcane plantation, oil palm plantation, rubber plantation, other forest type plantation, secondary forest, and primary forest. Earthworm fauna of each land-use was investigated from more than two localities. More than three quadrats (50 x 50 x 20 cm) were set from every land-use in each locality, after earthworms were collected by hand-sorting, two litter of 0.75 % mustard solution were applied to extract deep dwelling worms.

Results:

Total of 1,659 individuals were collected from 157 quadrats from 6 localities. We found sixteen species including 13 undescribed species. Earthworm diversity is high in primary forest (12 species), though those of the other habitat use in lowland of Sumatra was very poor (only 1-3 species). Except for primary forests, exotic *Pontoscolex corethrurus* was dominant in the most localities.

Discussion:

In Sumatra, 51 earthworm species has been reported, and only 3 from Lampung. Although our study sites were restricted only southern end of Sumatra, we found 13 undescribed species. Moreover, two described species had not been reported from Lampung. Threfore, research of earthworm diversity in Sumatra is insufficient, and many undescribed earthworms are expected in Sumatra. However, among the 51 known earthworm species from Sumatra, 33 considered as native and 18 as introduced species. Unfortunately, we found that *Pontoscolex corethrurus*, the most popular invading species in all tropical regions originated from Latin America, was dominant species in many localities even in secondary forests. Therefore native earthworm fauna of lowland Lampung has been largely modified and research for earthworm diversity in Sumatra is urgently needed.

Keywords: Pontoscolex corethrurus, introduced species, earthworm, Indonesia

[P2.114]

Distribution patterns of ground beetles along latitudinal gradients in Japanese forests

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The Ministry of the Environment, within the Government of Japan, has conducted the “Monitoring Sites 1000” project since 2003. As part of this project, we have investigated the species assemblages of ground beetles, and the litter accumulation on forest floors in Japan since 2004.

Because of their limited mobility, ground beetles are likely to reflect environmental conditions of local terrestrial ecosystems and, thus, may serve as useful indicators of ecosystem integrity. Moreover, ground beetles are effective predators, potentially controlling the dynamics and structure of terrestrial detrital food webs.

One of the goals of our project was to describe species assemblages of ground beetles along latitudinal gradients in Japanese forests, and to evaluate their usefulness as environmental indicators. A second goal was to scrutinize their roles as key-stone predators in terrestrial detrital food webs. In particular, we are interested in how local species compositions of ground beetles influence decomposition.

Ground beetles were sampled using pitfall traps at 22 sites. We found that litter accumulation and abundance of ground beetles, but not species diversity, were positively correlated with latitude. In northern high-latitude environments, most litter decomposes slowly with decreasing temperature, probably resulting in relative ground beetle abundance.

The abundance of ground beetles differed between deciduous and evergreen forests at a local scale, and also among years at a site where a typhoon occurred. Thus, ground beetles can be good indicators of local litter input dynamics in forests over the long term.

Keywords: Bioindicators, Carabidae, Litter accumulation, Monitoring

[P2.115]

Diversity of restored nitrogen cycling communities in the Athabasca oil sands

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The Athabasca oil sands deposit, located in the boreal forests of Northern Alberta, is one of the largest single oil deposits in the world. To date, an area of about 715 square kilometres has been disturbed by oil sands mining activity. Following surface mining, companies have the legal obligation to restore soil that can support the previous land capabilities. Because of its importance for site productivity, re-establishment of the nitrogen cycle between these reconstructed soils and plants is one of the most critical factors required to insure long-term sustainability of reclaimed boreal landscape. Soil microbial communities are the architects behind the nitrogen cycle; therefore knowledge about their diversity in the oil-sands-reconstructed soil is critical to assess the successfulness of reclamation processes.

N deposition rates on oil-sands-reclaimed sites were greater than in highly populated regions of Canada. MacKenzie and Quideau (2012) found that the rates of nitrogen mineralization in the reclaimed material were higher than anticipated for a N-limiting environment such as the boreal forest. Microbial community composition linked to the nitrogen cycle have been shown to be significantly different in reclaimed and in natural soils (Dimitriu et al., 2010). However, it is still unknown if these differences are ecologically significant. .

A series of 20 soils, covering different vegetation treatments both in reclaimed and naturally-disturbed sites were investigated. Gross nitrogen transformation rates were measured using ^{15}N pool-dilution (Müller et al. 2007). Microbial communities were characterized using pyrosequencing. Differences between nitrogen cycling processes and communities in the different vegetation treatments and in the naturally disturbed sites were found. The reasons for these variances will be discussed.

The oil sands will be Canada's environmental legacy. Recreating functional soils is fundamental to our ability to restore boreal ecosystems after disturbance. We believe that soil biota is key to that endeavour.

Keywords: nitrogen cycle, pyrosequencing, oil sands, restoration

[P2.116]

Effects of different land-use types on soil protist communities

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Soil protist microorganisms represent an important part of the soil microbial community being major players in providing ecosystem services. Changes in their community structure and dynamics may influence the rate and kind of soil formation and fertility. Corroborative studies indicate that protist microorganisms exhibit high levels of molecular and functional diversity in soils. However, studies questioning the protist diversity in soil and their variability across different soil land-use types, have received far less attention. The purpose of our study was to obtain relative abundances of flagellate, ciliates and amoeboid soil protists, and to relate the expected changes in community composition to space and land-use. Soils were collected from six long-term observatories (LTO's) scattered around Europe, covering different climatic zones and different vegetation types and land-use. These samples allowed us to explore the diversity of protist organisms geographically and study the hypothesis that different land-usage promotes different soil protist colonization, as seen previously for bacterial communities. We hypothesized that the diversity of soil protists with adaptation to specific abiotic and biotic conditions, such as flagellates will be comparatively limited by tilled agricultural soils compared with those in untilled soil. The use of 18S rRNA gene barcoding markers for determination of protist community becomes a challenge, due to the high proportion of plant and fungal sequences recovered within the 18S rDNA pool. Therefore, a PCR-DGGE fingerprint analysis, qPCR analyses and metabarcoding approach of the protist community composition and diversity was performed. Our results demonstrate that not only the geography but also the different land-use itself harboured unique soil protist communities. This suggests the great importance of protists in the soil food web and interaction with plants and soil microbes; an interaction driven by vegetation dynamics, moisture and organic nutrients availability and having impact on carbon turnover.

Keywords: Protist, 18S rDNA, Metabarcoding, Soil food web

[P2.117]

Persistence of *cry 1Ab* gene from genetically modified corn and structure microbial communities in agricultural soils in Brazil

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The environmental impact of genetically modified crops has been questioned due to the introduction of genes and proteins from *Bacillus thuringiensis* (Bt) in the soil. The incorporation of crop residues and release of root exudates of genetically modified plants will result in the release of engineered DNA into the environment, increasing the likelihood of horizontal gene transfer to soil microorganisms, and may promote rapid development and adaptation of exogenous genes to the environment. Thus, the objective of this study was to evaluate structure microbial communities in three Farms and the persistence of the *cry1Ab* gene from Bt in Brazilian agricultural soils. After sampling, DNA was extracted from soil using PowerLyzer Soil kit. We measured the abundance fragment corresponding to *hsp70* - *cry1Ab* from Bt corn was detected and quantified by qPCR technique and using T-RFLP of 16S rRNA bacteria, for to accesses bacterial communities of soil in different farm (1, 2 and 3). Bacterial 16S rRNA gene copy numbers, showed values up to 10^9 copies g^{-1} dry soil in farms. The size of *hsp70* - *cry1Ab* copies number of organisms genetically modified in soil resulted in several fold increases in farm 1 when compared to other farm. NMDS analysis showed communities bacterial associated in farm1 with 35S-hsp70 and *hsp70-cry1Ab* in harvest soybean and harvest maize showed copies number organisms *Bt* as drivers of bacterial communities. Index Shannon (*H'*), Simpson (*S'*) and Evenness (*J'*) resulted difference ($p<0.05$, LSD) between three farm after harvest soybean, but no resulted in significant results after harvest maize. These results indicate that microbial communities were shaped by after harvest maize. NMDS analysis indicated that functional community was primarily influenced by modifications crop systems, but not found affected the persistence of the *hsp70* - *cry1Ab* fragment, resulting in an decreasing number of fragment copies between samples.

Keywords: persistence, Microbial ecology, Bt, quantitative PCR

[P2.118]

Rapid microbial colonization alters carbon and nitrogen cycling in an Australian forest soil

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Microbial communities play a critical role in regulating the cycling, storage, and release of carbon (C) and nitrogen (N) in soil. Changes in land use (e.g. from forest to arable) are altering the composition of the soil microbial community. Under changing environments, the colonization of these soils by new microbial species may alter their nutrient status, however little is known about how rapid microbial colonization affect the soil C and N cycling.

Here, we conduct a microcosm experiment to evaluate how a hypothetical microbial colonization from two arable soils can affect the C and N cycling in a sterile forest soil, compare to the original community (re-introduced in the sterile soils). Soils were incubated for a month under sterile conditions. We then measured different C and N variables including soil respiration, substrate induced respiration (glucose and lignin), enzymes activities (glucosidase and cellobiose), dissolved organic C and N and N_2O emissions. We hypothesized that the entrance of new microbial species may bring new tools allowing the rapid mobilization of C and N which was not available for the previous microbial community. On the contrary, however, abiotic properties (e.g. pH) of the colonized soil may limit the entrance of new species restricting their impact on nutrient cycling.

Preliminary results showed a strong influence of the arable microbial communities on the C and N cycling of the forest soils. For instance, both arable communities enhanced soil CO_2 and N_2O emissions and enzyme production (e.g. cellobiose) in the forest soil compared to the original community, suggesting that at least part of the soil C and N was not available for the former microbial community. Our results provide evidence that changes in land use followed by rapid microbial colonization can alter both soil C (e.g. respiration) and N (N_2O emissions) cycles.

Keywords: Microbial colonization, Nitrogen cycle, Carbon cycle, Land uses

[P2.119]

Interactive effects of earthworm ecological strategies and manure application methods on soil leachate NO_3^- and N_2O emissions in a N-enriched agroecosystem

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Earthworms can enhance plant productivity and N_2O emissions by promoting nitrogen mineralization in N-limited agroecosystems and may enhance N_2O emissions and NO_3^--N leaching in N-enriched agroecosystems. However, direct evidence demonstrating the earthworm enhancement of N_2O emissions and NO_3^--N leaching is scarce, particularly in intensively managed systems with high organic inputs. Additionally, earthworm feeding strategies may profoundly modulate N cycling, but few studies have examined how these feeding strategies are related to N_2O emissions and NO_3^--N leaching. We examined these impacts using two earthworm species with distinct ecological strategies (i.e., epigeic *Eisenia foetida* and endogeic *Metaphire guillemi*) in combination with two application methods of manure compost amendments (i.e., surface mulch and incorporation into soil). Our results demonstrated that earthworm addition significantly increased the cumulative N_2O emissions by 19 to 25% depending on the earthworm ecological strategy. However, earthworm addition did not significantly increase the leachate NO_3^--N concentration. Additionally, earthworms did not affect the yield-scaled N_2O due to the tradeoff between the simultaneous promotion of both crop productivity and N_2O emissions. Earthworm-induced N_2O emissions were corroborated by the increased NO_3^--N concentration in N-enriched systems. The increased N_2O emissions were also related to the contents of soil macroaggregates, dissolved organic carbon and microbial biomass nitrogen, which are also promoted by earthworms. Taken together, understanding the trade-off between earthworm services and dis-services will contribute to the development of environmentally friendly integrative soil management by allowing full utilization of the potential roles of biological resources.

Keywords: Earthworm, Nitrous oxide, Nitrate leaching, Agroecosystem

[P2.120]

Soil-plant-microbe interactions in a grazed pasture under elevated atmospheric CO_2

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Introduction: An elevated concentration of carbon dioxide (eCO_2) in the atmosphere is the most predictable of the global changes. The initial impact of eCO_2 is on the physiology of individual plants. However, changes in the fluxes of carbon resulting from these physiological changes can propagate through an ecosystem resulting in altered relationships between plant and microbes and consequent effects on soil processes. We examined some of these potential changes in a grazed grassland after 14 years of exposure to eCO_2 in a Free Air Carbon dioxide Enrichment (FACE) experiment.

Methods: We measured soil and microbiological properties and bacterial community structure associated with a low fertility grass (*Agrostis capillaris*, brown top) and a high fertility grass (*Lolium perenne*, ryegrass) under ambient and eCO_2 (475 ppm) conditions. Soil samples were taken from under each grass on two occasions in May 2011 for DNA extractions and characterisation of soil properties. We used 16S metagenomic sequencing to identify the soil bacterial community.

Results: A nonparametric multivariate Adonis test carried out using the 468 most abundant operational taxonomic units (OTUs) (>1000 reads in all samples) indicated that the bacterial community structure at eCO_2 was different from ambient CO_2 ($P=0.06$). Correspondence analysis carried out using the 48 bacterial OTUs that were significantly ($P<0.05$) different at eCO_2 showed different responses under ryegrass and browntop. There was also a significant CO_2 x plant species effect for soil properties including dissolved organic C and N and microbial biomass C and N.

Discussion: Our results confirm that changes in microbial communities may be expected under eCO_2 are linked to changes in soil properties. Importantly, the nature of these changes is likely to be strongly influenced by the plant community leading to potentially complex effects as eCO_2 almost invariably influences plant community composition.

Keywords: Free Air Carbon dioxide Enrichment, Agrostis capillaris, Lolium perenne, grazed pasture

[P2.121]

Change in the community assembly rule of soil microarthropods along the decomposition processes of plant leaf and root litter

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Assessing how biological communities assemble has been a central theme in ecology, potentially helping elucidate the underlying mechanisms of biodiversity-ecosystem functioning relationships. The assembly processes of soil animals, however, have been relatively less-understood, despite their fundamental roles in soil ecosystem processes such as decomposition. We focused on temporal changes in the quantity and quality of decomposing litter, a primary resource for soil animals, and examined how different assembly processes contribute to organization of microarthropod communities over several stages of decomposition. We recorded collembolan species using litterbag method in a coniferous forest in Japan. Litterbags of leaves and roots were each placed at two positions (aboveground and belowground) in order to separate the effects of litter type and litter position. The four types of litterbags were collected seven times in three years. We calculated species turnover among 15 subplots (beta-diversity) for each type of litterbag at each time, and then used a null model to examine possible underlying processes of species assemblages. The values of beta-deviation, which represent the degree of deviation from random assembly, indicated that the collembolan community is assembled depending on the litterbag position (soil layers); stochastic processes were prevalent at soil surface (aboveground), whereas deterministic processes played a major role in the soil (belowground). These values were neither explained by litter mass (litter quantity) nor C:N ratio (litter quality). These results suggest that the difference in community assembly processes between aboveground and belowground may be mainly attributed to characteristics of soil physical structure, which largely limit the dispersal of animals especially at deeper soil layers. Our results suggest that, although relative importance between deterministic and stochastic processes changes along the stages of litter decomposition, the main driver of this shift is more tightly linked with the spatial variability of soil physical property rather than litter quality.

Keywords: beta-diversity, null model approach, deterministic process, stochastic process

[P2.122]

Microbial community characteristics of Montepulciano d'Abruzzo vineyard soils with different environmental conditions and in different seasons.

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In this work we studied the functional diversity of soil microbial community of six different type of "Montepulciano D'Abruzzo" soils. The aim of the study was to evaluate the effects that the vegetation diversity, solar exposition, weather conditions and physicochemical soils parameters, have on the diversity of soil microbial community. The study was conducted on two sampling, the first in winter and the second in summer. In the first sampling the Biolog Ecoplate systems were applied on samples untreated and treated with a temperature of 80°C for 48h. The results showed that the temperature treatment decreases the AWCD values. Therefore, the samples of second sampling were analysed without treatment. The results obtained from Biolog Ecolpate systems, showed that the Average Well Color Development (AWCD) were higher in samples of first sampling, probably because of the high microorganism concentration in soils. Also the Shannon index and Catabolic Versatility index, in the first sampling were higher than the indexes calculated for second sampling. The carbon sources mostly used by soil microbes, in both sampling, were carbohydrates and carboxylic acids, followed by amino acids and polymers. Phenolic acids and amines had the lowest utilization rate. Principal component analysis (PCA) on the samples of first sampling identified 2 principal component factors in relation to sources, explaining 71,68% of the variation. Principal component analysis (PCA) on the samples of second sampling identified 2 principal component factors in relation to sources, explaining 80,40% of the variance. The results of this study could provide basis for further approaching the relationships between environmental conditions and soil microbial community diversity and richness of the "Montepulciano d'Abruzzo" soil and soil in general.

Keywords: Microbial diversity, Functional diversity, Biolog Ecoplate, Montepulciano d'Abruzzo vineyard soils

[P2.123]

PCR-DGGE analysis for identification of genetic diversity of microbial communities of Montepulciano d'Abruzzo vineyard soils.

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In this work we studied the genetic diversity of microbial community of six different type of "Montepulciano D'Abruzzo" soils. The aim of the study was to characterise the composition of the microbial community of Montepulciano d'Abruzzo vineyard soils. The study was conducted on two sampling, the first in winter and the second in summer. The DNA was extracted by soil samples of six different vineyards and the than it was analysed by using denaturing gradient gel electrophoresis (DGGE) of PCR-amplified partial 16S rRNA genes.

The results were analysed by using the Pareto-Lorentz distribution curve, the Simpson's diversity index (1-D), Simpson's evenness index (Ed) and Range-weighted richness (Rr). The DGGE technique allowed also the identification of the microbial population through sequencing of excised bands. The results allowed the monitoring of the spatial/temporal changes in microbial community structure and provided a view of the dominant microbial species of the samples.

The detection of the microbial composition was useful for evaluate the possibility of the inoculation of vineyard soils with Plant Growth Promoting Rhizobacteria (PGPR).

The PGPR are a group of bacterial and yeasts that, interacting with the soil, root system and the tissues of the host plant, is capable of applying beneficial effects on it.

The results of this study could provide basis for a future substitution of chemical fertilization with the biofertilization, using PGPR.

Keywords: genetic diversity of microbial communities, PCR-DGGE, PGPR, Montepulciano d'Abruzzo vineyard soils

[P2.124]

Hidden puppet masters: Unproductive species shape ecosystem services of soil bacterial communities

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The importance of biodiversity for ecosystem functioning is a hotly debated topics in ecological research. Species loss may affect community function and stability. Some species have a keystone role and their disappearance disproportionally affects the remaining community. Identifying these species and their contribution to community function is crucial to predict the impact of environmental perturbations and altered species composition. Here we use constructed communities to identify microbial keystones. We set up communities along a diversity of one to sixteen bacteria and follow their ability to degrade organic pollutants in soil microcosms as a model ecosystem service. Contaminant degradation increased with species richness and breaking down this biodiversity effect into a network of pairwise interactions reveals that the less productive a species is in monoculture, the more neighbours it facilitates. Accordingly, the impact of selective species removal on ecosystem services directly depends on on productivity in monoculture. Removing productive species only marginally affected pollutant removal, but loss of less productive (and better networked) bacteria strongly reduced community performance. We propose that within a community species move along a gradient between “loners” performing well alone and “puppet masters” themselves unproductive but essentially stimulating the functioning of competing bacteria. This study calls for a new interpretation of species ecological relevance and offers new tools to selectively improve soil processes by adding “puppet masters” that will enhance the function of the resident soil communities.

Keywords: Interaction networks, bacteria, keystone species, biodegradation

[P2.125]

Linking microbial biogeography to agro-ecosystem health in Australian grape growing regions

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Australian soils are millions of years old and many are naturally saline and/or sodic. By global standards these soils are considered to be of inherently low fertility, yet they are under increasing pressure as agricultural production expands, both in area and in intensity. Soil salinity is of particular concern in agricultural industries that rely on drip-irrigation, including the grape and wine industry. Increasing salinity not only impacts productivity, but wine in some regions are exceeding NaCl thresholds, threatening a multi-billion dollar export industry.

As a starting point to develop strategies to overcome root-zone salinity, a national soil benchmarking program identifying key chemical and biological indicators was established. Within this program, we assessed microbial biogeography at 92 vineyards across the wine growing regions of southern Australia. At each site, soil samples were collected along a gradient of management impact: underneath vines, between vine rows, and from adjacent non-cultivated land. At one vineyard, an intensive sampling regime (192 samples across 0.13 ha) allowed us to characterize soils producing low-yielding but high quality vines and, conversely, high-yielding but low quality vines. Structural and functional shifts in microbial communities at the landscape and the field scale were measured using amplicon-based and metagenomic sequencing. Biogeochemical datasets were interpreted using ordination and neural network approaches. At the landscape scale, labile carbon and nitrogen pools, along with alkalinity and specific anion levels (Cl^-), were significant predictors of microbial biomass and taxonomy. At the field scale, these same parameters, when associated with specific microbial communities such as the Class Chloroflexi, were significant predictors of high-quality but low yielding vines.

We will report on progress made in selecting meaningful soil biodiversity measures for the grape and wine industry, including how this data is being uploaded to the soil quality monitoring web-based tool currently used by the Australian grains industry.

Keywords: Agro-ecosystem health, Microbial metagenomics, Biogeochemical cycling

[P2.126]

Influence of increasing soil salinity on diversity of arbuscular mycorrhizal fungi colonising winter barley

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Soil salinity is one of the most prevalent problems to crop productivity in arid and semi-arid regions. Increasing scientific and public attentions on soil salinization have been recently pointed to sustainable use of saline-alkaline soil resources. However, engineered approaches such as leaching of excessive salts or desalinizing seawater for irrigation are laborious and costly applications for developing countries. Little information has been available on how changing soil salinity influence arbuscular mycorrhizal (AM) fungal diversity and community structure. In these views, we investigated diversity of AM fungi associated with winter barley (*Hordeum vulgare* L.) using DNA-based technique in Central Anatolia located in the semi-arid climate zone in Turkey. The objective of this study was to evaluate how AM fungal species would be affected from soil salinity at different levels.

A pot experiment was conducted as follows: Soil samples were collected from three sites of winter barley cultivated area in Central Anatolia. Winter barley was grown in 1 kg of sterile soil with non-sterile soils as the inoculant of indigenous AM fungal consortia. Soil EC was adjusted to 2, 6 and 12 mS/cm before use. After 45 and 90 days, root samples were collected and DNA was extracted. Using the extracted DNA as the template, AM fungal 28S large subunit ribosomal DNA was amplified and AM fungal community structure and diversity were evaluated using a terminal restriction fragment length polymorphism (T-RFLP) technique.

Although the consecutive changes were not detected in 45 days, decrease of root AM fungal diversities were observed in all pots adjusted to the high EC level compared to the others after 90 days. The sequence types of *Rhizophagus* were dominant in all pots, followed by *Funneliformis* and *Claroideoglomus*. The results suggested that these indigenous AM fungi can maintain the symbiosis with the host plant under increasing salinity levels.

Keywords: arbuscular mycorrhizal fungi, Central Anatlia, Hordeum vulgare L., Molecular diversity

[P2.127]

Bacteria and plasmids involved in the spread of tetracycline resistance at a dairy farm and in manured soils

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Introduction: The soil antibiotic resistome has been enriched with manure-originating antibiotic resistance genes during the past 50 y, which may have consequences for both soil microbial interactions and human health. Concentrated Animal Feeding Operations have been recognized as a big contributor to this problem. Here we studied whether smaller dairy farms with more prudent antibiotic use also represent a risk for antibiotic resistance dissemination and which bacteria and plasmids are involved.

Methods: Manure from dairy cows that receive prophylactically (after each calving, intrauterinally) 1g chlortetracycline was screened (PCR/qPCR) for 12 tetracycline resistance (TC-r) genes. The TC-r gene persistence was monitored (qPCR) in soil-microcosms established from 3 soils mixed with the manure from chlortetracycline-treated cows. TC-resistant bacteria from manure and soil microcosms were screened for the presence of TC-r genes (PCR/sequencing). Plasmids that may be involved in the horizontal transfer of TC-r genes were captured by exogenous plasmid isolation from the manure.

Results: Seven classes of TC-r genes encoding efflux pumps (tetA, tetY), ribosomal protection proteins (tetM, tetO, tetQ, tetW) and TC-cleaving enzymes (tetX) were found in the manure, tetO, tetQ, and tetW being the most frequent. Screening of bacterial isolates from the manure revealed that tetM was harbored by lactobacilli and clostridia, tetY by *Acinetobacter*, tetA by enterobacteria, and tetX by *Wautersiella*. Plasmids carrying tetY (LowGC plasmids) and tetA (IncP or IncHI2) were captured into *Escherichia coli*. In a microcosm experiment, tetW, tetO (based on qPCR) and tetA (in enterobacteria) persisted for 3 months in manure-amended soils.

Discussion: Manure from a dairy farm with prophylactic antibiotic use is a reservoir of antibiotic resistance genes. Its application to land increases the diversity of the soil resistome over several months and may represent a risk for human health as the TC-r genes were found in possible human pathogens and on conjugative plasmids.

Keywords: soil resistome, tetracycline, antibiotic resistance, resistance plasmid

[P2.128]

Understanding linkages between soil microbial communities and plant roots influencing soil aggregate stability

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Careful management of land can prevent the detrimental consequences of farming on soils, but both fundamental and applied research are required to determine how best to manage depending on land use, climate and topography. The present study investigates the ecosystem service of soil fixation provided by different crop / forest systems examining root traits and soil microbial communities. The specific aim of this research is to determine the function of the root systems and the soil microbial communities in relation to aggregation properties of soils.

A combination of a field study and a laboratory inoculation experiment are used in this research. The philosophy of the field study is not to compare results from the different field sites, but to identify similarities depending on climate, soils and land uses. Field sites lie in hilly or erodible environments and represent natural forest, agroforest, arable and pasture fields in subalpine, temperate and mediterranean regions. Soil samples were collected on the different sites and aggregate stability, root traits, soil microbial communities, soil texture and soil chemical properties were studied. Bacterial and fungal community biodiversity was assessed using Terminal Restriction Fragment Polymorphism analyses (TRFLP) coupled with high throughput sequencing of 16S rRNA genes (bacteria) or the ITS region (fungi) to identify responsive taxa. The main root traits examined were density and biomass. Aggregate stability was studied using a standard method (ISO/CD 10930). The laboratory inoculation experiment was setup recently and results are not expected yet. The objective of this experiment is to test if soil microbial composition mediates the effects of roots and land use on soil aggregate stability. Reciprocal inoculations of microbial communities crossed with root systems (tap vs fibrous) are compared in their influence on the aggregation properties, root exudates and bio-films production. Preliminary findings of this research project will be presented and discussed.

Keywords: Ecosystem services, Soil erosion, Root systems, Land use

[P2.129]

Integrating soil biodiversity metrics into a national web-based soil quality monitoring tool for Australian primary producers.

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Prior to 2009, soil biodiversity measures had never been included in soil monitoring programs in Australia. A soil quality web-based decision support tool established in 2004 in Western Australia provided the ideal vehicle for more detailed measures of the soil microbial community. The existing tool monitors a minimum dataset of the physical, chemical and biological attributes considered by an expert panel to be significant in describing soil-based constraints to crop production. The current biological attributes are microbial activity and biomass, soil-borne pathogens (take-all, rhizoctonia bare patch, cereal cyst and root lesion nematodes) potentially mineralisation nitrogen, labile C, in a significant database comprising nearly 3000 agricultural sites covering the three major cropping regions (www.soilquality.org.au). The requirements for all soil quality metrics is that regional thresholds are set according to low, medium and high risk categories.

A five year Grains industry investment has enabled the development and ongoing validation of a new set of DNA-based microbial diversity measures, from low resolution TRFLP measures to higher resolution DNA sequencing methods (eg HiSeq/MiSeq). The initiative utilised, where appropriate, the commercial soil borne cereal disease diagnostics platform (PreDicta B; www.sardi.sa.gov.au/diagnostic services/predicta_b) for large scale soil DNA extractions. Soil biodiversity was characterised by sequencing soil metagenomes and group-specific amplicons, targeting 16S rRNA (bacterial and archaea) ITS (fungi) and 18s rRNA (nematodes). A subset of field sites, comprised of long-term agronomic experiments, were selected from each region for these analyses.

We will report on our progress to date and outline the challenges and pitfalls in selecting new microbial biodiversity measures for a web-based decision support tool. We will also illustrate some trends observed in three contrasting agroecological zones between soil diversity and edaphic features, and how we can apply predictive modelling to these data.

Keywords: monitoring, decision-support, Predicta B, agroecological zones

[P2.130]

Changes of bacterial diversity of soil under influence of oily waste containing radionuclides

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Oily wastes containing radionuclides are one of the serious environmental pollutants. Despite on the fact that negative influence of oily components and radioactive elements were widely studied, the question of complex effect of these compounds remains open. In Russia and other oil exporting countries, oily wastes are disposed on soil surface for further road building. Thus, compounds from these wastes can leak into soil.

In this study, we tried to distinguish the negative effects of the two main fractions of oily wastes – oily compounds and radionuclides – on soil microbial community. For this, raw oily waste containing 575 g kg^{-1} of hydrocarbons and 4.4, 2.8 and 1.3 kBq kg^{-1} of ^{226}Ra, ^{232}Th and ^{40}K, respectively and treated waste in which the content of oily components was reduced by washing by organic solvents - were loaded onto soil columns and the yearly amount of precipitation was simulated to determine the leakage of compounds from the waste. It was shown that only low amounts (up to 0.8%) of hydrocarbons and radionuclides leaked into the soil. However, compounds migrated from the raw waste sample caused changes in microbial biomass, basal respiration, metabolic coefficient and enzyme activity. No changes in microbiological parameters caused by radioactive elements leaked from the treated waste were observed.

In opposite, usage of PCR-SSCP method with common bacterial primers allowed estimating the negative influence not only of raw oily waste but also of radionuclides only. The Shannon-Weaver, Simpson and other biodiversity indexes differed significantly in raw- and treated waste polluted columns. Using MDS (Fig. 1) and clustering analysis of the SSCP patterns, three groups of samples – control, raw- and treated waste polluted – were distinguished. Phylogenetic analysis of SSCP-bands revealed strains similar to oily degraders – in raw polluted soil samples; and to uranium mining inhabitants – in treated wastes polluted soil samples.

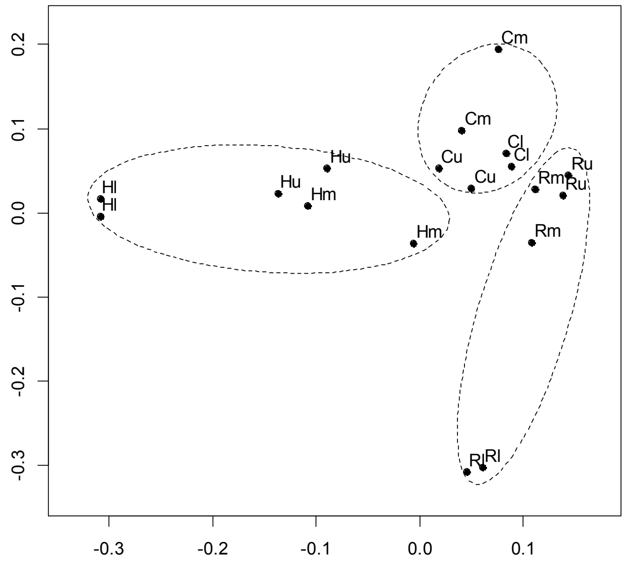

Fig. 1. MDS analysis based on distance matrix (Cu, Hm, Cl – soil samples from the control columns taken from the 0-20, 20-40, 40-60 cm, respectively. Hu, Hm, Hl – soil samples from

the raw waste polluted columns taken from the 0-20, 20-40, 40-60 cm, respectively. Ru, Rm, Rl – soil samples from the treated waste polluted columns taken from the 0-20, 20-40, 40-60 cm, respectively)

Keywords: oily waste, radionuclides, PCR-SSCP, biodiversity

[P2.131]

High throughput sequencing of oomycete communities in cultivated soil

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High throughput DNA sequencing is a useful tool to study complex soil microbial communities including oomycetes. Culture-independent studies using next generation sequencing has revolutionized microbial ecology studies but has until now only been used in very few soil oomycete ecology studies. This work was carried out to improve standard techniques for using high throughput sequencing as a tool for studying oomycete communities in soil. ITS1 was used as marker for species identification and sequencing was carried out using 454 pyro-sequencing technologies. Primer sets ITS4, ITS6 and ITS7 that are widely used in oomycete research were used to target the internal transcribed spacer (ITS) 1 of ribosomal DNA. Soil total DNA was extracted from 26 soil samples collected from different fields and sequenced together with 3 mock communities and 2 samples produced with lower annealing temperatures. Our sequencing data and resulting operational taxonomic units (OTUs) showed that 87.9% of the sequences assigned to oomycetes covering *Pythium*, *Aphanomyces*, *Hyaloperonospora*, *Saprolegnia* and *Phytophthora*. We found consistently high proportion of oomycetes sequence in our 26 soil samples. Moreover, a large diversity of *Pythium species* including pathogenic, neutral and saprophytic species were found to be dominating in cultivated soil. This study shows a successful approach for pyrosequencing of oomycete communities using ITS1 as a barcode sequence for species identification from soil using a culture-independent approach.

Keywords: Next generation sequencing, Oomycetes, ITS, diversity

[P2.132]

Detecting AM communities in high-altitude vineyards: a next generation sequencing approach

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Thousands of microbes are usually associated with plant roots, forming the so-called root microbiota which has crucial roles on plant health. Among them, the obligate biotrophs Arbuscular Mycorrhizal fungi (AMF) are pivotal for plant life, providing nutrient uptake and pathogen protection to the plant along several other benefits. AMF interact with more than 80% of vascular plant species, including *Vitis vinifera* (grapevine), an important crop plant due to wine production.

Given the agricultural importance of mycorrhizal symbiosis, we focused on the study of soil-dwelling and grapevine root colonizing AMF communities in three high altitude vineyards in Valle d'Aosta (Italy). These communities have been investigated through a NGS technique, *i.e.* Illumina MiSeq, by sequencing the ITS and the 18S rDNA regions.

The characterization of the 18S region yielded 148 OTUs, while 157 OTUs were obtained from the ITS analysis. In the three sites, the 18S and the ITS regions showed that the root communities shared 26 and 10 OTUs, respectively. Among these, the most frequent taxonomical rank was the *Rhizophagus/Sclerocystis* clade.

Notwithstanding both the 18S and the ITS regions produced biases in the determination of the α-diversity, the assessment of the β-diversity proved to be repeatable, since the two OTU-based sample distance matrices were shown to be correlated. Our results suggest the suitability of the ITS region, identified with universal fungal primers, for AMF-based β-diversity studies. However, the 18S region was demonstrated to be the best tool to describe the AMF-based α-diversity.

As a future perspective, the data collected aim to contribute to the development of sustainable viticulture. In fact, the ubiquitous taxa found could represent the backbone of a grapevine-specific inoculum that could be adopted as biofertilizer under poor soil conditions and/or strict climatic parameters.

Keywords: AM fungi, Fungal biodiversity, Grapevine, High altitude vineyards

[P2.133]

Physiological responses of a plant-associated bacterium *enterobacter* sp. strain EG16 to cadmium exposure

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Understanding the survival and adaptive strategies in response to heavy metals of the plant-associated, metal resistant bacteria is greatly important for their better assistance in phytoremediation. In this study, a soil-borne, Cd-resistant bacterium was isolated and identified as *Enterobacter sp.*. This strain, named *Enterobacter* sp. EG16, tolerates high Cd concentration (MIC>250 mg L^{-1}) and is able to produce siderophore and plant hormone indole-3-acetic acid (IAA) that contributes to plant growth promotion. Metal accumulation experiments and TEM-EDX analysis revealed that surface biosorption occupied 31% of the total Cd accumulated, while more than 50% of Cd were absorbed into the bacterial cells, suggesting that intracellular Cd accumulation is one of the main Cd-resistant mechanisms of EG16. From the RNAseq data, we identified 268 out of 4497 genes (6.0%) significantly regulated under Cd exposure and a global regulation at transcriptomic level was observed. EG16 switched to an energy-conserved mode by inhibiting some energy-consuming processes and paid more attention to produce stress-related proteins or enzymes and import more sulfur and iron that become deficient under Cd toxicity. Besides, EG16 started up a stress response system and redirected sulfur metabolism to maintain intracellular GSH level in response to Cd toxicity and Cd-induced oxidative stress. We also found Cd exposure significantly induced siderophore production while strongly inhibited IAA synthesis. Meanwhile, genes involved in iron homeostasis significantly regulated in response to Cd which may enhance iron uptake. EG16 appeared to produce siderophore at the expense of IAA synthesis since both them use chorismate as precursor so as to keep production of siderophore and defend against Cd-induced Fe deficiency in cells. Thus we supposed that siderophore production may be the main PGP mechanism of EG16 when associated with phytoremediation in Cd polluted soils, though EG16 possess ability to produce both siderophore and IAA in normal conditions.

Keywords:

[P2.134]

Impact of farmyard manure inputs on soil microbial diversity - Consequences on volatile organic compound emissions and carbon cycle

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By being involved in the decomposition of soil organic matter (SOM) and delivering nutrients readily accessible to plants, soil microorganisms are key players in agricultural soils. In addition to CO_2 and CH_4 emissions, it has recently been shown that microbial SOM breakdown generates volatile organic compounds (VOCs) which take part in greenhouse gases production in the atmosphere. The VOC emission rates from soil to atmosphere are still poorly documented compared to CO_2 and CH_4 fluxes. They depend on both SOM status and microbial diversity and functions involved.

The objectives of this study were to i) determine the response of soil microorganisms to farmyard manure inputs (pig slurry (PS) and methanised pig slurry (MPS)) and the consecutive diversity of VOCs emitted and ii) understand the link between SOM, active soil microorganisms and C-gas emissions (VOCs, CO_2, CH_4). Soil mesocosms were constructed with or without PS or MPS and incubated for 2 months. Control mesocosms with only PS or MPS were performed in parallel. Every 10 days the diversity of the VOCs emitted was determined (PTR-MS) and CO_2 and CH_4 emissions were quantified (µGC-MS). At the meantime soil was sampled to quantify and determine the composition of the SOM and analyse the active microbial community structure (T-RFLP based on RNA). Preliminary results allowed us to identify five main VOCs: acetone, 2-butanone, dichloromethane, 2-pentanone and toluene. Moreover, the VOC diversity emitted by the soil with the farmyard manures was significantly different to the gases produced by the PS and MPS alone indicating an impact of the soil microorganisms through SOM decomposition. Both SOM composition and microbial diversity structure analyses are currently running. These results will bring new insights into the impact of organic amendments on the soil components (SOM, microorganisms) and the consequences on C-gases emissions and C fluxes between soil and atmosphere.

Keywords: Soil microorganisms, Volatile organic compounds, Agricultural practices, Carbon cycle

[P2.135]

Understanding microbial mediated nitrogen cycling in Irish grassland soils

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A medium to high diversity of microbes in agricultural soils is often considered a good indicator of soil quality. However, species diversity per se may not be as useful an indicator as the abundance of functional genes present as different species can perform similar functional roles. The measurement of the abundance of key metabolic genes can provide insight into the functional capacity of a soil and assess the impact of management practice or environmental conditions on soil quality.

This study was concerned with examining key microbial nitrogen cycling processes across improved and unimproved grassland sites in Ireland. Nitrogen is frequently a limiting factor in crop productivity and the rates of microbially mediated nitrogen fixation, nitrification and denitrification are important for plant nutrient availability. This is of particular interest to Ireland where 4.2 million ha of 6.9 million ha total landmass are dedicated to agriculture.

Two genes, *amo*A and *nos*Z, were used as marker for nitrification and denitrification, respectively. The abundance of these genes was measured in 74 samples from a national soil survey, and results compared to the database of physicochemical soil properties created by the Irish Soil Information System. Information about possible environmental predictors identified will be shown and correlations and interactions between individual parameters presented.

Keywords: community structure, nitrogen cycling, functional genes, soil parameters

[P2.136]

Earthworm communities in grasslands of different cutting frequency and fertilization intensity

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Cutting frequency and the intensity of fertilizer application are the two main management factors in cultivated grassland in Central Europe. Earthworms are known to be affected by the amount and quality of plant residues in such systems. Hence, the number of seasonal cuttings in combination with fertilizer amounts is hypothesised to have direct and indirect effects on the size and structure of the earthworm communities. In a field experiment, we investigated the earthworm community response to different cutting frequencies and fertilization intensities. Two fertilizer treatments were established: (1) no fertilizer and (2) 180 kg ha^{-1} a^{-1} nitrogen, 30 kg ha^{-1} a^{-1} phosphorous and 100 kg ha^{-1} a^{-1} potasium. Within both fertilizer treatments, two cutting treatments were carried out: (1) only 1 cut per season and (2) 3 cuts per season. The resulting 4 treatment combinations were repeated 6 times in the field (24 plots). Earthworms were extracted from the soil using a mustard extraction method in May 2013 (3 extraction replicates on each of the 24 plots). In total, 5 different species (*Lumbricus castaneus, Lumbricus rubellus, Lumbricus terrestris, Aporrectodea caliginosa, Aporrectodea rosea*) were found covering all 3 ecological groups. *A. caliginosa* and *L. terrestris* were most abundant. Highest number of individuals was detected for the “no fertilizer/1 cut” treatment (180 ind. m^{-2}; average for all plots 161 ind. m^{-2}). Lowest biomass was recorded for the “fertilizer/1 cut” treatment (40 g m^{-2}; average for all plots 50 g m^{-2}). Significant effects were only found for the epigeic species, having lower numbers and biomass in the “no fertilizer/3 cut” treatment compared to the other treatments. Earthworms as a whole make use of both above and below ground plant litter but feeding preferences on the species level still remain unclear in most cases. This needs to be investigated in more detail to fully understand above-below ground interactions in complex grassland systems.

Keywords: Earthworms, Grassland, fertilization

[P2.137]

Soil macroinvertebrate communities as indicators of ecosystem services. A meta analysis of the MACROFAUNA data base.

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Soil macrofauna, the invertebrates that are visible to the naked eye, comprise 16 main orders that may locally comprise as many as 50-80 families, and 150-300 species, according to soil, climate and vegetation conditions as well as land management options. The MACROFAUNA database was built to accommodate data on communities of natural and disturbed ecosystems worldwide. In over 1500 sites distributed over 40 countries, ca. 15000 samples were taken in a great number of regional and international research projects using the standard Tropical Soil Biology and Fertility (TSBF) protocol now registered as ISO 23611-5.

A meta analysis showed considerable differences in soil macrofauna community structures from temperate and tropical climates and soil ecosystem processes regulated by these organisms.

Latitude: Earthworms and gastropods are dominant in temperate areas, while termites, ants and myriapods dominate in tropical areas. On the other hand, earthworms dominate the biomass in all land use systems in both temperate and tropical regions.

Soil texture: A co-inertia analysis showed a significant association of earthworms, isopods and ants with clayey soils with high organic matter content while termites were associated with sandy soils.

Land management: Macrofauna communities are highly sensitive to any option of soil management, degradation and contamination, which makes them excellent indicators of changes in soil function or conditions.

Synthetic Indicators of soil quality based on soil macroinvertebrate data are now widely used as proxies of soil biodiversity and health. In addition, indicator species have proved to be reliable indicators of levels of ecosystem service provision. Their mutual recognition by scientists and farmers and technicians might be a simple way to allow farmers to measure ecosystem services and access to the market of Ecosystem services and/or any public policy aimed at stimulating the conservation and proper management of soil natural capital.

Keywords: Macroinvertebrates, Communities, Ecosystem services, Meta analysis

[P2.138]

Soil biodiversity atlas: mapping earthworms of Europe

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Soil maps are increasingly used for nature conservation, spatial planning, environmental modelling and soil management issues, and have great potential in awareness raising. However, large area maps of soil biodiversity hardly exist, due to lack of data and harmonized methods, and the great variety of organisms thriving in soils. Still, some soil biodiversity datasets are available, although often not publically. Recently, German and Dutch data on soil biota were made freely accessible via the global diversity portal GBIF (Global Biodiversity Information Facility; www.GBIF.org).

As a spin-off of the FP7-EU EcoFINDERS project, we are producing a first European soil biodiversity map. We selected earthworms as the targeted soil organisms, as they appear to be one of the organism groups for which abundant data are available. Protocols for field sampling and analysis are rather straightforward and relatively common across different countries, and they are one of the more 'charismatic' soil organisms. Some earthworms species are considered as ecosystem engineers; their importance was already described in 1881 by Charles Darwin in his monograph 'The formation of vegetable mould, through the actions of worms, with observations on their habits (J. Murray, London).'

In order to arrive at reasonable surface coverage of countries for which abundant earthworm data are available (such as the Netherlands and Germany; Fig. 1) we applied a 'digital soil mapping' approach. Multiple regressions are used to relate scarce earthworm data to land use and soil characteristics (covariates) with a higher spatial resolution. Statistically significant relationships were used to build habitat response models for constructing earthworm maps with abundance, number of taxa (species) and some common species (e.g. *Aporrectodea caliginosa*). To our knowledge, this will be the first earthworm map of (parts of) Europe. Please join this initiative by providing yet unidentified data on earthworms elsewhere in Europe (michiel.rutgers@rivm.nl). The final map will be submitted for publication in the 1st Global Soil Bodiversity Atlas.

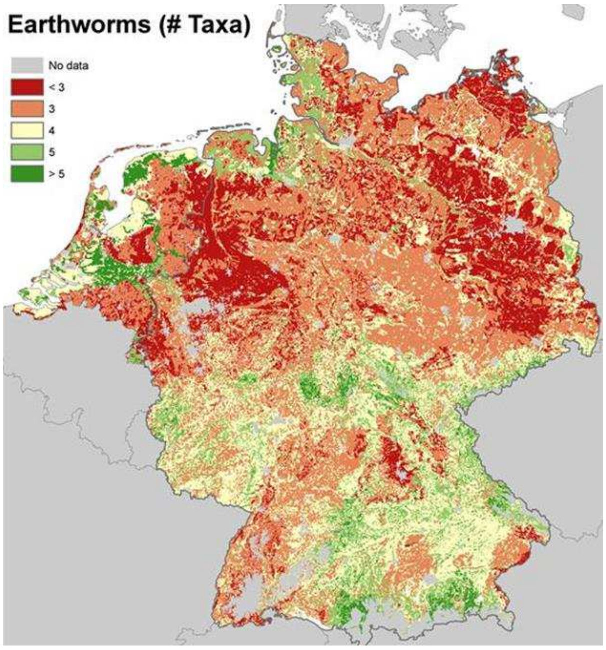

Fig. 1: Preliminary earthworm map of Germany and the Netherlands showing the extrapolated number of identified taxa of 100 individuals per site.

Keywords: Earthworms, Digital soil mapping, awareness raising, database

[P2.139]

A ground truthed DNA metabarcoding technique to determine fungal community structure and wider ecological applications

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Fungi are important for ecological function, biogeochemical cycles in soils and plant nutrition and some macrofungi are also of conservation interest. Here high throughput (Ion Torrent PGM) DNA sequencing was used to assess differences in fungal populations based on the LSU (28S) D1 variable region of the rRNA operon. The approach was initially validated then used to inform several land-use decisions.

To ground truth the methodology, firstly soils of woodland and adjacent grassland were differentiated on the basis of sequence data (by DCA, Permanova) and varied in predictable ways (e.g. ectomycorrhizal fungi detected in woodland but not grassland). Secondly, soil from established 900 m2 permanent quadrats on pristine (“waxcap”) grassland in Wales were analysed in conjunction with fruitbody surveys. All fungi identified during the fruitbody surveys were detected in NextGen datasets. Thirdly, fungal communities on plots at Park Grass, Rothamsted were found to vary in ways predicted from experimental treatments and fruitbody surveys; (eg. 50-fold lower Hygrocybe sequences on low nutrient control plots vs fertilized plots).

The approach has since been applied to inform conservation, restoration and commercial decisions. Soil cores from restored sites on former opencast sites in the south Wales coalfield were analysed. DCA showed that the community could not be differentiated from similar upland grassland sites but analysis at finer taxonomic scale showed differences (eg. more arbuscular mycorrhizal and pathogenic fungi in restored soil). Sequence analysis of soil from >12 protected grasslands was used to inform the success of conservation efforts, whilst engagement with ecological consultancies has led to the deployment of this methodology to inform planning decisions.

Keywords: NextGen, Fungi, Grassland

[P2.140]

Shifts in prokaryotic diversity and metabolic activity associated with plants in contaminated soils

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Dynamic synergy exists between plant roots and rhizosphere microorganisms – the soil in close proximity to roots (rhizosphere) is considered to be a “hotspot” of plant-microbe interactions. In contaminated soils, rhizosphere interactions are of extreme importance. Among others, processes such as root exudation and root turnover take place, which provide microbial growth substrates and secondary compounds that may function as inducers of enzymes of biodegradative pathways.

The primary objective of our research is to investigate the linkage between vegetation, fertilization, microbial diversity, and microbial functional activity in soils contaminated by diesel-range aromatics and polychlorinated biphenyls. Addressing these issues should help us better understand biodegradation and bioremediation mechanisms. In order to reach our goals, metagenomes were isolated from soil, followed by 16S rRNA gene and functional gene pyrotag analyses. Metabolically active populations were selected for via stable isotope probing.

Results of our research demonstrate that (i) different community structure patterns can be observed in bulk versus vegetated soil as well as in the rhizosphere of different plant species; (ii) microbial metabolic activity changes in response to the presence of plants; (iii) fertilizer appears to have an insignificant effect on community structure; (iv) different functional genes evolve in pristine and contaminated environments, potentially demonstrating an adaptation of the microbial populations' genes/enzymes to different substrates; (v) novel functional genes with as yet unknown substrate specificity can be retrieved from contaminated soil metagenomes. All of these findings will help us to better understand microbial ecological processes essential to soil functioning.

Acknowledgement: Funding is acknowledged of the Czech Science Foundation projects no. 13-20414P and 14-32432S and Ministry of Education, Youth and Sports project no. LH14004.

Keywords:

[P2.141]

Soil food web structure after wood ash application

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In 2006, the European Council established a mandatory target of 20 % renewable energy of the total energy consumption by 2020. Part of the replacement is burning biomass for heating and electricity instead of fossil fuels. Whole-tree biomass harvesting for biofuel combustion intensifies removal of nutrients from the ecosystem. This can be partly mitigated by applying ash from the combustion back to the system and thus recycle the nutrients. However, besides being rich in inorganic nutrients, ash is also very alkaline and contains heavy metals.

The ASHBACK project (www.ashback.dk) is a cooperation between three Danish universities, other research institutions and stake-holders that aims to investigate the consequences of returning wood ash to biofuel producing coniferous forest. We hypothesize that the change in pH and increased availability of nutrients after ash application to the forest floor can facilitate an increase in the bacteria to fungi ratio with possible cascading effects for the soil food web structure. This is tested by applying ash of different concentrations to experimental plots in a coniferous forest. During the course of the project soil samples will be collected with varying intervals and subsequently analyzed.

The food web analysis includes several trophic levels; bacteria/fungi, protozoa, nematodes, enchytraeids, microarthropods and arthropods. The initial results indicate that bacteria and protozoa are stimulated in the uppermost soil layer (0-3 cm) two months after ash application, whereas the enchytraeids are negatively affected. Generally, nematodes also appear to be negatively affected, although it differs slightly between feeding groups. The effects have not yet transferred to the lower soil layer (3-6 cm) at the site. On the higher trophic levels, we have not seen a direct effect thus far. Further sampling during the coming years will clarify the variability of both direct and indirect effects of wood ash application to a coniferous forest.

Keywords: Nutrient recycling, pH, Trophic levels, Biofuel

[P2.142]

Ash effects on arbuscular mycorrhizal fungi colonization, activity, diversity and their role in phosphorus and cadmium transfer

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Certain nutrients are required by plants to have a proper growth. One of the most limiting nutrients is phosphorus. The production of phosphorus fertilizers is becoming a problem due to the limitation of the supply compare to the demand. Several alternatives are being studied like the reutilization of biomass ashes. However, the effect of ashes on different microorganism's communities and the possible bioaccumulation of heavy metals need to be studied.

In this study different types and amounts of ash were mix with soil in barley crops. For each treatment the amount of phosphorus in barley shoots, the accumulation of Cd in roots and shoots, and the biomass of shoots and roots were analyzed. Besides, due to the role of arbuscular mycorrhizal fungi to acquire inorganic nutrients, the effect of ash in them was analyzed.

The results showed that there were no significant effects of the different types of ash in the growth of barley or in the root colonization or activity of arbuscular mycorrhizal fungi. In relation with the diversity, we do not expect any effects in the ash treatments. However, we could see a pattern where the highest concentration of ash enhance the amount of phosphorus in the shoots and root colonization, also the treatments with fertilizers tend to reduce the root colonization, in the same way it is expected some changes in the diversity in fertilizers treatments.

With these results we can conclude that fertilization with ash could be an alternative to phosphate fertilizers because it does not affect barley or arbuscular mycorrhizal fungi growth, activity or diversity, and it could improve crop yield.

Keywords: ash, arbuscular mycorrhizal fungi, heavy metals, phosphorus

[P2.143]

How roots influence soil properties and biotic processes across French agroforestry landscapes?

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In French agricultural landscapes, conventional farming is described as an amplifier of soil erosion. Recent policies have been encouraging agroforestry practices that are believed to provide a number of ecosystem services and improve biodiversity. However fundamental and applied research is still required to determine how best to plant and manage, depending on land use, climate and topography. Within this context, our project investigates ecosystem services provided by crop/forest systems, in relation to soil structural stability. We chose to study the following variables: stability of soil aggregates, root traits and presence, microbial activity and microbial metabolic diversity. The project involves eight field-sites representative of different agro-forests which have distinct ages and pedoclimatic characteristics. On each site, a systematic sampling was made to assess the influence of the tree line, the distance to the trees, and the perennial plant cover on the variables mentioned above. The relationship between soil aggregates and functional traits of plants and soil microbes is studied with substantial field measurements involving a large network in Agroforestry partnership. The preliminary results of this project suggest that the tree line and the proximity of trees are beneficial for soil aggregate stability. This may be related to the amount of roots. The magnitude of these effects seems however depending on the characteristics of the agroforestry systems. Finally, we hope that the results of this research will allow stakeholders and agroforesters to determine adapted spatial management strategies with regard to tree root traits and risks of erosion.

Keywords: root traits, soil aggregates stability, microbial metabolic diversity, agroforestry

[P2.144]

Effects of inoculation with *Serratia proteamaculans* S4 on community structure and allocation of plant-derived C in root and rhizosphere soil microbial communities of oilseed rape

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The rhizosphere is an active and dynamic niche in which plant-derived carbon supports microbial growth. Rhizosphere communities can be a source of high biodiversity but there are few studies of how this may be affected by applications of biological control agents. *Serratia* spp. have clearly demonstrated plant growth promoting and antagonistic effects, and should compete more successfully than indigenous communities for plant-derived carbon and alter C allocation patterns to root and rhizospheric microbial communities. A greenhouse study, using field soil, was performed to identify bacterial and fungal communities actively assimilating plant-derived C in the root and rhizosphere of oilseed rape plants following inoculation with *Serratia* bacteria and the fungal phytopathogen *Verticillium longisporum*. Oilseed rape seedlings were inoculated with *Serratia proteamaculans* S4 and were sown in soil artificially inoculated with *Verticillium*. Factorial combinations of *Serratia* and *Verticillium* inoculation were used, as well as additional plant-free soil treatments. Plants were grown for four weeks. Continuous labelling for 6 hours was initiated 4 weeks after the seeds were sown in pots. The first harvest took place 24h prior to labelling (SIP t0). Following $^{13}CO_2$ injection, 4 time points were decided for harvesting. No morphological differences or difference in shoot or root dry weight was observed between the treatments. However total ^{13}C enrichment in rhizospheric microorganisms was different between the different treatments suggesting a treatment effect on carbon allocation below-ground, either in the level of microorganisms or due to increased root exudation because of stress. The community structure of bacteria and fungi associated with the roots and rhizosphere was examined using 454 pyrosequencing and RNA-based stable isotope probing (SIP) of ^{13}C-labelled 16S rRNA fragments was used to identify taxa actively involved in the assimilation of root-derived carbon. The main focus of this study was to improve our understanding of the relationship between plants, indigenous microbial communities and externally applied biocontrol bacteria.

Keywords: Serratia biocontrol bacteria, RNA-SIP, Rhizosphere communities, Verticillium dahliae

[P2.145]
A simulation of the impact of earthworm bioturbation on soil structure

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Earthworms, as soil engineers, alter their environment and noticeably the soil structure. Indeed, they create burrow paths that they may maintain or refill more or less with their casts. Thus, earthworms create a porous soil structure and consequently impact on several soil functional properties such as hydraulic conductivity. Models of earthworm bioturbation are scarce and there is currently a need for models that account for the various species of earthworms and that explicitly simulate their impact on soil structure.

We built a model in which earthworms are allowed to *(i)* create new paths by ingesting soil particles, *i.e*. mineral and organic matter, *(ii)* move inside existing paths, *(iii)* wait or *(iv)* make a cast. Thus the model is able to simulate a network of burrows with their casts. The various endogeic and anecic species taken into account are represented by their probabilities of making any of these actions. As the stake is also to take into account the environment of the simulated earthworms, we also developed a simulator of soil structure used to provide features of the earthworms' close-environment and to save their impact on *e.g.* soil structure or organic matter content. To deal with the trajectory of earthworms a specific algorithm was implemented. Its principle is to divide the trajectory into segments and to save the links between them. The cast content of every segment and their length are also recorded. This implementation is compulsory to prevent earthworms from making new burrows into existing ones.

This model of earthworm bioturbation is been coupled with a simulator of tillage and settlement due to the rain. The goal is to assess the impact of various cultural practices on soil structure. Afterwards, this simulator and particularly the trajectory of earthworms could be used to simulate soil hydraulic conductivity.

Keywords: modelling, biological process, burrowing, cast production

[P2.146]

Changes of bacterial diversity in PCB-contaminated soil in rhizosphere of different plant species

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Rhizosphere microflora benefits from the compounds that plants release into soil through roots. Some of the compounds exuded are structurally analogous to some pollutants and can induce enzymes for the pollutants degradation. In our study, we isolated metagenomes from ten different plant species growing naturally in long-term PCB-contaminated soil. Our objectives were (i) to investigate bacterial diversity in the rhizosphere samples; and (ii) to identify plants stimulating bacteria potentially capable of PCB degradation by quantification of degradative genes in the rhizosphere samples. As a control, we used bulk soil from the same locality. Bacterial diversity was analyzed after metagenomic DNA was isolated from rhizosphere samples, and amplicons of prokaryotic 16S rRNA genes were prepared and pyrosequenced. The obtained sequences were processed with the Mothur software package and with R-project using vegan package. The same 16S rRNA gene amplicons were analyzed by terminal restriction fragment length polymorphism (T-RFLP). Both pyrosequencing and T-RFLP data revealed that bulk soil is significantly different from all rhizosphere samples. In the bulk soil, *Firmicutes* reads were the most abundant followed by those of *Proteobacteria* and *Actinobacteria*. In the rhizosphere samples, *Proteobacteria* reads were the most abundant followed by *Actinobacteria* and *Bacteroidetes*. Using qPCR, we were able to quantify the relative abundance of biphenyl dioxygenase (*bphA*) and 2,3-dihydroxybiphenyl-1,2-dioxygenase (*bphC*) genes in the samples. The highest 16S rRNA to *bphA* gene ratio was observed in the *Betula pendula* rhizosphere indicating more abundant population of PCB-degraders. This work brings new insight into the bioremediation mechanisms ongoing at the site.

Acknowledgements

Funding is acknowledged of the Czech Science Foundation project no. 13-28283S, Ministry of Education, Youth and Sports project no. LH14004 and specific university research MSMT No. 20/2014.

Keywords: bacterial diversity, plant secondary metabolites, pyrosequencing

[P2.147]

Development of metabarcoding for tracking changes of soil fauna community under stress by application of ash

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Ash is a waste product from combustion of bio-fuel in power plants. Application of ash on soil ensures nutrient recycling, but detrimental ecotoxicological consequences may arise since ash is a complex mixture that may contain compounds affecting soil invertebrates and their food and habitat condition. Here, we study the effects of ash on the abundance and composition of the soil fauna community. Over time, we will compare control plots with plots receiving three different concentrations of ash. Targeting soil fauna community includes protozoa, nematodes, enchytraeids, collembolans, mites and earthworms. For collembolans and mites, a morphospecies approach combined with DNA barcoding will be performed to quantify the species abundance.

Traditional morphological methods of identifying arthropods are (1) time consuming, (2) require trained taxonomists and (3) hampered by cryptic life stages and species. DNA metabarcoding, which couples the principle of DNA barcoding with next generation sequencing technology, has the potential to simplify community diversity monitoring. However, sampling and DNA extraction methods for the purpose of soil microarthropod metabarcoding have not been yet fully developed. We therefore will start out by comparing the morphospecies approach with three molecular approaches, differing in the types of DNA extracted from soil samples: total soil DNA, extracellular DNA and DNA gained from animals collected from the soil. In order to target all faunal groups, we use a set of three mini-barcodes based on the mitochondrial cytochrome oxidase I encoding gene (COI), histone 3 protein encoding gene (H3) and 18S regions, respectively. Community amplicon sequencing will be performed on the MiSeq Illumina platform. The extraction method with highest quality and efficiency will be used for long term monitoring of changes in the soil mesofaunal biodiversity under the stress of ash. Hopefully, the long term monitoring data could help maintain the soil ecology and improve the management of ash.

Keywords: Ash, Soil fauna, Metabarcoding

[P2.148]

Resistance and resilience of the forest soil microbiome to logging associated compaction

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Soil compaction is a major disturbance associated with logging, but we lack a fundamental understanding of how this affects the soil microbiome.

We assessed structural resistance and resilience of the microbiota using a high-throughput pyrosequencing approach in differently compacted soils at two forest sites and correlated these findings with changes in soil physical properties and functions.

Alterations in soil porosity after compaction strongly limited air and water conductivity. Compaction significantly reduced abundance, increased diversity, and persistently altered the structure of the microbiota. Fungi were less resistant and resilient than bacteria; clayey soils were less resistant and resilient than sandy soils. The strongest effects were observed in soils with unfavorable moisture conditions where air and water conductivities dropped well below 10% of their initial value. Maximum impact was observed around 6 to 12 months after compaction and microbial communities showed resilience in lightly but not in severely compacted soils four years post-disturbance. Bacteria capable of anaerobic respiration, including sulfate, sulfur, and metal reducers of the Proteobacteria and Firmicutes, were significantly associated with compacted soils. Compaction detrimentally affected ectomycorrhizal species, whereas saprobic, parasitic, and mutualistic fungi proportionally increased in compacted soils. Structural shifts in the microbiota were accompanied by significant changes in soil processes, resulting in reduced carbon dioxide, and increased methane and nitrous oxide emissions from compacted soils.

This study demonstrates that physical soil disturbance during logging induces profound and long-lasting changes in the soil microbiota and associated soil functions, raising awareness regarding sustainable management of economically driven logging operations.

Keywords: forest soil compaction, microbial diversity, ribosomal pyrotags, greenhouse gas fluxes

[P2.149]

Impact of microbial siderophore on the antioxidative enzyme activities and Al uptake of Jatropha curcas L. under Al stress

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Siderophores secreted by rhizobacteria have been proved to positively contribute to ferric acquisition and growth promotion of plants, yet their role in metal detoxification for plants has been seldom investigated. In this study, we hypothesized that the complexation of toxic metal ion by siderophore might lead to the reduction of metal bioavailability and hence less toxic challenge to plant.

Thus, a hydroponic experiment was conducted, in which 0, 100, 250 and 500 μM siderophore desferrioxamine-B (DFOB) were applied, respectively, to 0 and 500 μM Al stresses of *Jatropha curcas* L.. After 14 days of treatment, the antioxidative enzyme activities and translocation of Al in Jatropha curcas L. were investigated.

Results showed that lower DFOB concentration (100 μM) promoted the plants' growth although not significantly. Under Al stress, DFOM of all concentrations (100, 250 and 500 μM) positively reduced the activities of superoxide dismutase (SOD) and peroxidase (POD) in the roots and SOD in the leaves; Catalase (CAT) activities in both roots and leaves were alleviated by 500 μM of DFOB; The plasmalemma damages in roots and leaves were mitigated by reducing the production of malondialdehyde (MDA) by 250 and 500 μM of DFOM. DFOM of all concentrations promoted the root to shoot transfer of Al by reducing the Al accumulation in roots but increasing it in shoot.

In this study, the reduced antioxidative enzyme activities under Al stress were attributed to the exogenous siderophore DFOB applied, indicating a reduction of bioavailable Al due to the formation of DFOB-Al complex. Moreover, either Al or DFOB significantly inhibited the Fe uptake in the plants yet the co-existence of both substances led to a promoted Fe uptake. This synergetic effect might also contribute to tolerance of Al stress in plant and the mechanism is worth further studying.

Keywords: Siderophore, Detoxification, Al, Jatropha curcas L.

[P2.150]

Spatial variation and general patterns of soil microbial community structure across altitudinal gradients in arctic mountains - a study from petuniabukta, svalbard

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The temporal and spatial variation of soil microbial communities across altitudinal gradients was documented by several authors in temperate alpine ecosystems. However, there is lack of reports about the microbial community structure across altitudinal gradients from the Arctic ecosystems. In this study, we investigated spatial variation of microbial communities following three altitudinal soil transects in coastal mountains of Petunia Bay (Billefjorden, Svalbard; 78° 40´ N, 16° 35´ E) using phospholipid fatty acid (PLFA) analyses. The multivariate analyses of PLFAs specific to fungi, Actinobacteria, Gram-positive (G+) and Gram-negative (G-) bacteria revealed significant changes of relative abundances of these microbial groups with increasing altitude. We found twofold increase of F/B ratio with rising elevation within all gradients, which shifted the dominance of bacteria in lower elevations towards fungal dominated microbial community in upper parts of the gradients. The soil physico-chemical properties explained 56.8 % of variability in the microbial community structure (MCS) with pH, PO_4^-P, NO_3^-N, C_{tot}/N_{tot} and sitosterol (as proxy for plant residues) being the most important predictors (76.6 % of variation explained by the model). While the bacterial PLFAs were positively correlated with total and dissolved soil carbon, nitrogen, phosphorus and sitosterol contents, the best predictors for fungal and Actinobacterial abundance were pH and phosphorus availability. We found also general patterns connected with rising elevation in composition of PLFA specific to Actinobacteria, G+ and G- bacteria, which indicate different composition of these microbial groups across the gradients. Our results demonstrate that occupation of different niches by fungi and bacteria within the altitudinal gradients is pronouncedly driven by nutrient availability and pH. Bacteria are more proliferate in nutrient and substrate rich environments of lower elevations while fungi and Actinobacteria are more abundant in less favorable conditions of higher elevations with generally higher soil pH.

Keywords: phospholipid fatty acid, microbial community structure, altitudinal gradients, environmental gradients

[P2.151]

Abundance, richness and structure of soil fungal communities across an European transect

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In contrast with plants and animals, biogeographical patterns of fungal assemblages have been little explored. Consequently, the factors driving the diversity and the composition of these communities are poorly understood. The EcoFINDERS project aimed at (i) characterizing the soil fungal diversity according to soil types, land uses and climate, and (ii) determining environmental variables explaining the fungal richness and community structure. High-throughput sequencing of the ITS2 region was used to explore fungal assemblages in eleven countries along a latitudinal gradient in Europe. Parallel to the sequence based analyses, the fungal abundance was measured from the same DNA samples using qPCR targeting ITS2 region.

We showed that the European soil fungal diversity varies in terms of richness, relative abundance and distribution according to land uses (forests, pastures, arable soils), soil and climatic parameters. Remarkably, fungal diversity increases from forest to arable soils and this richness pattern was also positively correlated with pH, CEC, Ca and Clay. These High-throughput sequencing results have been partially confirmed by qPCR data. Indeed, also the fungal copy numbers in soils were affected by land-use and differed between climatic zones. The highest abundances were measured in (Boreal) forestry sites and the lowest in Mediterranean soils and in arable sites. However, the fungal abundance, unlike richness, was negatively correlated with pH, whereas the soil organic matter content seemed to have no affect on fungal abundance. Interestingly, along this large climatic gradient, we did not find relationship between richness and latitude, which could be a proxy of temperature. The usual ecological pattern between richness and thermic gradient did not appear transferable to soil fungi. Finally, the PCoA analysis revealed that the composition of fungi was largely explained by soil pH and climatic parameters. These results, with additional biogeographical studies, should help to predicting future distribution patterns of soil fungi.

Keywords: soil fungi, biogeography, High-throughput sequencing, ecology

[P2.152]

Co-occurrence patterns of ammonia and nitrite oxidizing communities in relation to edaphic factors and ecosystem functioning.

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Nitrification is a principal driver of nitrogen loss from agricultural soils, resulting in nitrate leaching into ground water as well as increased emission of greenhouse gases in the form of nitrous oxide (N_2O). Previous work examining the relationships between patterns of nitrifier diversity, abundance, and spatial distribution with large-scale ecosystem functions have focused primarily on ammonia oxidizing bacteria (AOB) and archaea (AOA), which perform the first step in the nitrification pathway. In contrast, substantial knowledge gaps exist on the relevance of differences in nitrite oxidizing bacterial communities (NOB), which perform the second step in the pathway, and whether non-random associations exist between NOB, AOB and AOA that may be linked to niche differentiation or ecosystem functioning. To address this, we explore the interaction between these communities in relation to spatial patterns of edaphic factors, process rates and ecosystem functioning in terms of nitrogen leaching, nitrogen use efficiency and potential nitrogen losses via denitrification across a 44-hectare farm. The diversity and abundance of AOA and AOB communities was determined by PCR amplification of the ammonia mono-oxygenase gene (*amoA*) variants for both communities, while recently developed molecular probes (Pester et al., 2013. *Environ. Microbiol*, doi:10.1111/1462-2920.12300) were used to assess NOB communities. The patterns of community structure for each group were significantly similar, suggesting an overall equivalent influence of edaphic factors on each community. However, only the AOB and *Nitrobacter*-type nitrite oxidizing communities showed a significant response to farm management practice, with correlations observed between soil moisture content and community structure, whereas the AOA and *Nitrospira*-type community structures were correlated to total soil carbon. Additional analyses will be presented on the relationship between community structure, diversity, abundance and associations between communities in relation to process rates and ecosystem functioning.

Keywords: nitrite oxidizing bacteria, ammonia oxidizers, co-occurrence, soil

[P2.153]

When citizens and scientists work together: OPVT, a french participative science project on earthworms

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Scientists have become more and more interested in earthworms because of their impact on soil functioning and their importance in provision of many ecosystem services. In order to improve the knowledge on soil biodiversity and integrate earthworms in soil quality diagnostics, it appeared necessary to gain a large amount of data. However, despite the huge number of research programs to collect these data, efforts are still needed.

In order to compensate for these missed data and accelerate their collect, the University of Rennes 1 developed in 2011 a citizen science project called **O**bservatoire **P**articipatif des **V**ers de **T**erre (participative earthworm observatory).

This project benefits both the work of scientists through the accumulation of a large set of data and also the education of citizens through awareness to scientific issues. It has several purposes: i) to offer, through earthworm assessment, a simple tool for soil biodiversity evaluation in natural and anthropic soils, ii) to provide simple sampling protocols, accessible to a wide range of citizens and adapted to the targeted public (farmers, territory managers, gardeners, pupils), iii) to build a databank of reference values on earthworms: participants can enter the data online and in return an individual reporting of results is proposed, iv) to offer trainings to farmers, v) to propose a website (http://ecobiosoil.univ-rennes1.fr/OPVT_accueil.php) providing for example earthworm identification guidelines and general scientific background on earthworm ecology and the impact of agricultural practices.

This project, initially available to anyone on a voluntary basis, was also recently used by the French ministry of agriculture to carry out a scientific watch throughout the French territory. Up to now, more than 2500 plots have been prospected since the opening of the project (fig 1). Details of this citizen project will be presented, meaning adaptation of the sampling protocols, tools for training, results and returns from end-users.

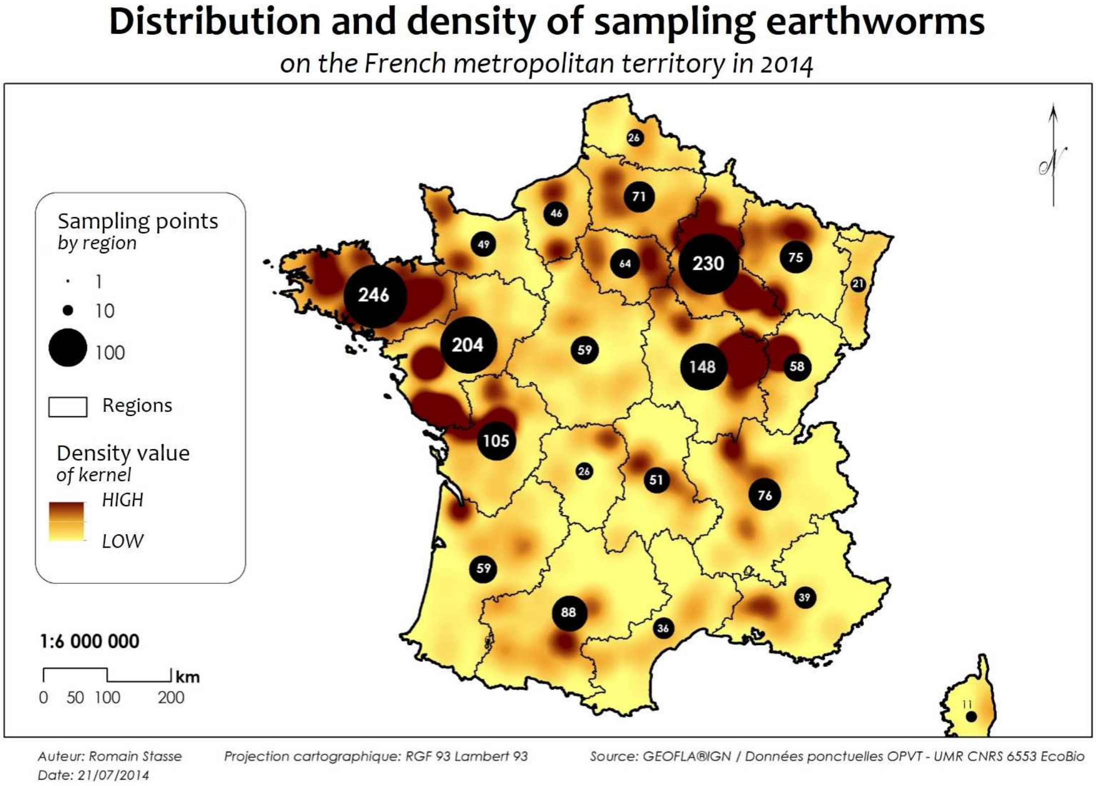

Figure 1 Distribution and density of sampling earthworms on the French metropolitan territory

Keywords: Earthworms, Observatory, Citizen science project, Sampling protocols

[P2.154]

Interaction between above and below ground biodiversity : mechanisms linking plant community properties to soil aggregate stability in an experimental grassland plant diversity gradient

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Introduction – Erosion is the most common source of soil degradation due to decreased stability of soil structure. Soil aggregate stability depends on plant community properties, such as functional group composition, diversity, and biomass production. However, little is known about the relative importance of these drivers and the role of soil organisms in mediating plant community effects. In the frame of an ANR-DISCOVER project we assessed how grassland plant diversity impacts on soil aggregate stability as an essential ecosystem service.

Methods – Soil aggregate stability was studied in an experimental grassland plant diversity gradient (the Jena Experiment, Germany). Experimental plots varied in plant species diversity (1, 4, and 16 species), functional group diversity (1, 2, 3, and 4) and identity (grasses, small herbs, tall herbs or legumes). Several explanatory variables (earthworms, microbial biomass, root biomass, soil organic carbon concentration) were considered to mechanistically explain effects of plant diversity and plant functional group composition. Three soil aggregate stability measures (slaking, mechanical breakdown and microcracking) were considered in path analyses.

Results – Soil aggregate stability increased significantly from monocultures to plant species mixtures and in the presence of grasses, while it decreased in the presence of legumes, though effects differed somewhat between soil aggregate stability measures. Using path analysis plant community effects could be explained by variations in root biomass, soil microbial biomass, soil organic carbon concentrations (all positive relationships), and earthworm biomass (negative relationship with mechanical breakdown).

Conclusion – The present study identified important drivers of plant community effects on soil aggregate stability. The effects of root biomass, soil microbial biomass, and soil organic carbon concentrations were largely consistent across plant diversity levels suggesting that the mechanisms identified are of general relevance.

Keywords: Grassland diversity, soil aggregate stability, soil biodiversity, drivers

[P2.155]

Pioneering microorganisms from a glacier forefield help to weather the granitic sediment and make trapped nutrients available

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Glaciers are retreating worldwide due to global climate change. In Europe, alpine glaciers lost about half of their total surface area and their total volume within the last 150 years. Consequently, fresh rock sediments are exposed at the surface and subjected to weathering processes. Rock surfaces that are freshly exposed to the atmosphere become rapidly colonized by microbial communities as the first settlers.

A 454-pyrosequencing approach was used to assess whether bacterial and fungal community structures differed between stages of soil development (10, 60, 80, 110 years) and depths (surface, 5 cm, 20 cm depth) along a soil chronosequence (Damma glacier forefield, Switzerland). Soil age significantly affected the bacterial and fungal community structures. In parallel to plant establishment, carbon and nitrogen contents increased with soil age, particularly in the surface, leading to higher bacterial activity and fungal biomass in vegetated soils.

A set of bacterial and fungal species isolated from fine granitic sediment of the non-vegetated forefield of the Damma Glacier in the central Swiss Alps showed a high potential to weather powdered granite material in batch experiments. In particular, four bacterial isolates and four fungal isolates were weathering associated. The presence of these strains caused a significant increase of granite dissolution (as measured by the release of Ca, Fe, Mg and Mn). These most promising weathering-associated bacterial species (one isolate each of *Arthrobacter* sp., *Janthinobacterium* sp., *Leifsonia* sp., and *Polaromonas* sp.) secreted large amounts of oxalic acid and they formed significant amounts of HCN. The combined action of oxalic acid and HCN appeared to be associated with enhanced elemental release from granite. The zygomycete fungi *Mucor hiemalis, Mortierella alpina, Umbelopsis isabellina* and the ascomycete fungus *Penicillium chrysogenum* dissolved the granite powder most efficiently, mainly due to the release of high amounts of the organic acids citrate, malate and oxalate.

Keywords: Pioneering microogansms, Glacier forefield, Weathering, Organic acids

[P2.156]

Potential methanotrophic and methanogenic activity of soil crusts in semi-arid Tabernas region

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Introduction: Arid and semi-arid regions occupy approximately one third of the Earth's land surface. Most often soil is covered by physical and biological soil crusts which play important ecological and functional roles. Nevertheless, little is known about potential methanotrophic and methanogenic activity of soil crusts. Mediterranean semi-arid ecosystems, with low mean annual rainfall and well- defined drought season, might contribute significantly to the terrestrial sink of atmospheric methane.

Aim: We focused on potential methanotrophic and methanogenic activities of physical and biological (cyanobacterial and lichen) soil crusts and compared them with adjacent soil from seven dominant shrub species at the Tabernas semi-desert in SE Spain.

Methods: In lab experiments we measured potential methanotrophic and methanogenic activity as well as basal respiration and substrate induced respiration, microbial biomass, and nutrient content in soil and crust samples. Extracted DNA/RNA was used for assessing diversity and expression of the pmoA and mcrA genes involved in methane oxidation and production processes.

Results: General microbial activity and nutrient availability changed along a successional gradient (physical crust - cyanobacterial crust - lichen crust - shrub), the highest values found in lichen crusts and under shrubs. Methanotrophic activity was in general relatively low, with the highest values in lichen crusts, while almost no activity was detected in physical crusts. On the other hand, potential methanogenic activity was highest in cyanobacterial crusts.

Conclusions: The studied semi-arid ecosystem does not likely play an important role as a terrestrial sink of atmospheric methane, as its methanotrophic potential is rather low. However, it could turn to significant source of methane during the wet season; especially under the predicted regional climatic scenario of larger rainfall events separated by longer drought spells.

Keywords: semi-arid zone, methane oxidation and production, soil crusts, nutrient content

[P2.157]

Acquisition of organic nitrogen by mycorrhizal fungi and cluster roots of plants in nitrogen-limited soils of the Cape Floristic Region, South Africa

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Soils of the Cape Floristic Region of South Africa are depleted of nitrogen (N) with over 99% in organic form. Given this limited N, we wished to determine the 1) extent that plants shift to a mycorrhizal symbiosis under N-limitation; 2) extent of organic N use by non-mycorrhizal (cluster-rooted Proteaceae), arbuscular mycorrhizal (various plant families) and ericoid mycorrhizal (Ericaceae) plants; and 3) the relative importance of mycorrhiza compared to cluster roots as root adaptations to low soil-N.

We used foliar delta ^{15}N as an indicator of N-sourcing at 13 field sites. Aware that foliar delta ^{15}N is a composite of various processes in the N cycle, we assessed foliar and soil ^{15}N across a rainfall gradient, while also determining mycorrhizal colonization and foliar N.

Contrary to previous studies that used only site-averaged results, we found that mean annual precipitation had only a weak negative effect (r^2=0.06 site-average; r^2=0.18 single species). There was also a weak positive effect of foliar N concentration (r^2=0.15 site averaged; r^2 = 0.17 single species), possibly reflecting changes in N allocation in the leaves as reported previously. Soil N being uniformly low (0.45% ± 0.04) was apparently not a driver of arbuscular or ericoid mycorrhizal colonization. Considering the weak confounding effects, we tentatively suggest that the foliar delta ^{15}N signatures could be mainly reflective of the organic N substrate in soils.

We further tested this hypothesis by supplying potted plants with organic nitrogen sources of known delta ^{15}N or ^{15}N-enrichment (plant litter, gelatine and doubly-labeled glycine). Arbuscular and ericoid but not non-mycorrhizal Proteaceae plants could acquire complex organic N.

Arbuscular and ericoid plants acquired greater amounts of glycine ($p<0.001$) than non-mycorrhizal counterparts and similar amounts to the non-mycorrhizal Proteaceae, confirming that both cluster roots and mycorrhiza utilize organic N sources in the N-limited Cape Floristic Region.

Keywords: organic nitrogen, natural abundance, arbuscular mycorrhiza, cluster roots

[P2.158]

Which vineyard practices in order to assure sustainable Champagne. Results from the VitiEcoBioSol programme, a long term study (25 years)

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Conventional vineyard practices have lead in many environmental disturbances as soil erosion, soil compaction, loss of organic matter and soil biodiversity, water contamination, … Therefore, there is an increasing interest to develop sustainable viticulture in the famous Champagne vineyard since 20 years: a huge program called “VITI 2000” has been developed since 1986 by CIVC (Inter-professional Committee of Champagne Wine) in collaboration with researchers. This program aims are i) to assess the impact of vineyard practices on soil functioning environmental properties and wine quality, ii) to advice sustainable practices to winegrowers. One strength of this program is to allow a long term field experiment.

In this program, earthworm communities, microbial biomass, soil and vine parameters were followed during 25 years in 19 plots representing 66 treatments which tested the impact of pesticides applications (nematicides, fungicides, herbicides), or organic matter inputs, or vine management (organic vineyard vs conventional vs integrated).

This program ended in a huge data collection e.g. the data table of earthworm communities (species, body mass, sexual stage) presents more than 39 000 lines. A database, compatible to others soil fauna databases developed by the laboratory EcoBio (University Rennes 1), has been developed.

First results indicate that i) grass strip between the vine rows and compost, quickly stimulate biological soil processes, while dried organic matter inputs have a slow positive impact, ii) fungicides containing copper alter in the same pattern, earthworm and microorganisms, iii) integrated management could be as positive as organic practices. Statistical treatments are still going on and further results will be discussed.

Keywords: Viticulture, Biostimulation, Ecological engineering

[P2.160]

Assessment of earthworm communities and associated ecosystem services in contrasting tillage systems in northwestern Europe

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Introduction – In response to soil structural degradation, organic matter and soil biodiversity decline associated with arable crop production, alternative approaches including reduced tillage systems have been developed. Farmers, researchers and policy makers in Europe are increasingly interested in exploring the possible benefits of these systems, both for conventional and organic crop production. Many studies worldwide have analysed the impact of tillage systems on soil properties and crop yields; however a comprehensive approach to linking soil management - soil biodiversity and ecosystem services is still lacking. This information, as well as the selection and monitoring of soil indicators, is crucial to guide practical implementation and policies.

Earthworm species have a central role in soil functioning in loamy agricultural soils of northwestern Europe, but generalization across geographical locations is challenged by differences in crop rotations, tillage practices and species communities composition. The SUSTAIN project is a collaborative project performed in France (Brittanny) and the Netherlands and addresses the following objectives (i) to provide a comprehensive understanding on how reduced-tillage systems impact earthworm communities in organic and conventional farming; and (ii) to quantify the effects of reduced tillage systems on ecosystem services (soil structure maintenance, water regulation, food production, greenhouse-gas mitigation).

Methods – Data have been collected from long term experiment fields (from 6 up to 13 years) and also from farm networks and approaches for data integration, including ecological trait-based approaches, have been explored and tested.

Results – The study will present results of this collaborative work, thereby shedding light on the benefits and trade-offs related to reduced tillage systems in NW Europe, and the role of earthworms for improved soil functioning and crop performance.

Conclusion – Recommendations for indicator selection and integrative approaches to improve understanding of earthworm community response to agricultural management will be provided.

Keywords: reduced tillage, earthworm, crop performance, physical properties

[P2.161]

Bacterial response to hydration-desiccation cycles in arid soils

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Although one quarter of the total land area of the world is dryland, these environments are poorly explored. Climate models predict that arid ecosystems will be strongly affected by changes in temperature and precipitation as air temperature will increase and precipitation events will be more intense but less frequent. The effect of hydration after long desiccation periods on the soil microbial populations is being debated for many years and different scenarios were suggested. Some suggest that hydration and the sharp increase in water potential would lead to severe physiological stress and massive death to members of the bacterial communities, while others suggested that the relief in water stress would revive the dormant populations and enhance activity. Different studies in arid and semi-arid ecosystems showed that precipitation pulses trigger rapid and massive carbon pulse, succeeded by mineralization of newly available nutrients, and it was widely accepted that the bacterial community is altered by the increase in the soil moisture content. However, in-depth analysis of the changes in desert soil bacterial communities starting from the rain pulse through the desiccation of moisture from the soil were never reported, bared a few scattered snapshots of microbial profiles in arid soil during hydration or desiccation events.

To fill this gap in knowledge we closely followed major rain events and the subsequent soil desiccation using controlled and field observations. We simulated rain on arid soil columns and linked changes in the active bacterial community to the soil water content. Concomitantly, we observed the hydration-desiccation pattern in the Negev Desert following a major rain event and sampling at intervals until the soil was fully desiccated.

Our collective data shows that under hydrated conditions active species richness and phylogenetic diversity plummet, while the total abundance of the active bacteria is unscathed. Desiccation of the soil restores the active bacterial diversity and richness while not affecting the abundance. In both the controlled soil environment and the field we have observed a shift in dominance during hydration and subsequent desiccation: from highly diverse Actinobacteria (40% relative abundance during desiccation to 5% during hydration) to a less diverse community of Firmicutes (10% during desiccation to 40% during hydration). From dominance of □- and □- proteobacteria (30%) during desiccation to □-proteobacteria (10%) population governed almost exclusively by Enterobacteriales during hydration.

We suggest that during hydration events, dryland bacteria are involved in complex community dynamics; as the moisture in the soil increase gaps between the soil particles are bridged by water, enabling interactions and competition between formally separated communities leading to a decrease in the overall bacterial diversity. When the soil desiccates the pores are again segregated and unique communities are established in each microhabitat thus stimulating bacterial dispersal and diversity.

Keywords: desert, rain, desiccation

[P2.162]

Soil fungal communities correlate with genotypic variation within an alpine cushion plant

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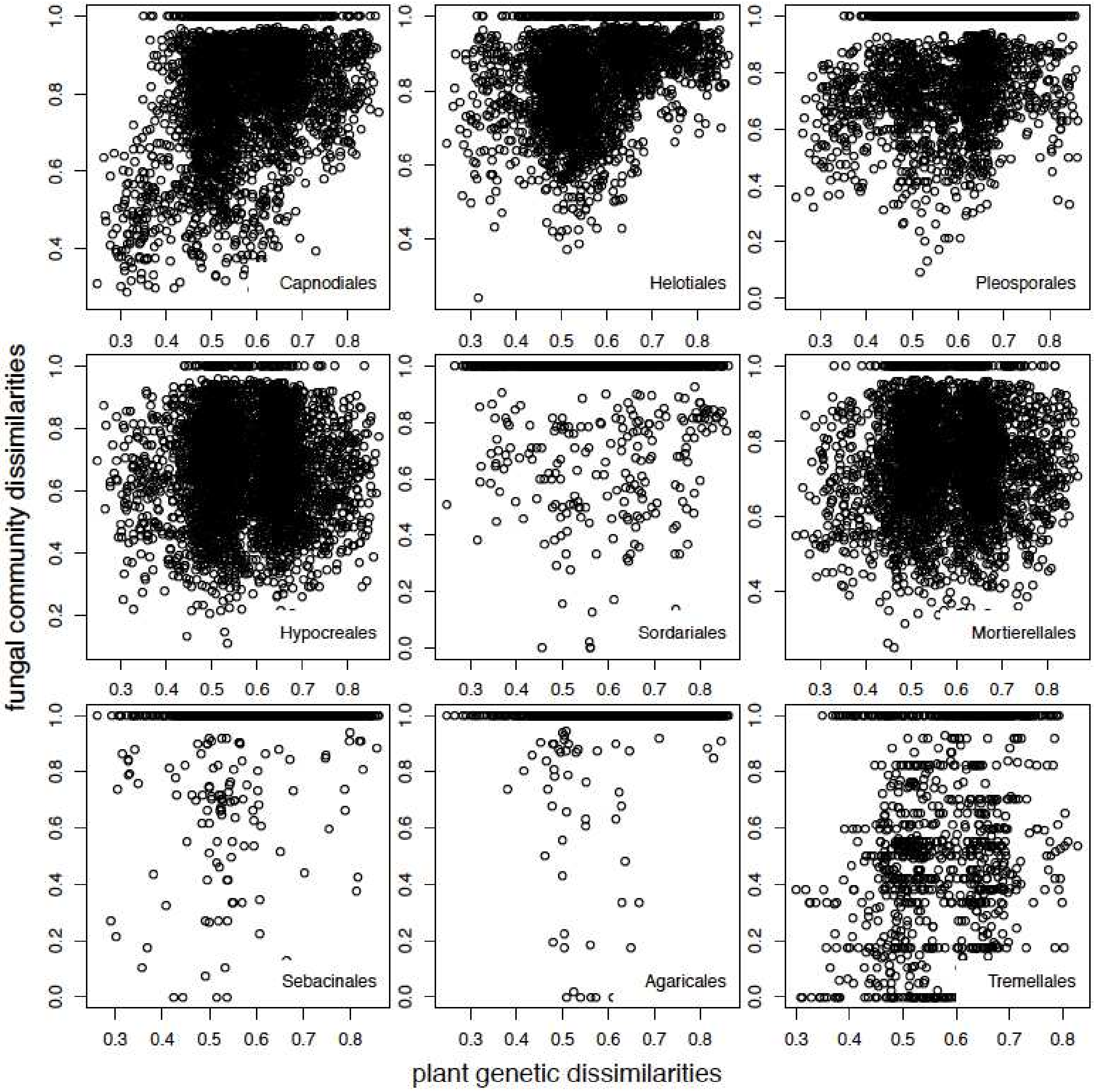
Fungi are intimately related to plants likely impacting positively or negatively their fitness and productivity. Our aim was to test whether plant divergence correlates with a shift in associated soil fungal communities by focusing on the cushion plant *Silene acaulis*, a particularly important foundation species of the alpine ecosystem. Ninety individuals were sampled along elevation gradients from two calcareous and siliceous mountains in the French Alps and genotyped using Amplified Fragment Length Polymorphism. Soil fungal communities within and outside cushions were characterized using MySeq paired-end sequencing of ITS1 amplicons. Population genetic analysis revealed 3 genetic clusters in *S. acaulis*. Cushions' fungal communities differed from the outside and depend on the plant genotype. We found that the more the cushions were genetically distant, the more their associated fungal communities differed. Furthermore, this effect predominates over environmental context in which plant grows. This correlation was particularly true for fungal lineages with biotrophic strategies (e.g. endophytes, pathogens) compared with lineages known primarily for saprotrophy, suggesting that this correlation is, at least in part, due to direct plant–fungal interactions. Further, closely related OTUs (some of which were assigned to the same species) showed contrasting preference to cushion genotype. Our results suggest fine scale ecological specialisation of fungi to intraspecific plant genetic variation and co-speciation. We conclude that biotic factors are more important in selecting plant-associated fungi than abiotic factors.



Correlation between fungal community dissimilarities (Bray-Curtis) and cushions genetic distance (Jaccard), for 9 abundant fungal lineages.

Keywords: plants-fungi interactions, intraspecific plant genetic variation, biotroph, next generation sequencing

[P2.163]

Changes of soil microbial community under multidirectional influence of non-traditional fertilizer

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Composting is one of the methods of utilization of organic wastes such as domestic waste or sewage sludge. Since in Russia a joint canalization of household and industrial waste water is realized, sewage sludge contains both nutrient elements and pollutants. Thus, compost produced from such a sewage sludge being used as non-traditional fertilizer affects the soil multidirectionally.

In this study we estimated the long term effect (five years) of compost (100, 150 and 175 t ha^{-1}) prepared from the sewage sludge on soil microorganisms. The compost contained 35% Corg, 2% Ntot, and toxic elements (67, 12, 77, 312, 166, 0.1, 646, 0.2 mg kg^{-1} of Cr, Cd, Ni, Cu, Pb, As, Zn, Hg, correspondingly). Implementation of the compost led to stimulated *Pinus silvestris* seedlings growth in 1.6-7.8 times in the first four years.

Soil microbial biomass increased in all variants in comparison with control immediately after compost implementation. Besides, composition of microbial community changed significantly. Thus, 9-fold decrease of total heterotrophic bacterial counts and 7-fold increase of fungi counts was observed. The microbial biomass remained significantly higher than control (1.8-4.7 fold) during three years and then stabilized. In opposite, respiration activity was inhibited or equal in comparison with control values but did not exceed them in none of the measurements. Similarly, potential nitrogenase activity was inhibited in compost-amended soil, especially during the first 30 days (~7, 10, 16-fold for 100, 150 and 175 t ha-1, correspondingly), and stabilized after two years. By analyzing of dehydrogenase and urease activities we did not observed significant differences of the average yearly values, whereas asynchronous effect of fluctuations of these parameters in comparison with control was revealed during the first three years.

Thus, implementation of composts from the sewage sludge improves ecosystem service function of soil while microbial community undergoes reversible changes.

Keywords: sewage sludge, compost, microbial parameters, Pinus silvestris

[P2.164]

The use of a functional approach as surrogate of springtail species richness in European forests

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Springtails are known indicators of soil disturbance. As for other groups of soil microarthropods, identifying them to the species level requires a huge effort and expert knowledge. On this study we evaluate whether their identification to morphotype level, using an eco-mophological index which classifies individuals based on their adaptation to the soil, can be used as a surrogate of species richness in an extensive monitoring scheme. The same evaluation is done also with taxonomic at genus and family levels. Additionally, sampling effort in order to sample 60, 70, 80 and 90% of a site's total richness was calculated. Species lists consisted of 35 sites (mainly southern european forests and perennial plantations) sampled within different projects and with the same number of samples (16 soil samples per site). Sampling effort results showed that, on average, 7 to 11 samples are enough to have a good estimate of a site’s species richness averaging 80-90% of the total site richness, but it varies considerably with site habitat heterogeneity and richness. The GLM models (using species richness as response variable) fitted for the family, genus or morphotype levels (used as explanatory variables) were all significant ($p<0.05$) but only the latter two had a pseudo R squared higher than 0.75. This indicates that when a rapid and cost-effective assessment of springtail richness in different sites is required, this eco-morphological approach could be used.

Keywords: springtails, morphology, monitoring, biodiversity

[P2.165]

Importance of agricultural practices on functional diversity of soil microbiota: first tracks of response with a diachronic study of biogeochemical cycles

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SOFIA project aims to provide new knowledge on environmental stakes linked to crop system management, in the context of biodiversity conservation, climate changes and biogeochemical cycles understanding. One aim of SOFIA is to understand impacts of agricultural practices on functional diversity of soil microbiota, particularly via a change in nutrients availability to soil organisms. SOFIA is set up on a LTER site “Agroécosystèmes, Cycles Biogéochimiques et Biodiversité” (SOERE ACBB) located at Estrées-Mons, Picardie, France. This field experiment consists in series of experimental treatments varying on anthropogenic pressure according to: crop rotation, fertilisation, residue management or soil tillage. This communication presents the diachronic response of microorganisms with modification of soil management, allowing predictive information of agroecosystem functioning.

Soils enzymes are interesting indicators to approach the release of nutrients for microbial and plants growth. This diachronic study (four years), following enzymatic activities linked to C, N, P and S cycles, allows hierarchizing firstly, the importance of the anthropic factors introduced and secondly the sensibility of each cycle to these factors.

Before application of different agricultural practices, enzymatic activities were homogeneous on the site, whatever the cycle considered. After four years, the amounts of active enzymes were lower with conventional tillage than under reduced tillage and zero tillage. Significant increases appear after two years in the 0-5cm surface layer with reduced tillage, for C and N cycles. P cycle evolution started after two years but significant effects on P and S cycles were observed only after four years. Increased enzyme activity under reduced tillage systems may be related to increased available carbon and/or functional diversity of soils.

Results will allow us to assess the ecosystem services potentially provided by the different cropping systems (habitat for biodiversity, maintenance of soil physical quality and nutrient cycles), and the rapidity of the turnover of the microbiota.

Keywords: agricultural practices, soil enzyme, functional biodiversity, biogeochemical cycles

[P2.166]

Symbiotic nitrogen-fixing bacterial populations trapped from soils under agroforestry systems in the Western Amazon

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Cowpea (Vigna unguiculata) is an important grain-producing legume that can forego nitrogen fertilization by establishing an efficient symbiosis with nitrogen-fixing bacteria. Although inoculating strains have already been selected for this species, little is known about the genotypic and symbiotic diversity of native rhizobia. Recently, *Bradyrhizobium* has been shown to be the genus most frequently trapped by cowpea in agricultural soils of the Amazon region.

The aim was investigating the genetic and symbiotic diversity of 148 bacterial strains with different phenotypic and cultural properties isolated from the nodules of the trap species cowpea, which was inoculated with samples from soils under agroforestry systems from the western Amazon.

Sixty non-nodulating strains indicated a high frequency of endophytic strains in the nodules. The 88 authenticated strains had varying symbiotic efficiency. The SPAD (Soil Plant Analysis Development) index (indirect measurement of chlorophyll content) was more efficient at evaluating the contribution of symbiotic N_2-fixation than shoot dry matter under axenic conditions. Cowpea nodulating bacteria exhibited a high level of genetic diversity, with 68 genotypes identified by BOX-PCR. Sequencing of the 16S rRNA gene showed a predominance of the genus *Bradyrhizobium*, which accounted for 70 % of all strains sequenced. Other genera identified were *Rhizobium, Ochrobactrum, Paenibacillus, Bosea, Bacillus, Enterobacter*, and *Stenotrophomonas*.

These results support the promiscuity of cowpea and demonstrate the high genetic and symbiotic diversity of rhizobia in soils under agroforestry systems, with some strains exhibiting potential for use as inoculants. The predominance of *Bradyrhizobium* in land uses with different plant communities and soil characteristics reflects the adaptation of this genus to the Amazon region.

Acknowledgements: FAPEMIG, CAPES, CNPq, and GEF/UNEP-GF2715-02 (CSM-BGBD).

Keywords: Legume-nodulating bacteria, Biodiversity, Symbiotic promiscuity, Chlorophyll content

[P2.167]

How is the olive grove management influencing soil sprintail communities?

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Olive grove is an important land-use type in the Mediterranean region, with significant socio-cultural, economic roles shaping the landscape of the areas where it is implemented. During the last years, high market pressures have led to the intensification of management practices such as the application of pesticides and soil tillage, causing degradation of natural resources and loss of biodiversity in these agro-ecosystems. Growing evidence has emphasized the crucial role of biodiversity on the provisioning of ecosystem services. In this study, the impact of land-use management and landscape features on the structure and composition of the springtails' community in olive groves was assessed. Nine olive groves were selected with different land-use management types. 16 samples were taken from each olive grove, 8 in the tree rows and 8 in between-rows. Springtails were counted, identified and different biodiversity and functional descriptors were calculated. Although rarely significant, the row of olive trees positively influenced richness and functional descriptors, possibly as a consequence of greater shading or decreased machinery pressure when compared to between-rows. Herbicide application and superficial cut on weeds showed no effects on the springtail community. Soil tillage inside exerted a strong negative impact on diversity and functional descriptors. Yet, from all the management variables, only grazing was responsible for significant differences between olive groves, while from soil parameters, the water holding capacity was the main driver for olive groves' differences, presenting a significant relation with springtail abundance. The partition of variance analysis assigns soil properties with the most explanatory power, followed by management type and landscape features. This data suggests that the traditional classification of olive groves between integrated production or organic farming are not the main drivers of springtail species or functional diversity.

Keywords: agriculture, land-use type, collembola, functional traits

[P2.168]

The circumpolar biodiversity monitoring program - Terrestrial plan

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The Circumpolar Biodiversity Monitoring Program, CBMP, Terrestrial Plan, www.caff.is/terrestrial, is a framework to focus and coordinate monitoring of terrestrial biodiversity across the Arctic. The goal of the plan is to improve the collective ability of Arctic traditional knowledge (TK) holders, northern communities, and scientists to detect, understand and report on long-term change in Arctic terrestrial ecosystems and biodiversity. This presentation will outline the key management questions the plan aims to address and the proposed nested, multi-scaled approach linking targeted, research based monitoring with survey-based monitoring and remotely sensed data.

The CBMP Terrestrial Plan intends to build upon and expand existing monitoring networks, engaging participants across a range of capacity and interests. The presentation will summarize the recommended focal soil ecosystem components and attributes to monitor in the plan related to soil invertebrates.

Focal Ecosystem Components (FECs) of the soil decomposer system include the soil living invertebrates such as microarthropods, enchytraeids and earthworms and the functions performed by microorganisms such as nitrification, decomposition, and humification (moisture and nutrient retention). As monitoring capacity is limited, we suggest requiring the monitoring of the mesofauna with collembolans at the species level, as this group hitherto is the most feasible concerning availability of expertise and equipment. DNA metabarcoding in conjunction with taxonomic studies are under development to become an invaluable tool in future monitoring efforts, and sample archives may be useful to provide baselines of soil ecosystem conditions.

Keywords: Arctic, Climate change, Monitoring, Soil biodiversity and ecosystem services

[P2.169]

Symbiotic efficiency and identification of rhizobia that nodulate cowpea in a rhodic eutrudox

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Cowpea (*Vigna unguiculata* (L.) Walp.) is one of the most important crops in the north and northeast regions of Brazil, where it is grown under the subsistence regime, mainly because of its adaptation to the local edaphoclimatic conditions. This species is an important legume in Brazil because of its significant nutritional value in the diet of lowincome populations. Moreover, it is able to benefit from the process of biological nitrogen fixation, which leads to a significant reduction in production costs.

The objective of this research was to evaluate the agronomic efficiency of bacterial strains approved by the Ministry of Agriculture, Livestock and Supply for commercial inoculant production when in symbiosis with cowpea in a Rhodic Eutrudox in Lavras, MG, as well as to identify and verify the efficiency of the native populations that nodulate cowpea.

Agronomic efficiency of nitrogen-fixing nodulating bacterial strains (UFLA 03-84, INPA 03-11B, and BR 3267) in symbiosis with cowpea was evaluated in the field. Subsequently, the efficiency and diversity of isolates from the nodules obtained in the field were evaluated under greenhouse conditions. The genetic diversity of the efficient isolates was determined by partial sequencing of the 16S rRNA gene.

Grain yields obtained by the inoculation of seeds in the field with the strains were similar to those of the controls without inoculation with and without mineral N addition indicating the existence of efficient native populations. In the native community, we identified isolates with similar or higher efficiency than the strains approved for cowpea inoculation and the control that received mineral N. The isolates subjected to partial sequencing of the 16S rRNA gene were phylogenetically related to the *Bradyrhizobium* genus.

Acknowledgments: FAPEMIG, CAPES and CNPq.

Keywords: Biological nitrogen fixation, Symbiosis, 16S rRNA, Vigna unguiculata

[P2.170]

Nitrification inhibitor effects on community structure and functional microbial communities in grassland soils

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Introduction:

Mitigation measures to reduce diffuse nitrogen (N) losses from agricultural soils are increasingly being sought. Nitrification inhibitors, which inhibit the conversion of ammonium to nitrate, are one such measure being considered. Nitrate is easily lost to water and can be reduced by microbial communities to gaseous forms, including the greenhouse gas nitrous oxide (N_2O). This study aimed to determine the impact of the nitrification inhibitor dicyandiamide (DCD) on microbial community structure and functional microbial communities involved in N cycling in grassland soils.

Methods:

Microcosms containing three contrasting grassland soils were incubated at 15°C for a 20 day period. Soils were amended with cattle slurry either with or without DCD treatment and ^{15}N isotopic labelling was employed to determine gross transformation rates. The community structure of the soil microbial community was determined by phospholipid fatty acid (PLFA) analysis while the abundance of ammonia oxidisers and denitrifiers were determined by qPCR.

Results:

DCD treatment significantly inhibited gross autotrophic nitrification by 79–90% across the soils. This was associated with significantly lower ammonia-oxidizing bacterial (AOB) populations. No effect was observed on ammonia oxidizing archaea (AOA). PLFA profiles indicated that community structure varied temporally but was not affected by DCD. Nitrite reductase populations NirK decreased with DCD while NirS, and nitrous oxide reductase (NosZ) populations were unaffected. N_2 fluxes and fluxes of N_2O from the nitrifying pool were both reduced by DCD treatment, which indicated effects of DCD on both nitrifier denitrification and coupled nitrification-denitrification. DCD significantly increased total gross mineralisation and immobilisation.

Discussion:

DCD proved to be an effective inhibitor of nitrification, with a resulting decrease in N_2O emissions from soil. It acted on AOB populations but not AOA. Community phenotype and denitrifiers were mostly unaffected by DCD. However, NirK populations were decreased and there were non-target effects on mineralisation and immobilisation.

Keywords: Ammonia oxidisers, Denitrifiers, Nitrogen, Community structure

[P2.171]

Disentangling relationships between soil organisms and soil processes under different land-use intensity systems and climate change scenarios

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The relation between soil biodiversity and ecosystem functioning is one of the Holy Grail's of Soil Ecology. The pathway "biodiversity–biological processes–ecosystem services" is well established for several organism groups, i.e., the importance of these groups in soil functioning is known. However, the level of biodiversity (structural, functional) needed for the system to function and to provide an ecosystem service (ES) at a desired rate (service providing units - SPUs) is still unknown. Furthermore, drivers like climate change and management have an influence on biodiversity and consequently on ecological processes and ES provision. Therefore is important not only to unveil the SPUs for several ES, but also to disentangle the effects of such drivers on biodiversity and ES provision. In this contribution a novel approach to tackle these aspects is presented, including manipulative experiments performed in two climatic zones (Mediterranean and Sub-tropical) and comparing two land-management systems (sustainable vs. conventional) at each zone. Mesocosm experiments are being conducted to improve knowledge regarding C and N cycles, emphasising key traits involved in resistance and resilience mechanisms under the influence of extreme climatic events (extreme rain and drought). Effects on soil fauna, soil microbial processes and community composition are being assessed. On a second phase, manipulations of soil fauna and arbuscular mycorrhizal fungi communities, aiming to create treatments with different functional dissimilarity levels, will be set up and similar parameters will be measured. It is expected to find higher structural and functional dissimilarities in the sustainably managed systems, enhancing traits of higher resistance and/or resilience against climate change. Additionally, it will be possible to understand the interactions between soil fauna and soil microorganisms in mediating soil processes related to C and N and to gain knowledge on which theoretical frameworks, mass ratio and niche overlap theories, could better explain these processes.

Keywords: Ecosystem services, Functional dissimilarity, Climate change, Trait based approaches

[P2.172]

Soil community composition shifts after an artificial heat wave in a natural system

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Extreme climatic events are increasing in frequency, duration and amplitude. As some species within ecological communities can be more sensitive to these extremes than others, it is uncertain how this will affect the outcome of species interactions. A mismatch in sensitivity can potentially disrupt the structure of soil food webs and communities. In this study we focus on the impact of heat waves on soil fauna. In a field study, we exposed soil fauna communities to artificial heat waves and we aim to answer three pressing questions: A) Does soil food web structure change after exposure to a heat wave? B) If structural changes occur, can we predict the direction of change in food web structure by measuring heat tolerance traits of the component species? C) Do individuals of these species show phenotypic plasticity in order to cope with the new situation?

This experiment was performed in the green beach ecosystem on the Dutch barrier island of Schiermonnikoog. Paired heated and control plots of 70x70cm were sampled at the end of a 5 day artificial heat wave. Our data suggests that exposure to heat waves results in: A) Shifts in the soil food web structure. Moreover, B) The upper thermal tolerance trait shows high inter-specific variation, suggesting that this trait is suitable to predict future changes in community structure. Whether this inter-specific variation is the main explaining factor of the observed shifts will be clear after additional analysis. And C) Plastic responses of soil organisms to exposure to heat waves appears to be limited, and is only observed in a subset of the species investigated.

In general we can conclude that extreme climatic events can induce shifts in soil food web structure, but that we can predict the direction of these shifts by measuring relevant traits.

Keywords: Extreme events, Heat wave, Soil food web, Traits

[P2.173]

Short term changes of soil biochemical parameters under organic and mineral soil fertilization in a potato field

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Soil fertilization is an agricultural practice that influences both crop production and soil quality. Effects of added mineral and organic fertilizers on soil biochemical parameters need to be assessed in order to choose the more sustainable agricultural practices.

The aim of our study was to assess the short term effects of organic (cattle manure) and mineral (complex $N_{15}P_{15}K_{15}$) fertilizers on microbial biomass, soil respiration, dehydrogenase activity, phosphatase activity and protease activity in a Chernosem soil seeded with potato.

A field experiment with three different treatments in three replicates was conducted during potato growing season. The treatments comprised 1) cattle manure fertilized soil with 100 kg N/ha; 2) mineral fertilized soil with 100 kg N/ha as complex $N_{15}P_{15}K_{15}$; 3) no fertilization as control. The experiment was conducted in a Chernosem soil with a pH 8.03, Corg value of 3.86%, Nt value of 0.32% and the C:N ratio of 12.

During potato growing season microbial biomass (SIR method), soil respiration (infrared analyzer CIRAS 2-PP System, USA), dehydrogenase activity (reduction of TTC to formazan), phosphatase activity (disodium phenylphosphate method) and protease activity (ninhydrin method) were measured monthly together with soil chemical parameters (pH, C_{org}, N_t, N-NH_4, N-NO_3, PO_4, K).

A seasonal dynamics of soil biochemical parameters was observed in our experiment. Phosphatase activity, soil respiration and soil nitrate content showed the highest values at the end of experiment, while potential dehydrogenase activity and protease activity were higher in spring than in autumn. Generally, soil biological parameters were higher in manure fertilized soil than in mineral fertilized soil and control. PO_4^+ and K^+ showed higher values in mineral fertilized treatments than in manure and control treatments.

According with our results, changes in seasonal condition (temperature, precipitations, vegetation) exert a greater influence on biological activity than type of fertilizers used. However, the use of organic fertilizer has been shown to be more beneficial to soil biotic activity compared with the use of mineral fertilizers.

Keywords: soil biochemical parameters, organic, mineral, fertilization

[P2.174]

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

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Here, microbial soil community structure, composition and functions were analyzed in two Brazilian sugarcane fields. The sugarcane fields, located in state of São Paulo, differed by mechanical harvesting of green sugarcane and trash retention as a surface 'blanket' (mechanized harvest – Site 1) and pre-harvest burning (conventional sugarcane harvest – Site 2). The Site 1 was under unburnt sugarcane cultivation for five years. This study used T-RFLP (*Terminal Restriction Fragment Length Polymorphism*) fingerprinting to reveal the soil bacterial community structure based on 16S rRNA gene, and shotgun metagenome sequencing to investigate the composition and potential functions of the microbial community in bulk soil from field and physical-chemical soil factors. The T-RFLP results pointed out for harvest management effects on bacterial community structure in bulk soil samples. Taxonomic analysis of the bacterial community based on shotgun metagenomic sequences confirmed the differences revealed by T-RFLP, and revealed Proteobacteria (37%), Actinobacteria (30%) and Firmicutes (7%) as the most abundant phyla present in bulk soil samples. Differences in relative abundance were revealed at class taxonomic level for Actinobacteria and Alphaproteobacteria when bulk soil samples from two sugarcane fields were compared. The bacterial classes Solibacteres, Planctomycetia and Chloroflexi showed differential abundance when bulk soil samples from both sugarcane harvest managements were compared. Functional analysis of metagenomic sequences showed that SEED subsystems (level 1) such as, 'sulfur metabolism', 'secondary metabolism' and 'membrane transport' were more related to unburnt sugarcane soils. In contrast, 'DNA metabolism' and 'cell division and cell cycle' was more related to pre-harvesting burning soils. The SEED subsystems (level 3) 'nitrate and nitrite ammonification', 'denitrification' and 'nitric oxide synthase' were more related to pre-harvesting burning soils. These results showed a clear effect of sugarcane harvest managements on the structure, composition and potential functions of the soil bacterial community in bulk soil from sugarcane fields. FAPESP, CNPq

Keywords: Shotgun metagenome, Harvesting sugarcane management, Soil microbial community

[P2.175]

Spatial patterns of soil bacterial communities at the European scale

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Here, soil bacterial diversity was studied at the European scale, under various environmental conditions (soil physico-chemical properties, climate, land use) in order to: (1) characterize the spatial distribution of this diversity and (2) identify and rank the environmental factors structuring bacterial diversity in European soils. Thus, 81 sites were selected along a transect spread across 11 European countries. Sites were selected on the basis of soil, climate and land use maps (Joint Research Council, LUCAS - land cover survey). For each site, one composite soil sample (5 soil cores) was taken, except for 17 sites in which a pseudo-triplicate sampling strategy was applied. A total of 115 soil samples was characterized regarding their physico-chemical and microbial properties. After microbial DNA extraction, pyrosequencing of 16S rRNA genes was performed to investigate soil bacterial richness, evenness, diversity (H') and community structure.

Along this European transect, a significant turnover of soil microbial community composition was observed, highlighting that they are distributed following non-random spatial patterns. Bacterial richness ranged from 653 to 1931 OTUs (95% similarity level), evenness ranged from 0.6 to 0.8, and H' from 4.0 to 6.2. A variance partitioning approach demonstrated that bacterial richness was mainly determined by soil texture and pH, whereas bacterial evenness and H' were first driven by land use and secondly by soil texture and pH. Land use, total C, pH and texture equivalently affected soil bacterial community structure. For soil bacterial richness, evenness, diversity and community structure, climatic factors were never significant, while remaining spatial autocorrelation was found. Soil bacterial community structure was also influenced by latitude. Altogether, this study helped to estimate the range of variation for bacterial richness, evenness and diversity; identify their distribution patterns and understand the environmental factors driving bacterial communities at the European scale.

Keywords: European scale, Soil bacterial communities, biogeography

[P2.176]

Abundance of methanogenic archaea in montane and subalpine forests and grasslands: effects of abiotic soil properties

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Methanogenic archaea are important key players within the global methane cycle and were long times thought to be restricted to anoxic environments only. Recent research, however, demonstrated that even well-aerated upland soils are inhabited by methanogens and possess the potential to produce CH_4. Nevertheless, there is still a lack of knowledge regarding the environmental factors regulating abundance of methanogens in these soils.

Therefore, 16 forest and 14 grassland soils located at the montane and subalpine belts of the Northern Limestone Alps as well as the Central European Alps were studied with respect to abundance of archaea and the methanogenic orders *Methanosarcinales* (MSL), *Methanococcales* (MCC) and *Methanobacteriales* (MBT) by using quantitative real-time PCR targeting 16S rRNA genes. Abundances of archaea, MSL and MBT were detected to be significantly higher in grassland soils compared to forests. Contrarily, sequences belonging to MCC were more abundant in forests and in soils which developed from calcareous parent materials. Multiple linear regression analysis identified soil pH as an important positive environmental predictor of methanogenic abundance, especially in forest soils, since it explained 76.2, 18.5, and 39.0% of the observed variation in MSL, MCC, and MBT gene copy numbers. In grasslands, pH only affected the abundance of MSL. Additionally, increasing soil dry matter led to a reduction of MBT in grasslands and of MSL in both grasslands and forests, whereas MCC were not influenced. This study provides evidence that methanogenic microorganisms belonging to other orders than *Methanosarcinales* and *Methanocellales* are also frequently present within well-aerated soils. Moreover, it was possible to gain insights into abiotic soil properties determining the presence of these anaerobic microorganisms in non-wetland ecosystems.

Keywords: methanogenic archaea, upland soil, qPCR

[P2.177]

Structure, composition and nitrogen-related functions microbial community in sugarcane rhizosphere

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The study aims at examining relationships between microbial community structure, composition and nitrogen-related functions in two Brazilian sugarcane rhizosphere from greenhouse mesocosm experiment. The sugarcane fields, located in state of São Paulo, differed by mechanical harvesting of green sugarcane and trash retention as a surface 'blanket' (mechanized harvest – Site 1) and pre-harvest burning (conventional sugarcane harvest – Site 2). The Site 1 was under unburnt sugarcane cultivation for twelve years. The experiment was conducted under controlled soil moisture for one hundred and eighty days. The upper part of all the pots was covered with sugarcane straw. Bacterial community structures were assessed by T-RFLP (*Terminal Restriction Fragment Length Polymorphism*). Shotgun metagenome sequencing investigated the composition and potential functions of the microbial community and both molecular techniques were for the bulk and rhizosphere samples. T-RFLP pointed out differences between harvest managements on bacterial community structure leading us to further investigation by soil metagenome correlation analysis and physical-chemical soil factors. Taxonomic analysis of the bacterial community based on shotgun metagenomic sequences confirmed the T-RFLP patterns, and revealed Proteobacteria (38%), Actinobacteria (30%) and Firmicutes (5%) as the most abundant phyla present in sugarcane rhizosphere samples. Differences in relative abundance were revealed at class taxonomic level for Gammaproteobacteria and Bacteroidiae when sugarcane rhizosphere samples from sites 1 and 2 were compared. Functional analysis of metagenomic sequences showed that SEED subsystems (Level 1) 'nitrogen metabolism' was more related to unburnt sugarcane rhizosphere samples. The SEED subsystems (Level 3) 'nitric oxide synthase' were more related to pre-harvesting burning sugarcane rhizosphere samples. Nitric oxide has also been implicated in plant responses to abiotic stress. The findings will help to understand better the effect of sugarcane harvest managements on the structure, composition and potential functions on the bacterial community inhabiting sugarcane rhizosphere. FAPESP, CNPq

Keywords: Harvesting sugarcane management, Shotgun metagenome, Rhizosphere

[P2.178]

Plant diversity and species composition effects on soil microbial diversity and communities in the rooting zone and below

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The effect of plant species diversity on soil microbial community composition has been studied extensively for both natural and managed vegetation due to the relevance of soil microorganisms for several essential ecosystem functions. However, most of these investigations focused on the upper 10 cm of soil, while it remains unclear how deep plant diversity effects reach in soils. We took advantage of the Jena Experiment, a long-term grassland biodiversity experiment, to compare microbial biomass, respiration, and community composition from distinct soil depth levels down to 1 m between plots planted with mixtures of 9 plant species and plots with monocultures of each of these plant species. We hypothesized that (i) soil microbial diversity and abundance differ between monocultures and the multispecies plots, and (ii) the effect of plant species composition decreases with increasing soil depth, leading to more uniform microbial community composition at the lowest depth level. PLFA analysis revealed a significant increase in bacterial and fungal biomass with higher plant diversity while soil microbial biomass and the fungal-to-bacterial ratio decreased significantly with soil depth. 454 pyrosequencing targeting bacterial 16S rRNA genes showed that microbial communities were dominated by Actinobacteria, Alphaproteobacteria, and Acidobacteria with the fractions of each group varying strongly with plant species composition and soil depth. Cluster analysis showed a clear distinction of microbial communities between upper and deeper soil layers across all plots. We found a clear influence of plant diversity on the diversity and abundance of soil microbes in soils at 1 m depth, suggesting that plant diversity may also affect soil microbial processes in deeper soil layers.

Keywords: Jena Experiment, microbial diversity, next generation sequencing

[P2.179]

AgrInnov : a national participative project with farmers to transfer an operational set of biological indicators to soil users

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This project aims at validating soil biological and agronomical indicators, as well as the transfer and training procedure to initiate an agricultural innovation network, and to monitor the impact of agricultural practices on soil biological life. The strategy used was based on selecting existing bioindicators, easily operational to be applied to a network of farming systems, in order to evaluate the environmental and agronomical impacts of agricultural practices. These bioindicators target three large groups of soil organisms, namely the earthworms, the nematodes, and the microbial communities. At the same time, agronomical indicators based on physico-chemical parameters, soil structure and organic matter decomposition were also used to better interpret the bioindicators. More than 230 private farms form the network (with an equal proportion of grapevine and arable farms), which therefore integrates a great variability of pedoclimatic and agricultural situations at the scale of the French territory. After a training on soil biology, soil observations and sampling, all these farmers sampled soil for laboratory measurements and characterized their soil structure and earthworms density.

This project enables to test the feasibility of monitoring soil bioindicators for farmers, their operability and their utility for end-users. One of the main deliverable of the project was to elaborate a handbook which could allow the farmers to understand the impact of their agricultural practices on the soil biological life, and therefore to evaluate the sustainability of their production system by mobilizing laboratory and field indicators. From this project, a new sector of analyses and agronomic advice based on biological indicators is raising, following the need expressed by farmers.

Keywords: soil biodiversity, sustainable agriculture, bioindicators

[P2.180]

Soil microbial communities reflects dominant plant biogeography and post-glacial re-colonisation history

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Plant species and plant-cover shape the soil microbial landscape at local and regional scales through biotic and saprophytic interactions. To assess the large-scale influence of dominant plant, we studied the microbial communities associated to the keystone grassland plants *Carex curvula, Carex rosae* and *Nardus stricta* in the Carpathians and in the Alps. We hypothesize that a large-scale soil microbial communities associated to a given dominant plant are more similar to each other than to those from other plant. Furthermore, the foundation plant *C. curvula* should keep a microbial "signature" of the biogeographical story. MiSeq Ilumina sequencing of ITS1 and V3-V4 region of 16SRNA gene were used to assess the composition of fungal and bacterial communities respectively. Using multivariate analysis of the variance, plant species was the major factor accounting for 15 (Bacteria) and 12% (Fungi) of the variance. *C. curvula* soil communities exhibited a beta diversity pattern with a tiny global core-community but consistent and specific ones for each Carpathians, East Alps and West Alps respectively (Fig. 1). This pattern overlaps with the post-glacial *C. curvula* colonisation story. *N. stricta* microbial communities did not exhibit such a pattern and the core microbial communities were homogeneous (Fig. 1), likely reflecting the influence of human activity. The composition of core-communities is specific for each plant; but *C. curvula* seems to select a cohort of microbes through biotic interactions (antibiosis/exclusion, pathogenesis, endophytism), rather than through saprophytic interactions.

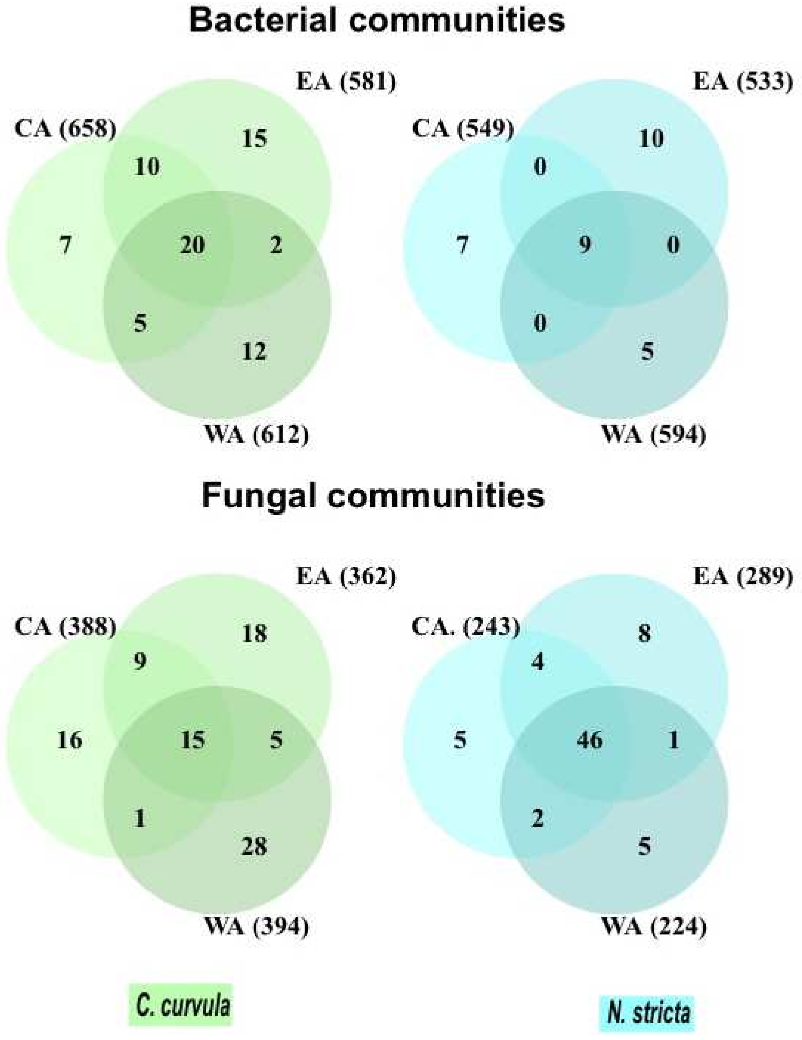

Figure 1. Microbial core communities of *C. curvula* and *N. stricta*. The specific MOTUs were found using the Chi^2 test with resampling for *P*-value <0.001. The number of MOTUs (between brackets for each massif) was calculated using *specpool*. CA, EA and WA for Carpathians, East and West Alps respectively.

Keywords: alpine tundra, foundation species, biotrophes, land use

[P2.181]

Microbial communities associated to rubber tree plantations along a chronosequence in North East Thailand

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Rubber tree (*Hevea brasiliensis*) is a crop of major socio-economic importance in Southern Asia as it represents a substantial source of income for small land holders. In Thailand (1/3 of world latex production) rubber tree plantations are currently greatly expanding in adverse eco-climatic zones, especially in Isan provinces, where soils have sandy texture, low fertility and are prone to erosion and leaching of applied fertilizers. A major potential for increased production in these conditions relies on the important roles of rhizosphere microbial communities in supporting soil fertility and plant nutrition. A chronosequence of 3, 6 and 16 year-old plantations was identified and cassava fields were used as no-rubber controls for comparison. Soils from each treatment were characterized for texture and chemistry. Using 454 sequencing, total bacterial and fungal communities as well as arbuscular mycorrhizal fungi (AMF) community were analyzed. Because they are known to contribute to plant P and N nutrition by increasing mineral nutrient availability or by enhancing plant nutrient uptake, root-interacting P-solubilizing bacteria (PSB) and free living N fixing bacteria were assessed after culturing on selective media. Nematodes populations were characterized as there are good soil fertility indicators. Functional traits were also analyzed by both qPCR and Ecoplates (Biolog) methods. Results showed significant differences between rubber and cassava associated communities but didn't reveal a strong impact of the age of the plantations on the different communities. For instance, the AMF community in cassava roots was twice as rich as in rubber tree samples but was not affected by the age of rubber trees. The improved understanding of the diversity of root-associated microbes will contribute to the development of alternative sustainable practices to improve and sustain soil fertility.

Keywords: Rubber tree, Microbial communities, Chronosequence, Northeast Thailand

[P2.182]

Root exudates can control soil N dynamics

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Agriculture represents both a dominant and recalcitrant source of the potent greenhouse gas nitrous oxide and a source of pollution through leaching of nitrate and other nutrient. This is largely due to the conversion of added nitrogen based fertiliser through the action of the microbial nitrogen cycle in soil. Denitrification represents a dominant source of nitrous oxide (N_2O) and is carbon driven, as it maintains respiration under low oxygen conditions with nitrogen oxides acting as alternative electron acceptors. Nitrification is also a source of N_2O, under more aerobic conditions, but primarily converts ammonium to nitrate resulting in potential loss of N through leaching and denitrification. Screens of barley (*Hordeum vulgare*) cultivars indicated that different cultivars support significant variation in N_2O emission from denitrification and/or inhibited nitrification from associated soil. Further experimentation using a limited range of contrasting cultivars has demonstrated that these effects are connected to root exudation difference rather than direct interaction or litter effects and may be mediated through manipulation of soil microbial community dynamics. Soil condition, through differential aerobic status and variability, also has a marked effect both on flux through denitrification and community dynamics. Further work is underway to dissect the role of exudation quality and composition, the interaction between soil aerobic status and flux through denitrification and the role soil community dynamics plays in driving alteration in nitrogen cycle flux and the end product of denitrification.

Keywords: root exudate, denitrification, nitrification, community dynamics

[P2.183]

High-throughput molecular mapping of biodiversity in tropical forest soils

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A major hurdle in predicting how biological diversity will respond to environmental changes is the difficulty to compile large, standardized species inventories that besides include crucial actors of ecosystem functioning (e.g. microbes or arthropods). This particularly holds true for tropical forests, where an enormous, yet largely unexplored soil diversity ensures extravagant nutrient cycles.

Taking advantages of next generation sequencing and DNA metabarcoding, we attempted to bridge this gap by compiling an extensive inventory of the whole soil biota in a tropical rainforest. To this end, we used a set of universal primers pairs targeting each Archaea, Bacteria, Eukarya, Plants, Fungi and Termites. The sampling was conducted at the Nouragues Biological Station (French Guiana). 361 soil samples were collected (top 10 cm) in a 1 ha-plot, with a grid step of 5 m. Extracellular DNA was extracted on the field, and then amplified and sequenced with the Illumina technology. Taxa-area relationships were obtained for each marker, and high-resolution maps of distribution were drawn for each molecular operational taxonomic unit (MOTU).

Plant MOTUs corresponded to 50-90% of the tree taxa occurring at the sampling site and their spatial distribution tightly corresponded to field observations. They also comprised lianas and understory plants that are usually not included in botanical inventories. Considering Archaea, Bacteria and Eukarya markers, the plot contained ca 11,000 MOTUs that mainly corresponded to α-, γ-, δ-proteobacteria and actinobacteria, as well as annelids, fungi and arthropods. Taxa-area relationships did not saturate at the plot-scale, and were the steepest for Archaea, Annelida and Plants.

This DNA-based cross-taxa inventory offers a rapid, cost-effective, and reliable method of biodiversity monitoring in the tropics. It further provides a global overview on the spatial distribution and co-occurrence of soil organisms, hence opening new research avenues for understanding diversity patterns and ecosystem functioning in a multi-trophic perspective.

Keywords: DNA metabarcoding, next-generation sequencing, multi-taxonomic diversity, tropical rainforest

[P2.184]

Ecofinders expert-systems: web-based platform for the identification of soil fauna

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In the last years, there has been an increased attention towards soil biodiversity. Several initiatives have been implemented and have increased the interest of different sectors of the population for the importance of soil biodiversity as key players in soil processes. Therefore, a higher awareness has been spent by the general public to simply recognize and/or to identify these organisms at different taxonomic levels. Soil invertebrates are an appealing group of soil organisms and also a good tool to be used on educational projects on biodiversity, targeting especially young students. This triggers the need for attractive and user-friendly tools to recognize and/or identify these organisms. Web-based platforms play a key role among them.

Aiming to fill this need, an interactive web-based platform allowing the identification of soil fauna organisms by a wide range of target audiences, according to their needs in terms of identification level, has been developed under the ECOFINDERS project. In this first stage, the platform allocates an interactive decision key with information to identify the most common soil macrofauna and mesofauna groups at Order level. At a more detailed taxonomic level, Collembola and Earthworms were used as examples to show the practicability of the platform. One appealing feature of this platform is the fact that it can be updated online by selected experts. It has been developed in two languages – English and Portuguese – but has the potential to add other languages. In sum, this platform allows the integration of the different groups of soil invertebrates in one single platform, thus facilitating the identification process of soil samples.

Keywords: Soil biodiversity, Interactive decision key, Educational tool, ECOFINDERS project

[P2.185]

Ectomycorrhizal and soil fungal biogeography: ecological patterns in European beech forests across energy gradients

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The relationship between energy gradients and community richness has been well documented in community ecology for numerous groups of organisms. However, little information exists concerning the impact of these thermic gradients on the fungal communities, a functional key component of forests. The aims of the two following studies were (i) to determine whether the diversity and composition of soil fungal assemblages vary with geographic energy gradients (ii) to investigate explanatory variables of this fungal diversity. High-throughput sequencing of the ITS-1 region was used to explore fungal assemblages, and particularly the ectomycorrhizal fungi, along three elevation gradients, located in France, and along a latitudinal gradient in Europe. Only beech forests were selected to minimise the host effect. In the elevation gradient study, our results showed that no clear relationship exists between fungal richness and elevation (from 180 to 1533 m). Nevertheless, the Ascomycota species richness peaked at mid-elevation, with richness declining both at higher and lower elevations, illustrating a mid-domain effect model. Interestingly, we did not find relationship between richness and temperature along the latitudinal gradient. However, the fungal richness was positively correlated with pH. Finally, in both studies, the composition of root-associated fungal assemblage was largely explained by soil pH and by temperature. Future studies that integrate geographical gradient approaches with experimental manipulations will provide powerful information that can improve models of climate change impacts in forest ecosystems.

Keywords: Energy gradient, Ectomycorrhizal fungi, Beech forest, High-throughput sequencing

[P2.186]

Good Taxonomic Practice for soil biodiversity research projects

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Knowledge and conservation of soil biodiversity is a growing concern in the Euroean Community, and several large-scale EU projects have addressed this issue in recent years. Part of the research activities result in species abundance lists, which are used to answer diverse questions such as the use of soil biota as indicators for soil quality or the influence of management practices on soil biodiversity. Apart from project-related questions, species lists also provide faunistic baseline data for the occurrence and distribution of species, thus contributing substantially to general biodiversity knowledge.

To assure the correct identification of specimens, taxonomic knowledge is required. Furthermore, a reference collection of specimens is necessary to allow the validation of species determinations. There is surprisingly little concern about the quality of species identification data in EU-funded and other ecological projects, and taxonomic expertise is often taken for granted.

We propose a number of criteria for Good Taxonomic Practice (GTP) that should be considered by funding bodies and project applicants as well. These include, among the citations of identification works and character lists to identify the species, the assignment of funds and working hours to (1) taxonomic expertise for identification, (2) formal descriptions of species (to avoid the inflation of "morpho-species"), (3) the establishment of well-labelled reference collections and their deposition in public and curated institutions such as Natural History museums, and (4) the preparation of voucher collections for the molecular characterization (DNA-barcoding) of selected specimens. GTP-rules will use as a template the well-known GLP-rules (Good Laboratory Practice), documenting all steps relevant for the handling, identification, storage and description of soil organisms. Technical guidelines will cover details of practical performance, which may differ considerably between organisms groups.

These measures will not only raise the quality of ecological data but also help a starving scientific discipline.

Keywords: taxonomy, standardization, data quality, validation

[P2.187]

Different approaches to analysis of functional gene pyrotags

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High-throughput amplicon sequencing of marker genes has become a standard technique for describing complex microbial diversity in environmental samples. The standard approach is to form operational taxonomic units (OTUs) as clusters of sequences defined by certain level of similarity. Such an approach is especially suitable for taxonomic marker genes analysis (e.g. 16S rRNA) where the emphasis is put not on actual sequence but rather on its taxonomic ranking. Clustering strategies efficiently mask intraspecies variability and also erroneous sequences derived from imprecisions of DNA polymerase or sequencing platform. On the other hand, when functional genes are studied an actual sequence is the item of interest. Insertions and deletions (indels) start to play a significant role as they cause frame shifts in protein sequences. 454 pyrosequencing is known to be prone to form indels while at the same time is it commonly utilized in ecological studies as it produces considerably long reads.

The aim of this work was to evaluate several bioinformatics tools designed for sequence correction of pyrotags – gene markers sequenced by 454 pyrosequencing – and their ability to reduce frame shifts. Genes encoding for alpha subunits of biphenyl and benzoate dioxygenases were used as model sequences. Results shows comparably low frame shifts numbers when data are treated by flowgram denoising or sequence quality trimming, followed by reference based frame shift correction tool FrameBot. To overcome reliance on references or extend the frame shifts reduction FrameBot was run in newly presented *de novo* mode.

Funding is acknowledged of the Czech Science Foundation project no. 14-32432S and Ministry of Education, Youth and Sports project no. LH14004 and specific university research MSMT No. 20/2014.

Keywords: pyrosequencing, functional genes, frame shifts

[P2.188]

Comparison of soil fauna community succession between different land uses in the south of Ecuador.

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We focus our research in the comparison of soil mesofauna between different land uses, having native forests as control, assuming that the mesofauna present in them is how it was before forests were cut down and changed into pasture land and secondary forests. In total 12 forest areas were chosen, 4 native ones as control, 4 alder and 4 pine forests. We collected soil samples from all studied forests to assess soil mesofauna, microbial activity and C/N ratio. We conducted a decomposition experiment using litter bags which were collected after 6 and 12 months, the colonizing soil mesofauna extracted and microbial activity and C/N ratio measured too.

We want to investigate if the abundance of decomposers and predators differ among vegetation types; how decomposition rates vary between forests and measure the quality of the organic matter (C/N ratio) to see differences among forests and time.

The preliminary results show that there are significant differences in the soil mesofauna among forests, having more abundance of oribatida, collembola, gamasida and prostigmata in alder forests. The decomposition rate was low, but it shows that alder litter decomposes faster than pine and the combination of both. We will seek for a correlation between litter and soil quality of all forests with the decomposition rate and soil mesofauna abundance (of functional groups like decomposers, predators, herbivores and omnivores).

Introduction

Global changes in land use and the resulting vegetation coverage have had an important effect on natural resources due to deterioration of soil and water quality, loss of biodiversity and changes in global climatic systems (Koning, G., 1998)

In Ecuador, primary forests remain unchanged according with the FAO (2006), and the Ecuador´s forest protection statistics shows 21% of primary forests as protected, therefore the deforestation occurs more in secondary forests. The reasons for the deforestation are the changes in land use, cutting of secondary forest areas for agricultural land and an increase of pasture land (Mosandl et al., 2008).

Soils perform several functions that support ecosystem services (food and water, biogeochemical and climatic cycles among some). These functions depend on belowground communities (Nielsen et al, 2010) which are responsible for decomposition of organic matter and nutrient mineralization (Birkhofer et al., 2012).

We studied the microbial activity (responsible for C and N cycling) and soil mesofauna among different land uses to assess community succession. The questions we wanted to assess are: (1) is the abundance of decomposers and predators different among vegetation types; (2) are the decomposition rates higher in native forests than in alder and pine forests, and (3) the quality of the organic matter (C/N ratio) differs among vegetation types and along time

Methods

We selected 12 forests areas: 4 native (control), 4 alder and 4 pine forests around the city of Loja, south of Ecuador. The alder and pine forests between 18 and 20 years old. We collected soil cores for soil mesofauna and microbial activity. The mesofauna was extracted using modified Kempson extractors (Kempson et al 1963) and the microbial activity was measured using using a O^2 microcompensation apparatus (Scheu 1992). We also collected alder and pine leaf material for a decomposition experiment using litter bags with 4 mm mesh size (to allow mesofauna colonization), we put 10 g of pine , alder and the combination of both in litter bags in all studied forests. The litter bags were collected after 6 and 12 months, the colonizing mesofauna was extracted and the ash free dry mass (AFDM) was measured to assess the decomposition rate. The C/N ratio from the soil cores for mesofauna extraction as well as the litter from the litter bags was analyzed to compare forest quality.

Results

(Preliminary results)

Soil mesofauna (base line).

We found a total of 27 genera in the 12 studied sites. The most abundant orders were oribatida, collembola, gamasida, uropodina y prostigmata; alder forests had more abundance of these orders, except for Uropodina that were more abundant in pine forests.

The colonizing mesofauna from the litter bags also showed a significant difference in forest type and litter bag type.

General linear models (GLM) showed that there is a significant difference between forest types (Table 1).

Decomposition experiment.

We collected litter from alder and pine forests and put them into litter bags and spread them around all 12 studied forests. We used the ash free dry mass to assess the litter decomposition and calculate the decomposition rate (*k*). It shows that alder litter decomposes faster than pine litter and the mixture of both (fig. 1). But in general, the decomposition rate was medium to low according with the classification of Graca 2005 [fast (k > 0,01), medium (k = 0,005) and slow (k < 0,005)].

Table 1. Multivariate test of significance of the soil mesofauna from the soil samples of all 12 studied forests and the colonizing mesofauna of the litter bags.

	Soil mesofauna		**Litter bags experiment**			
	Base line		**6 months**		**12 months**	
	F	***p***	**F**	***p***	**F**	***p***
Forest type	**2,58**	**0,0000**	**3,59**	**0,00000**	**3,47**	**0,0000**
Litter type			**2,24**	**0,00005**	**1,56**	**0,0167**

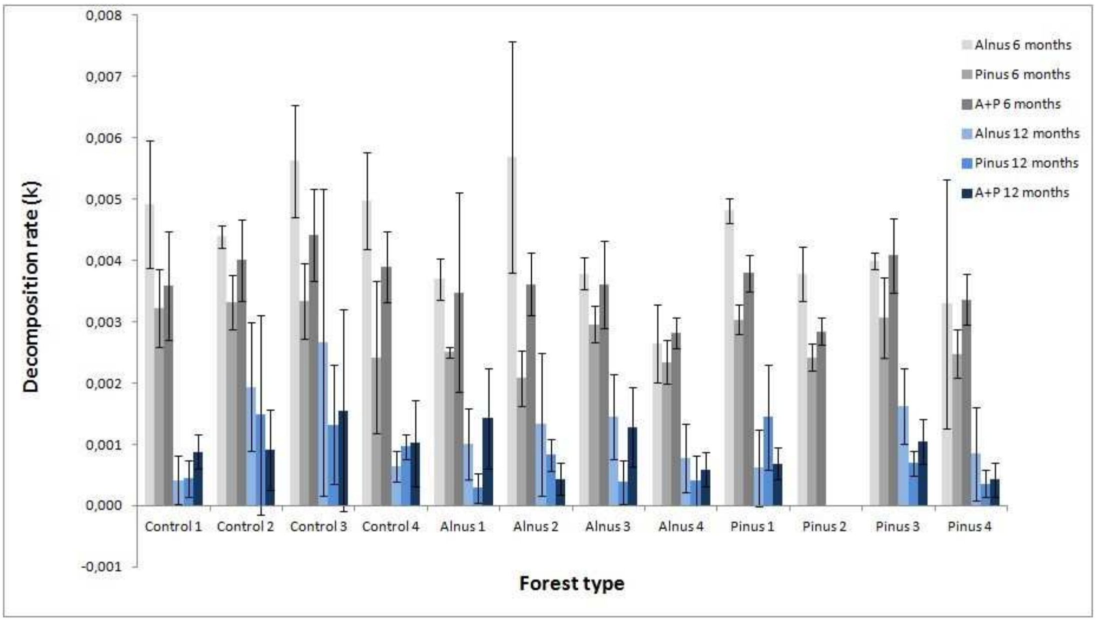

Figure 1.Decomposition rate of the litter bags in all 12 studied forests; note that forest Pinus 2 has just the dat from the first 6 months due to a fire which destroyed it and the data of the 12 months were lost.

Carbon and nitrogen ratio and microbial activity.

Those data are still in process of calculation and measurement, considering that they were collected recently, but they will be ready in time before the presentation for the symposium is finished.

Keywords: soil mesofauna, microbial activity, litter decomposition, C/N ratio

[P2.189]

Decomposition of fungal mycelium in podzol horizons of boreal forest-spatial distribution of bacterial and fungal communities

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Symbiotic ectomycorrhizal fungi form diverse communities in forest soils, allocating plant-derived carbon belowground to mobilise nutrients from organic polymers and mineral substrates. The distribution and activity of many species in vertically stratified forest soils is still poorly understood however. Cycling of nutrients in different organic substrates through decomposition is important to maintain growth and productivity. The extraradical mycelium of ectomycorrhizal fungi can be recycled by the ectomycorrhizal fungi themselves or decomposed by other fungi or bacteria, but the identity, activity and location of these organisms is still poorly characterized. Usually, only the composition of microorganism of the surface horizon has been studied because it is supposed to be the most active one.

In this study we have studied decomposition of ^{13}C-labelled mycelium in forest soil collected from the upper, organic (O), and lower, mineral (E & B) horizons of a *P. abies* forest at Jädraås in Sweden. Laboratory microcosms, with and without spruce seedlings, were used that allowed us to collect ^{13}C-labelled respiration products. 454 pyrosequencing and ^{13}C DNA- and RNA-based stable isotope probing (SIP) were used to characterize the bacterial and fungal communities and to distinguish the particular taxa that were active in decomposition of the mycelium and incorporating ^{13}C derived from the mycelium.

Our preliminary results suggest that: a) mycelium decomposition activity was highest during the first 7 days with some dynamic patterns of change in 'O', 'E' and 'B' horizon soil both with and without spruce seedlings, followed by clear decline in decomposition rate. b) Mg and Ca concentrations in seedlings grown in “E” horizon soil with added mycelium were higher than in control treatments without mycelium. These results suggest that decomposition of mycelial pools in the E horizon may supply base cations to forest trees.

Keywords: mycelium decomposition, forest podzol, microbial communities and activity, SIP analysis

[P2.190]

Developing a taxonomic scaffold to address questions of biodiversity, biogeography and phylogeography of a globally distributed suborder of plant-feeding nematodes.

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Addressing questions of nematode biogeography and biodiversity has been impaired by poor taxonomic resolution and ill-defined species boundaries. Biogeographic conclusions drawn from a perspective based solely on nematode morphology leads to the recognition of a multitude of cosmopolitan species. Furthermore it masks the biogeographic and phylogeographic patterns that exist among nematode communities. Using a combination of COI and 18s nucleotide sequence derived from individual nematodes we have constructed phylogenetic trees and visually display the trees as web pages that rapidly convey the link between morphology and phylogenetic relationships in the suborder Criconematina. This suborder was chosen because of its global distribution, abundance in native plant communities, lack of specialized dispersal stages, and an array of cuticular structures that allow convenient microscopic examination. To date over 3,000 specimens representing a majority of the described genera have been examined. It is apparent that cryptic species, as evidenced by genetically distinct lineages are common. Highly structured criconematid communities exist within native plant communities at the local and regional level. Cosmopolitanism is rare except in agricultural ecosystems. A significant proportion of criconematid biodiversity appears to be derived from ancient diversification, long predating Pleistocene glaciations. Haplotype diversity in former glaciated regions of North America is largely consistent with recolonization patterns exhibited by major tree species. Evidence supports the possibility that the Ozark Mountains and southern Appalachian Mountains served as refugia during the glacial period. Phylogeographic patterns south of these regions are complex and characterized by high levels of endemicity.

Keywords: Nematode taxonomy, distribution, historical biogeography, haplotype diversity

[P2.191]

Enchytraeid diversity across Europe (Oligochaeta, Annelida)

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A large-scale sampling program in the framework of the EcoFINDERS project aimed at describing and assessing the diversity of soil biodiversity across Europe. Among many parameters of diversity, abundance and function measured, Enchytraeidae (Oligochaeta, Annelida) as one of the key faunal groups were included as well. In three different sampling campaigns, more than 30.000 specimens of enchytraeids were extracted (using the standard ISO method) from 518 soil cores taken at 120 different sites in 11 countries of Europe, covering five bioregions (Boreal, Atlantic, Continental, Alpine, Mediterranean), three types of land use (forest, grassland, arable fields) and a wide range of soil pH, texture and carbon content. Specimens were identified to species *in vivo* and then fixed for morphological scrutiny or DNA barcoding.

About 170 species were registered, 79 of them previously undescribed. Most of the new species were found in previously unstudied regions of France, Sardinia, Slovenia or Portugal. Formal descriptions of the new species are underway and they include DNA barcodes. Diversity patterns have a regional component at the species but not at the genus level. Changes in enchytraeid communities (= species abundance patterns) correlate with changes of soil parameters such as pH and C:N ratios, and they are strikingly paralleled by changes in the microbial communities, which suggests predictable patterns of soil biodiversity across Europe based on soil properties and land use. Higher management intensity often reduced enchytraeid diversity, but the reverse was found as well. These effects were not always statistically significant.

Based on these experiences it is recommended to include the Enchytraeidae in monitoring programs aiming to evaluate biological soil quality (i.e. the habitat function of soil).

Keywords: enchytraeids, bioregions, new species

[P2.192]

Impact of agricultural extensification on the relation between soil biodiversity and ecosystem services (soil structure maintenance, water regulation)

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Introduction – There are increasing pressures on soil biodiversity and soil degradation remains a pertinent issue. In this context, one aim of the EcoFINDERS European project was to assess the impact of agricultural extensification, across a broad range of European land-use systems, on the relationships between soil biodiversity and ecosystem services. Special attention was given to the relation between i) soil biodiversity and aggregate stability, and ii) earthworms and soil macroporosity and water infiltration.

Method - Data from seven long-term field studies (France, Germany, United-Kingdom, Slovenia, Denmark) on replicated plots of different land management scenarios (grassland, arable cropping, mixed crop-grassland, reduced or conventional tillage) were analysed. Earthworms were sampled using hand sorting and chemical extraction. Aggregate stability was measured using wet sieving method. Macropore distribution (i.e. numbers and diameter of earthworm burrows) was quantified at different horizontal layers. Infiltration rates were measured as the saturated hydraulic conductivity.

Results – Data analysis demonstrated that earthworm community (species, ecological groups) was affected by land use and management practices. Aggregate stability in the top layer was significantly different among management treatments: higher under grassland than crop, and higher under reduced tillage than conventional tillage. Moreover, aggregate stability could significantly increase with earthworm biomass (anecic, endogeic). Burrow distribution was impacted by managements, likewise water infiltration capacity (permanent arable < mixed crop-grassland < permanent grassland; conventional < reduced or minimal tillage). Water infiltration capacity was related to functional diversity in earthworms, through the mediation of specific soil macropores by various species; pore systems and burrows that were connected to the soil surface contributed most efficiently to water infiltration rates.

Conclusion – These observations indicate that less intensive managements result in increasing earthworm functional biodiversity, providing better soil structure and water infiltration. These results provide more quantitative insights that allow for ecohydrological modelling (forecasting) and economic valuation.

Keywords: soil biodiversity, aggregate stability, macroporosity, infiltration

[P2.193]

Disentangling the fundamental underpinning of soil biological resilience

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The ability of soils to continue to function in the face of perturbation – their resilience – is key to safeguarding many of the ecosystem services which flow from them. However, the factors underpinning soil resilience (and indeed its definition) remain obscure and are complicated by the fact that soils are multi-functional. Many of these functions are inextricably linked to the soil microbial community and as such the reaction of this community is likely to have a strong influence on the resistance and resilience of soil functioning in general, and in relation to microbially-mediated processes in particular. We aim to untangle the linkages between different combinations of intrinsic (i.e. soil-based) and extrinsic (e.g. landscape context, management) factors to elucidate how they collectively determine the resilience of soil respiration to cycles of drying and rewetting, and the extent to which the soil microbiome relates to such resilience. A model experimental system based upon high temporal resolution respiration profiles following repeated drying:wetting cycles was applied to soils derived from tens of sites located across England which cover the spectrum of land-use, soil texture, geographic location and organic matter content. Soils were characterised in detail with respect to their resilience and a wide range of associated intrinsic and extrinsic biological, chemical and physical properties. Modelling approaches dealing with the resilience functions per se, based on an analogy with a mechanical spring and damper system are combined with Bayesian modelling approaches to determine the relative roles of the various soil-based and landscape contextual factors.

Keywords: resilience, intrinsic and extrinsic effects, modelling

[P2.194]

Above- and belowground plant traits help explaining fungal community composition shifts in mountain meadows of three countries

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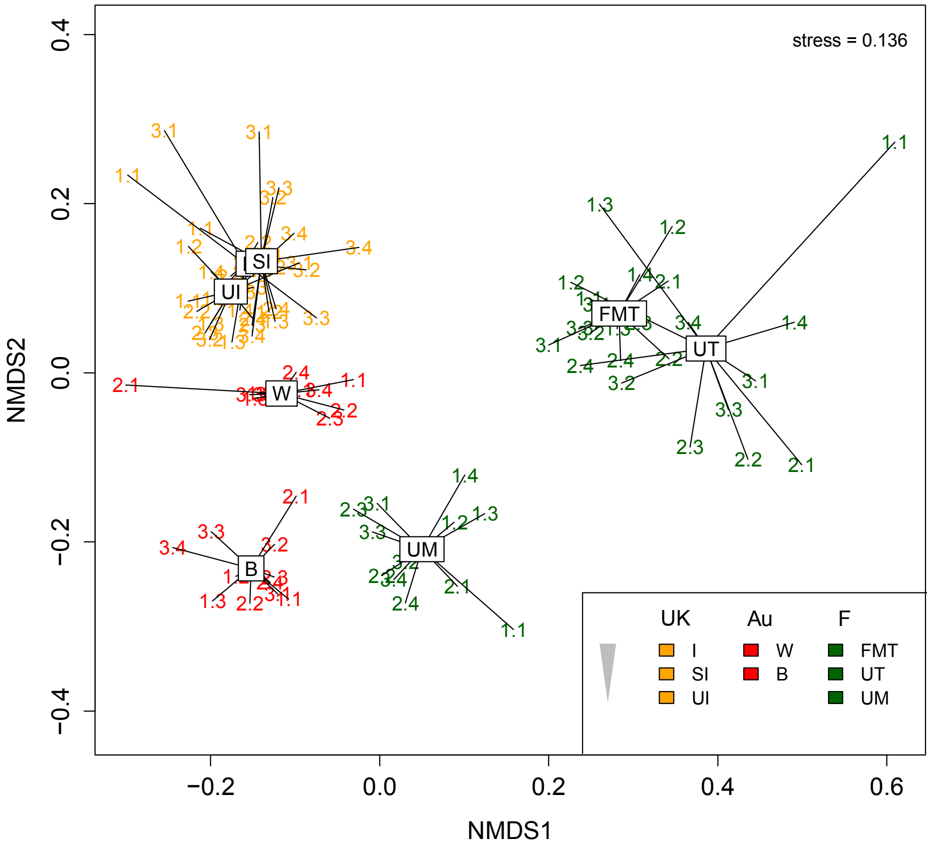
Soil fungal communities may be driven by abiotic- and biotic (plant and microbial) factors, which in turn can be shaped by land use. To identify these factors, we analyzed fungal DNA from meadows with contrasting types of agro-pastoral management. Sampling was performed in three sites of Lautaret pass (French Alps), two from Stubai Valley (Austria) and three from Yorkshire Dales (UK) across a land use extensification gradient. Fungal ITS1 DNA was amplified from 96 samples; >4 10^4 sequences were obtained for each and grouped into molecular operational taxonomic units (MOTUs). Of the 12275 identified MOTUs, the top 1000 accounted for 90% of the reads and 71% were assigned taxonomically at least at the phylum level. Along the extensification gradient in the three countries, we did not observe a shift in fungal diversity. There were however deep changes in fungal community composition for alpine sites (Figure 1). These changes were not reflected by consistent shifts in phylum abundances. We searched for fungal drivers among the 93 plant traits, microbial parameters and abiotic environmental variables that had been recorded on these sites. Overall, the combination of four variables accounting best for fungal composition variability included three plant traits (Leaf Carbon Content, Tabular Height and Root Diameter). The variables most correlated to fungal composition were selected in each of the four groups of aboveground- and belowground plant traits, abiotic and soil microbial parameters. Variance partitioning among these four variable subsets pinpointed specific contributions of plant traits and abiotic parameters, but not of prokaryotic parameters. Our work highlights the interdependency of herbaceous plant strategy and soil fungal composition.



NMDS ordination of the Bray-Curtis distances between fungal communities: a sharp pattern that does not fit the extensification gradient.

Keywords: High throughput DNA sequencing, grassland, bioinformatics

[P2.195]

Ectomycorrhiza-bacteria interactions in boreal forests

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Ectomycorrhizal fungi form diverse communities in boreal forests, allocating plant-derived carbon belowground to mobilise nutrients from organic polymers and mineral substrates. The continuous provision of energy-rich compounds, coupled with the large surface area of the fungal mycelium, suggests that it may constitute an important niche for bacterial growth and colonisation, however these microbial interactions are still poorly understood. We used single root-tip microbiomes to study the succession of bacterial and fungal communities, using Sanger sequencing for initial identification of dominant ectomycorrhizal fungi colonising individual root tips, and 454 pyrosequencing for subsequent profiling of the developing associated bacterial and fungal communities. In a microcosm experiment using field soil from a forest at Lunsen, Sweden *Phialocephala*, *Meliniomyces* and *Russula* spp. colonised at day 5 and persisted until week 24, *Rhizoscyphus* colonised at day 5 and persisted until week 16, *Piloderma* and *Paxillus* appeared at week 2 and persisted until week 24 whereas *Cenococcum* and higher abundance of *Russula* and *Meliniomyces* occurred later at weeks 8, 16, and 24. At week 8 the bacterial communities colonising roots predominantly colonised by *Piloderma*, *Meliniomyces*, *Russula* and *Paxillus* spp. were not statistically distinct from each other. At week 24 the roots colonised by these fungi harboured bacterial communities that were statistically distinct from each other. The abundance of *Burkholderia* on *Piloderma* colonized roots decreased from week 2 to week 24 whereas the abundance of *Dyella* roots increased during the same period. The results obtained support the idea that taxonomically distinct assemblages of bacteria develop with time on roots colonized by different ectomycorrhizal fungi and that the communities become more distinct with time. Changes in abundance may be related to patterns of assimilate allocation but the functional implications of the observed results need to be unravelled by further experiments.

Keywords: Ectomycorrhizal fungi, Bacteria, Succession, Root tips

[P2.196]

Strains of N_2-fixing bacteria from Zn-mining areas are efficient in symbiosis with Leucaena leucocephala

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The symbiosis between legumes and N_2-fixing bacteria (NFB) assures an important source of N to plants, which is relevant for establishing vegetation coverage in mine-degraded areas. One way to maximize the benefits of such symbiosis is to make use of tree species and NFB native to soils with high metal concentrations. This study aimed to: i) isolate and evaluate genotypic diversity and symbiotic efficiency of NFB from soils of a Zn-mining area in Brazil; and, ii) select strains with biotechnological potential for growing *Leucaena leucocephala*. Strains tolerance to heavy metals was assessed in 79 medium supplemented with 0.0142, 0.142, and 1.42 mM Cd; 0.6047 and 1.2094 mM Pb; 0.810 and 1.62 mM Zn. Strain authentication and symbiotic efficiency in *L. leucocephala* were assessed under greenhouse conditions, using sterile tubes containing sand+vermiculite. Treatments consisted of isolated strains and two controls (high and low mineral N), as well as the BR827 strain (*Sinorhizobium fredii*), which is approved as an inoculant for *L. leucocephala*. Symbiotic effectiveness was analyzed by number of nodules, nodule dry weight (DW), and shoot DW. The partial 16S rRNA gene identified the 19 NFB strains isolated from the mine area as belonging to the genus: *Mesorhizobium*, *Rhizobium,* and *Variovorax*. The nodulation ability was confirmed in 100% of the strains, with nine (52.94%) showing high efficiency of the N-fixation process. From these, eight were tolerant to all studied metals, irrespective of the concentrations. Most strains grew well in metal-contaminated media. Exceptions include UFLA01-774 with 1.2094 mM Pb and UFLA01-775 with 1.42 mM Cd, 1.2094 mM Pb, and 0.810 as well as 1.62 mM Zn. UFLA01-764 (*Variovorax* spp) and UFLA01-765 (*Mesorhizobium* sp), along with six additional strains showed high symbiotic efficiency and metal tolerance, with the potential to be tested in subsequent experiments aimed at revegetation of the Zn-mining area.

Keywords: mine-degraded areas, heavy metals, nodulation, symbiosis

[P2.197]

Towards a biodiversity monitoring program for Portuguese forests: operationalizing the use of soil macrofauna as an indicator tool

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Forest biodiversity is influenced by many drivers whose effects should be identified, evaluated and monitored. Extensive soil biodiversity monitoring schemes ought to be implemented and rely not only on good, cost-effective indicators but also on the possibility to use surrogates to model species richness. Estimating the relation between sampling effort and percentage of species richness at a site is also important, namely when considering trade-offs between costs and data robustness. To make operational the use of epigeal soil macrofauna in a monitoring programme of forest biodiversity and assess the feasibility of using surrogate groups/taxonomic levels as indicators, a set of 16 areas was defined considering dominant tree species in Portuguese forests. Sampling occured during Spring 2007, using 15 pitfall traps per area. 11551 individuals were collected and identified to family/order and species level (when that was not possible, morphospecies was used): the majority of individuals collected belonged to Formicidae, Coleoptera and Araneae. Species richness varied among areas, reflecting differences due to main tree species, location, management practices or interactions between these factors. GLM techniques modelling (morpho)species richness (S_Tot), and Coleoptera and Araneae species richness, delivered two significant models for S_Tot: one revealed Araneae and Coleoptera species richness can act as surrogates for S_Tot; the other, using total invertebrate family richness as explanatory variable, showed this can be a surrogate for S_Tot. Rarefaction models showed 8 samples on average per site are enough to attain 70% of maximum species richness (S_Max), incresaing to 11 and 16 samples for 80% and 90% of S_Max.. Our results suggest surrogates can be used in Portuguese forested areas to determine soil macrofauna richness. Furthermore, a range of baseline values of soil macrofauna richness for these areas can be obtained using our results, the first step towards the implementation of a monitoring program using these organisms

Keywords: Soil macrofauna, Monitoring programs, Forest biodiversity, Soil

[P2.198]

How an endogeic earthworm shapes soil nutrient availability: a study of the temporal and spatial dynamics of enzyme activity in the drilosphere

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Earthworms are known to affect microbial community composition and activity in the structures they create within the soil, namely casts and burrow linings. These changes are expected to be transient and therefore to lead to patchy patterns of nutrient availability. In order to assess the contribution of earthworms to nutrient availability in agroecosystems, a better understanding of the temporal and spatial distribution of earthworm-related microbial hotspots is needed.

We studied the heterogeneity of acid phosphatase, protease and amylase activity by zymography in experimental rhizobox systems in the presence and absence of endogeic earthworms (*Allolobophora chlorotica*) during a three-week period. Enzymatic activities were mapped 3 times during the study period, and analysed as proxies of microbial activity. The position and intensity of enzymatic activity hotspots were compared with the position and age of earthworm-related structures. In this way we established how earthworm activity affected the spatial distribution of enzyme activity and how this effect changed over time. These results are a step towards obtaining a quantitative characterisation of the drilosphere effect on nutrient mobilisation in bioturbated soils.

Keywords: endogeic earthworm, zymography, heterogeneity, soil organic matter dynamics

[P2.199]

Nematofauna as indicator of soil N availability in mixed plantations? A case study from tropical forest of Eucalyptus and Acacia in Congo

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Nitrogen is a limiting factor for the growth of Eucalyptus plantations, particularly in subtropical areas characterized by very low soil fertility (e.g.degraded pastures). The association with N_2-fixing species such as *Acacia mangium* is an alternative for ecological intensification of these ecosystems. Enhancement of Eucalyptus trees growth may happen by direct transfer of N fixed by Acacia trees or indirectly through litter decomposition. Field assessments in Congo showed that the productivity of Eucalyptus trees in mixed plantations was significantly increased compared with Eucalyptus alone. Higher N contents in soil of mixed plantations explained such positive impact. In a microcosm experiment, we measured N mineralization in soil sampled from pure stands of Acacia, pure stands of Eucalyptus and from the mixed plantations. The results showed an accumulation of nitrate in the rhizosphere of Acacia. We found that the introduction of Acacia trees changed significantly the structure of the community of nematodes by increasing the proportion of bacterial-feeding nematodes. Similar results were obtained in mixed-plantations in Brazil and in France, suggesting that nematofauna could be a key indicator of N availability in soil. Microbial communities involved in nitrification were also studied by targeting AOA and AOB genes using the quantitative PCR method. An increase of the number of copies of AOA gene was observed in the rhizosphere of Acacia while AOB gene was difficult to detect. This suggests that Archae communities may play an important role in N cycling in soil of Eucalyptus plantations. Our results demonstrate that the introduction of Acacia in mixed plantations systems influences the N cycle in the soil and associated biological activities.

Keywords: nematofauna, mixed plantation, N cycle, tropical soil

[P2.200]

Surprisingly evaluation of earthworm diversity in associative gardens of metropolitan areas

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Urban agriculture can be characterized by the culture or breeding, within or in periphery of urban zones, of products edible or not, that can be transformed and commercialized. It uses resources, services and products found in the immediate environment (Mougeor, 2006). The soils of these urban gardens can be considered as specific agricultural soils, intensely worked and with potential high fertility. Indeed, they contain on average 4% of organic matters, as compared to the 1 to 3% of agricultural soils Schwartz, 1993). These soils are heterogeneous because of their past usage that conditioned their nature (Putegnat, 2001) but also because of the great variety of cultural practices (Schwartz, 1993). Few studies were conducted on the soil fauna. This work is specifically turned towards earthworms because of their role as engineers in soil ecosystems. The aim of this work is to understand which mesological or anthropological factors influence earthworms in these special ecosystems.

In total, 73 gardens were sampled, from the 4 metropolis Nantes, Paris, Nancy and Toulouse. Results show large differences of abundance (from 0 to 1600 i/m²) related to historical factors of metallic contamination and other current factors of intense management. Despite these differences, gardens reveal a very large diversity (from 10 to 27 taxa) on relatively small areas (territory from 70 to 100 km²). These novel results will be discussed in comparison to the earthworm biodiversity found in agricultural soils of large farming plots, vine or natural habitats (grassland and forest).

Keywords: Earthworms, Diversity, Associative gardens, Metropolitan areas

[P2.201]

Fungal Biodiversity: Sustaining the Wood-Wide Web in Temperate Forests

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Soil is one of the most diverse habitats on Earth and one of the least characterized in terms of the identification and ecological roles of soil organisms. Soil also contains the largest repository of organic C in the terrestrial biosphere, and the activities of heterotrophic soil organisms are responsible for one of the largest annual fluxes of CO_2 to the atmosphere. A fundamental controversy in ecosystem ecology is the degree to which identification of microbial taxa informs our understanding of and ability to model ecosystem-scale processes. In this presentation, I will focus on fungi because they are the primary drivers of decomposition in temperate forests and because altered rates of organic matter decomposition will directly influence future trajectories of climate change. We have evidence that fungal identity does matter for understanding soil C dynamics, particularly in a global change context where soil microorganisms are subjected to selective pressures to adapt to changing conditions. Namely, our work at the Harvard Forest Long-term Ecological Research (LTER) site (Petersham, MA USA) shows that fungal community composition is a better predictor of microbial enzyme activity than are abiotic factors (%N, C:N, moisture). We have also observed that fungal community composition is fundamentally altered by chronic soil warming and simulated N deposition and that fungal taxa exposed to these global change stressors exhibit an altered capacity to degrade plant litter. This observed shift in physiology is evident even when these fungi are grown under ambient conditions, suggesting that they may have undergone evolutionary change that is not readily reversed (i.e., not a plastic response). These changes in the fungal community are associated with altered rates of plant litter decomposition and soil C storage. These results will be discussed in the context of conserving and sustaining the functionality of the wood-wide web in a changing world.

Keywords: fungi, global change, soil carbon, temperate forests

[P2.202]

Use of earthworm traits to understand link between species assemblages with their environment

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Species functional characteristics strongly influence ecosystem properties. Functional characteristics operate in a variety of contexts, including effects of dominant species, keystone species, ecological engineers and interactions among species. Most of studies in community ecology were based on species diversity and relative abundance but according to Hooper (2005), these parameters alone are not always a good predictor of species importance at the ecosystem-level. An understanding of how changes in species richness and composition, and biodiversity in general, influence ecosystem properties requires knowledge of the functional traits of the species involved. By definition, functional traits are those that influence ecosystem properties or species' responses to environmental conditions. A lot of studies are realized on links between plants species traits and their environment, but few studies have done on soil fauna. In this work we focus on temperate earthworm species because as engineer of soil ecosystem, they play an important role and make a lot of interaction with their environment. In this context, our aim is to determine which environmental variables control communities' assemblages using earthworm traits.

To reach this aim, we use data stored in Lombricien2000 database and EcoBioSoil database. These data concern earthworm taxa and environmental variables collected in France by M.B. Bouché and D. Cluzeau respectively between 1960-1980 & by co between 1985-2014. Environmental variables are characterized by carbon, nitrogen, pH, carbonates, altitude, soil texture, land use and land management. Several environments are investigated such as agricultural areas, forest and natural areas ... Species life history traits are selected among anatomical and morphological characteristic. We used a three-table ordination method (RLQ analysis) to identify the relationship between environmental variables and species traits. Results demonstrate gradient within environmental data (carbon and nitrogen opposed to pH and carbonates). The relevance of species anatomical and morphological traits used to link communities structures and environmental variables will be presented and discussed.

Keywords: Earthworms, Functional traits, Environmental variables, French species assemblages

[P2.204]

Agronomic and economic performance of common bean subjected to seed inoculation with rhizobium strains

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Soil biodiversity holds a relevant economic and social value. The common bean crop is quite expressive in Brazil due to the significant contingent of small rural producers involved in its production and since it represents an important source of protein in the Brazilian diet. Within this context, symbiosis with nitrogen fixing bacteria may reduce production costs and environmental impacts. Considering the diversity and territorial extension of Brazil, it is important to validate strains under different soil and climatic conditions with a view toward consolidating recommendation of these strains as inoculants.

The aim of the present study was to evaluate the agronomic and economic efficiency of strains of *Rhizobium* inoculated in seeds of the cultivar BRS-MG Madrepérola. Four field experiments were carried out in spring-summer 2012/2013 in four regions of the state of Minas Gerais, Brazil. A randomized block experimental design was used with 4 replications and 7 treatments, which were: inoculation with the strains CIAT 899^T of *Rhizobium tropici*, UFLA 02-68 of *R. etli* bv. *mimosae*, UFLA 02-100 of *R. etli*, UFLA 02-127 of *R. leguminosarum* bv. *phaseoli*, and UFLA 04-173 of *R. miluonense*, plus two controls, one without inoculation + nitrogen (N) from urea, at the application rate of 80 kg ha^{-1} N (½ at sowing and in topdressing), and the other without inoculation and without mineral N. The strain CIAT 899^T is already recommended for the manufacture of commercial inoculant, and the others, collected in the Amazon Forest, have exhibited high efficiency in biological nitrogen fixation.

We found that the symbiosis of common bean with the bacteria evaluated leads to good yields, with reduction in the application rate of mineral N and in economic and environmental costs. The greatest economic efficiency is obtained through the use of the strain UFLA 04-173.

*Financial support from CNPq, CAPES and FAPEMIG.

Keywords: Biological Nitrogen Fixation, Rhizobium spp, Phaseolus vulgaris, Economic efficiency

[P2.205]

Patterns in rhizobacterial and arbuscular mycorhizal fungal communities from a long-term climate change experiment

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The **Bio**diversity, **CO_2** and **N**itrogen (BioCON) experiment at the Cedar Creek Ecosystem Science Reserve (USA) was established in 1997 to determine plant responses to three globally occurring environmental changes: decreasing biological diversity, elevated levels of atmospheric CO_2 and increased nitrogen (N) deposition. Research has shown that plant productivity responds to aboveground species richness, climate or nutrient availability, and may be mediated by symbiotic microbial communities such as arbuscular mycorrhizal (AM) fungi and soil bacteria. Alternatively, plant responses can impose changes on these microbial communities via functional equilibrium mechanisms and plant-soil feedbacks (PSFs). The functional equilibrium model states that plants should preferentially allocate biomass to structures that optimize acquisition of essential limiting nutrients, and works well as a predictive hypothesis for plant-microbial responses from BioCON. In this study, we analysed the root/rhizosphere microbial communities from plots containing 1, 9 and 16 plant species using next-generation genetic sequencing to determine bacterial and AM community responses to elevated CO_2 and increased N enrichment. Our results indicate that both AM fungal communities and root-associated bacteria are altered similarly by N enrichment, less so by elevated CO_2, and these communities also respond strongly to species richness of the aboveground plant community. We propose that PSFs influence microbial community structure as a result of experimental treatments, but seasonal mechanisms driving PSFs are likely from the functional equilibrium between the environment, plants, microbes and soils. Studying the synergism of co-existing microbial communities from long-term experiments is of utmost importance and will further our understanding of resource trade markets that will shape future biological communities.

Keywords: Rhizosphere, Functional equilibrium, Plant-soil feedback, Soil metagenomics

[P2.206]

Structure of fungal and bacterial communities in a boreal forest podzol and their response to nitrogen fertilisation

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Symbiotic ectomycorrhizal fungi form diverse communities in boreal forests, mobilising nutrients from organic polymers with different degrees of recalcitrance and from mineral substrates that are weathered at different rates. These fungi may also sequester photosynthetically-derived carbon in the soil, but the different roles of individual taxa and their location within the soil profile are still poorly understood. The structure and activity of soil microbial communities are influenced by both atmospheric nitrogen deposition and applications of fertilizer but detailed knowledge of the community dynamics of these responses is still lacking. High throughput, massively parallel sequencing provides a new tool with which to investigate these effects. We investigated fungal and bacterial community structure in different horizons of a boreal forest at Lamborn, Sweden. Samples were taken in an 80 year old pine stand with two treatments (unfertilised control and fertilised with 150 kg N ha^{-1} 16 months prior to sampling). Ten replicate cores were taken from each plot, dived into O, E and B horizons and pooled prior to DNA extraction, PCR and pyrosequencing of both soil and root fungi. Sequences were quality filtered and clustered using the bioinformatics pipeline SCATA for fungi and the RDP pipeline for bacteria. A total of 807 fungal OTUs N>2 reads (496 OTUs with N>5 reads) was found in the soil samples with corresponding figures of 546 and 350 OTUs in the root samples. Fungal community structure in soil differed significantly between soil horizons but not between N treatments. Total numbers of OTUs declined significantly down the soil profile and were higher for soil DNA in N+ treatments in the O horizon than in the corresponding N- treatment. The horizon effect on OTUs from roots was not significant but there was a significant decrease in the number of root-associated OTUs in response to N.

Keywords: N-fertilisation, C-sequestration, ectomycorrhiza, diversity

[P2.207]

Long term minimum tillage as a driver for different response of ammonia oxidizing archea and bacteria to drought stress

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Climate change affects temporal and spatial distribution of the rainfall events and increases the frequency of severe droughts; which can influence soil microbial community structure and functioning.

The aim of our study was to evaluate the response of ammonia-oxidizing bacteria (AOB) and ammonia-oxidizing archaea (AOA) to intensive summer drought in 2013 under two different tillage systems; conventional moldboard plowing (CT) and minimum tillage (MT). Soil samples, exposed to natural summer drying-rewetting cycles, were taken from the 14 years tillage experiment at site Moskanjci, Slovenia at several time points according to the soil moisture conditions: moist (92-100% of WHC), dry (24-38% of WHC, 2 weeks without rain), and severe dry (14-20% of WHC, 4 weeks without rain).

MT tillage caused evident stratification of soil organic carbon and nutrients in the soil profile, which reflected in the total and active microbial biomass. Concentrations of the total extracted DNA and RNA were in the upper 0-10 cm soil layer of MT significantly higher at all sampling dates in comparison to CT, while in the lower 10-20 cm layer no differences were found. Although, the copy numbers of AOB *amoA* transcripts were always higher than those of AOA; during the drought period a significant increase of AOA *amoA* transcripts was observed under both tillage treatments. But under MT the increase of AOA was several times greater and coupled with a significant decrease of AOB *amoA* transcripts. Our results thus clearly show that resistance to drought in arable soil is higher in archaeal than in bacterial community, especially under minimum tillage.

Keywords: ammonia oxidising archea, ammonia oxidising bacteria, drought, minimum tillage

[P2.208]

The effect of carbon and phosphorus availability on soil microbial community

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Introduction:

Phosphorus is a macronutrient essential for plant growth. Microbial activities within soil are essential to release available phosphorus from organic matter, but require sufficient carbon and energy to do so. Studying the combined effect these growth limiting nutrients have on microbial community structure, whilst measuring biological, physical and chemical soil properties, could help optimize inorganic P (Pi) application rates. This study investigated the effect of Pi and carbon availability, and their interaction, on soil microbial communities in grassland soils.

Methods:

Pi application rates; Low (0 kg ha^{-1} yr^{-1}), Medium (15 kg ha^{-1} yr^{-1}) and High (30 kg ha^{-1} yr^{-1}) were applied to two grassland sites over 15 years. Sites differed in carbon availability, Site 1 having vegetation harvested, while in Site 2 vegetation was not removed. Biological, chemical and physical soil parameters were measured and the microbial community was profiled by T-RFLP.

Results:

When carbon input is not restricted, total soil phosphorus, microbial biomass P and plant available phosphorus increase linearly with Pi application rate. When carbon input is reduced, all Pi application rates remain relatively low and constant across application rates. The effect carbon input has on bacterial and archaeal community structures is similar, showing clear differences between sites. An effect of Pi is seen only when carbon availability is not limited, with Low and Medium Pi communities diverging from High Pi communities.

Discussion:

The results indicate that phosphorus release within the soils was restricted by carbon input. Carbon can be used by microbes to release inorganic phosphorus from soil organic matter and can incorporate more total phosphorus into the soil within microbial biomass. The differences in bacterial and archaeal community profiles between Pi application rates calls for further exploration. Targeting and quantifying key functional genes will determine if Pi application rates are affecting key nutrient cycles.

Keywords: phosphorus, carbon, soil microbial communities, grassland

[P2.209]

How affects the application of organic amendments to the richness of arbuscular mycorrhizal fungi in a trace element contaminated soil?

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In 1998 a toxic mine spill occurred in Aznalcóllar (Seville,Spain). Remediation works were carried out to remove the sludge from the surface of soil. However these tasks did not reduce the pollution until acceptable level. Afterwards, a study on the effect of organic amendments to restore the contaminated area has been conducted during 12 years. It comprises the use of two organic amendments: biosolid compost (BC) and leonardite (LE), a low grade coal rich in humic acids. Preliminary results showed differences in the restoration potential of the two amendments on soil properties. Next step includes the study of microbiological communities in the soil. Due to their important role for ecosystem functioning, the response of arbuscular mycorrhizal (AM) fungal communities has been studied in the treated soils.

The AM fungal colonization of the two most abundant plant species in the experimental area :*Lamarckia aurea (L.) Moench* (Poaceae), and *Chrysanthemum coronarium L.*, (Asteraceae), was investigated. *C. coronarium* roots showed a higher AM fungal colonization level whereas the concentration of trace elements (e.g. As, Cd, Cu, Zn) incorporated in the aerial part of the plant was higher in *L. aurea*.

Resulting from a subsequent molecular analysis of the AM fungal community colonizing the root of target plants, we expect to observe an increased diversity of AM fungi associated to *C. coronarium* and in the treatments using LE (the more effective amendment). Disentangling the contribution of AM fungal diversity to the survival and fitness of plant species in polluted areas can be valuable information when carrying out restoration programmes.

Keywords: arbuscular mycorrhizal fungi, restoration, contaminated soils, amendment

[P2.210]

Earthworms abundance and diversity within a range of permanent and temporal moisture condition in biofuel crops

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Use of marginal, abandoned lands for bioenergy production can prevent the food vs. fuel issues that exist when prime farmland is used for energy production. In the northeast USA, marginal lands are typically seasonally wet, and there is concern over the environmental impact associated with land use conversion and management, for instance regarding greenhouse gas emissions. As earthworms have important effects on soil hydrology and biogeochemical processes, we investigated the effect of land use change on earthworm abundance and diversity, near Ithaca, NY, USA, using a factorial design of land cover (3-yr old switchgrass, 3-yr old reed canarygrass, and a 50-yr unplowed control; n=3 per cover) and wetness (classified based on 3 years of soil moisture and water table depth data; n=3 per wetness class). Earthworms were collected by hand-sorting in July 2014 using two 25x25x30 cm monoliths for each replicate land cover x wetness combination. They were preserved in 3.7% formaldehyde, counted, weighted and identified into species. Litter biomass, standing biomass and monolith soil moisture and rock fragment content were determined. Linear mixed effect models (wetness class x cover) for earthworm biomass and diversity were performed and canonical analysis was also developed. Cover surprisingly did not significantly affect earthworm biomass and diversity, though highest earthworm biomass was found in control plots with medium wetness (Figure 1-2). *Aporrectodea tuberculata* and *A. trapezoides* responded to soil moisture, while *Lumbricus rubellus, Dendrodilus ribidus and A. longa* responded to standing biomass (Figure 3). Further analyses will be performed taking additional soil health data; preliminary findings suggest that the effect of wetness is greater than the effect of land cover.

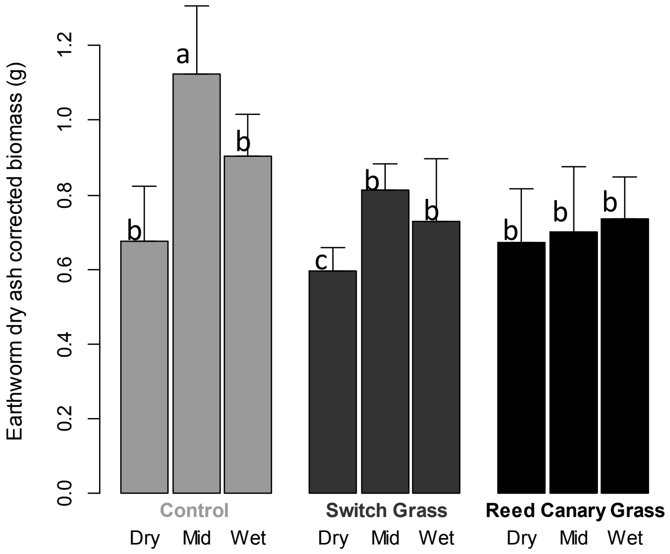

Figure 1. Dry earthworms biomass among treatments. Different letters indicate significant differences ($p<0.05$).

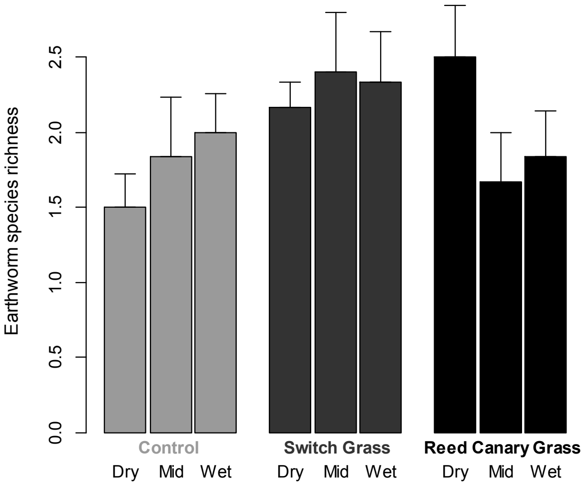

Figure 2. Number of earthworm species per treatment.

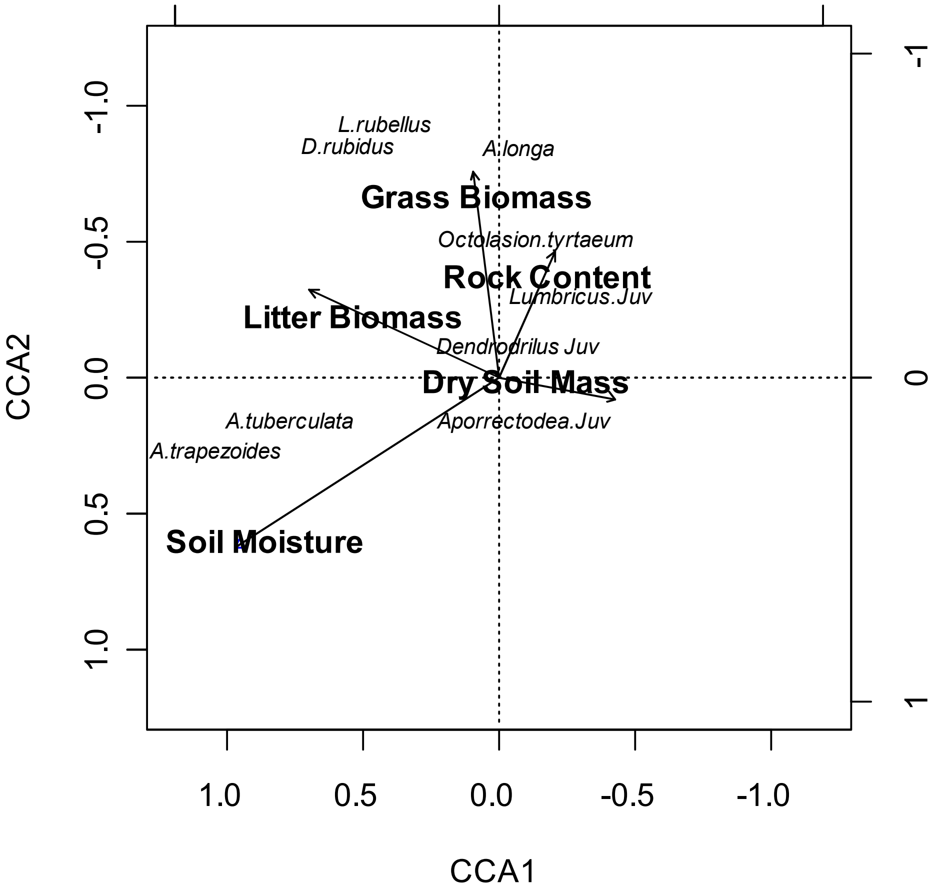

Figure 3. Environmental and species variables over the factorial plan. After canonical analysis.

Keywords: biofuel crops, wetness class, earthworms, abundance and diversity

[P2.211]

Soil bacterial community response to elevated air humidity under silver birch stand growing in an experimental free air humidity manipulation facility

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A free air humidity manipulation facility (FAHM, Estonia) was established in 2007 to study the effect of increased air humidity on plants performance and functioning with respect to rising air humidity predicted for Northern Europe. To evaluate the effects of increasing air humidity to the bulk and rhizosphere soil bacterial communities of silver birch (Betula pendula Roth.) stands, massively parallel sequencing of 16S rDNA V6 variable region on Illumina HiSeq2000 and quantification of 16S rDNA, nirS, nirK, and nosZ genes was used. Soil samples from 0-10 cm soil layer of control and fumigated plots in two replicates were collected in October 2009 and 2011.

Permutational analysis of variance (PERMANOVA) showed significant differences in bacterial community structure between control and fumigated plots both in bulk soil and rhizosphere soil. Bacterial community structure was related to soil moisture content and pH value both in bulk and rhizosphere soil. According to LDA effect size (LEfSe) analysis abundance of Geobacter and Gordonia increased, while abundance of Rhodobacter and Xanthomonadaceae decreased in soils of fumigated plots. In case of rhizosphere soil samples in addition to Geobacter the abundance of Clostridia increased due to treatment. Abundances of measured bacterial gene abundances did not differ between treatments. In comparison with fumigated plots overall temporal changes in bacterial community structure were larger in control plots indicating stabilization effect of fumigation on soil microbial communities during the study period.

In conclusion, the increased air humidity lead to altered and less diverse bacterial community structure in bulk soil and rhizosphere under silver birch stands.

Keywords: elevated air humidity, soil bacterial community, silver birch

[P2.212]

Changes in forest soil invertebrates community along a post-fire chronosequence

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Forest harvesting and fire were widespread in the upper Great Lakes region of North America. The effects of this ecological disturbance on soil invertebrate assemblages require careful consideration due to their important functional roles in the soil and in the providing of forest ecosystem services.

We propose to assess the soil invertebrates long-term post-fire response (15 to 102 years) by studying a forest chronosequence in northern lower Michigan (USA). Six one hectare plots that were one time experimentally clear-cut harvested and burnt were sampled. For soil and litter dwelling macro- and meso-invertebrates, hand sorting and Tullgren funnels methods were done in fall 2012 (N=16 per plot). For active invertebrates at the soil surface, pitfall traps were left for one week in fall 2012 and in spring 2013 (N=16 per plot each year). Moreover, the forest understory and the soil cover were characterized in a 1 m² square around each pitfall trap.

Fairly small difference of taxa richness and density of the meso and macro invertebrates were found across the chronosequence. At the soil surface, for a given pair of plots a higher percentage of taxa was shared if their burning dates were close together. A Principal Coordinate Analysis showed that community structure of active macroinvertebrates was strongly affected by chronosequence stage for both sampling dates with a clear dissimilarity between the extreme stages. Canonical Correspondence Analyses showed that the shifts of community composition across plots were due to dependence of certain taxa to aboveground characteristics. For instance, the *Stelidota octomaculata* beetle density was higher in the oldest forest stage because of the oak dominance in this plot.

This post-fire chronosequence study highlighted the indirect impact of the late-recovery of the aboveground composition after forest harvesting and fire disturbance on the belowground communities that might have effect on the ecosystem functioning

Keywords: disturbance, spontaneous succesion, pyrogenic landscape

[P2.213]

Where the small ones have big roles: linking biocrusts and ecosystem services in drylands

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Functional traits and functional diversity have been identified as fundamental targets in ecological research to disentangle the link between biodiversity and ecosystem services. Contrary to species identity or species diversity (e.g. number of species), the functional approach make the link between effect traits and trait diversity and ecosystem processes, which in turn allows to better assess the contribution of organisms to ecosystem services delivery. However, there is a necessity to complement the existing science on functional diversity about vascular plants with that of other soil organisms present in ecosystems where vascular vegetation is scarce, namely drylands.

In drylands, “biocrusts” formed by soil lichens, bryophytes, and other microbial organisms such as cyanobacteria and fungi, may dominate plant interspaces. Biocrusts perform key functional roles; such as carbon and nitrogen fixation, nutrient cycling, soil surface protection and formation, and they also take part in numerous biotic interactions.

The overall objective of the project “BSCES” (*Functional diversity of Biocrusts: towards ecosystem services quantification in drylands*) is to quantify the contribution of biocrusts to ecosystem services. To address this objective, we selected 3 regions (Portugal, Italy and south-western USA) to measure biocrust functional traits and diversity, and evaluate the relation between these biodiversity components and ecosystem properties (such as topsoil carbon and nitrogen, soil micronutrient concentration, soil water relations, surface reflectance, seed bank), along aridity gradients.

Up to date, we recorded biocrust distribution and abundance along aridity gradients in two Mediterranean drylands and in two contrasting microenvironments (shrub and intershrub spaces). We measured biocrust functional traits and collected soil samples beneath different functional groups. Our aim is to have a more precise measure of the ecosystem properties related to the “biocrust effect”, and to model the contribution of this complex component to ecosystem services such as soil fertility, topsoil-water regulation, heat exchange and microhabitat provision.

Keywords: Biocrusts, Drylands, Functional diversity, Traits

[P2.214]

Assessment of biological soil quality indicators of the Harran Plain under continuous cropping design

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Soil microbiological activities are key components in soil ecosystems playing role in the cycling of nutrient elements and maintaining soil quality. They respond rapidly to changes in soil conditions and are sensitive to management practices thus proposed as early and sensitive indicators of soil ecological stress and soil quality alone or in combination with other chemical or physical properties. As a part of soil quality initiative project, this study has been performed in the Harran Plain which is one of the largest agricultural areas of the country and has been extensively used since the irrigation started in 1995. The plain is dominated with continuous cotton and wheat-corn cropping design. The Plain suffers from degradation due to extensive tillage, fertilizer and chemical usages and salinity. Over 400 soil samples were collected across the plain covering saline and non-saline areas and samples were analyzed for soil biological quality indicators. As parallel to the degradation of soils and the loss of soil organic part induced from intensive agriculture, soil biological activities were low. In soils the catalase, dehydrogenase, urease enzyme activities, alkaline phosphatase, total fungi, bacteria, actynomyces and soil microbial biomass carbon ranged from 0.7 to 8.8 mg O_2/5 g soil, from 0.14 to 118.1 µg TPF g^{-1} dry soil, from 7.5 to 186.25 mg N/100 g soil, from 0.47 to 244.7, from 23 x10^3 to 3.4 x10^6 cfu/g soil, from 0.1 to 59 10^6 cfu/g soil, from 0.1 to 59 10^6 cfu/g soil and from 10.61 to 7145.7 µg g^{-1} dry soil, respectively. Soil biological variables were found to have significant correlations among themselves and with other variables. The PCA analysis showed that soil biological parameters such as microbial biomass and dehydrogenase enzyme activities are significant and should be available in the least minimum data set for the characterization of soil qualities.

Keywords: Microbial activity, Soil quality, Soil ecology, Degradation

[P2.215]

Abundance and diversity of *phoD* alkaline phosphatase genes and transcripts in soil bacteria

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Biological transformations of phosphorus (P) in soil are largely dependent on soil microbial functions. As part of the pho regulon in bacteria, the *phoD* gene produces extracellular alkaline phosphatases, a non-specific enzyme that catalyses the hydrolysis of phosphomonoesters. This study examined the effect of long-term management and P amendment on potential alkaline phosphatase activity (ALP), P bioavailability and the abundance and diversity of bacterial *phoD* genes and transcripts. Management treatments at the Glenlea Long-term Rotation near Winnipeg MB, Canada included no-input organic (ORG), organic with composted manure (ORG+M), conventional (CONV) and restored prairie (PRA). A negative correlation was found between ALP activity and bioavailable soil P in 2011 (r^2=0.68; P=0.03) and 2012 (r^2=0.51; P=0.02), suggesting that ALP activity increased under P limiting conditions. Significantly higher ALP levels in ORG plots corresponded with increased *phoD* gene abundance. A greenhouse experiment assessed if manure or mineral P treatment suppressed ALP activity and *phoD* gene and transcript abundance after 30 days. ALP activity, although similar at day 0, was higher for all treatments in the ORG (5.38 to 6.23 µmol PNP g^{-1} hr^{-1}) and responded to manure, but not mineral P, for CONV (5.63 to 3.26 µmol PNP g^{-1} hr^{-1}) and PRA (4.71 to 3.22 µmol PNP g^{-1} hr^{-1}). The abundance of bacterial *phoD* genes, but not transcripts, was significantly correlated with ALP activity. A resulting negative correlation was observed between $NaHCO_3$-extractable organic P and both ALP activity and *phoD* gene abundance. Transcript abundance was not correlated to other measured variables although we were able to confirm expression of the *pho*D gene in all soils, thus indicating that gene abundance is a better indicator of potential ALP activity. Illumina sequencing showed differences in community composition between management systems for both genes and transcripts in soils with no added P.

Keywords: phoD abundance, bacterial communities, alkaline phosphatase, bioavailable P

[P2.216]

DRILOBASE 2.0, the first comprehensive and collaborative database system on the earthworms of the world.

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Today, treatment and analysis of a growing body of data on earthworms needs new approaches and computer tools. While traditional database management systems are usually built around non-collaborative data storage and query interfaces, such as Microsoft Access or the couple MySQL/PHP, a new philosophy in the data production, organisation and use has emerged during the 2000s with the program Mediawiki. This new type of interface is becoming increasingly popular worldwide for the building of collaborative databases. Building on a previous version, which focused on the earthworms of South America, DRILOBASE 2.0 has become a wiki-based system dedicated to all earthworm taxa of the world. It presents a list continuously updated of the accepted families, genus and species. To date, up to 6000 taxa have been added, distributed among 23 families. For each taxon there corresponds a page accessible by search engine or browsable by taxonomic tree. Each page for each taxon is divided in 3 parts: General data, thematic references, and distribution references. Complete cited references appear in a dedicated module and a discussion forum promotes the communication between contributors. A hypertext system based on the simple Mediawiki language facilitates the navigation between taxonomic pages and all compartments of the database. Access and modification of the database requires password authorization while viewing content is open to all. A series of appropriate Creative Commons licenses is associated to the content of the database for copyright protection. Future additional functions are considered, such as the possibility of establishment of bridges to other existing databases dedicated to soil fauna. DRILOBASE 2.0 aims at becoming a collaborative platform by which scientific knowledge regarding earthworms may be accessible to the scientific community and the general public.

Keywords: Earthworms, Database

[P2.218]

Microeukaryote communities along a gradient of drainage and productivity in the coastal temperate rainforest of Calvert Island (British Columbia, Canada)

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Although widely recognized as key players in ecosystems and representing a large part of the Earth's biodiversity, unicellular eukaryotes (protists) are still poorly characterized, particularly in soil ecosystems. In this study, we assessed protistan diversity and community structure along a gradient of productivity on Calvert Island (British Columbia, Canada). Soil samples have been collected from blanket bogs, bog woodlands, bog forests and zonal forests and three different soil depths were investigated: the soil surface (moss/litter), the organic horizon and the mineral horizon. To analyze the composition and diversity of the protistan communities, we amplified the hypervariable V4 region of the SSU rRNA gene with universal eukaryotic primers and generated sequences on an Illumina MiSeq. In addition, we used a microscopy-based approach to characterize the composition and biomass of testate amoebae (Arcellinida, Euglyphida and Amphitremida), one of the most important and abundant groups of protists on the soil surface.

Microscopy-based results indicate testate amoeba community structure on the soil surface differs between ecosystems and are particularly abundant in bog ecosystems. High-throughput sequencing analyses reveal an extensive diversity of protists across distinct terrestrial ecosystems and for the first time, provide comparative data from different soil depths. This study also highlights which environmental factors structure protistan communities in soils of the temperate rainforest.

Keywords: Protists, High-throughput sequencing, Soil depth, Temperate rainforest

[P2.219]

BIOTIC SOIL-EFFECTS CONTRIBUTE TO THE CONTROL OF POTENTIALLY DOMINANT PLANTS AND ENABLE SPECIES COEXISTENCE AND BIODIVERSITY IN GRASSLANDS

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Interactions between soil microorganisms and plants seem to play an important role for plant productivity, plant fitness and therefore possibly also for plant-community composition and diversity. However, the mechanisms how biotic plant-soil interactions putatively influence biodiversity, i.e., local dominance and abundance of plant species, is not well understood yet.

Using 35 model plant species, we tested i) the impact of soil-microorganisms on the competitive ability of plants classified into different plant functional types (hypothesizing that especially large and non-dominant plant species are held in check by negative biotic soil-effects) and in addition, (ii) how combined effects of soil-microorganisms and plant-plant competition affect local plant abundances and diversity in grasslands.

We observed more negative biotic soil-feedback effects for large non-dominant plant species in comparison with small and locally abundant species. Furthermore, combined and synergistic effects of soil biota and plant-plant competition in our experimental systems were congruent with patterns of local abundances of plant species observed in the field.

These results indicate that soil biota by differently affecting growth of plant species and plant functional types influence competitive abilities among plants and therefore affect productivity and biodiversity as well as ecosystem functions and ecosystem services in grasslands.

Keywords: grassland diversity, local dominance, plant community-composition, plant-soil interactions

[P2.220]

Arbuscular mycorrhizal fungi diversity along a land-use and biogeographical gradient in southern Brasil.

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Given the large crop and pasture area cover in Santa Catarina-Brazil, climatic conditions and the occurrence of low fertility soils, is important to evaluate the influence of different soil management practices on arbuscular mycorrhizal fungi (AMF), since the presence of these fungi and the associations they establish with the host plants may be an indicator of soil quality and ecosystem sustainability. The aim of this study was to evaluate AMF species richness in five different land-use systems: native forest (NF), eucalyptus plantation (EP), pasture (PA), crop-livestock integration (ICL) and no-tillage cropping (NT), in twelve municipalities, three replicates of each land-use system at each one. The municipalities were distributed along a biogeographic gradient embracing four major zones within Santa Catarina State with different soil and climatic conditions: West (W), Plateau (P), South (S) and East/Coastal (E). Sampling was conducted between 2011 and 2012 in winter and summer. At each site (a patch of a certain land-use system) a sampling grid was established with nine points totaling 100 m^2 area. The AMF species were identified through spores recovered in trap cultures. In total 24 species of AMF were found, predominantly of the genus *Acaulospora*. The pattern of species richness was different between land-use systems and between regions. Species richness was higher on no-tillage cropping, pastures and crop-livestock integration, non-forested areas where management intensity was not so high. These findings confirm that these microorganisms are sensitive to management practices that may exert an effect with the AMF-plant symbiosis and on their added value for the increased productivity of the system.

Keywords: arbuscular mycorrhizal fungi, soil diversity, land-use, biogeographical gradient

[P2.221]

Impact of riparian forest degradation on Isoptera and Formicidae (Hymenoptera) abundance and richness in Eastern Amazon

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Eastern Amazon is the oldest and more deforested forest frontier in the Brazilian Amazon. About 76% of forest cover was converted for agriculture. Most of remnant forest patches are less than 1000 ha and surrounded by a matrix of degraded pasture or young secondary vegetation. Despite their extreme importance for water resource and legal protection, riparian forests are also strongly degraded in the region. In order to limit water resources degradation and prevent a large scale ecosystem collapse, an ambitious restoration effort is urgent for these fragile ecosystems. In this study, we focus on the soil degradation in the riparian zone and evaluated the effect of forest degradation on the abundance and diversity of two determinant soil ecosystem engineer groups: ants and termites. A gradient of forest degradation was established in two streams of Alcantâra (Maranhão State), “Rio Grande” and “Rio Pepital”. The gradient has four levels: D1=Conserved forest; D2=Secondary forest>15m; D3=Young secondary forest<7m; D4=Open vegetation dominated by bare soil. Each level was repeated three times (blocks) in each river. Ants and termites were collected with the Tropical Soil Biology and Fertility method in the dry (2012) and wet (2013) season. Insects were identified until specie or morphospecie and the effects of the river and degradation level on abundance and diversity were tested through two-way ANOVA and Tukey test ($P<0.05$). Eighty five ant and 37 termite species were identified for both rivers. Abundance and diversity of both ants and termites were higher in the dry season and in the D4 and D3 compared to D1. Rio Grande had the highest richness despite a higher overall degradation. Both groups revealed a high adaptation capacity to dryness and degradation but the severe degradation caused by slash-and-burn agriculture may impair the soil resilience provided by the ant and termites soil engineering.

Keywords: Diversity, Restoration, Tropical forest

[P2.222]

A comparison of soil amendment with either anaerobically digested or fresh cattle manure and its impact on genetic diversity, microbial activity and physiological community profile

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Agricultural soils are subjected to recurring external disturbances such as tillage, crop cultivation, harvest, and soil fertilisation (e.g. application of manures). In recent years, small- and mid-scale biogas plants have thrived in Europe and led to a change in land-use. Manures that used to be applied to agricultural soils are now used for energy generation in biogas reactors and instead digestate is applied to agricultural soils. Here we present the results of a study simulating soil amendment with either anaerobically digested or fresh cattle manure. The aim was to investigate the resistance and resilience of the resident microbiota and to detect differences in the microbial biomass and activity after fertilizer amendment. Furthermore discrepancies of the physiological community profile were evaluated and the role of the indigenous microbial community was elucidated.

We applied a single amendment of either treatment to agricultural soil (non-sterilized or sterilized by gamma-irradiation) in a microcosm experiment. The effect of amendments on the community structure was tested immediately and after 1 and 3 months by PCR-DGGE, CLPP through MicroResp^{TM} (6 sugars, 5 amino acids, 4 carboxylic acids) and measurement of basal respiration, microbial biomass and the metabolic quotient.

The community strucure of dominant fungi and bacteria was not affected by either amendment, indicating the ability of the indigenous microbiota to outcompete allochthonous microorganisms. Soil microbial biomass was not changed, whereas basal respiration was significantly higher after amendment, especially when using fresh manure. CLPP revealed initially higher substrate utilization and reduced utilization of citric and malic acid after either amendment compared to the control. Differences were generally more pronounced for digestate application. After one month, both treatments returned to control levels for all parameters. In conclusion, the amendment with anaerobically digested manure did not have a greater impact on soil microbial parameters than fresh manure.

Keywords: soil amendment, cattle manure, anaerobic digestate, microbial community

[P2.223]

Seasonal variation in the soil macrofauna community along a gradient of degradation of riparian forest in the humid tropic

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Soil fauna have seasonal rhythms regulated by temperature and humidity. In the tropics, where the temperature is stable and high over the year, the most important factors of seasonality for macrofauna is food resources availability and precipitation. The objective of this study was to assess the seasonal variability of soil macrofauna community in a gradient of degradation of riparian forest in the humid tropic for selection of bioindicators of soil degradation. The study was conducted in the watershed of Pepital and Grande rivers, in Alcântara, Maranhão, Brazil. The region is characterized by two well-defined seasons (dry and rainy) and original vegetation typical of Eastern Amazon forests. Four levels of degradation were defined in the riparian forest: D1=Conserved forest; D2=Secondary forest>15m; D3=Young secondary forest<7m; D4=Open vegetation dominated by bare soil. Soil macrofauna was sampled according to the Tropical Soil Biological and Fertility methodology and identified to the order. Two-way ANOVA and SNK tested for the effects of river and degradation level on each macrofauna group and between-class principal component analyses (BCA) were performed to study the effects of river, degradation level and season on the whole community. The season effect on macrofauna was small but highly significant (5.1%; P=0.003). In the dry season, the abundance and richness of macrofauna and densities of Hymenoptera, Isoptera, Oligochaeta, Isopoda, Diplopoda, Gastropoda, Coleoptera, Blattaria, Chilopoda, Opiliones and Diplura were sensitive to degradation (25.5%; P=0.003). In the rainy season, degradation had significant impacts on the richness of macrofauna and densities of Oligochaeta, Diplopoda, Orthoptera, Acari, Araneae, Pseudoscorpiones, Isoptera, Isopoda, Gastropoda and Chilopoda (19.7%; P=0.007). The impact of degradation in the riparian forest on the composition and diversity of soil macrofauna was more pronounced in the dry season. Oligochaeta, Isopoda and Diplopoda are potencial good indicators of soil degradation in the riparian zone for the region.

Keywords: Restoration, Diversity, Bioindicators

[P2.224]

Do root mycobiota recruitment differ from the one acting for the bacterial microbiota? The tomato case

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The current wealth of studies on the plant microbiota reflects the widespread interest in this topic, since root-microbe interactions are not only crucial for better understanding plant growth and health, but also for sustainable crop production in a changing world. To date, such studies focus almost exclusively on the bacterial dimension of the root-associated microbiota. However, given the unique biological and ecological features of fungi, recruitment of the fungal microbiota may deviate from the relationships documented for bacteria. For instance, due to the mycelial growth form, the distinction among the different rhizosphere compartments (root surface/tissues vs rhizosphere soil) may be less clear-cut for fungi than for bacteria.

Within the framework of a project combining meta-barcoding and systems biology to infer the principles underlying the interactions between tomato and its root mycobiota (Mycoplant), we addressed the relative importance of different factors (soil type, cultivar-specificity, abundant pathogen presence) shaping this fungal microbiota. Approx. 900 000 ITS2 and EF1-alpha amplicons obtained from the roots of four tomato cultivars grown in two different soils under greenhouse conditions were analyzed. Tomato genotypes either susceptible (Moneymaker, Cuore di Bue) or resistant (Heinz; Battito) to Fusarium oxysporum f. sp. lycopersici were used; the two resistant cultivars had been grown either in the presence or in the absence of the pathogen. Rhizosphere and bulk soil samples were also analyzed. Both soil type and plant genotype were significant drivers of the structure of root mycobiota, the magnitude of the impact of the two factors being comparable in some cases. Inoculation with the pathogen also significantly affected the communities associated with the resistant cultivars.

Keywords: plant microbiome, fungal communities, plant pathogen, Fusarium wilt

[P2.225]

Patterns of soil macrofauna diversity in agricultural land uses from rain forest conversion in the Los Tuxtlas Biosphere Reserve, México.

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The purpose of this work was to study the alpha (α), beta (β) and gamma (γ) diversity of soil macrofauna invertebrates in order to evaluate the impact of i) land use change on its diversity and, ii) to find out taxa as habitat quality indicators. This work was part of the project "Conservation and Sustainable of the Below Ground Biodiversity" funded by GEF.

In the Santa Marta region (Los Tuxtlas), three sites were selected and, within each of them, three land uses (agro forestry, A; maize, M; pasture, P) and the primary forest (RF), were sampled to collect macrofauna and soil, 106 points were sampled.

A total of 73 species and 328 morph species were recorded. The groups with the greatest species richness were Coleoptera (178 sp) and Formicidae (141)., The trend in alpha diversity for the majority of the taxonomic groups was that RF and A had higher richness than M and P. Alfa diversity of most groups was positively correlated with total carbon, and nitrogen, and negatively correlated with clay and bulk density. Larger forest fragments sampled seemed not to be able to preserve the whole current soil macrofauna diversity; the anthropogenic habitat complements the landscape diversity. Only 52.9% to 77.7% of the gamma diversity was found in RF fragments, whereas the remaining 22-47% was complemented by the diversity of anthropogenic habitats. Species of beetles, ants, millipedes and centipedes seemed to be most affected by anthropogenic habitats and would be useful as habitat quality indicators. The distance from the anthropogenic areas to the primary forest is crucial to maintain high macrofauna diversity in anthropogenic habitats; the greater the distance, the lower the alpha diversity. We concluded that primary forest (RF) maintains the higher macrofauna diversity, however, in fragmented areas a mosaic of both habitats, i.e. natural and anthropogenic, is necessary to preserve the macrofauna gamma diversity at the landscape level.

Keywords: macrofauna, land uses, Mexico, alfa beta gama diversity

[P2.226]

Grassland N addition and rainfall drive variation in microbial community structure and functio

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Introduction:

In Southern California, nitrogen deposition is increasing due to agriculture and industry and precipitation rates are predicted to decrease due to climate change. We investigated the relationships between precipitation change, increased nitrogen deposition, soil microbial diversity, and greenhouse gas fluxes in a Southern California grassland.

Methods:

This factorial study consists of 48 large plots, which have been treated over the last 7+ years with increased (+50%) and decreased rainfall (-50%), crossed with increased nitrogen deposition. Gas and soil samples were collected bi-weekly to bi-monthly from October 2011 through March 2013. We analysed the trace gas fluxes using a static vented chamber, and ran all samples on a gas chromatograph (GC) with flame ionization detector for methane and carbon dioxide fluxes, as well as on a GC with a electron capture detector for nitrous oxide (N_2O) fluxes. We performed Roche 454 barcode sequencing of 16S rRNA genes across all collection dates.

Results:

Across all measurements, N_2O production was more than twice as high in the increased nitrogen treatment relative to the control. In particular, the difference between N added and control plots was greater after mid-winter rainfall events. We found that the profiles for methane and carbon dioxide were more complex, with rainfall timing becoming an important factor. Overall, the microbial community varied more in the control than the N addition plots, and the drought treatment led to a less diverse microbial community, dominated by the Actinobacteria.

Discussion:

The microbial community structure and functional response to climate changes, such as drought, and environmental changes, such as increased N deposition, will be varied and complex.

Keywords: methanotrophy, nitrification, greenhouse gases, grassland

[P2.227]

Soil bacterial and fungal community composition along a plant species richness gradient

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Abundance and diversity of microbes in soil is extremely large, yet their distribution is not totally random. Several studies have shown how particular microbial groups (arbuscular mycorrhizal fungi, plant pathogens, plant pathogen suppressive microbes) respond to increasing plant species richness but it remains unclear how similar or different their relations are with plant species richness and composition. We hypothesised that 1) the fungal community is more responsive to variation in the plant community than the bacterial community, 2) alpha diversity (richness within the community) of soil microbes increases and 3) beta diversity (turnover of species between communities) decreases with plant species richness. To test the hypotheses we sampled soil from the long-term Jena biodiversity experiment comprising a plant species richness gradient of 1, 2, 4, 8, 16, and 60 grassland species, replicated in 4 blocks. We used 454-pyrosequencing of 16S and 18S to identify the soil microbial community composition.

We found that the majority of species of bacteria and archaea occurred in few plots and at low relative abundance, while a minority of species were highly abundant and occurred in nearly all plots. In contrast several fungal species occurred in only few plots and at high relative abundance, indicating that fungal species respond stronger to the local plant community than bacteria, confirming the first hypothesis. Plant species richness increased the minimum value of alpha diversity of bacteria and archaea, while the beta diversity of bacteria and archaea decreased between plots within the same plant diversity level, confirming the second and third hypotheses. These results indicate that the more plant species are present the more similar the community composition of bacteria and archaea becomes in terms of species identity and relative abundance. The analysis of the (dis)similarities of the fungal communities is in progress but will be included on the poster.

Keywords: Soil microbial diversity, Plant-soil interactions, 454-pyrosequencing

[P2.228]

Neighbouring landscape and land use shape the local functional diversity of soil fauna

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The aim here is to study the respective influences of land use and neighbouring landscape on functional diversity of soil fauna (earthworms, woodlices and millipedes).

Soil fauna was sampled in 184 plots. At each one, land use (open vegetation: crop or grassland, closed vegetation: deciduous or coniferous forest) and neighbouring landscape (forested, wood-pasture mosaic, pasture-crop mosaic) were registered. Functional traits considered were habitat, microhabitat, diet, body size and pigmentation. Functional diversity and community weighted mean were calculated. Statistical analyses were performed on trait assemblages from closed or open vegetation by constrained multivariate analyses and non-parametric tests.

In both vegetation types, we found that the functional diversity increases with landscape contrast while the functional redundancy decreases with the intensification of land use. In both vegetation types, intensification of land use lead to a loss of species without a modification of functional diversity, meaning that intensification of land use lead to a loss of functional redundancy. The landscape contrast, whatever the type of vegetation, increases functional diversity without modification of species richness, which is going with a increase of endogeic individuals and a decrease of litter individuals in closed vegetation, while is the reverse in open vegetation: more litter individuals, zoophagous or detritivore and less endogeic individuals, geophagous and larger. The impact on the trait assemblages is done in a complementary way: the ecological traits are filtered by landscape contrast while the morphological traits are filtered by the intensification of land use.

A more heterogeneous neighbouring landscape increases the probability to locally encounter species from a different habitat still able to tolerate the local habitat, which is the case of generalist species. The increase of functional diversity without increase of species richness, when the landscape contrast increase, therefore indicates a local replacement of species from specialist to generalist ones.

Keywords: functional diversity, soil fauna, landscape contrast, land use intensification

[P2.229]

The application of the contingent value method on inhabitants of Los Tuxtlas (Mexico) Biospshere Reserve who collaborated in a project of soil biodiversity conservation.

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The soil biota plays a main role in maintaining ecosystem functions and productivity in agriculture and forestry. In Mexico, there is little research about the below ground biodiversity. This study used the contingent valuation (CV) method which is used to estimate economic values for all kinds of ecosystem and environmental services. Here we used it 1) to estimate the availability, amount and perception of the below ground biodiversity for its conservation by the inhabitants of Los Tuxtlas Reserve and 2) to measure the impact associated with education on soil conservation and friendly land use decisions. We worked in three localities in the Biosphere Reserve "Los Tuxtlas", Veracruz, Mexico, which participated in the project "Conservation and Sustainable Management of Below-Ground Biodiversity (CSM-BGBD)", financed by the Global Environment Facility (GEF) and administered by the Tropical Soil Biology and Fertility Institute of CIAT (TSBF). This project elaborated an inventory of the belowground biodiversity focused on taxonomic groups that have an evident impact on soil fertility from the micro to the macroscale. A contingent valuation survey was applied to estimate the economic values associated with the soil biota conservation. The estimated economic value of belowground biodiversity per household ranged from $20.03 US for household that participated in the project to $19.06 US for the rest of the households. If we apply the average willingness to pay per household to the whole Los Tuxtlas Reserve inhabitants we are talking of around $497,434.43 dollars. We appraise that if all Tuxtlas residents pay the value they had given to the soil biodiversity, thus alone would nearly be enough for restoring the soil…

Keywords: valuation, soil organisms, knowledge

[P2.230]

Effect of four previous crops on potato yield and tuber quality and their impact on soil and rhizosphere bacterial communities.

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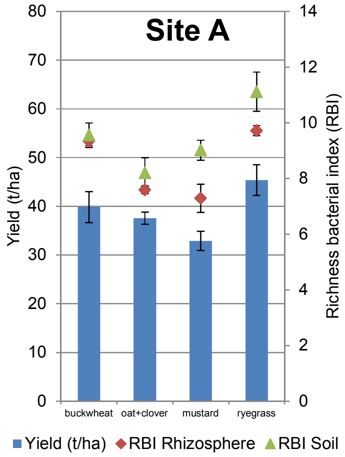
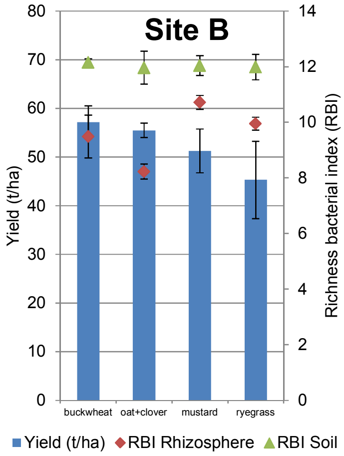
We studied the effect of four previous crops (oat + clover; mustard; ryegrass; buckwheat) at three potato production sites. The objectives were to improve the potato yield and the tuber quality, and to evaluate the impact of each management system (rotation crop - potato) on bacterial communities in soil and rhizosphere. Among the physical and chemical parameters of the soil, the three sites were mainly differentiated by their organic matter level that varied (A = 4.9, B = 8.9 and C = 6.2).

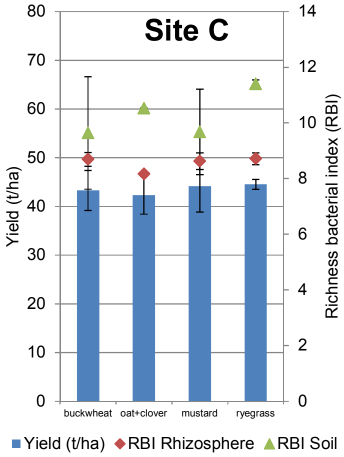
Previous crops at sites B and C had no impact on potato yields. The highest potato yields were obtained at site B in buckwheat and oat + clover sub-plots. The highest yields obtained at sites A and C from the ryegrass sub-plots were almost similar to the lowest yield obtained at site B.

The tuber quality was evaluated against four potato diseases. Previous crops had far less impact than the production sites on the mean Disease Index of Black scurf (A=0.37; B=1.14; C=0.18), Silver Scurf (A=5.67; B=0.95; C=0.08), Common Scab (A=0.44; B=0.51; C=0.28), and Powdery Scab (A=0.03; B=0.02; C=0.92).

The bacterial communities were extracted from soil and rhizosphere samples. Their DNA were extracted and amplified using primers targetting 16SrDNA V6-V8 region. The amplified products were analyzed by pyrosequencing. Based on rarefaction curves, richness bacterial index (RBI) values were calculated. Soil samples obtained higher RBI values. Previous crops showed lesser impact on RBI values than the sites. At site A, where the potato yields were the lowest, the previous crop had an impact on the richness of bacterial populations. Principal component analysis (PCoA) differentiated bacterial diversity settling in the soil and in the rhizophere, while relative abundance of several bacterial families, (*Xanthomonadaceae; Flavobacteriaceae; Streptomycetaceae; Hyphomicrobiaceae; Chitinophagaceae; Oxalobacteraceae; Sphingobacteriaceae)*, could be putatively linked with few agronomic traits.







Keywords: ecology, metagenomic, bacterial, yield

[P2.231]

Genetic diversity of *Porcellionides sexfasciatus* (Isopoda) in a metal contaminated habitat

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In 1993 the Convention on Biological Diversity considered different levels of biodiversity: diversity of ecosystems and landscapes, species richness and genetic variation within species. Genetic diversity may be affected by toxic substances, such as metals, widely spread in terrestrial ecosystems, due to anthropogenic activities. The way metal contamination changes the genetic diversity of exposed populations depends on its influence on evolutionary processes: mutation, genetic drift, migration and selection. In contaminated environments mutation rates may be higher resulting in increased genetic diversity, however, most mutations are deleterious which may affect the population viability and fertility and consequently the population size, ultimately reducing the genetic diversity. If metal pollution causes a decrease in population size, random changes in allele frequencies may be enhanced and genetic diversity decreases. Genetic diversity may, however, be maintained if individuals migrate between metal-contaminated and clean sites. Metal contamination of soils is considered to be a continuous, strong, directional selective pressure. Thus a reduction on genetic diversity may occur, by the elimination of homozygote genotypes that lack the increased tolerance. It is considered that the loss of genetic diversity reduces the ability of populations to evolve and to cope with further environmental changes. In this study, the effects of metal contamination on genetic diversity and differentiation were assessed in three populations of *Porcellionides sexfasciatus* collected at an abandoned mine area, using Random Amplified Polymorphic DNA (RAPD). No differences in genetic diversity were found, however moderate levels of genetic differentiation were observed, possibly due to genetic drift or local selective pressures (metal contamination). The lack of reduced genetic diversity using neutral markers may be due to the limited capacity of neutral markers to identify contamination-induced changes on genetic variation, since a decrease in genetic diversity will only be detected when population size is reduced and gene flow is restricted.

Keywords: Genetic diversity, Metal contamination, Terrestrial isopods

[P2.232]

Technical considerations for the construction and interpretation of co-occurrence networks inferred from massive sequencing data.

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High-throughput sequencing (HTS) approaches have been used to characterize microbial diversity in different ecosystems. However, we lack understanding of the interactions among microorganisms. Here, we combined the use of co-occurrence network analyses with HTS published data[1] of soils from three types of ecosystems (forest, prairie and cultivated field) and explored potential interactions among microorganisms. We propose that the resulting networks will reveal properties or attributes of the different communities that will be associated with the community structure and the ecosystem origin.

Decision on OTU identity threshold must consider a balance among problem treatability and OTUs biological significance. The number of OTUs increases with the identity threshold. Furthermore, low-occurrence OTUs can generate noise and ambiguous interactions during network inference [2]. First, we investigated the effect that different OTU identity thresholds had on network inference. We tested for 67%, 82%, 94% and 97% sequence identity thresholds using QIIME. OTUs determined with 82%, 94% and 97% thresholds showed similar taxonomic resolution, but the 94 and 97% OTUs had more than 50% low-occurence OTUs (<10 occurrences). Taking into account: computational efficiency, inclusion of genetic diversity, and potential confounding effects of low-occurrence OTUs, we used the 82% threshold and eliminated low-occurrence OTUs to infer the networks with Cytoscape's CoNet plugin [**FIG1**]. The resulting networks were analyzed using python's NetworkX package.

The comparison of the networks showed that while the three communities have 47% of OTUs in common, only 2% of the interactions are shared [**FIG2**]. Node´s (OTU) degree and betweeness centrality were not correlated with relative abundance for any ecosystem [**FIG3**]. Altogether, the analyses demostrate that microbial communities uniqueness is more evident when we look beyond inventories of species or OTUs and explore the interactions among members.

[1]Portillo, *et al*. *Appl.Environ.Microbiol*. 79(24), 7610-7617 (2013).

[2]Faust, *et al*. *PLOS.Comp.Biol.* 8(7), e1002606 (2012).

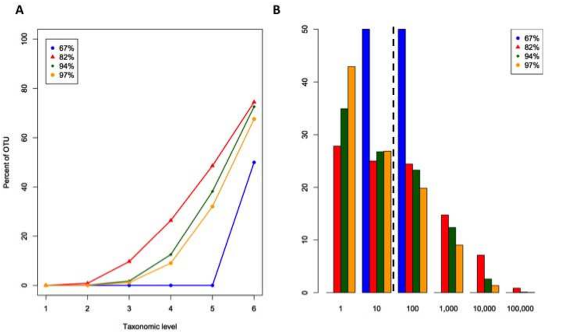

FIG1. Technical considerations for data selection for network inference. **(A)** Percentage of OTUs with non-determined taxonomy. **(B)** Distribution of OTU occurrences across different identity thresholds.

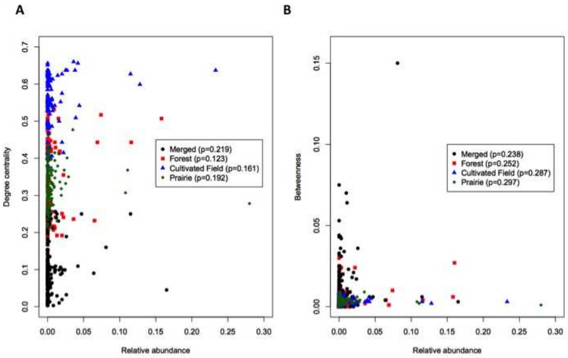

FIG3. Relation between relative abundance and degree centrality **(A)** and betweenness **(B)** for OTUs in each type of soil. Spearman correlation coefficients for the plotted variables are indicated in brackets.

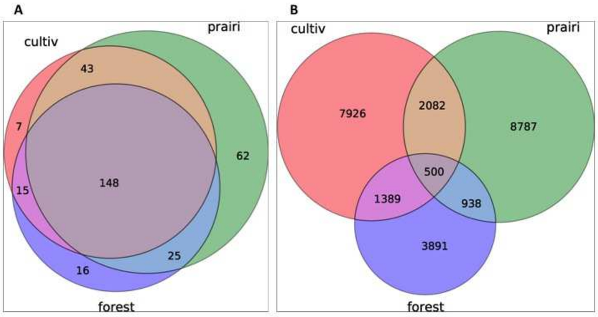

FIG2. Venn diagrams for shared nodes **(A)** and edges **(B)** between the networks associated to three types of soils. ***forest*** = forest, ***prairi*** = prairie, ***cultiv*** = cultivated agricultural field.

Keywords: High-throughput sequencing, Co-occurrence networks

[P2.233]

Do arbuscular mycorrhizal fungi exhibit phylogenetic conservatism in their response to drought?

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Diversity of arbuscular mycorrhizal fungi (AMF) in soil is considered as one of the major factors contributing to the maintenance of plant biodiversity and to grassland ecosystem functioning. It is therefore of great interest to understand how AMF communities respond to disturbances expected with climate change, such as drought. Thus far, however, the impact of drought on AMF diversity in soil has been largely overlooked.

By means of a tag-assisted MiSeq (Illumina) sequencing approach, we addressed changes in the composition of soil AMF communities in the field-based mesocosm experiment by de Vries et al. (this meeting), after imposing an experimental drought. Approx. 800,000 AMF 18S amplicons (ca. 420 bp-long) obtained from soil samples collected under different plant assemblages at four time-points (before, at the end, and two and eight weeks after ending the drought treatment) were analyzed. The AMF diversity covered by the primers used was (almost) saturated in most samples (per sample Good's coverage estimator ranging 0.873-1.000). 97% sequence identity OTUs were identified as Virtual Taxa (VTX) using a customized reference repository, derived from the MaarjAM database (http://maarjam.botany.ut.ee/).

Most (80%) of the 60 VTX retrieved following subsampling at even sampling depth were unaffected by the treatment. However, sequence abundances of 12 VTX significantly increased or decreased at either the end and eight weeks after drought (METASTATS, 1000 permutations). At both time points, VTX exhibiting a significant increase in the treated samples belonged to the Glomeraceae or Claroideoglomaceae (Glomerales), whereas VTX exhibiting a decrease belonged to the Acaulosporaceae or Gigasporaceae (Diversisporales). This finding suggests a certain degree of phylogenetic conservatism in the response of AMF to drought disturbance.

Keywords: Glomeromycota, bioindicators, drought disturbance

[P2.234]

European index for sustainable and productive agriculture. The Inspia project

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The concept of sustainable development has evolved from a mere movement for the protection of the environment, to a holistic approach, seeking to preserve not only the environment, but also to achieve sustainability in economics and social wellbeing. Using a more efficient use of natural resources whilst preserving biodiversity are the main challenges for agriculture. Indeed, soil biodiversity is widely recognized as an indicator of soil health and quality, and as a relevant factor for the soil to fulfill its ecological functions. The decrease of soil biodiversity has been identified as one of the major threats to European soils. Within the upcoming rules of the Common Agricultural Policy there are some special measures to preserve a minimum degree of biodiversity on farmland, which oblige to maintain part of the cropland out of production, such as the ecological focus areas.

Inspia project is a win-win for European agriculture. Inspia will demonstrate sustainable agriculture through the implementation of Best Management Practices (BMPs) and the measurement and monitoring of a set of defined indicators. Inspia promotes sustainable practices that protect ecosystems services provided by biodiversity, as well as soils and water. BMPs based on minimum soil disturbance, permanent soil cover, and crop rotations, are considered as a valuable option, capable of enhancing soil biodiversity. The implementation of the BMPs deliver ecosystem services, and recognize the value of natural resources such as biodiversity, water quality, soil quality, among others.

The project is present in over 50 farms in Belgium, Denmark, France and Spain and its main objectives are:

Demonstrate that BMPs help to achieve sustainability in European agriculture.

Provide an index of farm sustainability based on a set of verifiable indicators.

Create a farm network to enable the validation, demonstration and communication of BMPs.

Promote sustainable agricultural practices.

Raise awareness among EU stakeholders.

Keywords: BMPs, index, farm network, indicators

[P2.235]

Ecological diversity of arthropod fauna in the soils of some agricultural and natural landscapes in Romania

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Agricultural policy reform, after Romania joined the European Union, proposed (according with the Communitarian Agricultural Policy) a model of sustainable development based on various forms of agriculture, rich in traditional practices, like multifunctional farms focused on rethinking of some indicators such as diversification, productivity, biodiversity conservation, ecotourism, rural tourism.

Based on a wide variety of soil types, Romania has a very rich source of soil biodiversity, especially in the arthropods fillum. However, studies about soil biodiversity (in natural ecosystems or agrosystems) are poor and connected only with some ecological peculiar aspects of some regional areas.

Our research is based on many original studies performed by the authors and on the review of other important investigations carried out during 1983-2014. Our main goal is to show some preliminary data on soil arthropods biodiversity in different soil types from Romania and in different landscapes - natural ecosystems and main types of agrosystems: maize, wheat, sunflower, sugarbeet, potato, alfalfa and pastures crops. The method for collecting the biological material was the use of the soil pit-fall traps for the mobile epigeous arthropods fauna from the ground level. The sampling period was monthly, from Mars to November, each year. For each ecosystem, 25 traps were placed in different sampling sites, depending on the environment heterogeneity. The second method used was the soil survey in a hole with 25 cm^2 surface and 30 cm depth. For every research site a number of 30 each soil survey was performed. All arthropods in a pit represented a sample.

The main groups of arthropods were listed from a case study, with the values of their relative abundance in every soil type in connection with two important drivers: host plant and soil type.

Keywords: soil type, arthropods, ecology diversity, host plant

[P2.236]

Effects of the earthworm Aporrectodea caliginosa and the plant Lolium perenne on microbial communities of a technosol

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Technosol is a recent technology based on the assemblage of technogenic materials which had started to be used for ecological remediation of polluted soil environments (Farhan et al., 2012). Soil construction is an innovating option to do remediation by a process based on the assemblage of already treated soil, recycled waste, and industrial residual products; which are treated, formulated and layered in order to build a new soil profile, so the technosol, in the polluted area which need remediation. Little is known about the effects of earthworms in interaction with plants on the microbial communities' structure and activities. In this study, we used six different ratios of ballast lime material (BLM) with 0, 10, 20, 30, 40 and 50% of compost (Co). Each technosol was submitted to four treatments: 1) control formed by only the different ratios of BLM and Co, 2) with the earthworm (*Aporrectodea caliginosa*) 3) with the plant (*Lolium perenne*), and 4) with both the earthworm and the plant. After a 5 month incubation in phytotron (20°C, 80% of the WHC), samples were collected to analyses the microbial communities structure and activities. To this aim, the environmental DNA was extracted and quantified, the abundance and the diversity of bacteria, fungi and archae were estimated using qPCR and T-RFLP. In addition enzymatic activities were measured as well as catabolic profiles using Biolog Ecoplates®, Results show a strong and positive correlation between the number of bacteria and the amount of compost in all technosol treatments, and also suggest an effect on the fungal diversity. The effect of *Aporrectodea caliginosa* and *Lolium perenne* were both significant on microbial activities but the effect of the latter was more important. This study provides new insight into our understanding of the influence of plant and earthworm on the microbial communities of technosols.

Keywords: Technosol, Soil Microbial Communities, Earthworm, Plant

[P2.237]

The MCM TON: A research program to understand terrestrial ecosystem response to rapid environmental and ecological change

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There is considerable interest in understanding how terrestrial ecosystems have, and are continuing to respond to rapid environmental and ecological change. Research at the McMurdo Long Term Ecological Research site in Taylor Valley, Antarctica takes advantage of the extremely dry, windy, cold and saline environments in order to study soil biodiversity at its physical limits. These environments are extremely sensitive to natural and anthropogenic drivers of ecological change, but they are also very sensitive to research activities.

Recent efforts to coordinate ecological studies associated with the major landscape features have been highly successful. To efficiently move these research programs towards informing predictive models of how Antarctic soil ecosystems and their biodiversity will respond to future global changes, we are developing a multinational, interdisciplinary, long-term data monitoring and observation network (MCM TON). With the participation of researchers and program managers from the United States, New Zealand, Italy, Korea, and Australia, we have developed i) the minimum core set of measurements required to assess and address environmental change on Dry Valley ecosystems (and other terrestrial ecosystems in Antarctica), ii) the requisite standards and protocols for gathering the most critical biotic and abiotic measurements associated with the dominant terrestrial landforms, iii) a draft data coordination and development plan that will maximize the utility of these data, and iv) tools for assessing the effectiveness of current McMurdo Dry Valley environmental protection guidelines.

By coordinating international experimental and observational measurements through the MCM TON, we have significantly increased our ability to measure key processes associated with environmental change in Dry Valley ecosystems, as well as assess the effectiveness of existing environmental stewardship and management policies.

Keywords: Long-Term Monitoring, Observation Networks, Rapid Environmental & Ecological Change, Measurement Standards & Coordination

[P2.238]

Can arbuscular mycorrhizal fungi be used as bioindicators of land use?

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Being abundant in nearly all soils and less diverse than other soil organisms, Arbuscular Mycorrhizal Fungi (AMF) are potential indicators of land management legacies and soil quality degradation. It has been pointed out that these are critical factors for understanding and supporting the sustainable use of soils, but can be difficult to measure directly (Jansa et al. 2014). To serve as broadly applicable bioindicators, AMF should exhibit consistent patterns in a range of soils.

In the framework of the EcoFINDERS project, soil AMF assemblages were described in four European long term observatories (mainly grasslands), located in different climatic and geological zones, subjected to either low or high management intensity. AMF communities were described, in both spring and autumn, by means of high-throughput metabarcoding targeting the ITS2 region. AMF community structures were related to soil properties, land management intensity and geographic distances to address the relative importance of these factors in shaping the composition of AMF communities.

As expected, our results indicate significant effects of management type ($p=0.000999$), soil chemical and physical properties (such as pH, soil texture, organic carbon content and available phosphorus), and among-site geographic distances on community composition (Mantel tests). Indicator species analysis (presence/absence data) retrieved some taxa (or their combinations) characteristic of specific land uses (or their combinations) in both seasons.

Jansa J. et al. 2014 - Soil and geography are more important determinants of indigenous arbuscular mycorrhizal communities than management practices in Swiss agricultural soils. Molecular Ecology 23: 2118–2135

Keywords: Glomeromycota, bioindicators, land use

[P2.239]

Earthworm abundance in land-use systems in Santa Catarina state, Brazil*

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Little is known of the earthworm communities (abundance and diversity) of the state of Santa Catarina (SC), Southern Brazil. Therefore, the present study evaluated earthworm species richness and abundance in various land-use systems (LUS) in four regions (West, Plateau, East, South) of Santa Catarina. Five LUS were sampled in three counties per region: native forest (NF), *Eucalyptus* plantation (EP), pasture (PA), integrated crop-livestock (ICL) and no-tillage cropping (NT). Nine TSBF sized holes (25x25cm, 20cm deep) were taken in each LUS in summer and winter seasons, totaling 1080 samples. The earthworms were fixed in alcohol 92.8%, counted and identified to family, genus and species level. Considering the LUS independently of region, higher annual mean abundance was found in RE and PA (125 and 89 ind m^{-2}), while the other LUS had much lower abundance (ICL=69 ind m^{-2}, NF=65 ind m^{-2} and NT=49 ind m^{-2}). Exotic earthworm species dominated in all LUS (EP>NF>NT>ICL>PA = 95>88>69>66>61% exotics). Considering each region separately this scenario changes. PA (West) and ICL (Plateau) had higher abundance (118 and 60 ind m^{-2}, respectively), while the other LUS ranged from 5-30 ind m^{-2}, with smallest abundance in RE in both regions. Several LUS in the West (NF, PA and NT) and Plateau (NF, EP and PA) regions had 100% native species. The East region had higher abundances in EP, NF, PA and NT (300, 228, 191 and 113 ind m^{-2}) and all these LUS had >90% exotics (RE=100%). EP in the South had the highest abundance (185 ind m^{-2}), followed by PA (88 ind m^{-2}). The other LUS had <50 ind m^{-2}, with NF only 11 ind m^{-2}. Exotics dominated in the South in NF and EP (89 and 92%), while ICL and NT had more native spp (60 and 66%).

Keywords: Oligocheata, soil management, anthropic impact, agroecosystems

[P2.240]

Soil macrofauna denisty in different land-use systems in Santa Catarina state, Brazil*

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Soil macrofauna communities are strongly affected by soil and land-use management, with biodiversity patterns at local and regional level being dependent on management activities In Santa Catarina (SC), Brazil, little information is available on soil macrofauna, so during the SisBIOTA project (2011-2013), five land-use systems (LUS) were sampled (native forest - NF, *Eucalyptus* plantation - EP, pasture - PA, no-tillage cropping - NT and integrated crop-livestock - ICL) in 12 counties in 4 regions of the state (West, Plateau, East and South), totalling 60 sites (12 for each LUS). At each site, nine 25 x 25 x 20 cm monoliths (TSBF method) were collected in the winter and summer seasons using a 3x3 grid scheme. The soil macrofauna was fixed in alcohol 92.8%, counted and sorted at group level. Annual group richness ranged from 9 to 17 in all regions and LUS. Highest group richness was found in NF in the West (15), East (17) and South (16) regions and NT (15) in the Plateau. Macrofauna annual mean density was usually higher in all regions in the less impacted LUS (Region = NF, RE and PA – West = 612, 816 and 226 ind m^{-2} – Plateau = 913, 476, 1500 ind m^{-2} – East = 847, 984 and 1156 ind m^{-2} – South = 277, 1296 and 2368 ind m^{-2}), but in the West and South regions NT also had high soil macrofauna abundance (642 and 648 ind m^{-2}). Soil ecosystem engineers (Oligochaeta, Formicidae and Coleoptera) predominated in abundance in all regions. Isoptera were frequent in the West and Plateau regions. These groups accounted more than 88% in the West, 90% in the East, 92% in the Plateau and 95% in the South region of all the soil macrofauna density and varied considerably among the regions and among the LUS.

Keywords: soil organisms, soil management, anthropic impact, agroecosystems

[P2.241]

Case studies of evaluating soil microbiota on reclaimed sites in the Athabasca Oil Sands Region, Alberta, Canada

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Environmental practitioners and stakeholders are increasingly recognizing the critical roles soil organisms perform in fulfilling key ecological functions and providing ecosystem services, leading to higher demand for incorporation of soil biodiversity and ecology in assessing environmental degradation and improving restoration outcomes. This is limited, however, by the lack of standard methods and knowledge of linkages for incorporation into existing models and frameworks. While our understanding is growing rapidly, it is not yet possible to routinely predict effects of altered soil biota on ecosystem structure and function across ecosystems and soil types.

In Canada's Oil Sands region, novel initiatives involving soil organisms were applied to evaluate and improve reclamation outcomes. Case studies utilizing soil organisms and/or biodiversity to resolve environmental problems include a morphometric assessment of ectomycorrhizal diversity and abundance on tree roots on reclaimed tailings slopes with varying degrees of revegetation success; and the detection of sulphur oxidizing bacteria in stockpiles and reclaimed soils to evaluate the potential to convert elemental sulphur into sulphate. Despite the success of these studies, the current generation of molecular tools (e.g., metagenomics, DNA barcoding) presents a greater opportunity to incorporate measures of soil biodiversity and function in environmental monitoring and restoration programs, provided that standard procedures can be developed. To this end, assessing heterogeneity of soil biodiversity and function within and between soils and ecosystems likely to be affected, as well as effects of typical disturbances on soil biodiversity and corresponding changes in the provision of ecosystem services, is required. Potential studies of value include before-after-control-impact (BACI) studies incorporating reference, disturbed, and reclaimed soils.

Keywords: soil biodiversity, ecosystem services, metagenomics, reclamation and restoration

[P2.242]

Inclusion of soil biodiversity metrics in environmental impact and ecosystem function assessments - perspectives from the consulting industry

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Global impact assessment guidelines and governments require resource-development companies to assess impacts on biodiversity, along with ecosystem services. Currently there is no requirement to include biological aspects of soil in environmental impact assessments (EIAs). There are increasing requirements by regulators and expectations by stakeholders to mitigate project impacts and restore ecosystem function. As an example, Canadian Oil Sands operators are mandated to return the disturbed land to an equivalent capability with minimal loss of ecosystem functions, which requires healthy starting soils. Knowledge of soil biodiversity baseline conditions and how it is affected by industrial disturbance in Oil Sands is scarce, due to limited information on success of current reclamation projects (which take decades to achieve in cold, northern climates) and a lack of defined ecologically relevant soil health indicators. Local communities in Canada have expressed concerns with such limitations and are starting to request mining and oil companies to include additional data in EIAs, including soil biological assessments. Application of knowledge and procedures that can enhance and/or accelerate reclamation in this region is of great interest for all stakeholders.

To this end, there is a need for consulting professionals who understand and can translate technical and regulatory information to resource-development companies, as well as facilitate transfer of such information to key stakeholders. Environmental consultants have a key role to play in informing companies of the value of the inclusion of soil biodiversity data in EIAs, as well as contributing to the body of knowledge on soil biota pre *vs*. post disturbance.

We present considerations and approaches for conducting soil diversity assessments as part of EIAs to guide the implementation of scientifically sound, practical and cost effective solutions to ecosystem disturbances.

Keywords: soil biodiversity, environmental impact assessment, ecosystem function

[P2.243]

Predation by litter ants in a brown food web: diminishing effects from microbivory to decomposition rates

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Ants (Hymenoptera:Formicidae) are predators within tropical brown food webs, with important trophic interactions with other litter invertebrates and impacts on nutrient cycling. In a two-month field experiment, we used a sucrose supplementation assay to increase litter ant abundance. Then, we tested the general hypothesis that ants reduce the numbers of litter predators, shredders, and grazers, and ultimately, shape the rate of litter decomposition. After one month, ant abundance increased in sucrose plots. This increase was accompanied by significant reductions in the abundance of two shredder taxa and one predator taxa. After two months, the native form of the invasive ant, *Wasmannia auropunctata*, came to dominate sucrose plots, decreasing the overall abundance of the remaining ants and that of grazers. During the length of this experiment, there was no evidence of changes in litter depth or rates of decomposition. Our study highlights the importance of temporal scales in the study of trophic interactions among tropical litter taxa. We conclude that effects of predation by litter ants on other litter taxa may be limited by nutrient availability and molded by growth-defense tradeoffs among detritivore taxa.

Keywords: Formicidae, Tropical ecosystems, Brown Food Webs, Defense-growth trade-offs

[P2.244]

Climate variation impacts antarctic McMurdo dry valley soil food web structure and complexity

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Soils of the McMurdo Dry Valleys, Antarctica are some of the oldest, coldest, driest and most oligotrophic on the planet. Despite extreme conditions, relatively complex soil food webs exist. Yet, potential climate change impacts on these food webs are poorly understood. We asked: Is climate variation over a scale of 20 years reflected in soil food web complexity and structure? Dry valley soil food webs are composed of basal levels: cyanobacterial mats, bacteria, archaea, and fungi; and higher levels: protozoan and metazoan consumers (i.e., two mite, one springtail, two rotifer, two tardigrade, and four nematode species). Previous studies showed that soil habitats' physical and chemical compositions are primary drivers of community structure. However, soil invertebrates have mixed responses to interannual temperature and moisture trends, and it is unclear how soil food webs respond to these soil environment changes. We hypothesized that climate change (e.g., increased temperature, solar radiation, moisture pulses) will lead to higher food web complexity belowground. To test our hypothesis, we measured organisms' natural abundances of 15N and 13C isotopes and determined trophic positions of key taxa. Then, we examined food web structure changes for the McMurdo Long Term Ecological Research's elevational transect study near Lake Hoare in Taylor Valley. Using link density and connectance methods, we analyzed trophic complexity through time (1993-2013) for three elevations (83m, 121m, and 183m A.S.L.) and compared these results to climate data. Our results confirmed wetter, lower elevations had greater complexity (3+ linkages), but lower stability; while drier, higher elevations had less complexity (1 linkage) and higher stability over time. While trophic complexity was positively correlated with moisture, it was negatively correlated with air temperature. Overall, shifts in trophic complexity were related to climate variation over 20 years, and sites of greatest initial complexity experienced the largest fluctuations in structure over time.

Keywords: trophic, connectance, nematodes, desert

[P2.245]

Effects of the mound-building termite (*Macrotermes bellicosus*) on iron (oxyhydr)oxide mineralogy in a tropical savannah of Central Nigeria

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Termites (Isoptera) are regarded as one of the major ecosystem engineers which modify soil biophysicochemical environments and resource availability to other organisms in tropical ecosystems. It is well known that the termites manipulate soil material trough preferential selection of finer soil particles, but their influences on soil mineralogical composition have not been examined extensively. There have been several reports in the literature on this issue but most of them have assessed phyllosilicate minerals only and much fewer have addressed free iron (oxyhydr)oxides in the soil. In my previous paper (Abe and Wakatsuki, Pedobiologia, 2010), the selective dissolution analysis suggested that the mound-building termite (*Macrotermes bellicosus*) altered forms and composition of free iron (oxyhydr)oxides in a soil catena overlying the Basement Complex rocks of Southwest Nigeria due to altered moisture regimes in soil material incorporated into the termite mounds. However, detailed mineralogical analyses are still needed for further research. Therefore, X-ray diffraction analysis and differential thermal analysis were performed to analyse iron (oxyhydr)oxide mineralogy deeply by comparing soils that constitute termite mound structures with those of surrounding soil horizons free of any visible sign of termite activities. Findings obtained from the present study will be discussed in this presentation.

Keywords: soil iron (oxyhydr)oxides, termite mounds, X-ray diffraction analysis, differential thermal analysis

[P2.246]

Microbes at the top of the world: microbial diversity along a high altitudinal gradient soils in the Himalayas.

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Elevational diversity gradients of plants and animals are a well-established ecological phenomenon. Yet despite few attempts to describe microbial diversity along altitudinal transects it remains unclear if and to what extent do microbes mirror the changes seen in plants and animals. In addition, most studies focused on mountains in temperate regions where temperature decrease with elevation is the primary abiotic gradient affecting biodiversity. We studied the bacterial diversity and population size of various microbial groups along an extreme-high elevation gradient ranging from 4700 to 6450 m.a.s.l in the western Himalayas, where a precipitation gradient exists inversely to the temperature gradient.

Population densities of bacteria, archaea, fungi and cyanobacteria (determined using qPCR) and alpha diversity estimates for bacteria (determined using Illumina sequencing) all displayed a humped-shape trend peaking at around 5800 m.a.s.l, just below the subnival zone, coinciding with maximum plant diversity. Below this altitude, microorganisms were likely water limited; they were about 10 times less abundant and the bacterial community was about 30—50% less diverse. Above this altitude, temperature was likely the key limiting factor. Population sizes were up to 100 time lower and the bacteria were up to 70% less diverse.

Members of the orders Sphingomonadales, Sphingobacteriales and Solirubrobacterales were abundant throughout the gradient and together with Burkholderiales prevailed in the subnival soils, similarly to soils from hot and cold deserts. In contrast, lower elevations were dominated by Rhizobiales, Rhodospirillales, Micrococcales and Cytophagales. In addition, distinct communities dominated the different vegetation belts, desert and alpine grassland, found at lower elevations.

Our results show that soil microbes react to contrasting gradients of precipitation and temperate similarly to plants, and demonstrate clear and predictable changes in dominant taxonomic groups with increasing altitude. In addition, we demarcate the importance of Sphingomonadales, Sphingobacteriales, and Solirubrobacterales as pioneer species dominating deglaciated soils.

Keywords: Microbial diversity, Elevational Diversity Gradient, Deglaciation, High-throughput sequencing

[P2.247]

Enhancing soil animal biodiversity return to revegetated sites in Australia

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Problem. Since European settlement southern Australia has experienced much vegetation clearance for agriculture pastoralism, leading to soil erosion, loss of top soil, sediment increase in the water resource, increased vulnerability to flooding and reduced protection for stock from adverse weather.

Solution. In the last few years, considerable government funding has been directed to revegetation efforts by farmers, land managers and conservation organisations. Programmes such as planting 3 million trees and the Green Corps etc have assisted.

Audits. The “success” of revegetation efforts in recreating functioning ecosystems carrying a fauna of native species has not been assessed until recently. In the last few years, an attempt has been made to assess invertebrate abundance and species composition on selected sites particularly for Formicidae and Collembola also in two southern states, South Australia and Victoria. Both untreated, revegetated and remnant vegetation sites have been investigated in approximately equal numbers of each.

Results. Return of native invertebrates appears to be less affected by years since revegetation and more by location, original land use, climate and weather, plant species used, topography and current management. Examples of sites that have been monitored for the return of decomposer invertebrates and found to be successful and those not so successful will be documented and illustrated.

Keywords: Revegetation, invertebrates, Collembola, Formicidae

[P2.248]

Phages as biological and colloidal vectors of mass and genetic information in the Earth's Critical Zone

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Although viruses represent the most abundant entities on earth, research has focused mainly on marine ecosystems neglecting terrestrial habitats. Viruses that infect specific host bacteria, (i.e. bacteriophages), influence their hosts mortality, evolution, physiology and community structure, and thus on biogeochemical cycles. Despite their relevance still little is known about their transport behavior in terrestrial habitats and the implications of (transported) phages for the genetic landscape of the terrestrial deep subsurface biosphere.

Here we would like to present our recently started 'PHAGE' project in the framework of the DFG Collaborative Research Center 1076 – AquaDiva. The overall aim for the following three years is to study (transducing) phages as biological and colloidal vectors of mass and genetic information in the subsurface zone between the plant roots and the first aquifers (up to 100 m), known as the Earth's Critical Zone. As both mobility and the ability of infection determine the contribution of phages in ecosystems, we will assess their diversity and their role as drivers and indicators for microbial diversity and subsurface transport. More specifically 'PHAGE' aims at:

(i) Identifying bacteria participating in transduction-mediated gene transfer in different layers of the Critical Zone using Illumina sequencing of 16S rRNA genes isolated from phage heads. Using 454 shotgun sequencing we will investigate the viral functional metagenome in selected field core samples. These approaches will be complemented by transmission electron microscopy and PCR- fingerprinting techniques.

(ii) Investigating the factors driving subsurface phage transport and assessing the eligibility of marine phages as specific markers of hydrological flow and reactive transport of colloidal particles in the Critical Zone. Laboratory column experiments will be applied to test the possible effects of different factors such as phage morphology, different flow regimes as well as the role of eukaryotic (fungal, plant root) networks on phage transport and infection ability.

Keywords: virus diversity, virus transport, bacteriophage, networks

[P2.249]

Using terrain analysis and remotely sensed data to prediction of soil texture (A case study in the Southwest of Iran)

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In the recent decade a large part of Iran because of the rapid changes in land use due to overgrazing, over using of agriculture area and also the effect of climate change are prone to land degradation. *In many* qualitative modelling for assess of soil erosion and land degradation the spatial of soil texture is an important factor. Therefore the need for a digital soil map for assessment of land degradation with available data is very necessary because this information is practical for monitoring landscape change and the rate of soil erosion. There is various legacy soil maps in Iran that were produced based on traditional approaches that are not available for all the area and also with spending much time and cost to prepare those products. In this study we present a digital soil mapping approach with using of satellite images and terrain analysis. Terrain analysis with GIS and remote sensing technologies can be useful tools to predict the spatial distribution of soil texture. Therefore we delineated the topographies indices as basis for a subsequent soil map modeling, for this reason a high digital elevation model (DEM) with 10 m resolution has been processed in SAGA2.01 for extraction of these indices, Furthermore the information from satellite images (Landsat ETM, 2007) have been used to extraction of vegetation and land use indices. Finally the stochastic modeling has been used to regionalization of soil texture map in this study area. The result shows that the integration of data derived from DEM and satellite images allowed a detailed assessment of soil spatial distribution.

Key words: Soil map, Terrain analysis, Remote sensing

Keywords: Soil map, Terrain analysis, Remote sensing

P2.250]]

Effect of a bacterial polysaccharide on the structural stability of the soil

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The addition of bacterial polysaccharide (*Burkholderia fungorum* strain BF01) to the soil of Biskra (South of Algeria) at 2 concentrations (0,5 and 1%), allows a significant increase in the proportion of aggregates > 2mm stable to water and alcohol. We called this fraction coarse fraction which is representative of aggregation. This latter represent about 60% of the mass of the soil in soils added with EPS after water test and was about 7% prior to the addition of EPS. When we submit aggregates to a pretreatment with alcohol, the coarse fraction is estimated at 61% and 88% for soils enriched to 0.5% and 1% respectively EPS. The control lacks this fraction.

Rewetting soil by capillary, a less abrupt test operated under vacuum, is less destructive to soil aggregates unlike previous tests (water test and water test after alcohol pretreatment). The coarse fraction appears in soils treated with EPS in considerable proportions (96% and 99% for soils enriched to 0.5% and 1% respectively EPS). Unlike the two previous tests, this fraction appears as well in the control soil but is much smaller (about 8 times less than the two treated soils).

The bursting indices (IE) of the different samples provide the following classification:

$IE_{\text{control soil}} > IE_{\text{soil (0.5\% EPS)}} > IE_{\text{soil (1\% EPS)}}$.

We show that the polysaccharide produced by *Burkholderia fungorum* strain Bf01 has significantly strengthens the integrity of soil aggregates of Biskra.

Polysaccharides are transient agents that aggregate fine soil particles to form micro-aggregates. Microaggregates bind together to form larger aggregates. A combination of aggregate size and stability is needed to build soil structure.
The use of bacterial polysaccharides proves this fact very interesting for structural stabilization and improvement of the physical properties and the impact on water retention and soil fertility.

Keywords: soil, bacteria, structure, stability

[P2.251]

Structure and successional changes in communities of bacteria, archaea and fungi colonising granitic rock surfaces in a boreal forest

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In boreal forest ecosystems, bedrock outcrops and boulders are generally covered by mor-layer soil, with distinct mycelial mats at the interface between the rock surface and mor-layer. Using such rocks as model systems, we are studying microbial diversity and patterns of colonisation in relation to biogeochemical weathering processes that lead to mobilisation of mineral nutrients essential for plant growth and ecosystem function. The nutrients released from the rocks are utilised by the microbial community, taken up directly by roots or transported to roots via mycelia of ectomycorrhizal fungi forming symbiotic associations with tree roots.

We hypothesise that both microbial diversity and abundance will be greater on rocks receiving higher amounts of recently fixed photosynthetic carbon (to produce weathering agents such as organic acids or siderophores) compared to bare rocks. To test this we sampled rock surfaces that were either: 1) bare or colonised only by lichens, 2) colonised by mosses or 3) colonised by tree roots and fungal mycelia. We analysed communities of bacteria, archaea and fungi using high-throughput 454-pyrosequencing.

Significant differences were found between fungal and bacterial communities colonising the three rock-types. Lichen forming fungi were dominant on bare rocks while rocks with tree roots were dominated by ectomycorrhizal fungi and also exhibited higher fungal diversity than the bare rocks or rocks with mosses. A decline in abundance of lichens from bare to ectomycorrhizal rocks suggests that lichens may have facilitated the colonisation of mosses and subsequently ectomycorrhizal mycelia and tree roots during the course of boreal ecosystem development. Rocks with mosses and ectomycorrhizal roots had higher numbers of bacterial sequences than the bare rocks. Extremely low abundance of archaea on rocks suggests that they probably have little or no direct role in biological weathering. However crenarchaeota appear to have a specific association with rocks colonised by mosses.

Keywords: Microbial communities, Biological weathering, Ectomycorrhizal fungi, Boreal ecosystem

[P2.252]

Rhizosphere microbial community manipulated by 2-year consecutive bio-fertilizer application associated with banana Fusarium wilt disease suppression

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Banana production in China has been severely hindered by the *Fusarium* wilt disease. The effects of chemical fertilizer (CF), pig manure compost (CM) and the bio-fertilizer (BIO) for 2-year continuous application on the banana *Fusarium* wilt disease incidence, crop yield and rhizosphere microbial community were investigated in this study under the field condition. The field experimental results demonstrated that 2-year consecutive bio-fertilizer application significantly suppressed the banana *Fusarium* wilt disease and improved the banana yield. Moreover, rhizosphere microbial community responded differently to the application of bio-fertilizer (BIO), pig manure compost (PM) and only chemical fertilizer (CF) as revealed by 16S rRNA and internal transcribed spacer (ITS) deep pyrosequencing. In total 104,201 bacterial 16S and 154,953 fungal ITS sequence reads were obtained after basal quality control and *Acidobacteria*, *Actinobacteria*, *Bacteroidetes*, *Firmicutes*, *Proteobacteria* and *Ascomycota* were the most abundant phyla across all samples. Compared to the PM and CF treatments, after 2-year consecutive bio-fertilizer application, the alpha diversity of bacteria significantly increased while that of fungi significantly reduced. Moreover, the abundance of *Acidobacteria*, *Firmucutes*, *Gp1*, *Gp3*, *Leptosphaeria* and *Phaeosphaeriopsis* significantly elevated while that of *Proteobacteria* and *Ascomycota* significantly depleted in BIO treatment compared to PM and CF treatment. Furthermore, the abundance of *Fusarium*, a causal pathogen for *Fusarium* wilt disease, reduced significantly in BIO treatment compared to CF control and reduced slightly without significance compared to PM treatment. Interestingly, the disease incidence was also negatively correlated with *Acidobacteria* and *Firmicutes*, *Gp1*, *Gp3*, *Leptosphaeria* and *Phaeosphaeriopsis* while positively correlated with *Proteobacteria*, *Ascomycota*, *Fusarium*, *Cylindrocarpon*, *Gymnascella*, *Monographella*, *Pochonia* and *Sakaguchia*. Overall, this study suggests that a 2-year bio-fertilizer application manipulated the rhizosphere microbial community and induced a general suppression by increasing bacterial diversity and stimulating some possible microbial consortia taxa , such as *Acidobacteria*, *Firmicutes*, *Gp1*, *Gp3*, *Leptosphaeria* and *Phaeosphaeriopsis*.

Keywords: Bio-fertilizer, Fusarium wilt disease, Microbial community, Banana

[P2.253]

Are assemblages of Springtails (Arthropoda) from spoil tips distinct from those of surrounding environments?

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In North of France, spoil tips are similar to “islands of schist” within a "silty clay ocean”. Thus, the flora and fauna of aboveground dumps are unique and distinct from the surrounding environment (Petit 1980; Cohez and Derolez 2007). In order to study communities of springtails, samples of soil were carried out under four different vegetation types (an area without vegetation, an herbaceous area, a shrub area and a forest one) on twelve spoil tips and under similar vegetation types in their environments.

Microclimate, original substrate, exotic vegetation cover and geographic isolation affect the community of soil organisms of these dumps. Indeed, the community structure of Collembola in dumps differs from one observed in the environment with different dominant species. Moreover, we have already noted the presence of taxa in habitats which differ from their recognized ecological niche. We have found on zones without vegetation, Monobella grassei, usually observed in forest and Seira domestica, usually seen in human habitations. These observations suggest a particular ecological functioning of these anthropic soils. Discussion about causes and consequences at the local and regional scale of such difference is proposed.

Keywords: Springtail, spoil tip, community, ecological adaptation

[P2.254]

Effect of different types of insecticide (indoxacarb and pyrethroid) on functional groups of soil fauna in rape crops

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Practices to maintain and enhance ecosystem services provided by soil biodiversity

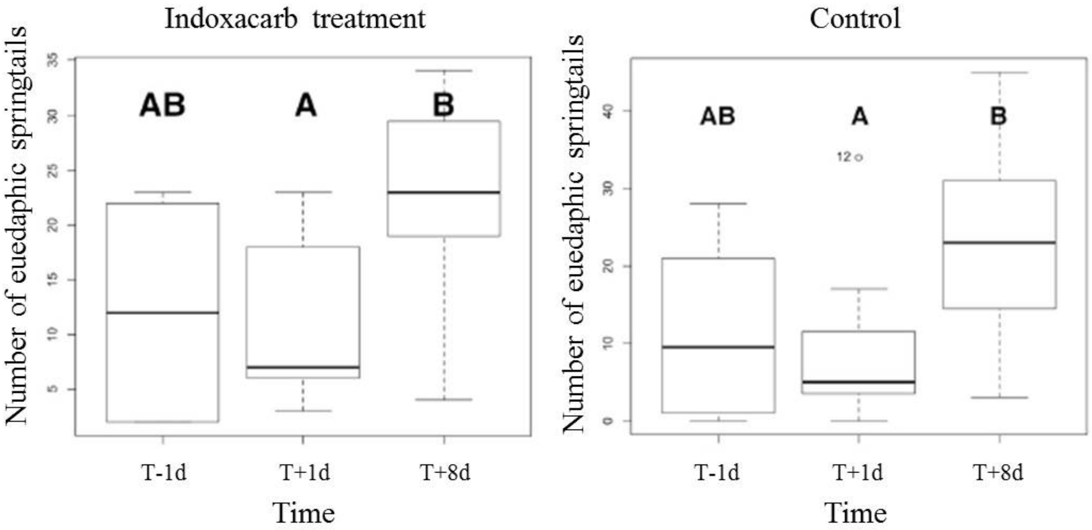
Elucidating relationships between soil biodiversity and ecosystem functioning and ecosystem services

The challenge of our time is to preserve the quality of our environment while maintaining our technical, social and economic achievements. Agriculture is known to have an important impact on ecosystem functioning and ecosystem services, especially through the generalized use of pesticides. However, the apparition of a new generation of pesticides, supposed to be more environmentally friendly, represent a promising step. Otherwise, ecosystem services provided by soil fauna represent an understudied, but nevertheless essential, aspect to consider ensuring the success of agriculture in the future.

We conducted an experiment to evaluate the effect of different types of insecticide used against rape crop pests (*Brassicogethes* spp) on soil fauna (springtails and earthworms). A new generation insecticide (indoxacarb) was compared with a classic insecticide (pyrethroid) and a control without any insecticide. The study was carried out in Picardie (North France) in 7 rape crop stands. Functional diversity of springtails and earthworms was assessed in each insecticide modality, using respectively Berlese extractor on soil samples and chemical extraction (with allyl isothiocyanate), before (1 day) and after (1 day and 8 days) insecticide treatment.

Results show that indoxacarb-based insecticide seems to be more effective in controlling rape crop pests (observable trend, but not significant). A positive development of euedafic springtails was observed between 1 day and 8 days after treatment (figure 1), but there was no significant difference of neither springtail nor earthworm functional diversity between insecticide treatments.

These results are promising, considering the impact of insecticides on soil fauna and the ecosystem services they provide. However, this kind of study has to consider sublethal effects.



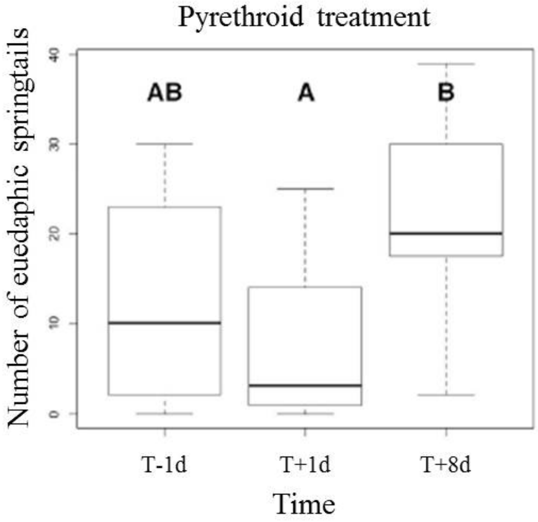


Figure 1 : box plots presenting the evolution of the number of euedaphic springtails overtime (1 day before, 1 day after, and 8 days after insecticide treatment). Different letters indicate differences in post-hoc Wilcoxon tests.

Keywords: insecticide, rape crop, springtails, earthworms

[P2.255]

Biodiversity of smelter wasteland reclaimed with biosolids and by-product lime

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Metal smelting wasteland sites are serious sources of secondary metal pollution. The sites are usually barren due to metal toxicity and harsh physical conditions which causes metal dispersion through wind erosion and runoff. Revegetation of such sites is a substantial challenge and involves a number of technical and cost difficulties.

The pilot site in Piekary, Poland was revegetated in mid 90s using municipal biosolids and limestone treatments along with pre-selected grass mixture. It was tested if such approach would support persistent functioning of the revegetated metal waste ecosystem. Total zinc content in top layer ranged from 6.9 to 128 g kg^{-1}. The reclamation work resulted in vegetation of 3 ha pilot areas. The site was reclaimed by application of biosolids at the rates 150-300 tons per hectare (dry matter basis) combined with the incorporation of high rates of by-product lime. The grass mixture consisted of the local cultivars of Festuca rubra, Poa pratensis, Festuca arundinacea and Festuca ovina. Additionally 23 other local grass cultivars was tested for their effectiveness in the wasteland revegetation.

The most crucial question is how persistent and sustainable are such constructed ecosystems. The long term site monitoring included chemical (e.g. metals extractability) and biological parameters (plant biomass, plants species diversity, microbial activity and community structure, insect biodiversity). Plant diversity assessment involved both original grass species and spontaneous vegetation. Samples for the analyses were collected in a regular grid and in various periods.

This paper will present trends in evolution of biodiversity over 19 years period as related to waste toxicity and their implications to risk to humans and wildlife.

Acknowledgements: The financial support by FP-7 project GREENLAND contract No. 266124 is greatly appreciated

Keywords: wasteland, revegetation, biosolids, biodiversity

[P2.256]

Impact of novel combinations of soil amendments on biodiversity of contaminated soils and reaction of soil organisms

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Metals can be stabilized in contaminated soil by amendments increasing metal adsorption or altering their chemical form. Few experiments compare different amendments under similar environmental conditions, or consider whether all soil properties or functions (microbes, soil fauna, plant growth, retention, colloid stability, etc.) are similarly protected. Within the EU FP7 Greenland project (266124) we compared the impact of novel soil amendment combinations and traditional materials on metal solubility and response of plants, soil organisms and microbial activity.

One-year greenhouse pot experiments were established on toxic agricultural soil contaminated through long-term Zn/Pb smelter emissions in Poland. Amendments were tested individually and in novel combinations: compost, drinking water residue, iron grit, Ca-phosphate, LD slag, Thomas basic slag, gravel sludge and siderite, cyclonic ash (CA). Soils were planted with grasses or lettuce. Soil metal extractability, pH, EC and enzymatic activity were measured. Determinations of microbial activity included intensity of dehydrogenases and acidic and alkaline phosphatases.

Parallel tests evaluated earthworm behaviour and metal accumulation. Eisenia veneta earthworms were put into jars stored at 20° C. Earthworms were removed from the soil after 4 weeks, weighted and analysed for metals content. The soil was thoroughly mixed and samples were taken for the determination of metal solubility and pH.

The earthworms were removed from soil and kept on moist filter papers in glass vessels for 3 days for full depuration of worms. Then they were washed in deionized water, dried on paper towels, and killed by dry-freezing. The dry weight of the earthworms was recorded and the samples were dissolved in concentrated nitric acid (Baker Analyzed Instra). Metal concentrations in earthworm extracts were measured with inductively coupled plasma mass spectrometry (ICP-MS, AGILENT 7500CE).

Acknowledgements: The financial support by FP-7 project GREENLAND contract No. 266124 is greatly appreciated.

Keywords: contamination, amendments, earthworms, enzymes

[P2.257]

EST (expressed sequence tag) analysis on soil mite, Nanhermannia verna (Nanhermanniidae: Oribatida).

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There area many papers about food habits of oribatid mites studied as a decomposer by morphological and ecological view. Siepel and deReuiter-Dijikman (1993) reports seven types of guilds in oribatid mites based on several patterns of biochemical enzyme activities, cellulase (digestive enzyme of cellulose, main component of plant cell wall), chitinase (chitine, main component of fungal cell wall) and trehalase (trehalose, main component of cytoplasm).

Our purpose was an exhaustive investigation on gene expression of *Nanhermannia verna*, as a model of oribatid mites. The data set was neither taken from isolated gut cell of mites nor used isolated microbes, however, the data set could be based on several expanded studies (e.g. *in situ* hybridization). The database of EST analysis was established by cDNA library and a massive sequencer. The 589,151 reading 56.4M bases was determined by Ion 318 chip, Ion PGM 200 sequencing Kit (Life Technologies) with Ion Torrent PGM (Life Technologies). *De novo* assembly was carried out by CLC genomic workbench (CLC) and obtained 4,849 contigs. These contigs was analyzed free soft, blastX and Blast2go. Finally, expressed eleven cellulase genes was detected and was suspected to originated from Arthropoda (36%), Protista (9%) and Bacteria (55%). Similarly, other two expressed gene was suspected these origin as that gene 36 expressed trehalase gene from Arthropoda (8%), other organisms of Animalia (2%), Fugi (8%) and Bacteria (79%), 14 expressed chitinase gene from Arthropoda (79%), and Bacteria (21%). Actually, so many origins of expressed gene in such tiny oribatid mites. For studies of oribatid mite function as a decomposer, we would like to take next step based on these results of gene expression.

Keywords: function, soil mites

[P2.258]

Re-evaluated testate amoeba fauna by soil inhabiting species

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For the first time in the vast population of soil material investigated testate amoebae in mountain and lowland forests of Japan. An analysis of 152 samples of forest soil from each island - Honshu, Yaku, Kitadaitou-jima, Minamidaitou-jima and Kume-jima. The territory of Japan is of interest to protistology as an example of a unique island biogeography of large and small islands. It is part of the eastern part of the Holarctic. The island of Honshu comes in two biogeographic provinces - Japanese Evergreen Forest and Oriental Deciduous Forest. The most southern islands make up the local biogeographical unit: Ryukyu Archipelago.

The samples found about 250 taxa of testate amoebae, included almost 150 species was new record to Japan. We describe two new species - *Deharvegia japonica* and *Assulina discoides*. The bulk of the population belongs to evribiontnoy and cosmopolitan group of testate amoebae. While the findings are not specific to species of the Holarctic, such as *Centropyxis deflandriana, C. latideflandriana, C. stenodeflandriana, C. sacciformis, Cyclopyxis lithostoma, Distomatopyxis couillardi, Hoogenraadia humicola, Planhoogenraadia daurica, Assulina discoides, Deharvengia japonica, Quadrulella quadrigera, Q. quadrigera v. africana, Wailesella* sp. can raise the question of the uniqueness of the southeastern part of the Holarctic.

We believe that such a high frequency of species common to the Indo-Malayan, Australian and Neotropical regions gives reason to raise the question from the standpoint of Protistology on the special status of biogeographic Japan.

Keywords: soil protists, diversity

[P2.259]

Do arbuscular mycorrhizal fungi improve productivity and nutrient uptake of field-grown wheat? A numerical analysis of published field trials from 1975 to 2013

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Arbuscular mycorrhizal fungi (AMF) can benefit the growth and yield of agriculturally significant crops by improving mineral uptake, disease resistance and drought tolerance of plants. We conducted a meta-analysis of 38 published field trials with 333 observations to determine the effects of root colonization by inoculated and native AMF on nutrient uptake, growth, and yield of field-grown wheat. Field AM fungal inoculation increased grain yield (28%), P content in straw and grain (57 and 30%, respectively), N content in grain (58%), and Zn concentration in grain (7%). Grain yield and plant P concentration were strongly positively related to mycorrhizal colonization, while straw was negatively related. The most important drivers of the growth response of field-inoculated wheat were soil organic matter, pH, total N and available P concentration, and texture, as well as the identity of the inoculated AMF. When inoculation was not performed, the positive association between root colonization by natural AMF and plant traits was still present, but weaker than in inoculation trials. In addition to soil parameters, climate strongly affected wheat response to native AMF. Our analysis showed that AM fungal inoculation of wheat in field conditions can be proposed as an effective agronomical practice although its economic profitability should still be addressed for large-scale applications in sustainable cropping systems.

Keywords: AM fungal root colonization, Field-grown wheat, mycorrhizal field inoculation, Grain yield and nutrient uptake., Meta-analysis

[P2.260]

Functional traits and community structure of arbuscular mycorrhizal fungi in 10-year old rainfead Arundo donax and Miscanthus x giganteus energy crops under Mediterranean conditions

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Bioenergy crops play a key role in current agriculture. Changes in the European policies promoted the use of renewable energy and several researches were performed on the *non-food* sector. So far, the agronomical aspects and economics of such crops have been largely evaluated, but few studies have been performed on the quality of soil after their long-term plantation. Here, we studied the effects of long-term giant reed (Gr) and miscanthus (Mis) plantations on the root development, functional traits and community structure of arbuscular mycorrhizal fungi (AMF) in comparison with a wheat monocropping system (wheat). The AM fungal functional traits were studied using the root colonization percentage and density and the mycorrhizal infection potential (MIP) of the *non-food* crops respect to the wheat, while the within root AM fungal assemblages were assessed by the primers of Kruger et al. (2009). All these parameters were studied at different soil depths (0-15 cm; 15-30 cm; 30-60 cm and 60-90 cm).

Keywords: arbuscular mycorrhizal fungi, biomass crops, biofuel plants, giant reed and miscanthus.

[P2.262]

Tripartite symbiosis in intercropping systems

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Arbuscular mycorrhizal fungi (AMF), belonging to the phylum Glomeromycota, form symbiotic associations with more than 90% of all plants and are well known to improve their mineral content and productivity. Photosynthetic rates of mycorrhizal plants increase as nutrients are supplied by the AMF, increasing the amount of photosynthates available for fungal growth and maintenance. In re-turn for carbon (C), the fungus provides the host with mineral nutrients, such as phosphorus (P) which is present in the form of insoluble phosphates and hence cannot be directly utilized by the plants. The assessment of AMF diversity and spore density in agricultural soil confirms the existence of considerable amounts of inoculum.

Leguminous plants have the ability to fix N from the atmosphere through a symbiosis with soil bacteria belonging to the family Rhizobiaceae. Rhizobia N_2 fixation in legumes can reach up to 97% of the total plant N, reducing the need for mineral N fertilizer, increase yield and increase seed protein content. Moreover, several studies have shown that legume/rhizobia interaction can increase N availability to non fixing crops.

Legumes can co-host N_2-fixing rhizobia and AMF, which can form common mycelium networks with other plants such as non-legumes. Traditional agricultural practices such as intercropping legumes with non-legumes crops were developed to increase yields and reduce costs. Such practices have shown to enable savings of energy, reduction of greenhouse gas emissions, global warming, ozone formation and ecotoxicity.

The effects of intercropping maize with soy (leguminous crop), in the presence of microbial inoculants, on productivity and nutritional status of plants are to be assessed, under the hypothesis that the leguminous crop inoculated with rhizobia will enhance N availability for the non-leguminous crop by shared AM fungal hyphal networks.

To that, we established an experiment with split-pot containers with two plant root-hyphal compartments followed by two compartments accessible only to AMF hyphae and not to roots (Walder et al. 2012). The host plants were maize (*Zea mays* L.), for its socioeconomical importance, and soy (*Glicine max*), for its ability to support N-fixing rhizobia. Microbial inoculation consisted of *Rhizophagus irregularis* (AMF) and *Bradyrhizobium japonicum* (N-fixing bacteria). After 8 weeks of plant growth, 15N-labeled $(NH_4)_2SO_4$ was supplied to the farthest root excluding compartment.

Response variables consist of plant biomass, %N, %C, d15N and d13C isotopic signatures of maize leaves and soy seeds.

Results show a tendency to an increase on maize biomass in the presence of AMF and of soy biomass in the presence of both AMF and N-fixing bacteria. AM fungal mycelium growth was confirmed and d15N and d13C isotopic signature analyses results point to the establishment of a hyphal network between soy, maize and the d15N source. Altogether, d15N and d13C isotopic signatures results show that maize benefits from being in an intercropping situation, inoculated with both N-fixing bacteria and AMF, as it receives higher amounts of d15N.

Keywords: mycorrhiza, N-fixing bacteria, maize, symbiosis

[P2.263]

Correlations between soil bacterial community and black pepper (Piper nigrum L.) replant obstacle under continuous cropping systems

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Black pepper long-term cropping systems lead to the soil pH and organic matter significant decline. The present study compared the soils from 5 black pepper replanted orchards with different cropping history and their nearby grass land. A total of 202, 265 bacterial operational taxonomic units (OTU) were identified by 454 pyrosequencing analysis based on 16S rRNA genes. *Acidobacteria* and *Proteobacteria* were the main phyla in both the black pepper replanted orchards and the grass land soil, comprising up to 73.27% of the total sequences. The *Bacteroidetes* and *Actinobacteria* were more abundant in grass land than in black pepper replanted orchards, while the *Acidobacteria* showed an opposite result. Moreover, the abundance of *Actinobacteria*, *Chloroflexi* and *Nitrospirae* showed significantly ($P < 0.05$) positive correlation with black pepper shoot weights. In addition, at genera level, *Nitrospira, Pseudomonas* and *Bradyrhizobium* exhibited significantly ($P < 0.05$) positive correlation with black pepper shoot weights. Compared to the black pepper replanted orchards samples, α-diversity index of grass land is obviously higher, and among the 5 different continuous cropping history black pepper orchards, the 14y orchard with the lowest pH value showed the lowest diversity index. Both weighted and unweighted principal coordinates analysis (PCoA) showed that the bacterial community structure of grass land soil was significantly different from black pepper replanted orchards soil, and PCoA plots revealed the variation in bacterial community structure across 5 different continuous cropping history black pepper orchards could be attributed to the monoculture time. In sum, continuous cropping in black pepper cultivation changed soil microbial community membership and structure, and this change might result in soil weakness and black pepper replant problem.

Keywords: Soil bacterial community, Continuous cropping systems, Black pepper, Replant obstacle

[P2.264]

Human activites and their relative threats to biodiversity at selected forest reserves in Nigeria

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Thousands of years of cutting and burning, especially in Africa have so transformed vegetation and subsequently land that it bears little resemblance of its original state in which tree cover was probably denser than it is today. Concern has developed about the rapid rate of tropical deforestation, the temporary or permanent clearance of forest for agriculture and other purposes. This study evaluates the degree of pressure and threats imputed by human activities on protected areas in Yewa Division of Ogun State, Nigeria. Four forest reserves out of seven in the division were randomly selected as representative samples. They are; Ilaro forest reserve, Imeko forest reserve, Oja odan forest reserve and Aworo forest reserve.

Primary data were used for this study. Data were collected through the use of Rapid Assessment and Prioritization of Protected Areas Management (RAPPAM) designed questionnaire that was recommended for evaluation of threats and Pressure on protected areas (WWF, 2003). Descriptive statistics and ANOVA were the statistical tools used for data analysis in this study. The findings show that all the reserves are severely threatened by logging while only Oja- Odan F.R. is severely threatened by conversion of land use. In addition, Oja-Odan and Imeko are the only reserves that are severely threatened by hunting, although Aworo F.R. is also highly threatened. Oja-Odan F.R. and Imeko F.R are severely threatened by harvesting of non-timber forest products while Aworo is also highly threatened by same activity. Furthermore, all the forest reserves are highly threatened by grazing except Ilaro F.R. while cross boundary influence severely threatened Oja-Odan F.R., although severity of threat in Ilaro F.R. and Aworo F.R. is high as well. Result also revealed that there is no significant difference (LSD = 9.04; $p<0.05$) between activities in each forest reserves; although analysis of variance shows a significant difference between the pressure and threat across the forest reserves. Policy recommendations were made based on the outcome of this study.

KEYWORDS: Management Effectiveness, Protected Area Pressure, Conservation, Competing Useage

Keywords: Management Effectiveness, Protected Area Pressure, Conservation, Competing Useage

[P2.265]

Deciphering the potential biocontrol mechanism of bio-organic fertilizer application to Panama disease in a new reclaimed field based on culture-dependent approaches

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A novel healthy fertilization mode based on bioorganic fertilizer (BIO) in parallel to banana planting was carried out to manage the banana fusarium wilt in a reclaimed filed for three years. The functional capacity and community structure of the culturable rhizobacteria were evaluated through the combined utilization of Biolog Ecopaltes and culture dependent DGGE. Results showed that a significant reduction in disease incidence and promotion in crop yield were achieved by BIO application. The Biolog Ecopaltes analysis showed the metabolic capacity of rhizosphere soil induced by BIO application was significantly improved for the later two years, especially in utilization of carboxylic acids and phenolic compounds. The DGGE fingerprinting profiles demonstrated the obvious shift in community structure of healthy and infested rhizosphere soils in CK treatment along with the planting years, while on the contrary, the community structure of culturable part in soil applied by BIO was relatively stable. In addition, the higher richness and diversity index were observed in the rhizosphere soil collected from BIO treatment and more abundant culturable bacteria affiliated to Fimicutes, Gammaproteobacteria and Actinobacteria were also detected in these samples. All the results confirmed that application of bioorganic fertilizer effectively suppressed fusarium wilt disease in field condition by improving metabolic potential and stabilizing culturable microbial community. This novel healthy fertilization mode should be a useful strategy for suppressing banana fusarium wilt disease in an ecologically sustainable manner.

Keywords: Bio-fertilizer, Fusarium wilt disease, Banana, Rhizobacteria

[P2.266]

Global diversity and biogeography of soil fungi

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The fungal kingdom comprises some 100,000 described species, but little is known about general patterns of fungal diversity or functional roles over large geographic scales. We used a global dataset to disentangle the roles of climatic, edaphic, floristic, and spatial variables governing global-scale patterns of soil fungal diversity. We collected 40 soil cores from natural communities in each of 365 sites (2500 m2) across the world following a uniform sampling protocol.

DNA was extracted from 2 g of pulverized soil and subjected to ITS2 amplification using multiplex primers that match perfectly nearly all Fungi. Pyrosequencing 5 half-plates and clustering at 98% sequence similarity revealed 1,019,514 quality-filtered sequences belonging to 94,255 species-level OTUs, of which 85.4% were classified as Fungi. The 44,563 non-singleton fungal OTUs numerically correspond to approximately half of the described fungal species on Earth. Of fungal taxa, Ascomycota (48.7%), Basidiomycota (41.8%), Chytridiomycota (2.3%), and Cryptomycota (2.1%) were the most OTU-rich phyla. Only 24.2% fungal OTUs exhibited >98% sequence similarity to pre-existing ITS sequences in public databases, emphasizing our poor overall knowledge of global soil biodiversity.

Climate has both a strong direct effect on plant and fungal richness and functional groups, but indirect effects by altering edaphic conditions. Diversity of saprotrophs, parasites and pathogens peaked at low latitudes, whereas richness of EcM fungi peaked at mid-latitudes. Plant and fungal richness were positively correlated, but modelling indicated that this is best explained by similar response to climatic and edaphic variables rather than by direct effects of plants on fungi. The ratio of plant-to-fungal richness decreased exponentially with increasing latitude, challenging the present global fungal richness estimates. Consistent with Rapoport's rule formulated for macro-organisms, the mean latitudinal range of fungi strongly increased towards the poles, indicating greater endemicity at low latitudes.

Keywords: Global diversity, macroecology, DNA metabarcoding, Fungi

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