

Abstract EJP Soil Science Days 2022

Session: #4: Soil Biodiversity and Ecosystem Service

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### **Modelling the impact of the soil microbiome on carbon sequestration in the AGROECOseqC-project**

Soil fauna and microbial communities drive key ecosystem functions such as carbon sequestration and nitrogen mineralisation. The soil microbiome itself is shaped by land-use and soil management, e.g. plant diversity. Detailed knowledge about the relationships involved would provide options for baseline accounting and/or soil management. However, current models for assessing carbon sequestration are poorly equipped to represent the soil biota composition, functional diversity and activity. We hypothesize that the effect of plant diversity on carbon sequestration, playing a key role on shaping soil microbiome, may be differentiated from its effect as a mere source of carbon. To test the hypothesis, a modelling exercise will be carried out using the RothC-model and data from EU long-term experiments (LTE). Data collection in the LTEs will include all relevant aspects of the soil microbiome, i.e. particularly regarding its composition and activity. The RothC-model includes a BIO pool that represents carbon stored in the microbial biomass. Not only have pool size and turnover rate of the BIO pool been poorly validated, but the concept falls short in taking soil biodiversity into account. Furthermore, the model may be extended to include C from plant roots. Based on the outcomes of a multivariate analysis focusing on carbon use efficiency (CUE), the inclusion of the effect of the soil biome may be improved. Several possible adaptations of the RothC model will be tested with data from selected LTEs and evaluation made relative to time series of measured SOC from selected LTEs reserved for validation. Then conclusions may be drawn for a policy-relevant indicator, e.g. regarding the impact of the soil microbiome on carbon sequestration. This approach for model development will be discussed.

## Do we need an ISO standard on the valuation of ecosystem services provided by soils?

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Soils host an enormous biodiversity, both in terms of abundance, number of species and functions of organisms. These organisms and their interactions are fundamental to many soil processes and ecological functions, as organic matter decomposition, nutrient and water cycling, soil structure formation, pest regulation, filtration and biotransformation of contaminants. All those processes and functions can be related to ecosystem services that are of direct benefit to humans, such as food production, climate regulation or provision of clean water.

Ecosystem services are quite easily understandable and communicable: the way Nature provides you a service. Very quickly policy makers and even citizens have asked for valuations of ecosystem services provided by land (not only soil). As a consequence several world, EU, national or local experiments have been conducted leading to a great number of publications, the most famous one being the Millennium Ecosystem Assessment. All those valuations have more or less proposed their own definitions and methodologies leading to a wide diversity of results. For more than 10 years several approaches and frameworks were developed by research units around the world to assess soil functions and the related ecosystem services. As a consequence various minimum datasets of parameters were proposed for those assessments including at least soil biological, physical and chemical parameters, but also integrating land use, land management or climate information. Now it appears there is a need to gather all those experiences to provide a consensual methodology to evaluators.

Methods and models developed by scientists for investigating and deciphering processes in soils need to be translated into practical and transparent procedures. International standardization is a way to achieve such objective, as the aim is to share knowledge and reach agreement on a document (e.g., standard, guideline, technical report) that can be used worldwide. Having an international common way to assess soil functions and related ecosystem services is crucial to further compare valuations made in different countries, soil types and land uses (from degraded or contaminated land to agricultural or natural land) for management or remediation purposes.

ISO/TC 190 has developed from the 1980's more than 180 standards dealing with soil description and soil analysis. Until the 1990's most of the standards were dedicated to the characterization of soil

quality regarding fertility in relation to food production. Subsequently, the main emphasis shifted to the analysis of soil contaminants (e.g., trace elements, organic molecules) and their respective impact on soil living organisms (e.g., microorganisms, soil invertebrates, plants). More recently the issues of climate change and ecosystem services were raised. Last year during the plenary meeting ISO/TC 190 asked a group to decide about the need of standardization in the field of ecosystem services. We want to take the opportunity EJPS SOIL Annual Science Days to discuss this question with a broad range of research communities, coming from ecology, pedology, climatology, economics, agronomy...: do you think we can reach an agreement on definitions, indicators, models... to develop standards and by the way will you join us?

# Tuning the soil microbiome to support sustainable crop systems

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Soils provide 99.9% of the food consumed by humanity. Wheat is the most widely grown crop in agricultural system and is the staple crop for 35% of the world population, providing 20% of daily protein and food calories. To meet the sustainable development goal of 'food security' it is necessary to maintain healthy soils and to restore degraded agricultural land. Effective strategies require identifying, and targeting, the parameters that define a healthy soil but also the effectors. One of the WISH-ROOTS project goals addresses a main markers of soil health: the capacity to provide essential nutrients to plants and soil organisms while maintaining a balance, focusing on nitrogen cycling.

Application of nitrogen (N) fertilisers to agricultural soils supports half of the world's food production. However, approximately 50% of this N worldwide is transformed by soil microbes (through nitrification/denitrification) and lost to the environment by leaching/gaseous emissions. Biological nitrification inhibitors (BNIs) exuded from the roots of certain varieties of plants can reduce loss of N-fertilizer. Particularly, some historic landraces of bread wheat (*Triticum aestivum* L.) have shown evidence of BNI activity in their root exudates. Introducing this agronomic trait into modern cultivars could improve the efficiency of use of N-fertilizer by crops while reducing N losses to the environment.

Performing 16S sequencing analysis for rhizosphere soil from a modern wheat variety (Paragon) and an ancient landrace with BNI capacity has revealed a significant segregation in microbiome composition in the rhizosphere with significant differences in the abundances of several bacterial communities, particularly for guilds involved in the transformation of N in soil. The prediction of the functions of these communities using PICRUSt2 and shotgun sequencing has confirmed differences for several functions related to N transformation between Paragon and Persia.

Microbiome diversity in rhizosphere soil and associated functionality can be used for quantitative trait loci (QTL) mapping of agronomic traits such as control of soil nitrification. We have sequenced (16S and ITS) rhizosphere soil from 88 recombinant inbred lines of bread wheat derived from parentals with contrasting capacity to control nitrification in the rhizosphere. We have identified genomic regions in the wheat genome significantly linked to the abundance of specific nitrifying communities (*Nitrospiraceae*, *Nitrosomonadaceae* and *Nitrosococcaceae*) and associated ecological functions: aerobic ammonia oxidation and nitrification (PICRUSt2).

We are currently using wheat gene expression databases to identify potential target genes in the wheat genome which are expressed at high levels in root tissue and may influence soil microbial communities. This will be used to develop breeding targets for wheat breeders to incorporate BNI activity into modern bread wheat varieties. This strategy can provide advantageous varieties for farmers that support a more sustainable use of land improving soil microbial biodiversity and N cycling while ensuring wheat production for food security.

**Keywords:** rhizosphere, soil microbiome, nitrogen, wheat

# Microorganisms as biological indicators of soil quality under different tillage systems in *Retisol*

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Soil microorganism diversity have a close relation with soil function, and the changes in the composition of soil microbial population can directly affect it. To meet increasing human food demands, scientists and farmers face new challenges that result from significant ongoing climate changes which includes mild winters, prolonged vegetation period, extreme temperatures, and intense rain in the Northern part of Europe. Sustainable soil management and biodiversity conservation may be the key actions for the soil health maintenance. The aim of this study was to identify bacterial community composition and to determine the main soil chemical and physical properties formed by the different tillage systems. The experiment was set up in the year 2013 and had a split-plot design where the whole-plot treatments were laid out in a randomized design with three replicates. The whole-plot treatments consisted of three tillage methods – deep ploughing (22–25 cm) (DP), ploughless tillage (7–10 cm) (PT) and ploughless tillage (7–10 cm) with additional deep loosening (up to 40 cm), which was applied every 4 years (PTS). The split-plot treatments involved four types of additional organic fertilizers: stubble (S), chopped straw + N<sub>10</sub> (ChS), chopped grass (1<sup>st</sup> cut) + N<sub>10</sub> (G) and farmyard manure 40 tha<sup>-1</sup>(M). Soil samples were taken from the two layers of the soil profile, the upper 0–10 cm, and the lower 10–20 cm. Composition and diversity of soil bacterial communities were assessed by the sequencing of 16S rRNA genes. Results revealed that acidification process was determined in all analysed soils except in the soil with shallow ploughless tillage and additional loosening, however, this method significantly increased soil density and humidity but adversely affected aeration and general porosity of the soil. The highest biodiversity was found in the soil with shallow ploughless tillage and enriched with farmyard manure. *Actinobacteria* and *Proteobacteria* were the dominant bacterial species across all treatments. Their total abundance varied between 26% and 36% in the different analysed agroecosystems. In the conditions of western Lithuanian climate, the process of mineralization in *Dystric Bathyglyeyic Glossic Retisol* takes place all year round but becomes the most intensive in autumn. Neither the application of different organic fertilizers, nor tillage methods have any significant effect on the rate of mineralization of the substrate samples. Shallow ploughless tillage is the most suitable tillage technology, as it creates favourable conditions for the accumulation of organic carbon in the soil. Additional loosening promotes the loss of organic carbon in soil and increases the number of unsaturated compounds, which leads to soil degradation. These experimental results showed that great opportunities exist to change deep ploughing with alternative more environmentally friendly techniques, but further research is encouraged to determine the soil fungal and mesofauna biodiversity.

**Keywords:** bacterial communities; biodiversity; 16S rRNA sequencing; *Dystric Glossic Retisol*.

# ***Scanning soil biodiversity in long term Agroforestry system in temperate climate: results from central Italy***

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Soils have recently become part of the global carbon agenda for climate change mitigation and adaptation through the launch of high-level initiatives. Last year, FAO launched the RECSOIL program with the intention of increasing attention to management practices that increase soil organic carbon (SOC) and can partially mitigate carbon emissions. Recarbonisation of soil by current SOC stocks maintenance and fostering SOC sequestration, has positive effects on soil structure, water retention and nutrient supply and is critical for supporting ecosystem services and agricultural productivity (FAO). In this context, agroforestry, one of the most ancient agricultural practices of the Mediterranean culture and partly lost due to agricultural intensification, has recently been reintroduced for its positive effects on the SOC sequestration (FAO and ITP 2021).

In fact, agroforestry systems positively improve the resources of the agroecosystem by providing numerous advantages as reported in experiments performed, in recent years, on tropical areas. By contrast, long-term agroforestry (LTA) studies in temperate climate are still lacking. Temperate LTA studies focusing on the soil biota communities and relative roles of the ecological drivers of organic carbon dynamics are extremely interesting and deserve to be analyzed.

This survey aims to provide monitoring tools and to highlight specific "biological traits" and / or ecological relationships for the assessment of soil quality and to define appropriate biodiversity indicators useful for providing functional information relating to ecosystem services.

During spring and autumn 2021, we analyzed some components of soil biota: mesofauna and microbial fungal communities. Particular attention was given to collembola and possible relationships with fungi, as these can significantly influence the soil carbon cycle and the related trophic network.

The study was conducted inside an area of " Tenuta di Paganico", an extensive farm devoted to organic agro-zootechnical productions in central Italy based on silvopasture practices of the local Maremmana cattle breed. The methodology was developed along a gradient based on land use (Mediterranean forestry, Silvopastoral and Grassland) and on the intensity of grazing as a function of the maximum distance that animals usually reach from the main feeding stations (high density pastures with lower distance from the station feeder and low-density pasture at greater distance).

The first results showed a substantial trend in how some silvopastoral practices can better preserve soil biodiversity, with a high level of abundance of mesofauna and fungal biodiversity, as well as soil biological quality and ecological stability, if managed in a way rational.

If forest pasture is not properly managed and livestock is persistently on the ground, biodiversity levels drop dramatically and the benefits of silvopastoral practice are not realized.

Further analyses will be necessary to 1) deepen understand and highlight the complex interactions between biological communities and physicochemical variables, all of which contribute to the overall quality of soils; 2) explore if interactions can be reliable enough to be applied for soil quality monitoring and management.

**Keywords** long-term agroforestry (LTA), mesofauna, Fungi, soil monitoring

# Effect of Plant Probiotics and Biochar Application on Rhizosphere Biodiversity and Maize Growth in the Field

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**Keywords:** microbial consortia; biochar; maize rhizosphere; soil microbiome

Many efforts in the recent years are being made in developing new inoculants microbial consortia not only for growing crops sustainably but also for preserving soil health; in this context, the question of whether natural soil microbiomes are negatively or positively affected by adding foreign microorganisms needs to be addressed. The main objective of the present work is to exploit the potential of three microbial consortia, developed within the frame of the Horizon 2020 SIMBA, for sustainable crop production of maize and to assess the impact of their application in field on indigenous rhizosphere microbial diversity. Microbial consortia were applied alone or in association with Arbuscular Mycorrhizal Fungi (AMF) and biochar in open field under conventional and organic management and compared with commercial microbial products. The diversity and composition of bacterial communities in maize rhizosphere soil was investigated at different maize growth stages and with different fertilization levels via partial 16S rRNA gene amplicon sequencing. The application of SIMBA microbial consortia had clear effects on biomass growth, yield and N content of maize, especially at lower fertilization levels while did not significantly affect species diversity and richness of native rhizospheric microbial communities. A significant change in rhizospheric microbiota diversity was found following application of commercial Micosat F1, AMF and biochar as well as increased fertilization level. Overall, our results suggested that SIMBA microbial consortia may be effectively exploited as biofertilizer in sustainable maize cultivation without altering the biodiversity or the resident microbiota, thus removing risks of long-term impacts on natural soil biodiversity.

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## Designing sustainable agrosystems to promote plant-soil synchrony

S. Fontaine

Understanding how natural ecosystems may reach equivalent levels of productivity to high-input annual crops whilst providing key regulating services such as carbon storage is critical for both theoretical and applied biology. Using the latest advances in biogeochemistry and ecology, I propose that the capacity of natural ecosystems to be sustainably productive largely results from a coordination between multiple plant- and soil-related processes, synchronizing the supply of soluble nutrients by soil biota to fluctuating plant nutrient demand. This synchrony limits deficiencies and excesses that usually penalize both biomass production and the environmental performance of agrosystems. I outline four systems of plant-soil synchrony, and discuss their importance in regulating nutrient and carbon cycles depending on the environmental context. Finally, I discuss the implications of this framework for the design of sustainable agrosystems.