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Book of Abstracts

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Soil microorganisms encompass archaea, bacteria, fungi, and protozoa. They maintain the majority of enzymatic processes in soil and preserve energy and nutrients in their biomass. The assessment of the microbial community structure can be divided into two main approaches: The first approach is the differentiation of the microbial biomass into a small number of large functional subgroups such as fungi and bacteria. The second approach is to measure the large diversity on a genotype, phenotype or functional level. The knowledge about the diversity of the soil microbial community has much increased over the past years, but the contribution of fungi and bacteria to the soil microbial biomass is still controversial. This is especially due to the strong focus on soil bacteria in the new molecular and physiological methods for characterizing microbial diversity. The repertoire of methods for differentiating between fungal and bacterial biomass has remained essentially unchanged over the past decade. Three different approaches can be distinguished (1) microscopic methods, (2) selective inhibition (3) biomarkers (ergosterol, PLFA, glucosamine, muramic acid). Data obtained from the literature were compiled for these three methodological approaches. The advantages and disadvantages of the different methodological approaches are highlighted and discussed. In the majority of experiments, a fungal dominance has been observed, with a proportion ranging from 60 to 80% fungi of the total soil microbial biomass in comparison with 40 to 20% bacteria.

S08.G.02

Influence of pH-heterogeneity of fertiliser effects on microbial biomass in a long-term field trial of ecological agriculture

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This research project focuses on the comparison of mineral (MIN), organic (CM) and organic fertiliser with biodynamic preparation (CMBD) in terms of microbial biomass in a long-term field experiment of organic agriculture. The data showed a high variation in the pH values, which are not caused by different fertiliser but influenced by the heterogeneity of the fluvial sandy sediments. This influence of the highly varying pH values was reduced by the geostatistical methods to improve the comparison of microbial biomass in the different treatments. The organic treatments were characterized by nearly 10.7% higher contents of Cmic (CM: 149 mg kg⁻¹; CMBD: 152 mg kg⁻¹) and Nmic (CM: 18 mg kg⁻¹; CMBD: 22 mg kg⁻¹) compared with the mineral ones (136 mg Cmic kg⁻¹; 17 mg Nmic kg⁻¹). These results were consistent with the significant (P < 0.05) lower Cmic/Nmic-ratios (MIN: 9.2; CM: 8.4; CMBD: 7.5) of the treatments with organic fertiliser addition. Furthermore, the Pmic contents showed 25% higher values (6.5 mg kg⁻¹) in the CM treatment and 44 % in the field with CMBD addition (7.5 mg kg⁻¹) than in the mineral treated soil (5.2 mg kg⁻¹). The Cmic/Pmic-ratio was 26 with mineral fertilisation compared with 23 (CM) and 20 (CMBD) in the organic treatments. This points to a higher P-availability in the soils with organic fertilisation. This suggests that the addition of organic fertiliser generates higher microbial biomass and higher nutrient availability of nitrogen and phosphorus in comparison with the addition of mineral fertiliser. Microbial sulphur (Smic) will be determined to give additional information about the role of microbial sulphur transformation in soil with mineral and organic fertilisation.

S08.G.03

Soil microbial community structure, diversity and functionality in integrated livestock-crop production systems compared to continuous cotton

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Many regions of the world are facing soil quality and sustainability problems due to monoculture. In the Texas High Plains of US, cotton (*Gossypium hirsutum*) production under continuous monoculture and conventional tillage (since the 1940's) has contributed to wind-induced soil erosion and organic matter reduction. This study is part of a larger project to develop and evaluate integrated crop and livestock systems that reduce dependence on underground water while optimizing productivity and enhancing soil quality. A clay soil (Fine, mixed, thermic Torrertic Paleustolls) was studied during the first 10 years under continuous cotton compared to an integrated livestock-crop system with a perennial warm-season grass pasture (*Bothriochloa bladhii*) and two stages of a rotation (wheat (*Triticum aestivum*)-fallow-rye (*Secale cereale*)-cotton). After 5 years, total C (0-5 cm) was only higher under perennial pasture, but total C (avg: 17.3 g kg⁻¹ soil) and total N (avg: 1.5 g kg⁻¹ soil) were higher in all the integrated crop-livestock systems compared to continuous cotton (11.4 g C kg⁻¹ and 1.1 g N kg⁻¹ soil) after 10 years. After 5 years, soil microbial biomass C (MBC) was greater in perennial pasture (193 mg kg⁻¹ soil) and in the rotation when sampled under rye or cotton (237 mg kg⁻¹ soil) compared to continuous cotton (124 mg kg⁻¹ soil), but MBC became significantly higher in all the alternative systems after 7 years. Similar trends were found for enzyme activities of C (β -glucosidase, α -galactosidase), P (alkaline phosphatase, phosphodiesterase), N (β -glucosaminidase), and S (arylsulfatase) cycling. The integrated crop-livestock systems had higher protozoa (20:4w6c=1.98%) and fungi (18:3w9c=1.30%) than continuous cotton (20:4w6c =1.09%; 18:3w9c= 0.76%) after 5 yrs. Higher mycorrhizal fungal fatty acids (18:1w9c, 16:1w5c) were detected under ungrazed areas compared to grazed areas in pasture at 0-5 cm. Bacterial diversity as affected by the integrated-crop livestock systems will be discussed.

S08.G.04

Microbial-biogeography of France by the use of molecular tools applied to the French soil quality monitoring network (RMQS)

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Although microorganisms are the most diverse and abundant type of organisms on earth, the determinism of microbial diversification and the distribution of microbial diversity from small to large scale are poorly documented. Ecologists studying macroorganisms have long recognized that beta-diversity (how community composition changes across a landscape) is central for understanding the environmental factors driving the magnitude and the variability of biodiversity. However, this conceptual vision is also relevant for microorganisms since patterns of beta-diversity can offer valuable insights into the relative influence of dispersal limitations, environmental heterogeneity, and environmental and evolutionary changes in shaping the structure of ecological communities. Despite the statement that spatial patterning of microbial diversity can have important consequences regarding to plant community structure and ecosystem functioning, microbial beta-diversity patterns