Principles and Applications of Soil Microbiology - Environmental and Agricultural Perspectives

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Abstract
Soil microbiology has constantly been stimulated by the need for a greater understanding of microbial activities related to soil fertility, such as the decomposition of organic matter and cycling of nutrients, or the biotransformation of contaminants. The microbial community in soils is highly heterogeneous and consists of fungi and bacteria belonging to various taxa. Studies published so far revealed evidence for microbial populations being controlled by soil physicochemical properties, besides impacts from different types of vegetation, or climate. Furthermore, human impacts on soil microbial abundance and activities, such as land use management including fertilization or tillage, have been studied intensively. Although considerable knowledge accumulated about the role of microbial activities in sustaining or improving soil biochemical processes, the assessment of functional groups of microorganisms and of specific microbial activities need further study. Results from three projects in applied microbial ecology of arable soils (project 1), forest soil (project 2), and soil under bioremediation (project 3) will be presented:

I. Project 1
Diversity and activity of cellulose-decomposing bacteria, isolated from a sandy and a loamy soil after long-term manure application (Ulrich, Klimke & Wirth)
The community of culturable cellulolytic bacteria was analysed in two long-term experimental field sites on Albic Luvisol and Haplic Phaeozem treated with and without farmyard manure. Against the background of significant differences in soil properties, the bacterial community structure differed clearly between sites and was affected by manure treatment, as analysed by T-RFLP of 16S rDNA. The population densities of cellulolytic bacteria were significantly increased by manure treatment in Phaeozem. Cellulose decomposing potentials of 537 isolates were tested on soluble, colloidal and crystalline cellulose. The results showed some evidence of a greater proportion of isolates with high decomposition activity in Luvisol, but no impact from manure treatment could be observed in both soils. Restriction analysis and sequencing of 16S rDNA of isolates revealed a rather simple community composition dominated by Streptomyces (67%). The composition of pattern groups was affected by manure treatment, which was most clearly evident in Luvisol, whereas an effect of the soil type could not be found. Although predominant pattern groups were assigned to phylogenetically different bacterial classes (Actinobacteria, Betaproteobacteria and Gammaproteobacteria), cellulolytic activity could hardly be differentiated. All in all, cellulolytic capabilities of the isolates were highly variable and did not map to phylogenetic affiliation.

Fig. 1: Dendrogram showing the similarity between the T-RFLP profiles derived from the manured (m) and control (c) plots of the Albic Luvisol (L) and Haplic Phaeozem (P) sites. The samples were taken in spring with three field replicates (first number) and investigated by two independent analyses (second number).
II. Project 2:

Response of soil microbial biomass, activities and community structure at a pine stand in north-eastern Germany, five years after thinning (Maassen, Fritze, Wirth)

A 62-year old pine stand located in north-eastern Germany (Brandenburg, Ost-Prignitz, Revier Beerenbusch) was studied with respect to a thinned vs. an unthinned treatment (year of thinning: 1999, degree of canopy opening: 0.4). Samples of the organic layer (O) and the mineral horizon (Aeh) of an acid brown earth were collected along a transect at each treatment in November 2003 and April 2004. Substrate induced respiration, basal respiration, as well as a suite of enzymes involved in the degradation of lignocellulose (endo-cellulase, exo-cellulase, β-glucosidase, endo-xylanase, exo-xylanase, phenoloxidase, peroxidase) were assayed. Microbial community structure and relative biomass of bacteria, actinomycetes, and fungi were assayed by phospholipid fatty acid (PLFA) analysis. Five years after thinning, microbial biomass, basal respiration, and enzyme activities in both soil layers did not differ significantly, when comparing thinned and unthinned treatments. However, the analysis of soil microbial community structure revealed a significant difference between the thinned and unthinned treatment at both sampling dates. Thus, it was concluded that thinning did not yet result in any response in soil microbial activities at the site under study, but since early evidence of change in the microbial community was detected, long-term monitoring and additional studies on mineralization activities are required.

III. Project 3:

Soil microbial monitoring of a mineral oil contaminated, former military airbase site before and after bioremediation by landfarming (Genske, Benter, Simonis, Ulrich, Wirth)

Soil pollution with mineral oil hydrocarbons provides serious environmental hazards to ecosystem functioning and human health. As a concept for on site bioremediation of polluted sites, landfarming relies on the activity of indigenous soil microorganisms degrading hydrocarbons. By using a deep plough technique in combination with the application of nutrient solutions, soil ecological conditions such as aeration, substrate distribution and availability are altered, inducing an increase of microbial over-all activities. The aim of our study was to monitor selected soil microbiological properties immediately before and after the beginning of a bioremediation project, with special emphasis on assessing soil ecological impacts and efficiency of landfarming. A kerosene and diesel fuel storage tank farm at a former Soviet military airport located in north-eastern Germany was studied with respect to a heavily contaminated vs. an unspoiled area, respectively. After begin of bioremediation, mineral oil hydrocarbons (MOHC) contents sharply decreased at the unspoiled area (over-all mean = 168 ppm), but increased in the deeper soil layers at the contaminated area (mean = 9.317 ppm). C_muc was significantly higher in the contaminated (over-all mean = 618 μg g⁻¹ soil) vs. the unspoiled area (over-all mean = 361 μg g⁻¹ soil) and decreased in both variants with soil
depth at both sampling dates. Soil respiration activity was significantly higher in the contaminated vs. the unspoiled area and increased after bioremediation in the contaminated area with maxima in the deeper soil layers. The contents of MOHC were highly correlated with contents of Cmic and respiration activity in soils, both before and after bioremediation, highlighting the role of soil microbes in MOHC decomposition. Soil enzyme activity displayed a decrease with soil depth at the unspoiled area and a higher activity at the contaminated vs. the unspoiled area in the deeper soil layers only after the begin of bioremediation. In conclusion, long-term soil ecological monitoring is required to assess further progress of bioremediation at the site under study. Moreover, studies of decomposition rates of mineral oil hydrocarbons and of the composition of soil microbial communities are essential.

Fig. 3: Soil basal CO₂ respiration in low-contaminated area (left figure) and in high-contaminated area (right figure), with respect to soil depth (Tiefenstufe 1: 0-15cm, 2: 15-30cm, 3: 30-45 cm) before and after beginning of bioremediation (dark and light columns, respectively).

IV. Acknowledgements

Projects 1 and 2 were funded by the German Science Foundation, DFG (UL 179/1 and Wi 1798/4-1). I am grateful to Mrs. Sigune Weinert and Mrs. Martina Wiemer for their skilful technical assistance, and furthermore, to the ZALF Central Laboratory for soil chemical analyses.