



Microbial community changes as a possible factor controlling carbon sequestration in subsoil

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In order to gain more knowledge regarding the microbial community and their influence on carbon sequestration in subsoil two depth profiles with different soil organic carbon (SOC) concentrations were sampled. The SOC concentrations developed naturally due to deposition and erosion. This experiment offers the opportunity to investigate to which extend natural SOC availability or other subsoil specific conditions influence the composition and the functional diversity of the microbial community and in return if there is any evidence how the microbial community composition affects carbon sequestration under these conditions.

Soil samples were taken at four different depths on two neighbouring arable 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 functional diversity of the microbial community along the depth profiles. Amino sugars Muramic Acid and Glucosamine 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 17 substrates used in 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 composition 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.