Geophysical Research Abstracts
Vol. 20, EGU2018-2698, 2018
EGU General Assembly 2018

Microbial regulation of carbon cycling within soil profiles: A reciprocal soil translocation experiment separated the response to root addition from environmental conditions

Sebastian Preusser, Christian Poll, Sven Marhan, and Ellen Kandeler

University of Hohenheim, Institute of Soil Science and Land Evaluation, Stuttgart, Germany
(ellen.kandeler@uni-hohenheim.de)

Microorganisms in subsoils are less abundant and diverse as well as more heterogeneously distributed in subsoils than in topsoil environments. Especially in deeper soil, the impact of changes in habitat conditions on microorganisms is largely unexplored. We conducted a reciprocal soil translocation field experiment with topsoil (5 cm soil depth) and subsoil (110 cm) samples of an acid and sandy Dystric Cambisol from a European beech (Fagus sylvatica L.) forest in Lower Saxony, Germany. The design of this experiment allowed disentangling the response of soil microorganisms and C flow from labelled root litter into different C pools to either substrate addition and/or altered micro-environmental conditions. In total 144 samples were buried into three depths (5 cm, 45 cm and 110 cm) for up to one year and 13C-labelled root litter was added to expose the samples to different environmental conditions and to increase the substrate availability, respectively. Whereas measurements of Cmic, PLFA and ergosterol in the reciprocal soil experiment yielded information about the abundance of specific groups of microorganisms, SIP techniques (EO13C, 13Cmic, 13C-PLFAs) elucidated the C flow from root litter into different C pools within the soil profile. PLFAs of gram-positive and gram-negative bacteria as well as fungi showed highest relative 13C incorporation in 110 cm depth and samples with root addition had generally higher microbial abundances than those with no root addition. Here, especially fungi benefited from the additional C source with highly increased abundances in all incorporation depths. The altered environmental conditions in the different incorporation depths significantly influenced soil microorganisms. Abundance of fungi decreased strongly with depth, while bacteria were less affected and increased in relative abundance in soil samples incorporated into subsoil layers. The highest seasonal variability in microbial abundance was determined in 5 cm incorporation depth due to the amplitude in micro-climatic and micro-environmental conditions in this habitat. In summary, this experiment demonstrated that C quality and quantity were the main factors restricting fungal abundance in deeper soil layers, while bacterial decomposer communities were adapted to a wider range of habitat conditions.