Geophysical Research Abstracts
Vol. 12, EGU2010-4164, 2010
EGU General Assembly 2010

Metaproteomics to investigate the impact of sampling-site biogeochemistry on structure and functionality of leaf-litter degrading microbial communities

Thomas Schneider (1), Katharina Keiblinger (2), Bertran Gerrits (3), Emanuel Schmid (1), Leo Eberl (1), Sophie Zechmeister-Boltenstern (2), and Kathrin Riedel (1)

(1) University of Zurich, Institute of Plant Biology, Microbiology, Zurich, Switzerland (thomas.schneider@botinst.uzh.ch), (2) Federal Office and Research Centre for Forests – BFW, Vienna, Austria, (3) Functional Genomics Center, University of Zurich/ETH Zurich, Zurich, Switzerland

The composition of organic matter in natural ecosystems is strongly influenced by the microorganisms present. Conversely, bacteria and fungi are limited by the amount and type of organic matter available in a given environment, most of which is ultimately derived from plants. Changes in the stoichiometry and biochemical constituents of plant litter may therefore alter species composition and elicit changes in the activities of microbial communities and their component parts. The identification of the microbial proteins of a given habitat together with the analysis of their phylogenetic origin and their spatial and temporal distribution are expected to provide fundamentally new insights into the role of microbial diversity in biogeochemical processes.

To relate structure and functionality of microbial communities involved in leaf-litter decomposition we determined biogeochemistry, community structure by phospholipid fatty acid (PLFA)-analyses, enzymatic activities, and analysed the protein complement of different litter types, which were collected in winter and spring at various Austrian sampling sites, in a semi-quantitative proteomics approach by one dimensional polyacrylamide gel electrophoresis (1-D-SDS-PAGE) combined with liquid chromatography/tandem mass-spectrometry (LC-MS/MS). Protein abundances were determined by counting the number of MS/MS spectra assigned to each protein. In samples with high manganese and phosphor content a significant increase of fungal proteins from February to May was observed, which was in good agreement with the PLFA-analyses showing similar trends towards an increase of the fungal community. In contrast, the PLFA analysis revealed no temporal changes in the community at Achenkirch and even a decrease in the fungal/bacterial ratio at Klausen-Leopoldsdorf, two sampling sites low in P and Mn; similar trends are reflected in our spectral counts. In conclusion, semi-quantitative proteome- and PLFA-analyses suggest that fungal and bacterial abundance positively correlates with the total amount of P and Mn within the different litter types. Spectral counts of extracellular enzymes demonstrated a significant increase of these enzymes in the May, which was also mirrored by measurements of total enzymatic activities. The finding that almost all hydrolytic enzymes identified from litter were of fungal origin suggests a prominent role of fungi during aerobic litter decomposition.