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Metaproteome analysis of the microbial community during leaf litter decomposition - the impact of stoichiometry and temperature perturbations

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Leaf litter decomposition is the breakdown of dead plant material, a terrestrial ecosystem process of paramount importance. Nutrients released during decomposition play a key role for microbial growth and plant productivity. These processes are controlled by abiotic factors, such as climate, and by biotic factors, such as litter nutrient concentration and stoichiometry (carbon:nutrient ratio) and activity of soil organisms. Future climate change scenarios predict temperature perturbations, therefore following changes of microbial community composition and possible feedbacks on ecosystem processes are of key interest; especially as our knowledge about the microbial regulation of these processes is still scarce.

Our aim was to elucidate how temperature perturbations and leaf litter stoichiometry affect the composition of the microbial decomposer community. To this end a terrestrial microcosm experiment using beech (Fagus sylvatica) litter with different stoichiometry was conducted. In a semi-quantitative metaproteomics approach (1D-SDS PAGE combined with liquid chromatography and tandem mass spectrometry; unique spectral counting) we used the intrinsic metabolic function of proteins to relate specific microbial activities to their phylogenetic origin in multispecies communities.

Decomposer communities varied on litter with different stoichiometry so that microbial decomposers (fungi and bacteria) were favoured in litter with narrow C:nutrient ratios. The fungal community was dominated by Ascomycota (Eurotiomycetes, Sordariomycetes) and Basidiomycota (Agaricomycetes) and the bacterial community was dominated by Proteobacteria, Actinobacteria and Firmicutes. The extracellular enzymes we detected belonged mainly to classes of xylanases, pectinases, cellulases and proteases and were almost exclusively of fungal origin (particularly Ascomycota). Temperature stress (heat and frost) evoked strong changes in community composition, enzyme activities, dissolved organic nitrogen and litter pH. Freeze treatments resulted in increased fungal abundance and a decline in residual plant litter material, indicating slightly accelerated decomposition. Extracellular enzyme activities were especially blocked by heat treatment. Using metaproteomics enabled us to link the composition of the microbial community to its ecosystem function.