

Abstract

The abilities of fungi and bacteria to degrade simple and complex carbon compounds derived from different sources, such as root exudates, litter, soil organic matter or fungal mycelium were studied in this dissertation. Knowledge of functional traits, especially degradation abilities of fungi and bacteria, are important for deciphering the black box of microbial functioning in topsoil and thus aiding in modeling and predicting future directions of microbial communities development in face of global changes. Among fungal cultures from culture collection representing strains with different taxonomy and ecophysiology, the ecophysiology of fungi was more important in manifestation of functional traits than taxonomy. Among bacterial isolates from the litter and soil of spruce forest, Acidobacteria were confirmed to express multiple decomposition enzymes in high rates *in vitro* and were also abundant and active degraders in acidic spruce forest soil. The expression of degradation capacities of both bacteria and fungi were further studied *in situ* in spruce forest topsoil, that represents an important environment due to the ubiquity of coniferous forests on the Northern hemisphere. There is an obvious gap of knowledge, when comes to our understanding of seasonal effect on microbial functioning, and this is why the effect of seasonality on transcription of all functional genes of fungi and bacteria was also addressed. The same experimental set-up was used to compare the encoded and transcribed capacity of enzymes involved in carbon cycle as well as seasonality of their production by fungi and bacteria including β -glucosidase, the enzyme involved in the last step of complete cellulose degradation. The focus on seasonality is motivated by the expectation that the seasonal change in the amount of photosynthates produced by trees in forest and thus the changes in the amount of root exudates between summer and winter affect diverse soil microbiota but mostly ectomycorrhizal fungi (ECM). Indeed, lower transcription activity of ECM and higher abundance of bacterial transcripts in metatranscriptome was observed in winter. It was shown that summer and winter microbial communities use different enzyme sets, especially in soil, which probably reflects distinct C compounds available to microorganisms through the year, although microbes did not change their abundance or composition. In winter, the usage of storage compounds and higher abundance of bacterial transcripts was observed, while in summer, complex C sources were used mostly by Basidiomycota that largely represented ECM members in studied soil. When targeting β -glucosidase, PCR amplicons of partial gene sequence were demonstrated to be a useful proxy of

diversity and the involvement of both bacteria and fungi in cellulose degradation and seasonal patterns of enzyme transcription were observed. However, the full diversity could not be obtained by amplicon sequencing since amplification primers miss some organisms. Overall, the result indicate that simple C compounds have priming effect on and are required for the fungal degradation of recalcitrant soil organic matter.