

Abstract

Deadwood is a hotspot of microbial diversity and its decomposition contributes to carbon and nitrogen cycling in temperate forests. The historically recognized importance of fungi in the decomposition of deadwood has recently been complemented by the description of bacterial functions thanks to the rapid progress of culture-independent methods based on the analysis of nucleic acids. To study different aspects of deadwood decomposition, a temperate mixed forest in Zofinsky prales National Nature Reserve was selected as a site with rich historical forestry data where deadwood decomposition represents an important process in wood turnover. The aim of this thesis is to describe role of bacteria in deadwood decomposition at fine scale resolution with respect to community composition, enzyme transcription, and metabolic potential of dominant species. Effects of deadwood age together with pH and water content on the bacterial community composition proved to be more important than tree species identity. Bacteria showed distinct composition between early and late community in decomposing deadwood. The bacterial community was also under a significant influence of fungal community composition. Despite being in a close contact, bacterial and fungal communities differed significantly between deadwood and the underlying soil horizons. Bacteria in deadwood contributed to the nitrogen (N) cycling with an important role in N₂ fixation. Bacterial utilization of carbon (C) via degradation of recalcitrant polymers was present, but less important than fungal degradation. The decomposition potential of abundant bacterial taxa in deadwood can be delineated from the presence of carbohydrate active enzyme (CAZy) set which was found to be rich in *Acidobacteria*, *Bacteroidetes*, and *Actinobacteria* in contrast to less CAZy-equipped *Alphaproteobacteria* and *Gammaproteobacteria*. The latter taxa depended on mycophagy, low-molecular-mass C sources and were able to perform several N-cycling steps including N₂ fixation. Deadwood is a unique habitat with interkingdom interactions among prokaryotic and eukaryotic microorganisms and in which individual bacterial groups show adaptations to specific habitat conditions characterized by high C:N ratio, recalcitrant C sources, extracellular activity of degradative enzymes, and substrate impermeability.