Summary

My thesis is focused on soil saprotrophic basidiomycetes, their role in the decomposition of dead plant biomass and interactions with other members of microbial community since these fungi play a particularly important role in biotransformation of soil organic matter and therefore also in the cycling of carbon and mineral nutrients. Three litter-decomposing basidiomycetes isolated from *Quercus petraea* forest: *Hypholoma fasciculare*, *Rhodocollybia butyracea* and *Gymnopus* sp., efficiently degraded oak litter under both sterile and nonsterile conditions, but the rate of degradation and lignocellulolytic enzyme production considerably differed among isolates. Generally, the degradation caused by these isolates resembled decay caused by white-rot fungi. The fungi produced a broad range of lignocellulose-degrading enzymes: laccase, Mn- peroxidase, endo-1,4-β glucanase, endo-1,4-β xylanase, β-glucosidase and β-xylosidase. Saprotrophic basidiomycetes thus probably contribute to the observed spatial variability in extracellular enzyme activities in the upper soil horizon in oak forest. Spatial differences in enzyme activities were accompanied by differences in the microbial community composition, the relative amount of fungal biomass decreased with soil depth. The vertical gradients in soil occured at a small scale even within separate soil horizon. Physicochemical conditions of decomposing litter and wood such as pH, abundance of reactive radicals and enzymes and amount of available nutrients, were considerably changed during its decomposition and transformation as shown for *Piptoporus betulinus* and *Hypholoma fasciculare*. It was hypothesized that these changes will affect abundance and composition of microbial community due to intensive selective pressure on microorganisms' physiology. However, neither *H. fasciculare* nor *R. butyracea* affected total soil bacterial or fungal biomass quantitatively during soil colonization. Bacterial community in *H. fasciculare* -colonized wood was rich and diverse, dominated by *Proteobacteria* and *Acidobacteria*. Selection of bacterial community was more likely due to selective pressure of environment rather than specific effects of *H. fasciculare*. Bacteria inhabiting decayed wood seemed to be acid tolerant and relied on growth substrates released by fungal decay activities, although some may also utilize cellulose. No interference competition (antibiosis) or mutualism (nitrogen-fixation) became apparent in interaction between *H. fasciculare* and wood-inhabiting bacteria.