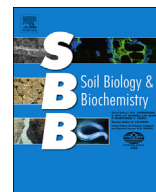




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How do microbial communities in top- and subsoil respond to root litter addition under field conditions?



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ABSTRACT

Contrasting microbial community composition and activity at different soil depths may affect root litter decomposition. These effects have up to now been investigated mainly in laboratory studies, which may not be able to take into account complex *in situ* conditions. Our study aimed to analyze the composition and activity of microbial communities after addition of ¹³C labeled wheat root litter to a loamy soil under grassland at 30, 60 and 90 cm depths, during a three-year field experiment. We investigated the dynamics of bacterial and fungal abundances and community structures by DNA genotyping and pyrosequencing of 16S and 18S rDNAs. The genetic structures of bacterial and fungal communities were evaluated by automated ribosomal intergenetic spacer analysis. The functions of these communities were analysed by determination of extracellular enzyme activities and viable microbial communities involved in ¹³C labeled organic matter decomposition studied by ¹³C PLFAs.

The abundance of fungal and bacterial communities (16S and 18S rDNAs and PLFA) and the potential activities of enzymes involved in the C- and N-cycles were significantly higher at the top 30 cm compared with deeper soil throughout the experiment. Both were stimulated by fresh litter input. A trend to decreasing bacterial and fungal richness was noted after root litter addition at 30 cm, while richness of bacteria at 90 cm and those of fungi at 60 and 90 cm increased. Moreover, root litter addition caused a reduction of the Shannon Weaver Diversity index and a shift in microbial community structure at all three depths, which was more pronounced for bacteria at 30 and 60 cm and for fungi at 90 cm. The changes during litter degradation resulted in similar dynamics of most enzyme activities at all depths. Chitinase activity was enhanced after 29 months compared to initial conditions indicating the availability of high amounts of microbial detritus. The degrading microbial community as assessed by ¹³C PLFA showed similar temporal dynamics at all three depths. Fungal contribution to this community decreased during later stages of litter degradation, while the contribution of Gram+ bacteria increased. We conclude that litter addition led to convergence of microbial communities of top- and subsoil through stimulation of copiotrophic populations. Soil microbial community structures are thus connected with the amount of fresh litter input. Enzyme activities and ¹³C PLFA reflect to some extent the changes occurring during degradation, i.e. exhaustion of fresh plant material and accumulation of detritus.

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1. Introduction

Heterotrophic microbial community abundance and composition is closely related to plant growth, especially in rhizosphere and detritosphere. It is assumed that the highest microbial abundance,

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