

# Active fungal-bacterial interactions and functional patterns are governing deadwood decay in temperate forests

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## ABSTRACT:

Microbial community members are the primary microbial colonizers and active decomposers of deadwood. This study placed sterilized standardized beech and spruce sapwood specimens on the forest ground of 8 beech- and 8 spruce-dominated forest sites. After 370 days, specimens were assessed for mass loss, nitrogen (N) content and <sup>15</sup>N isotopic signature, hydrolytic and lignin-modifying enzyme activities. Each specimen was incubated with bromodeoxyuridine (BrdU) to label metabolically active fungal and bacterial community members, which were assessed using an amplicon sequencing. Fungal saprotrophs colonized the deadwood accompanied by a distinct bacterial community that was capable of cellulose degradation, aromatic depolymerisation, and N<sub>2</sub> fixation. The latter were governed by the genus *Sphingomonas*, which was co-present with the majority of saprotrophic fungi regardless of whether beech or spruce specimens were decayed. Moreover, the richness of the diazotrophic *Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium* group were significantly correlated with mass loss, N content and <sup>15</sup>N isotopic signature. In contrast, presence of obligate predator *Bdellovibrio* spp. shifted bacterial community composition and were linked to decreased beech deadwood decay rates. Our study provides the first account of the composition and function of metabolically active wood-colonising bacterial and fungal communities, highlighting cross-kingdom interactions during the early and intermediate stages of wood decay.

## KEYWORDS:

Beech, Bromodeoxyuridine, Diazotrophs Deadwood decay, Enzyme Activity, Microbiome, 15N signature, Spruce