

Publication

Functional Profiling and Distribution of the Forest Soil Bacterial Communities Along the Soil Mycorrhizosphere Continuum

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An ectomycorrhiza is a multitrophic association between a tree root, an ectomycorrhizal fungus, free-living fungi and the associated bacterial communities. Enzymatic activities of ectomycorrhizal root tips are therefore result of the contribution from different partners of the symbiotic organ. However, the functional potential of the fungus-associated bacterial communities remains unknown. In this study, a collection of 80 bacterial strains randomly selected and isolated from a soil-ectomycorrhiza continuum (oak-*Scleroderma citrinum* ectomycorrhizas, the ectomycorrhizosphere and the surrounding bulk soil) were characterized. All the bacterial isolates were identified by partial 16S rRNA gene sequences as members of the genera Burkholderia, Collimonas, Dyella, Mesorhizobium, Pseudomonas, Rhizobium and Sphingomonas. The bacterial strains were then assayed for beta-xylosidase, beta-glucosidase, N-acetylhexosaminidase, beta-glucuronidase, cellobiohydrolase, phosphomonoesterase, leucine-aminopeptidase and laccase activities, chitin solubilization and auxin production. Using these bioassays, we demonstrated significant differences in the functional distribution of the bacterial communities living in the different compartments of the soil-ectomycorrhiza continuum. The surrounding bulk soil was significantly enriched in bacterial isolates capable of hydrolysing cellobiose and N-acetylglucosamine. In contrast, the ectomycorrhizosphere appeared significantly enriched in bacterial isolates capable of hydrolysing glucopyranoside and chitin. Notably, chitinase and laccase activities were found only in bacterial isolates belonging to the Collimonas and Pseudomonas genera. Overall, the results suggest that the ectomycorrhizal fungi favour specific bacterial communities with contrasting functional characteristics from the surrounding soil.

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