



Spatiotemporal diversity and activity patterns of laccase genes in a forest soil

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Accumulation and stability of Soil Organic Matter 'SOM' results from a balance between two biologically driven processes, i.e. humification on the one and mineralization on the other hand. Soil microorganisms are largely involved in these processes and besides bacteria fungi are the key players.

Laccases, one of the most universal of different exoenzymes in fungi, catalyse the oxidation of phenolic compounds and aromatic amines coupled with the reduction of molecular oxygen to water. Therefore they are able to degrade complex organic substrates such as lignin and appear to be of importance in the SOM cycle. The presented work aims at investigating this role at the molecular level and is embedded in the priority program SPP 1090 'Soils as source and sink for CO₂ – mechanisms and regulation of organic matter stabilisation in soils', founded by the German Research Foundation (DFG).

Special degenerated primers were optimized and tested, that allowed us to show the diversity [1] and expression [2] patterns of fungal laccase genes compared to the total laccase activity in soils. The specificity of these primers was assessed on cultured fungal strains.

Replicated soil cores of a Dystric Cambisol were taken in spring, summer and autumn. They were divided into Oh and Ah horizon before extraction of DNA and RNA. PCR techniques were used to amplify a target region of approx. 140 bp within cbs1 (copper binding site) and cbs2 of the laccase gene. Based on sequence analysis and cladistics, the spatiotemporal appearance of fungal laccases (based on DNA) and their expression (based on cDNA) was analysed. Additionally the ecological position, e.g. saprotrophic

or mycorrhizal, of soil fungi will be determined.

[1] Luis P., Walther G., Kellner H., Martin F., Buscot F. (2004) Diversity of laccase genes from basidiomycetes in a forest soil. *Soil Biology and Biochemistry* 36, 1025-1036.

[2] Luis P., Kellner H., Martin F., Buscot F. (accepted) A molecular method to evaluate basidiomycete laccase gene expression in forest soils. *Geoderma*.