

Analysis of microbial diversity and green-house gases production of pine decaying logs

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Abstract

In Sustainable Forest Management decaying wood plays an important role in biodiversity conservation, carbon balance, nutrient cycling and bioenergy production. The management of this important component of forest ecosystems is limited by the fact that little is known about relationship between substrate quality and community structure of wood-inhabiting microorganisms. During decomposition carbon stored in deadwood is lost either in the atmosphere or in the soil, but to our knowledge few information on the quantity of CO₂ and other green-house gases emitted are available. In the present research was investigated the correlation between the decay of logs (lying deadwood), the decomposer microorganisms and their activities, in terms of greenhouse gas production and enzymes, in a black pine degraded forest. The decomposition of deadwood was visually assessed using a five decay-class system and for each decay class four wood samples were collected. CO₂, CH₄ and N₂O potential production from each decay class was measured in closed systems by means of gas-chromatography. Enzyme activities related to carbon, nitrogen, sulphur and phosphorus cycling were measured fluorometrically. The composition of decomposer microbial communities (fungi, bacteria and actinobacteria) was assessed by using PCR-DGGE fingerprinting. CO₂ production and enzyme activities were significantly higher in the last decay classes of deadwood. The molecular approach highlighted differences in microbial community structure both at species and abundance level, depending on the rate of decay.

Keywords: pine deadwood decomposition, green-house gas emissions, hydrolytic enzyme activities, microbial communities, biogeochemical cycling

Acknowledgments

Financially supported by the LIFE program, in the context of FoResMit project (LIFE14/CCM/IT/905) "recovery of degraded coniferous Forests for environmental sustainability Restoration and climate change Mitigation".)