Forest soil microbial composition is driven by the influence of tree species

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The linkage between tree species influence and soil microbial community remains uncertain. We investigated the soil microbial composition, using phospholipid fatty acids (PLFA) profiles, for the forest floor and three mineral horizons (0-5 cm, 5-10 cm, 10-30 cm) at six sites including monocultural stands of pine (Pinus nigra), spruce (Picea omorika), Douglas fir (Pseudotsuga mienziesii), beech (Fagus sylvatica) and red oak (Quercus rubra) as well as a mixed deciduous stand site consisting mainly of hornbeam (Carpinus betulus), linden (Tilia cordata) and common oak (Quercus robur).

The study was carried out at the spoil heap and recultivation area Sophienhöhe, Rhineland, Germany, where afforested sites were established since 1980 following lignite mining. There, boundary conditions including climate, soil type, texture, exposition, stand age and management type were similar at the different forest stands.

Within 35 years after afforestation the grand mean of total PLFAs content for all tree species increased from 112 % in soil depths from 10-30 cm up to 2900 % in the forest floor compared to the initial soil material. The most pronounced differences between tree species were detected in forest floor horizons, where pine stands (increased by 5900 %) show the highest and oak stands (1387 %) the lowest total PLFAs content. For forest floor layers the total PLFAs increased in the order oak < spruce < mixed stand < beech < Douglas fir « pine. With increasing depth the differences became less pronounced with highest PLFAs contents at Douglas fir (200 %) and the mixed deciduous stands (185 %). The strongest increase was found for PLFAs representing fungal communities in the forest floor, where under coniferous species a higher amount was determined compared to the deciduous species. Similar to the total PLFAs, the highest fungal PLFAs were determined under pine stands (15000 %) and the lowest under oak stands (3000 %). With increasing depth the bacterial PLFAs content including PLFAs representing gram-positive and gram-negative bacteria, respectively, was most developed at Douglas fir and mixed deciduous stands, whereas in the forest floor the pine stands showed the highest contents. Furthermore, the ratios of fungi to bacteria increased in all depths after afforestation, which indicates that the relative establishment of fungal communities is more promoted in the first decades after afforestation compared to the bacterial ones. Principal component analysis (PCA) of PLFAs displayed distinct differences between soils under coniferous and deciduous species but also stand specific patterns in microbial community composition which are mainly contributed by the fungal biomarkers C18:2ω6 and C18:1ω9c. PCA also revealed that a different microbial community was established under the mixed deciduous stand compared to the monocultural stands. This interplay of vegetation and soil microorganisms will have consequences for the formation and composition of soil organic matter.