Response of soil microbial community composition to afforestation with pure and mixed tree species

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Afforestation of agricultural land affects soil ecosystem functions by inducing carbon (C) and nitrogen (N) sequestration and promoting shifts in microbial community structure. Soil C and N stocks undergo progressive changes over several decades after forest establishment, particularly in successional forests. In contrast, microbial community structure can be shifted already in the first decade and thus, direct effect of tree species can be revealed. Thus, the aim of this study was to determine how soil microbial community composition is altered by afforestation with either one, two or three species mixtures of trees, which possess strongly contrasting functional traits.

The study was conducted at the BangorDIVERSE temperate forest experiment established in 2004 on a former arable soil. Soil samples were collected under single, two and three species mixtures of alder, birch, beech and oak, while contiguous field was chosen as a control. Soil samples were analysed for key quality indicators (total C and N, pH, nitrate and ammonium), and microbial community structure was determined by phospholipid fatty acids (PLFAs) analysis.

Ten years after afforestation, total soil C, N and C/N ratios were not strongly affected, with the highest positive changes (up to 20%) for the birch, alder+oak and birch+beech plots. Decrease of C and N contents were observed for the pure beech plot. pH decreased by 1-1.2 units for all forest plots compare to the control soil. Total PLFAs content (370-630 nmol g^{-1} soil) increased in comparison to the control (315 nmol g^{-1} soil), resulting in the changes in total PLFAs content from 20 to 100%. Thus, changes of chemical properties (C, N) occur slower than changes of microbial biomarkers at the early stage of afforestation.

Bacterial PLFA content was shifted by 20-120%, whereas fungal PLFAs were changed by 50-300%, reflecting stronger impact of afforestation on the recovery of fungal communities than on bacterial. Principal component analysis of PLFAs composition revealed that microbial composition in soils under two species mixtures forests were different from the mono- and three species mixtures. Gram positive PLFAs (a15:0 and i16:0) and actinomycetes PLFAs (10Me16:0 and 10Me18:0) contributed mainly to differentiation of two species mixtures from other forests. In contrast, gram negative biomarkers contributed to the separation of mono- and three species mixtures.

Thus, the study revealed the changes of microbial communities at the early stage of afforestation, and impact of various tree species and forest biodiversity on the main microbial functional groups.