



## Effects of land use on the level, variation and spatial structure of soil enzyme activities and bacterial communities

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### ABSTRACT

The aim of this study was to evaluate the long-term influence of contrasting rural land use types on the level, plot-scale variation and horizontal spatial structure of decomposition activities and the bacterial community in soil. Experimental data were collected in the southern boreal zone from topsoil layers of adjacent spruce forest, unmanaged meadow (former field) and organically cultivated field that all shared the same soil origin. The forest soil was sampled separately for the organic and mineral layers. A geo-statistical design comprising 50 sampling points per plot area of  $10 \times 10 \text{ m}^2$  was used. The measured microbiological characteristics included eight different hydrolytic soil enzyme activities involved in C, P and S cycles, bacterial 16S rDNA length heterogeneity profiles (LH-PCR) and total DNA yield as a relative estimate of microbial biomass.

Effects of land use were pronounced on both the bacterial community structure and soil enzyme activities. Soil organic matter (SOM) content predicted well the major differences in soil enzyme activities and microbial biomass. Highest enzyme activities were generally found in the forest organic soil whereas the underlying mineral soil showed significantly lower activities with a pattern similar to those of the other mineral soils, especially the cultivated field. Bacterial LH-PCR fingerprints were distinct but at the same time remarkably similar between field and meadow soils whereas the forest organic layer differed clearly from the mineral soils. Within-plot variation of soil microbiological characteristics was best explained by the variation of SOM. Relative standard deviations of soil microbiological characteristics typically decreased in the order: forest organic layer  $\approx$  forest mineral layer  $>$  meadow  $>$  field. However, bacterial fingerprints showed lowest variation within the meadow. Most of the microbiological variables studied showed no or only weak spatial structure at the scale sampled.

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### 1. Introduction

Land use conversion from natural ecosystems to agriculture is the major driver of global environmental change associated with e.g. climate change, species extinctions and loss of ecosystem services (Tilman et al., 2001). As microorganisms play key roles in nutrient cycling and ecosystem functioning, it is well recognised that more knowledge on the specific effects of different land use practices on soil microbial communities is needed (Macdonald et al., 2009). Hitherto, most studies on the microbiological effects of land use have focused on differences in soil microbial community

structure or in the level of microbial activities, whereas only little attention has been paid to land use-associated differences in the spatial variation of these properties.

Predicting the effects of land use change on soil microbiological characteristics is a challenging task as microbial communities are affected by multiple interrelated factors that operate at different spatial and temporal scales. Conversion of forest to cropped field alters ecosystem properties fundamentally. Plant biomass and species diversity are drastically reduced. Removal of plant cover, stones and tree roots together with tillage practices increase the physical homogeneity of surface soils. Soil organic matter (SOM) can be depleted through erosion, harvest and increased respiration losses or diluted by repeated mixing of topsoil layers. Also the quality of SOM is changed due to change in plant cover and organic inputs. Soil porosity, aggregation and water storage capacity are affected by

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tillage and the use of heavy agricultural machinery. Although previous studies have shown that SOM, vegetation and tillage are important regulators of soil microbial community composition and its activities (e.g. Sinsabaugh et al., 2008; Hartmann et al., 2009; Ceja-Navarro et al., 2010; Lamb et al., 2011; Stursová and Baldrian, 2011), we still have a poor understanding of the relative importance of these factors as determinants of the level, variation and spatial structure of soil microbiological characteristics.

Soil organic matter is the main arena of interactions between plants, microbes and soil fauna. Most microbiological processes take place in SOM, as it is a reservoir of carbon and nitrogen sources, a water absorbent and a binding agent for microbial biofilms and soil aggregates. Successive decomposition of SOM with heterogenous origins (derived from plant, animal and microbial material) and high variation in spatial and temporal input, produces diverse substrates for microbiota and thus helps generate high species richness. Since land use practices alter both the quantity and quality of SOM and its distribution in soil, it is probable that the level and spatial location of microbial activities differ between cultivated and non-cultivated lands. Fresh litter is more easily degraded than aged and stabilised organic matter. It is therefore expected that forest floor raw humus as well as a dense grass rhizosphere are locations of high decomposition activity and microbial biomass. As a result of acidic litter material, boreal coniferous forest soils typically have relatively low pH, which favours fungi over bacteria (e.g. Rousk et al., 2009). A different ratio of fungal and bacterial biomass between land use systems is expected to lead to differences in the characteristic enzyme activity patterns. Fungi are proposed to be the predominant source of certain enzymes, e.g.  $\beta$ -glucosidase (Hayano and Tubaki, 1985). On the other hand, fungal biomass is a substrate for chitinolytic enzymes, e.g.  $\beta$ -acetylglucosaminidase.

Plants influence microbial communities through several mechanisms. Quality and amount of leaf and root litter together with root exudates affect the variety, availability and quantity of carbon substrates in soil. In addition to carbon inputs, plant communities may affect soil pH, moisture and temperature, all of which are important regulators of microbial activity. Several authors have reported plant species diversity to correlate positively with the diversity of soil microbiota and their catabolic potential (Stephan et al., 2000; Loranger-Merciris et al., 2006), although this connection is highly complex and needs further investigations (Lamb et al., 2011). Size of the plant affects the extent of root system and litter production and thereby the spatial distribution of carbon sources. Forest and cultivated land differ with respect to the size of their dominant plants, which is probably reflected as differences in the spatial patterns of various microbiological variables. Saetre and Bååth (2000) demonstrated that the microbial community composition measured as phospholipid fatty acid patterns was influenced by the position of trees in a mixed spruce–birch stand. In their study, individual fatty acids had spatial patterns (range of spatial autocorrelation) at scales from 1 m to 11 m. For comparison, spatial patterns of fatty acids have been reported to range from 0.25 m to 1 m in an agricultural field (Cavigelli et al., 1995) and from 0.7 m to 6 m in an unimproved grassland (Ritz et al., 2004). Saetre and Bååth (2000) suggested that the different scales of spatial structure could be explained by the more widely spaced vegetation in forests and the long-lived nature of trees compared to annually harvested crops on agricultural fields.

Intensive tillage and heavy machinery are known to increase the risk of erosion and compaction of soil and thereby to hamper plant productivity and microbial activity (Welbaum et al., 2004) and to reduce microbial species richness (Ceja-Navarro et al., 2010). Fungi have been shown to be especially vulnerable to soil disturbance (Frey et al., 1999). Tillage also counteracts the formation of horizontal gradients in surface soil. This probably contributes to

narrower ranges of autocorrelation of microbiological variables in tilled agricultural soil compared to non-tilled forest soil.

In this study soil enzyme activities were used as indicators of the soil's potential for biodegradation of organic molecules. Decomposition of organic matter occurs at the lowest trophic level and is crucial to all other soil functions, e.g. nutrient cycling, soil structure maintenance, biological population regulation and plant growth (Kibblewhite et al., 2008). As the diversity of the soil microbial community is vast, it is difficult to measure and interpret the relevance of changes in community structure. Therefore, it is advisable to look at the key processes mediated by microbes. However, in order to make full use of enzymes as indicators of soil quality, more reference datasets are needed on their response to different land use and management practices under diverse geographic conditions and soil types (Gil-Sotres et al., 2005; Trasar-Cepeda et al., 2008).

According to our general hypothesis, long-term contrasting land use (e.g. forest vs. cultivated field) leads to clearly distinct functional and structural patterns of the soil microbial community. We expected the different land use systems to differ not only with regard to the level (L) of decomposition activities but also in their plot-scale variation (V) and spatial structure (S). More specifically, we hypothesised that these three dimensions of soil microbiological properties are governed in the land use context as follows:

(L) **Level** of soil enzyme activities and microbial biomass is primarily determined by the concentration of SOM and secondarily by the quality of SOM and the density of rhizosphere.

(V) Within-site **variation** of soil microbiological characteristics is primarily determined by the within-site variation of SOM content and secondarily by plant diversity and tillage intensity.

(S) The range of **spatial autocorrelation** of soil microbiological characteristics is primarily determined by the size of the dominant plant and secondarily by tillage intensity.

To test these hypotheses, we collected spatial data on selected microbiological characteristics from topsoil layers of adjacent spruce forest, unmanaged meadow and organically cultivated field on an ancient seafloor area in south-western Finland. The habitats shared the same origin of soil but differed in vegetation, SOM content and tillage. Eight common hydrolytic enzyme activities, contributing to the decomposition of cellulose, starch, xylose, chitin and acquisition of organic phosphorus and sulphur, were analysed to yield information on how different land use systems affect important biochemical functions in soil. Bacterial fingerprint data, measured as LH-PCR profiles in our study, were used to reveal structural differences in the bacterial community.

## 2. Materials and methods

### 2.1. Site and soil

The studied habitats, spruce forest, meadow and organically cultivated field, are located in Jokioinen in south-western Finland (N60°51.647', E23°31.597') on an ancient seafloor area with even topography. All habitats are within 300 m of each other on the same soil series classified as Vertic Cambisol (WRB classification) with approximately 60% clay content in the topsoil (Soinnie et al., 2009). The area is +100 m above sea level. The growing season is approximately 170 days and the accumulative temperature sum is 1200 degree days. The mean annual precipitation is 600 mm.

Cultivation in the area began at the end of the 19th century. The first hundred years of cultivation resembled modern organic farming, with only minor use of fertilisers. The main crops were hay and cereals. The present-day organically cultivated field and the meadow sampled in this study shared the same cultivation history until 1991, when management of the farm was transferred to MTT Agrifood Research Finland. Since then, the sampled field site has

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