



Soil property and management effects on grassland microbial communities across a latitudinal gradient in Germany



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ARTICLE INFO

Article history:

Received 30 January 2013

Received in revised form 3 July 2013

Accepted 10 July 2013

Keywords:

Temperate grasslands

Degraded peat soils

Land-use intensity

Phospholipid fatty acid (PLFA)

Specific enzyme activities

ABSTRACT

There is much interest in the identification of the main drivers controlling changes in the microbial community that may be related to sustainable land use. We examined the influence of soil properties and land-use intensity (N fertilization, mowing, grazing) on total phospholipid fatty acid (PLFA) biomass, microbial community composition (PLFA profiles) and activities of enzymes involved in the C, N, and P cycle. These relationships were examined in the topsoil of grasslands from three German regions (Schorfheide-Chorin (SCH), Hainich-Dün (HAI), Schwäbische Alb (ALB)) with different parent material. Differences in soil properties explained 60% of variation in PLFA data and 81% of variation in enzyme activities across regions and land-use intensities. Degraded peat soils in the lowland areas of the SCH with high organic carbon (OC) concentrations and sand content contained lower PLFA biomass, lower concentrations of bacterial, fungal, and arbuscular mycorrhizal PLFAs, but greater enzyme activities, and specific enzyme activities (per unit microbial biomass) than mineral soils in the upland areas of the HAI and ALB, which are finer textured, drier, and have smaller OC concentrations. After extraction of variation that originated from large-scale differences among regions and differences in land-use intensities between plots, soil properties still explained a significant amount of variation in PLFA data (34%) and enzyme activities (60%). Total PLFA biomass and all enzyme activities were mainly related to OC concentration, while relative abundance of fungi and fungal to bacterial ratio were mainly related to soil moisture. Land-use intensity (LUI) significantly decreased the soil C:N ratio. There was no direct effect of LUI on total PLFA biomass, microbial community composition, N and P cycling enzyme activities independent of study region and soil properties. In contrast, the activities and specific activities of enzymes involved in the C cycle increased significantly with LUI independent of study region and soil properties, which can have impact on soil organic matter decomposition and nutrient cycling. Our findings demonstrate that microbial biomass and community composition as well as enzyme activities are more controlled by soil properties than by grassland management at the regional scale.

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1. Introduction

Soil microorganisms play a significant role in many ecosystem processes such as soil organic matter decomposition, nutrient cycling, and organic carbon (OC) sequestration. At the same time, they are important drivers of plant diversity and productivity in

terrestrial ecosystems and thus of sustainable land use (Van der Heijden et al., 2008). The link between soil microbes and their function can be made by studying the activity of extracellular enzymes involved in the C, N and P cycling (Caldwell, 2005). Extracellular enzymes are responsible for the breakdown of large polymeric compounds and thus control many metabolic pathways in soils. There are various factors regulating the abundance, composition and activities of soil microorganisms such as edaphic factors (soil type, texture, moisture, pH, nutrient availability) or land management practices. In order to understand soil processes at larger spatial scales and management effects, it is therefore necessary

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to know more about the main edaphic drivers that determine the composition and functions of soil microorganisms.

In Europe, grasslands cover about 13% of the land area (Eurostat, 2011), and have great potential to sequester C by improving grassland management practices (Conant, 2010). Grasslands in Germany exist in different geographical regions such as in lowland areas in northern Germany or in low mountain ranges (upland areas) in central and southern Germany (Fischer et al., 2010). As a result of differences in climate, topography, and parent material, various soil properties such as OC concentration, texture, soil temperature, soil moisture, nutrient availability, and pH vary across these larger regions. All these soil properties have been shown to impact microbial community composition and related enzyme activities in mineral soils (Grayston et al., 2001; Brodie et al., 2002; Lauber et al., 2008; Sinsabaugh et al., 2008). However, most of these studies have focused on the relation between soil properties and microbes in only one study region. It has been shown that results obtained at one site with specific soil characteristics cannot be generalized and transferred to other sites/regions with different soil properties (Gianfreda et al., 2005). So far, little is known about relationships between soil properties and biota shared among different regions with their specific abiotic conditions (Birkhofer et al., 2012). Thus, studies on larger spatial scales are needed to derive general patterns.

In lowland areas of northern Germany, former peat soils were frequently drained and subsequently managed as grasslands, resulting in grassland sites with large soil OC concentrations. Waterlogged conditions were shown to inhibit microbial activities (Kang and Freeman, 1999). Periodically, waterlogged conditions still occur at these managed grasslands, but at present, little is known about the microbial community structure and activity at these sites, and how they deviate from other grassland soils in upland areas. Soils in upland areas in Germany, in contrast, often contain much less OC and soil moisture (Chen et al., 2009).

Grasslands in lowland and upland areas in Germany are all subject to similar management practices such as nitrogen (N) fertilization, mowing, and grazing. The effect of different management practices on soil microbiological properties has usually been studied using field manipulations. Such experiments have shown that N addition and high grazing intensities favor the growth of bacteria as indicated by lower fungi to bacteria ratios (Bardgett et al., 1999, 2001; Grayston et al., 2001), and decrease the overall abundance of microorganisms (Lovell et al., 1995; Bardgett et al., 1999, 2001). In contrast, mowing has been found to increase soil microbial biomass (Uhlirová et al., 2005). In comparison to microbial community composition or growth, enzyme activities show no clear pattern in response to inorganic N fertilization, mowing, or grazing. Some authors reported that inorganic N fertilization stimulated activities of C, N and phosphorus (P) acquiring enzymes (Stursova et al., 2006; Keeler et al., 2009), while others found that N fertilization inhibited activities of enzymes involved in the N cycle (Dick, 1992; Olander and Vitousek, 2000). Mowing and grazing has been reported to increase (Le Roux et al., 2003) or decrease (Holt, 1997) the activities of soil enzymes that are fundamental to N cycling. Although experiments help to understand the effects of single management practices, farmers commonly apply a number of different management practices simultaneously. The combination of several management practices can lead to additive, neutralizing or completely different effects on soil communities and functions compared to each single practice in isolation. However, field studies to analyze these combined effects are rare (for instance, Grayston et al. (2001)). In addition, many experiments run for only a few years, and therefore long-term effects of grassland management are not well known.

In this study, we analyzed the effects of soil properties and grassland management on microbial biomass, soil microbial community

composition (measured as phospholipid fatty acids (PLFAs)), and enzyme activities in topsoils from three German regions. All plots have experienced a long history of management and differ in their soil characteristics (degraded peat soils in lowland areas, mineral soils in upland areas). Grassland management in each study region included N fertilization, mowing, and grazing. The combined effect of these management activities was examined using a land-use intensity index. With this study, we aimed to determine (1) general relationships between soil properties and total PLFA biomass, microbial community composition, and enzyme activities and (2) the impact of long-term grassland management on total PLFA biomass, microbial community composition, and enzyme activities.

2. Materials and methods

2.1. Study sites

We studied 27 continuously managed grassland plots located in the Biodiversity Exploratories comprising Schorfheide-Chorin (SCH) in northern Germany, Hainich-Dün (HAI) in central Germany and Schwäbische Alb (ALB) in southern Germany (Fischer et al., 2010). These three study regions differ in climatic conditions and parent materials (Table 1) and constitute a latitudinal gradient of 800 km. The predominant soil groups in the three study regions are Histosols in the SCH, Stagnosols in the HAI, and Leptosols in the ALB (IUSS Working Group WRB, 2006). In each region, nine grassland plots with different land-use intensities were established. For each plot i , the land-use intensity (LUI_i) (Table 2) was calculated according to Blüthgen et al. (2012), and is defined as

$$LUI_i = \frac{F_i}{F_R} + \frac{M_i}{M_R} + \frac{G_i}{G_R}$$

where F_i is the intensity of N fertilization ($\text{kg N ha}^{-1} \text{ yr}^{-1}$), M_i is the mowing frequency and G_i is the grazing intensity (livestock units days (LU d) of grazing $\text{ha}^{-1} \text{ yr}^{-1}$) for the year 2007, and F_R , M_R , G_R are their respective mean within its region R for that year.

2.2. Soil sampling

In spring 2008, five soil samples were taken at each grassland plot ($20 \times 20 \text{ m}$), one at each corner and one in the plot center, and mixed to obtain a composite sample for each plot. Prior to the sampling, the aboveground vegetation was cut and removed. The soils in the HAI and ALB were sampled down to the bedrock (mean soil profile depth HAI $45 \pm 1.7 \text{ cm}$, ALB $20 \pm 1.4 \text{ cm}$) using a motor driven auger (8.3 cm diameter). In the SCH a split tube sampler (4.8 cm diameter, 40 cm length) was used to sample Histosols and Gleysols. The uppermost soil horizon, the Ah horizon in the HAI and ALB, and the Ha horizon of the Histosols in the SCH was separated from the soil core, stored in ice boxes and transported to the field lab facility. The mean horizon depth in the HAI was $10.4 \pm 3.0 \text{ cm}$, in the ALB $12.6 \pm 0.8 \text{ cm}$, while only the 0–10 cm depth increment of the Ha horizons were sampled. After removal of coarse roots and stones one sub-sample of the soil sample was air-dried, a second was stored at -20°C and another one was stored at -80°C .

2.3. General soil properties

Air-dried sub-samples were sieved to $<2 \text{ mm}$ and used to determine soil texture, pH, organic carbon (OC), total nitrogen (TN), labile inorganic P (P_i), and labile organic P (P_o) concentrations. Soil texture was determined according to Schlichting and Blume (1964). Soil pH was measured in the supernatant of a 1:2.5 mixture of soil and 0.01 M CaCl_2 using a glass electrode. Sub-samples for elemental analysis were ground in a ball mill. Total C and N concentrations

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