Soil Biology & Biochemistry 77 (2014) 221–232

Contents lists available at ScienceDirect

Soil Biology & Biochemistry

journal homepage: www.elsevier.com/locate/soilbio

Contrasting development of soil microbial community structure under no-tilled perennial and tilled cropping during early pedogenesis of a Mollisol

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ARTICLE INFO

Article history:
Received 26 November 2013
Received in revised form
4 July 2014
Accepted 6 July 2014
Available online 9 July 2014

Keywords:
Soil microbial community structure
Phospholipid fatty acid
Organic amendment
Mollisol
Soil formation
Soil restoration

ABSTRACT

A range of agricultural practices influence soil microbial communities, such as tillage and organic C inputs, however such effects are largely unknown at the initial stage of soil formation. Using an eight-year field experiment established on exposed parent material (PM) of a Mollisol, our objectives were to: (1) to determine the effects of field management and soil depth on soil microbial community structure; (2) to elucidate shifts in microbial community structure in relation to PM, compared to an arable Mollisol (MO) without organic amendment; and (3) to identify the controlling factors of such changes in microbial community structure. The treatments included two no-tilled soils supporting perennial crops, and four tilled soils under the same cropping system, with or without chemical fertilization and crop residue amendment. Principal component (PC) analysis of phospholipid fatty acid (PLFA) profiles demonstrated that microbial community structures were affected by tillage and/or organic and inorganic inputs via PC1 and by land use and/or soil depth via PC2. All the field treatments were separated by PM into two groups via PC1, the tilled and the no-tilled soils, with the tilled soils more developed towards MO. The tilled soils were separated with respect to MO via PC1 associated with the differences in mineral fertilization and the quality of organic amendments, with the soils without organic amendment being more similar to MO. The separations via PC1 were principally driven by bacteria and associated with soil pH and soil C, N and P. The separations via PC2 were driven by fungi, actinomycetes and Gram (−) bacteria, and associated with soil bulk density. The separations via both PC1 and PC2 were associated with soil aggregate stability and exchangeable K, indicating the effects of weathering and soil aggregation. The results suggest that in spite of the importance of mineral fertilization and organic amendments, tillage and land-use type play a significant role in determining the nature of the development of associated soil microbial community structures at the initial stages of soil formation.

1. Introduction

Soil losses due to erosion processes in some locations around the world are up to 100 times faster than the associated rates of soil formation (Montgomery, 2007). This can result in soil parent materials being closer to the ground surface, or even exposed to the air, which in turn can affect the ability of soils to support food production, since such parent material is inherently less fertile than a fully-formed soil. Such phenomena occur widely, e.g. from the south (Zhang et al., 2004) to the north (Liu et al., 2011) of China and around the world (Lal, 2003; Quinton et al., 2010). Therefore, there is a considerable need for large-scale restoration programs to develop strategies for restoration, sustainable use and protection of soils (Cairns, 1999; Hobbs and Harris, 2001; Schulz et al., 2013). Many large-scale restoration programs have proven successful in terms of above-ground ecosystem properties. However, our understanding of soil development in vegetation restoration contexts

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http://dx.doi.org/10.1016/j.soilbio.2014.07.002
0038-0717/

is still very poor (Griffiths et al., 2008; Harris, 2009; Yao et al., 2009), possibly because it may take more than hundreds of years to develop a high level of soil fertility under natural conditions (Harrison and Strahm, 2008). Although agricultural use is one of the most important objectives of restoration in arable regions, and agricultural practices can rapidly influence soil properties and fertility in contrast to 'natural' successional processes (Knops and Tilman, 2000), such management approaches have rarely been considered as a restoration technique *per se*.

Soil microbes play critical roles in soil formation. They drive the essential processes of mineral weathering (Chorover et al., 2007), the formation of soil structure (Feeney et al., 2006; Rillig and Mummey, 2006), organic matter decomposition and nutrient cycling (Paul and Clark, 1989; Schimel, 1995). Therefore, they further regulate plant productivity and community diversity (Wardle et al., 2004; van der Heijden et al., 2008). During above-ground ecosystem succession, soil physico-chemical properties, such as organic matter, pH, and redox conditions change with time. This can further influence soil microbial communities (Lombard et al., 2011). Therefore, there are complex interactions between soil biota and abiotic conditions at different stages of above-ground ecosystem succession and below-ground soil development (Schulz et al., 2013). Consequently it can be difficult to distinguish whether the soil microbial communities act as 'facilitators' or 'followers' for ecosystem succession and restoration (Harris, 2009; Schulz et al., 2013). Measurement of soil microbial communities can indicate the status of the ecosystem development in relation to targets and the effectiveness of management intervention (Harris, 2009).

Most microbial functions arise not as the result of actions of particular single organisms, but of microbial communities which closely interact with each other (Aneja et al., 2006). Phospholipid fatty acid (PLFA) analysis has been widely used to reflect a broad measure of active biomass with various groups of soil microorganisms (Liu and Ristaino, 2003; Girvan et al., 2004; Mckinley et al., 2005; Feeney et al., 2006), and to reveal changes in biomass of the various components of microbial communities (Vestal and White, 1989; Zelles, 1997). Profiles of community-level PLFAs indicate relative proportions of particular phenotypic groups of organisms in soils, which will deliver different functions such as decomposition of plant litter, or the development of food web structures and closed nutrient cycling (Zak et al., 1994; Ringelber et al., 1997; Aneja et al., 2006). PLFA profiles have been used to reveal changes in microbial communities at the primary stage of soil development in many studies using soil chronosequences after vegetation restoration (e.g. Inglett et al., 2011) or glacier recession (e.g. Hahn and Quideau, 2013; Schulz et al., 2013).

Agricultural practices such as the particular nature of different cropping systems, organic amendments, mineral fertilization and tillage can strongly influence soil microbial community development and dynamics. Different crops provide different resources that vary in quality and quantity and can be exploited by different microbial consortia, causing changes in microbial communities (Miethling et al., 2000; McKinley et al., 2005; Goldfarb et al., 2012). Soil microbial community structure can change in the presence of pioneer N-fixing plants due to the influence of plant species' on soil pH and N availability (Tscheko et al., 2003; Lauber et al., 2008; Deng et al., 2010). With an increasing amount of organic amendments such as plant residues, incorporation of crop straw and application of organic manure, soil physico-chemical properties, and microbial activity and biomass can be significantly modified (Fröberg et al., 2003; Bronick and Lal, 2005; Brant et al., 2006). There are a few studies demonstrating the effects of the quantity of added organic matter on soil microbial communities in the laboratory (Griffiths et al., 1999; Eilers et al., 2010) or in the field (Zhang et al., 2013). Chemical fertilization influences soil pH, availability and deficiency of nutrients such as N and P as well as soil organic matter due to more biomass being produced and returned to soil with increasing fertilization (Marschner et al., 2003; Zhong and Cai, 2007; Zhong et al., 2010). Tillage may have detrimental effects on soil organisms (Lenz and Eisenbeis, 2000; Berkelmans et al., 2003) as it disrupts fungal mycelia and hyphae, thus reducing fungal biomass (Beare et al., 1997; Frey et al., 1999; Simmons and Coleman, 2008). Moreover, tillage is frequently integrated within chemical fertilization and organic amendments, which can extend effects on soil microbial communities into deeper soil layers (Treonis et al., 2010). Root penetration depths may also influence soil microbial communities in deep soil possibly through impacts on spatial heterogeneity of physico-chemical properties in relation to root penetration depths and tillage depth (Blume et al., 2002; Deng et al., 2010; Eilers et al., 2010). However, most of knowledge is gained in the context of well-developed soils, which are often limited to the surface zones. We were unable to locate reports about the effects of agricultural practices on changes in soil microbial communities at the initial stages of soil development. Accordingly, a field experiment was established in 2004 to examine soil development from the parent material (PM) of a Mollisol. The objectives of this study were: 1) to determine the effects of field treatment and soil depth on soil microbial community structure; 2) to elucidate the shifts of soil microbial community structure in relation to PM and an arable Mollisol (MO) without organic amendment; and 3) to identify controlling factors of such relationships. The treatments included no-tilled perennials and tilled soils under the same cropping system, with or without chemical fertilization and different amounts of aboveground biomass incorporated into soil. It was hypothesized that agricultural practices facilitate the development of microbial community structure in soil profiles through soil tillage, interacting with organic and inorganic inputs. Such knowledge may identify factors that allow accelerated restoration and development of critical soil functions that are governed by soil microbial communities.

2. Materials and methods

2.1. Study site and experimental design

The experiment was established in 2004 at the State Key Experimental Station of Agroecology, Chinese Academy of Sciences, Hailun, Heilongjiang province (47°26′N, 126°38′E) (Hailun Station). The experimental site is located in the center region of the Mollisols in Northeast China. The region has a typical temperate continental monsoon climate with a hot summer and a cold winter. The mean annual temperature is 2.2 °C, with the highest monthly temperature (35 °C) in July and lowest in January (−38 °C). The mean annual rainfall is 550 mm, with about 65% occurring from June to August. The soil is classified as Pachic Haploborolls according to the USDA Taxonomy (Soil Survey Staff, 2010) and as Phaeozems according to WRB (IUSS Working Group WRB, 2006). The Mollisol was derived from the parent materials that were sedimentary materials of loamy loess (Xiong and Li, 1987). The soil profile consists Ap1 (0–0.15 m) – Ap2 (0.15–0.25 m) – Ah1 (0.25–0.40 m) – Ah2 (0.40–0.70 m) – AB (0.70–1.00 m) – BC (1.00–1.70 m) and C (>1.70 m). The parent materials contained 420 g kg^{-1} clay (<0.002 mm) and 356 g kg^{-1} silt (0.02–0.002 mm), with a blocky structure and dominant clay minerals of vermiculate, chlorite and illite.

In June 2004, the soils from the surface down to 0.8 m were excavated from an area of 9.8 m long and 5.0 m wide. In the open area, twenty-four plots (1.4 m length, 1.0 m width and 0.8 m depth for each plot) were constructed and separated by cement barriers (0.2 m wide and 0.1 m above the ground) to set up six different