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Linking macroaggregation to soil microbial community and organic carbon accumulation under different tillage and residue managements

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ABSTRACT

The formation of aggregates plays a key role in shaping soil microenvironment, which in turn influences microbial community structure and organic carbon (C) dynamics in soil. The objective of this study was to identify the linkages between soil macroaggregation and microbial community as well as organic C accumulation using field samples following 9 years of conservation tillage. A wet-sieving method was used to fractionate soil aggregates and soil microbial abundance and community composition were determined using phospholipid fatty acid (PLFA) analysis. Compared to continuous tillage, reduced/no-tillage and straw returning significantly promoted soil macroaggregation and consequently increased organic C, C/N ratio and soil moisture but decreased the porosity and computed effective oxygen diffusion coefficients. The changes in these soil characteristics were closely related to the abundance and composition of microbial community. The abundance of microbial PLFAs in reduced/no-tillage soils was 30.0% higher in Gram-positive bacteria, 11.6% higher in Gram-negative bacteria, 71.7% higher in fungi and 45.4% lower in actinobacteria, whereas straw returning significantly increased all microbial PLFA abundances relative to straw removing. The ratios of bacteria/fungi (B/F) and monounsaturated/branched (M/B) PLFAs were significantly correlated with the volumetric soil water content, porosity, or computed effective oxygen diffusion coefficients. Soil macroaggregation and microbial community composition collectively explained 82.4% variation in organic C accumulation and their interaction made the largest contribution. Overall, soil macroaggregation under conservation tillage might cause a shift in microbial community to more fungi and anaerobes through primarily influencing soil moisture and aeration, which could effectively promote organic C accumulation in soil.

1. Introduction

Soil aggregation can enhance the physical inaccessibility of organic carbon (C) for decomposing microorganisms (Jagadamma et al., 2014) and meanwhile, changes of aggregate formation under different management regimes influence soil microenvironment (Kong et al., 2011). Sessitsch et al. (2001) and Helgason et al. (2010) have found significant effects of soil macroaggregation on water infiltration and oxygen availability. Soil characteristics such as soil total porosity, water- and air-filled pore space, organic substrates, temperature etc., are responsible for the changes in soil microbial community structure under different agricultural management practices (Macdonald et al., 2009; Kuntz et al., 2013). For a conservation tillage system, the reduced physical disturbance, increased soil moisture and altered distribution of organic substrates in the soil profile could cause great shifts in bacterial and fungal biomass ratios (Strickland and Rousk, 2010; Zhang et al., 2015a). After adding crop residues to the soil, Aneja et al. (2006) found that the decomposing residues, as a carbon source, exerted the most pervasive effects on soil microbial activity and community. When conservation tillage practice was operated over an 8-year period, the pathway of organic C decomposition in surface soil was altered from bacteria-dominated to fungi-dominated decomposition (Griffiths et al., 2012). Whereas, some conflicting results reported by Sun et al. (2016) that long-term conservation tillage had potential for improving microbial abundance but might not alter their community composition, seem to be related to the effect of individual pedo-climatic conditions (Kuntz et al., 2013).

In recent years, C sequestration in soil has been gaining increasing

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recognition for its role in increasing crop yields, improving soil quality and maintaining agricultural sustainable development (Panettieri et al., 2014; Zhang et al., 2015b). The turnover of soil organic C is not only determined by the physical protection offered by aggregates, but also by the abundance and community of microorganisms (Miltner et al., 2009). Sun et al. (2004) and Karolien et al. (2009) reported that microorganisms strongly influence a wide range of soil processes, and their abundance and composition in soil are being increasingly recognized as crucial for determining C cycle processes such as organic C turnover, stabilization and accumulation in soil. Accumulated evidence (Moore-Kucera and Dick, 2008) suggests that soil microbial communities dominated by fungi have greater capability to degrade recalcitrant organic C like lignin and cellulose than soils dominated by bacterial communities because fungi release a broader range of extracellular enzymes. In contrast, the actinobacteria are well-adapted to metabolize nutrient-poor soil organic compounds (MacKenzie and Quideau, 2010), and thus the decrease in their abundance could reduce the decomposition of old soil organic matter or newly formed relatively recalcitrant organic C (Billings and Ziegler, 2008). Because aerobes can decompose organic C more efficiently, the shift in microbial communities towards facultative and obligate anaerobes seems to be favorable to stabilize soil organic C (Zhang et al., 2014).

A direct link of the development of soil microbial communities with soil aggregation was revealed in an incubation experiment by Blaud et al. (2012). Soil environmental conditions controlled by soil structure and aggregation affected the community and activity of soil microorganisms and the connectivity between organic C and potential decomposers, which in turn influenced the turnover of soil organic C (Kong et al., 2011). The formation of macroaggregates is driven by conservation tillage directly through decreasing physical disruption, and indirectly by enhancing organic matter inputs (Melero et al., 2009; Xu et al., 2011). Consequently, macroaggregation, microbial community and organic C accumulation are related through dynamic feedback mechanisms which inextricably link these three primary foundations of soil functioning under conservation tillage.

The North China Plain is dominated by fluvo-aquic soils that are characterized by poor structures and low organic matter. Continuous tillage and the removal of postharvest residues from conventional tillage practices have seriously degraded the soil. It has been suggested that conservation tillage systems including reduced and no-tillage coupling with straw returning, could effectively promote soil macroaggregation and reverse the disadvantages of conventional tillage in accumulating C through altering the abundance and community of soil microorganisms (White and Rice, 2009; van Capelle et al., 2012; Zhang et al., 2013a). Thus, to investigate the linkages between soil macroaggregation and microbial community composition as well as organic C accumulation in soil following conservation tillage, the present study was conducted based on a continuous 9-year conservation tillage experiment in the North China Plain. Furthermore, considering the significant increase and slight decrease of soil organic C storage caused by conservation tillage in the same site at the 0–10 and 10–20 cm depths, respectively, which was reported by Zhang et al. (2017), this study was primarily focused on the 0–10 cm surface soil. We aimed at evaluating microbial community and organic C accumulation in the topsoil related to soil macroaggregation under different tillage and residue management. Consequently, we examined (1) how macroaggregation regulated soil characteristics and therefore, influenced bacterial and fungal communities, and (2) how such changes in microbial community could be related to organic C accumulation in soil following conservation tillage.

2. Materials and methods

2.1. Experimental site and design

The long-term field experiment was established in June 2006 in a well-drained field where winter wheat (*Triticum aestivum* L.) has been annually rotated with summer maize (*Zea mays* L.). The site is located in Fengqiu, Henan province, China (35°00′N, 114°24′E), which belongs to the Fengqiu National Agro-Ecological Experimental Station, Chinese Academy of Sciences. The area is semi-arid, with a warm temperate continental monsoon climate. The mean annual precipitation is 615 mm (mainly from July to September) and the mean annual temperature is 13.9 °C. The soil, derived from alluvial sediments of the Yellow River, is classified as an Aquic Inceptisol with 52% sand, 33% silt and 15% clay. At the beginning of the experiment, soil had been cultivated for > 50 years in a similar agricultural cropping system, so the spatial heterogeneity of soil fertility across the field was considered to be minimal. In 2006, soil had an average pH of 8.3, bulk density of 1.44 g cm^{-3}, porosity of 0.46 cm^3 cm^{-3}, 6.09 g organic C kg^{-1}, 0.55 g total N kg^{-1}, 0.81 g total P kg^{-1}, 18.08 g total K kg^{-1}, and 8.01 cmol CEC (cation exchange capacity) kg^{-1}.

The long-term conservation tillage experiment was based on a completely randomized design with eight treatments in triplicates including two factors. The first factor was tillage regime including T (continuous tillage), 2T (tillage every two years), 4T (tillage every four years) and NT (no-tillage); and no residue (-S) or all crop residues (+S) were added to the soils of four tillage practices and regarded as the second factor. Different tillage regimes were applied only to wheat and the land was never tilled for maize. T treatment involved one moldboard plowing (20–22 cm) in October followed by secondary seedbed preparation (7.5–10 cm) with a disk harrow. Under NT treatment, the soil was undisturbed except when the crop was planted using a no-till planter. In the 2T and 4T, moldboard plowing was employed in the tillage-year, whereas no tillage disturbance occurred in the no-tillage-year. After harvesting, residues were crushed into 2–3 cm pieces for maize straw and 6–7 cm pieces for wheat straw, and were then returned to the soil surface under + S treatments. The residue amounts were related to the crop yield in each plot. And under –S treatments, all crop residues were removed from the plots. The plot size was 7 m × 6.5 m. Each treatment plot received the same amount of fertilizer. Further details of fertilizer application have been reported by Zhang et al. (2017). Other field management practices were the same for all treatments during the experiment.

2.2. Soil sampling, fractionation and analysis

In September 2015 immediately after the maize harvest, five soil core samples were collected from each replicate plot by inserting a cylindrical metal core of 5 cm in diameter to 10 cm depth, and then mixed as one composite sample. Fresh samples were stored at 4 °C in the field and transported immediately to the laboratory. Moist soils were gently broken apart along the natural break points and passed through a 10-mm sieve. By dividing each sieved soil sample into three subsamples, one subsample was used for PLFA analyses and aggregate fractionation; another one was dried at 105 °C to measure soil moisture; and the last one was air-dried for the analyses of organic C and total N using a Vario MAX CN elemental analyser (Elementar, Germany). Due to the presence of carbonate, the soil was pretreated with 1.0M HCl to determine organic C content. Soil bulk density was determined using the core method (Grossman and Reinsch, 2002). According to the wet-sieving protocol of Elliott (1986), the tested soil was fractionated into macroaggregates (> 250 μm), microaggregates (250–53 μm), and the silt + clay fraction (< 53 μm). All separated aggregates were oven-dried at 60 °C for determining their properties.

2.3. Phospholipid fatty acid (PLFA) analysis

Soil PLFA extraction was conducted following the methods described by Zhang et al. (2015b), which were based on a modified Bligh-Dyer technique (Brant et al., 2006). Briefly, total lipids were extracted in a single-phase methanol-chloroform-phosphate buffer (2:1:0.8)