



Microbial crop residue decomposition dynamics in organic and conventionally managed soils



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ABSTRACT

Agricultural practices can influence soil microbial communities, which are the primary regulators of soil carbon and nutrient cycling processes. Differences in microbial community composition have the potential to affect the fate of carbon and nutrients during decomposition and may therefore influence the retention of C and provisioning of crop nutrients in agroecosystems. Long term management-induced shifts in microbial communities and resource availability may interact to affect the microbial utilization of fresh inputs of crop residues in the short term, with lasting impacts on soil C accrual and fertility. The objective of this study was to investigate whether long-term organic and conventional management resulted in differences in microbial residue decomposition. Soils under conventional and organic management planted with annual crops or with a mix of annual crops and three years of perennial alfalfa were collected from a long-term (19 y) field study in Saskatchewan, Canada and were incubated in the laboratory with and without ¹³C-labelled barley residues for 98 d. We measured extracellular enzyme activities (EEAs) and the incorporation of crop residue-derived C within major microbial groups (fungi, actinobacteria, and Gram positive and negative bacteria) during decomposition. Total PLFA biomass and EEAs were highest in soils from the conventional-annual system, similar between the conventional and organic perennial systems, and similar or lowest in the organic-annual system. Crop residue additions alleviated these differences; that is, in residue-amended soils total PLFA biomass, EEAs, and the abundance of the fungal biomarker increased in the organic systems compared to the unamended soils to become similar to the conventional systems. In contrast, residue additions induced small or no changes in biomass and EEAs in the conventional-annual soils. Using ¹³C-PLFA-SIP we showed that the general pattern of microbial succession during decomposition was similar among soils, but that fungi and especially actinobacteria were relatively more dominant in organic compared to conventionally managed soils during early and later stages of decomposition, respectively. Thus, shifts in the decomposer community composition were greater in soils originating from organic management, possibly as a result of larger changes in resource availability during the incubation that advanced the rate of microbial succession. This may reinforce long term differences in SOC quality and nutrient availability between management regimes. Organically-managed cropping systems are particularly reliant on biological cycling of organic nutrients to support crop growth. This work reinforces the importance of adequate crop residue returns for maintaining soil function, particularly where external organic amendments are not applied to balance nutrients exported as crop products.

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1. Introduction

Organic management is often observed to improve measures of soil quality in agroecosystems relative to conventional management. Higher soil organic carbon (SOC) stocks (Gattinger et al.,

2012; Kong and Six, 2010), microbial biomass (Mäder et al., 2002), enzyme activities (García-Ruiz et al., 2008; Mäder et al., 2002; Reeve et al., 2010), and distinct microbial communities (Dai et al., 2014; Kong et al., 2011; Li et al., 2012) have been reported in on-farm experiments as well as in long-term field studies under organic management. These increases in SOC and microbial activity are attributed to a greater reliance on inputs of organic materials, particularly manure (Flieβbach et al., 2007), and the planting of forage legumes (Leithold et al., 2015). Organic

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management systems also tend to utilize more diverse crop rotations (Dai et al., 2014), which can increase soil microbial biomass and SOC (McDaniel et al., 2014b), alter microbial community composition, and enhance aggregate formation and biogeochemical cycling (Tiemann et al., 2015). However, there is controversy surrounding the improvement of soil quality with organic management (Leifeld et al., 2013). Indeed, the benefits of organic farming to soil quality may not be ubiquitous among regions or systems.

In the Canadian prairies, organic farms are predominantly managed as large-scale intensive grain operations. Livestock are rarely integrated into these systems and as a result, application of manure is uncommon or sparse (Knight et al., 2010). In addition, whereas no-till has been adopted on 68% of land in this region (Awada et al., 2015), organic farmers still rely on tillage for weed control and green manure termination (Dai et al., 2014). Therefore, the gains in SOC often found with the adoption of no-till (VandenBygaart et al., 2003) in this region may not be realized on organic farms. Previous studies comparing organic and conventional systems in the Canadian prairies suggest that tillage and lack of manure inputs could negate other potential positive effects of organic practices to soil quality such as the use of diversified and extended crop rotations that include perennials, cover crops, and green manures. Previous work in this region indicates nutrient limitation and declines in SOC quality and quantity in organic systems (Bell et al., 2012; Knight et al., 2010; Malhi et al., 2009). Even with tillage, SOC stocks were higher in a conventional compared to a similarly tilled organic system, reflecting lower plant litter inputs over the course of an 18 y field trial in Manitoba, Canada (Bell et al., 2012). Light fraction (LF) organic matter was higher in soils after 12 y of no-till conventional compared to tilled organic management in Saskatchewan, Canada, despite no differences in total SOC (Malhi et al., 2009). This indicates that soil organic matter (SOM) composition, and thus resource quality and availability, diverged between the organic and conventional systems.

Differences in SOM characteristics can account for variations in microbial community composition and function between contrasting soils (Ng et al., 2014) and alterations in soil resource availability due to changing environmental conditions and land management can shift community composition (Allison et al., 2013; Fierer et al., 2012; Hartmann et al., 2014). The role that microbial community composition plays in regulating complex processes such as decomposition is not well understood (McGuire and Treseder, 2010), but it is increasingly recognized and demonstrated to be an important factor (Strickland et al., 2009; Waring et al., 2013; Wickings et al., 2010). Microbial community composition can affect decomposition and associated nutrient cycling as a result of varied life strategies and physiologies that affect the substrate utilization patterns of the microbial taxa comprising the community (Fierer et al., 2007). As a result, distinct communities can allocate substrate differentially to catabolic respiration and to anabolic processes that support growth as well as the production of molecules important to soil functioning such as extracellular polysaccharides that bind SOM or enzymes that mineralize organic nutrients (Schimel and Schaeffer, 2012). Thus, agricultural management-induced changes to microbial community composition may reinforce differences in SOC accrual, SOM composition, and nutrient availability between farming systems.

Stable isotope probing (SIP) coupled with phospholipid fatty acid (PLFA) analysis can be used to identify metabolically active microbial decomposers, providing direct insight into the role that the soil microbial community plays in decomposition (Watzinger, 2015; Yao et al., 2015). PLFA-SIP has been useful in quantifying successional changes in microbial C utilization during crop residue

decomposition (Bai et al., 2016; Helgason et al., 2014; Marschner et al., 2011; McMahon et al., 2005; Moore-Kucera and Dick, 2008), and has indicated that the shift in dominance of microbial groups over the course of decomposition can vary among soils and residue types (Herman et al., 2012; Williams et al., 2006) and as a result of cropping system management (Helgason et al., 2014). Moreover, the dominant microbial group involved in decomposition can also depend on nutrient availability. For example, manipulating N availability was shown to induce a shift in the incorporation of substrate-derived C within PLFA microbial groups; N addition enhanced fungal and reduced Gram negative bacterial incorporation of substrate-C (Koranda et al., 2014). Yet under high, non-limiting nutrient conditions, there was no difference in the incorporation of residue-C within microbial groups among organic, low-input, and conventional tomato-maize cropping systems in spite of variations in community composition (Kong and Six, 2012). Characterizing microbial community composition using PLFA-SIP may have utility in elucidating differences in decomposition and the fate of crop residue-derived C in soils of contrasting nutrient availability.

The Alternative Cropping Systems (ACS) trial established in 1994 in Saskatchewan, Canada, has demonstrated lower nutrient status in organically managed soils and diverging quality of SOM between organic and conventional management systems (Malhi et al., 2009). Lower LF organic matter content in organic compared to conventionally managed soils in the ACS trial might indicate a depleted supply of easily degradable substrate (Janzen et al., 1992) for the microbial community as well as a reduced enzymatic potential to cycle organic materials (Veres et al., 2015). Soil microbial communities shift extracellular enzyme production to acquire the most limiting element (Moorhead et al., 2013; Schimel and Schaeffer, 2012). The hydrolytic enzymes, β -glucosidase (BG), N-acetyl glucosaminidase (NAG), and phosphatase (Phos) have been proposed to stand in as proxies for groups of enzymes responsible for holocellulose, chitin and peptidoglycan, and organic P degradation, respectively, and their ratios could be linked to the relative availability of C, N, and P (Moorhead et al., 2013). Differences in organic substrate and nutrient availability have been shown to reflect differences in β -glucosidase (Lagomarsino et al., 2009) and phosphatase (Fraser et al., 2015) activities between organic and conventionally managed soils. As such, differences in resource availability may also affect extracellular enzyme activities in soils under contrasting management regimes within the ACS trial.

In the absence of manure and fertilizer inputs, crop residues are particularly important sources of energy and nutrients to soil microorganisms in Prairie organic grain farming systems. Therefore, understanding how microbial communities process crop residues is vital to predicting, and thus managing, the fate of C and the provisioning of crop nutrients in these systems. The objective of this laboratory incubation study was to assess whether microbial community composition and function in soils collected from the ACS field trial differs after 19 y of contrasting management. Specifically, we investigated whether microbial community composition was linked to crop residue decomposition and extracellular enzyme activities (EEAs) important for C (BG), P (Phos), and N (NAG) cycling. PLFA-SIP was used to quantify the distribution of incorporated crop residue-derived C into microbial groups (fungi, actinobacteria, Gram negative and Gram positive bacteria) during decomposition. Microbial succession and the temporal dynamics of enzyme activities were monitored over the course of the incubation to determine whether these factors followed similar trajectories in soils that varied in initial nutrient and C characteristics. We hypothesized that distinct microbial communities would develop in soils with different management histories due to altered resource availability and that this legacy

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