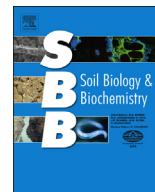




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Soil enzyme activities, microbial communities, and carbon and nitrogen availability in organic agroecosystems across an intensively-managed agricultural landscape[☆]



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ABSTRACT

Variability in the activity and composition of soil microbial communities may have important implications for the suite of microbially-derived ecosystem functions upon which agricultural systems rely, particularly organic agriculture. An on-farm approach was used to investigate microbial communities and soil carbon (C) and nitrogen (N) availability on 13 organically-managed fields growing Roma-type tomatoes, but differing in nutrient management, across an intensively-managed agricultural landscape in the Central Valley of California. Soil physicochemical characteristics, potential activities of nine soil enzymes involved in C, N, phosphorus (P), and sulfur (S) cycling, and fatty acid methyl esters (FAMES) were measured during the growing season and evaluated with multivariate approaches. Soil texture and pH in the 0–15 cm surface layer were similar across the 13 fields, but there was a three-fold range of soil C and N as well as substantial variation in inorganic N and available P that reflected current and historical management practices. Redundancy analysis showed distinct profiles of enzyme activities across the fields, such that C-cycling enzyme potential activities increased with inorganic N availability while those of N-cycling enzymes increased with C availability. Although FAMES suggested that microbial community composition was less variable across fields than enzyme activities, there were slight community differences that were related to organic amendments (manure vs. composted green waste). Overall, however, the general similarity among fields for particular taxonomic indicators, especially saprophytic fungi, likely reflects the high disturbance and low complexity in this landscape. Variation in potential enzyme activities was better accounted for with soil physicochemical characteristics than microbial community composition, suggesting high plasticity of the resident microbial community to environmental conditions. These patterns suggest that, in this landscape, differences in organic agroecosystem management have strongly influenced soil nutrients and enzyme activity, but without a major effect on soil microbial communities. The on-farm approach provided a wide range of farming practices and soil characteristics to reveal how microbially-derived ecosystem functions can be effectively manipulated to enhance nutrient cycling capacity.

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1. Introduction

Agricultural landscapes exhibit a high degree of spatial variability, including variation in soil physicochemical characteristics and agroecosystem management (Drinkwater et al., 1995; Vasseur et al., 2013), which can affect the activity and composition of the soil biota (Acosta-Martínez et al., 2008; Schipanski and Drinkwater, 2012). Soil microbes mediate the biochemical transformations of organic matter that underpin essential ecosystem functions, including decomposition, mineralization of plant available

nutrients, and nutrient retention. Organic production relies on these microbially-derived ecosystem functions and thus may be a model system for ecological intensification of agriculture (Jackson et al., 2012). By focusing on building and utilizing soil organic matter (SOM) as opposed to using synthetic fertilizers, organic production systems differ greatly from conventional systems; organic management in many research station trials has been shown to improve soil fertility (Burger and Jackson, 2003; Gattinger et al., 2012), reduce nutrient losses (Drinkwater and Wagoner, 1998; Kramer et al., 2006; Syswerda et al., 2012), and reduce global warming potential (Burger et al., 2005; Cavigelli et al., 2013) while supporting similar crop yields in certain contexts (Seufert et al., 2012).

Yet, such research station-based experiments may belie the challenge of evaluating multiple ecosystem services on working organic farms across actual landscapes that vary in topography, soil type, commodities, and motivations of farmers for making the organic transition (Darnhofer et al., 2005; Williams and Hedlund, 2013). Organic farms also use many different nutrient management strategies (Guthman, 2000; Darnhofer et al., 2010) even when growing the same crop in the same region (e.g. Drinkwater et al., 1995; García-Ruiz et al., 2008). While this heterogeneity could help explain some of the ambiguous results of landscape-scale comparisons of organic and conventional farms relative to site-specific experiments (e.g. Williams and Hedlund, 2013), we lack basic understanding of how heterogeneity affects soil microbial activity and community composition and the implications for soil ecosystem functions and agroecosystem management.

The quantity and quality of SOM and carbon (C) and nitrogen (N) inputs are the overriding controls on soil microbial biomass and activity (Fierer et al., 2009; Kallenbach and Grandy, 2011). Thus, distinct organic amendments (e.g. manure, leguminous cover crops, and composted materials) can stimulate microbial biomass differently through increases in labile organic matter (Marriott and Wander, 2006; Smukler et al., 2008; Kallenbach and Grandy, 2011) and/or total soil C on time frames from months to decades (Drinkwater and Wagoner, 1998; Kong et al., 2005). However, little is known about how the quantity and composition of SOM and nutrient inputs (e.g. C:N ratio) affect microbial communities and their enzyme activities, and in turn, transformations of C, N, phosphorus (P), and sulfur (S) on organic farms. The total enzymatic activity of soil, derived from active microorganisms and the stabilized pool in clay–humus complexes (Tabatabai, 1994; Burns et al., 2013), plays a major role in the depolymerization of structurally diverse polymeric macromolecules, which is considered the rate-limiting step in decomposition and nutrient mineralization potential of soil (Schimel and Bennett, 2004).

Organic management increases overall enzyme activity (Mäder et al., 2002; García-Ruiz et al., 2008; Moeskops et al., 2010), but activities of specific enzymes may change depending on the composition of the amendments and the relative availability of nutrients, as well as other factors, such as soil type and its unique characteristics, e.g. pH and texture (Acosta-Martínez et al., 2007; Sinsabaugh et al., 2008; Štursová and Baldrian, 2010). Given the relatively constrained C:N:P ratios of microbial biomass (Cleveland and Liptzin, 2007), enzymatic activity might be expected to enhance the availability of the most limiting nutrients in order to meet microbial metabolic demands (Sinsabaugh et al., 2008; Allison et al., 2011). For instance, in grassland and forest soils, long-term N fertilization increased the activity of soil enzymes involved in labile C breakdown (Ajwa et al., 1999; Saiya-Cork et al., 2002; Tiemann and Billings, 2010) with similar trends in conventionally-managed agricultural soils (Bandick and Dick, 1999; Piotrowska and Wilczewski, 2012).

Properties of SOM and organic amendments may also influence microbial community composition and in turn, microbial activity and associated ecosystem processes (Fraterrigo et al., 2006; Reed and Martiny, 2013). Increases in the fungal:bacterial ratio have been linked to increases in soil C and the C:N ratio across landscapes (Fierer et al., 2009; de Vries et al., 2012) and in response to organic management (Bossio et al., 1998) as well as various organic amendments, such as conifer-based compost (Bernard et al., 2012) and vetch cover-cropping (Carrera et al., 2007). Other studies have shown increases in phospholipid fatty acid biomarkers for arbuscular mycorrhizal fungi (AMF) in response to composted green waste as well as long-term organic management (Bossio et al., 1998; Moeskops et al., 2010, 2012). While management that supports fungal communities has been suggested as a means of increasing agroecosystem N retention and other functions (de Vries and Bardgett, 2012; Jackson et al., 2012), changes in microbial community composition may be relatively constrained in agricultural landscapes with a legacy of intensive agricultural management (Fraterrigo et al., 2006; Culman et al., 2010), even in response to organic management (Williams and Hedlund, 2013). Indeed, in agricultural soils that are intensively managed, microbial activity tends to change more quickly in response to organic management than community composition (Burger and Jackson, 2003).

The overall objective of this study is to examine how soil physicochemical characteristics and nutrient management practices affect soil microbial activity and microbial community composition in organic agricultural systems, using an on-farm approach with several participating farmers. This study is part of a larger project examining plant–soil–microbial interactions and multiple ecosystem functions across a set of organic farms selected to be representative of the local landscape using geographic information system (GIS) techniques (Bowles et al., ms. in preparation). Thirteen organically-managed fields growing Roma-type tomatoes (*Solanum lycopersicum* L.) were selected in Yolo County, part of the Sacramento Valley of California, an agricultural landscape dominated by high-input conventional agriculture with a diverse array of crops. The focus is on the period of maximal tomato nutrient demand when microbial activity is most important for crop productivity. There were two main hypotheses. First, farm fields would differ in soil microbial biomass and enzyme activities, and these differences would depend on the quantity and composition of SOM as well as other factors related to the type of organic amendments. Second, microbial community composition would be influenced by nutrient management practices but with fewer differences across the fields relative to enzyme activities given the overall lack of diversity in the soil biota in this landscape, which appears to be related to high disturbance and low complexity (Culman et al., 2010).

The specific objectives of this study are to: 1) characterize the variability of soil properties and organic management practices across a number of organically-managed Roma-type tomato fields; 2) determine patterns of soil enzyme activities and fatty acid methyl esters (FAMES) to indicate microbial community composition and relate them with soil properties and management practices; and 3) consider the implications for microbially-derived ecosystem functions for management of different types of organic farms across this landscape. On 13 organic fields differing in nutrient management practices, soil physicochemical characteristics; microbial biomass C and N; activities of soil enzymes involved in C, N, P, and S cycling; and FAMES were measured and analyzed with multivariate techniques to model the relationships among these factors. The on-farm approach provided a wide range of farming practices and soil characteristics to reveal how microbially-derived ecosystem functions can be effectively manipulated to enhance nutrient cycling capacity.

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