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Evaluating the diversity of soil microbial communities in vineyards relative to adjacent native ecosystems

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ABSTRACT

Agricultural land use disturbs soil microbial communities, which can reduce crop production and impair ecosystem functioning. We investigated the effects of viticulture on the diversity and composition of three soil microbial communities: bacteria, fungi and arbuscular mycorrhizal fungi, by comparing communities in vineyards and nearby unmanaged areas. All three communities were influenced by land use. Bacteria had higher species richness in vineyards whereas arbuscular mycorrhizal fungi had higher richness in unmanaged areas. Differences between vineyards and unmanaged sites in community composition for the three microbial groups were related to both abiotic and biotic factors. In particular, bacterial communities were most sensitive to soil pH, whereas fungal (including AM fungi) communities responded more to changes in plant diversity. Other abiotic factors (cation exchange, temperature and soil texture) were correlated with community compositional changes, regardless of land use. These results indicate that viticulture practices influence key factors controlling soil microbial communities and possibly affect nutrient availability and other services provided by natural soil communities.

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1. Introduction

Soil microbial communities, which include bacteria and fungi, are major ecological players in both below and aboveground ecosystems (van der Heijden et al., 2008, 1998; Wardle et al., 2004). While sequencing technology has allowed for greater insight into the diversity of microbial taxa in soil, we have yet to understand exactly how much variation exists and what is driving it. This challenge is compounded when considering that soil microbial populations include both prokaryotes (bacterial and archaea) and eukaryotes (fungal and protozoan). These diverse groups have such different ecologies and life histories that it is unlikely their variation results from a single influence or small set of factors. Nevertheless, understanding how environmental factors influence patterns in below-ground communities may help elucidate aspects of ecosystem functioning that are important in the performance of crop production systems.

Given the extent to which natural landscapes have been converted to managed systems (38.47% worldwide as of the 2011 FAO statistics), soil communities of today may be substantially influenced by choice of land use practices. Although managed agricultural landscapes share common features such as the addition of resources (e.g., water and nutrients) and reduced plant species richness, other practices that cause disturbance and influence microbial diversity such as tillage, (Frey et al., 1999; Garcia-Orenes et al., 2013; Lupwavi et al., 1998) and biocide application (Campisano et al., 2015; Viti et al., 2008; Whitelaw-Weckert et al., 2007) vary among systems and management styles. Improved knowledge of how management choices affect microbial communities and their influences on crop performance would benefit the design of efficient and sustainable production systems.

Considering the various ways crop production systems can change a landscape and underlying soils, it is unlikely that all soil microbes are impacted similarly. Our current understanding of how different microbial taxa respond to land use practices is not clear. There is ample evidence that some practices can impose strong selection pressures on soil bacteria (Buckley and Schmidt, 2001; Fierer et al., 2013; Garcia-Orenes et al., 2013; Tian et al., 2012) and fungi (Garcia-Orenes et al., 2013; Oehl et al., 2010; Tian

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et al., 2012,), but how microbial communities change in concert is not well understood.

Soil bacteria exist in various habitats, as free-living microbes in bulk soil and in the plant rhizosphere and as endophytes within plant tissues (Coleman et al., 2004; Wardle, 2002). In soil their distribution has been shown to respond primarily to soil chemical properties such as pH (Fierer and Jackson, 2006; Lauber et al., 2009). Unlike bacteria, which feed on a wide variety of carbon sources, soil fungi depend almost entirely on living or dead plant tissue (Coleman et al., 2004; Wardle, 2002). Fungi can exist as free-living saprobes influenced by the quantity and quality of organic matter entering the soil food chain (Holland and Coleman, 1987; Nicolardot et al., 2007; Kendrick, 2000), or as participants in mutualisms ranging from parasitic to mutualistic (i.e., arbuscular mycorrhizal (AM) fungi), in which they exhibit strong preference for particular plant hosts (Johnson et al., 1997; Klironomos, 2003). Thus, the identity, diversity and abundance of plants have important implications for fungal community structure. However, complex interactions can occur among the communities of bacteria, fungi and plants, which influence the soil environment and their community structures (Bever et al., 1997; van der Heijden et al., 1998; Reynolds et al., 2003).

Given the complex interrelationships among soil microbes and site conditions, it is difficult to predict how bacterial and fungal communities will respond to land use. In this study, we characterized soil microbial communities in vineyard ecosystems (referred to as 'managed') and adjacent largely undisturbed native ecosystems (referred to as 'unmanaged'). Like other perennial cropping systems, viticultural systems in British Columbia are characterized by low levels of soil disturbance (little or no tillage) and relatively diverse plant communities that include grapevines along with grass and forb species grown as cover crops in vineyard inter-rows, all of which are influenced by inputs of water and fertilizers. When considering soil bacterial and fungal communities in viticultural systems compared to unmanaged, natural systems we predict:

a Differences in bacterial communities will be driven primarily by soil chemistry (i.e., pH and possibly concentrations of mineral nutrients)
b Differences in fungal communities will be driven primarily by plant communities. This effect should be more pronounced for mutualistic fungi (i.e., AM fungi) than for the general fungal community.

2. Methods

2.1. Study area and sampling design for soil microbes

Soil microbial populations were compared under two contrasting ecosystems types: established vineyards, and adjacent unmanaged ecosystems inhabited by native plants and invasive alien species. The study was conducted in grape growing regions in south-central British Columbia, Canada (Fig. 1). These regions lie within the Okanagan Valley and Similkameen Valley geographical indications (GI) for viticulture (British Columbia Wine Authority, 2014), extending ca. 150 km from the Canada–US border northward to near Vernon B.C. Native plant assemblages inhabiting these areas suitable for grape production range from shrub steppe dominated by *Artemisia tridentata* and *Pseudoroegneria spicata* in the south to open ponderosa pine (*Pinus ponderosa* C. Lawson) forests with grass understory dominated by *Festuca* spp., *Pseudoroegneria spicata* and *Achillea millefolium* in the north (Lloyd et al., 1990). The Similkameen Valley GI lies west of the Okanagan Valley and extends north-westward from the Canada–US border. Currently vineyards in the Similkameen Valley GI extend from near the border to approximately 10 km north and west of Keremeos B.C. Native plant assemblages in this GI are similar to those in the southern Okanagan Valley GI (Lloyd et al., 1990). Annual rainfall in the Okanagan Valley GI averages 386 mm in the north, 329–346 mm in the mid latitudes, and 323 mm in the south. The Similkameen Valley GI receives 325 mm of annual rainfall (Environment Canada, 2015). The soils of the northern Ponderosa Pine vegetation zone are generally classified as Brunisolic soils, while those formed under the grassland communities of the southern Bunch Grass zones are classified as Chernozemic soils according to the Canadian System of Soil Classification (Soil Classification Working Group, 1998). These soil orders would approximate the Inceptisol and Mollisol orders within the USDA Soil Taxonomy (Soil Survey Staff, 1999).

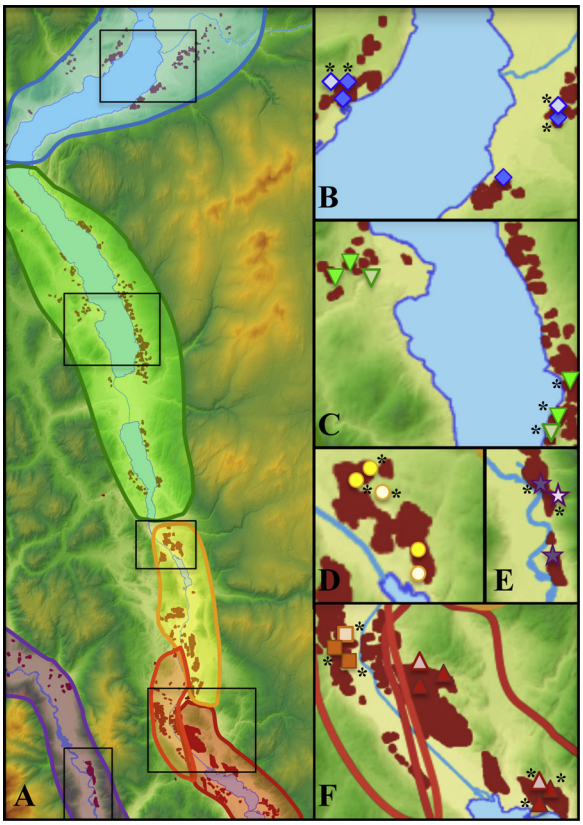

Fig. 1. Soil sampling areas within the six viticulture regions of the South Okanagan and Similkameen valleys: Kelowna (blue), Penticton (green), Vaseaux-Oliver (yellow), Golden Mile (orange), Black Sage–Osoyoos (red) and Similkameen (purple) (A, as defined in Bowen et al. 2005). Enlargements (B–F) of the areas outlined in A show the locations of the 10 unmanaged (white symbols) and 19 vineyard (closed symbols) sampled sites. Asterisks indicate sites where soil texture and chemistry were characterized (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.).

Soil was sampled for microbial analysis from ten unmanaged sites and nineteen vineyards within the six grape growing regions (Fig. 1). Five of the regions (1–5) fall within the Okanagan Valley GI and one (region 6) within the Similkameen Valley GI.

For comparative analyses, vineyard sites were chosen based on their proximity to unmanaged sites and similarities in soil texture, aspect and slope. The unmanaged sites were suitable for vineyard development, but had no apparent recent human disturbance or inputs. These sites were mainly inhabited with native plant communities and few invasive or alien plant species. In each of three regions (Kelowna, Penticton and Black Sage—Osoyoos) there were two unmanaged and four vineyard sampling sites. Two regions (Golden Mile and Similkameen) each had one unmanaged

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