



Vineyard soil bacterial diversity and composition revealed by 16S rRNA genes: Differentiation by vineyard management



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ABSTRACT

Little is known about the hierarchical effects of management practices, soil attributes and location factors on structure of vineyard soil microbiota. A hierarchical effect occurs when the specific influence of an experimental factor (e.g. cover crop type, compost application) on soil-borne bacterial communities is greater within a subset composing the larger set but not across the entire set (e.g. bacterial communities only respond to a management practice within a subset of soil types but not across the entire set composed of all soil types). To address this concept, we measured differences in soil bacterial and archaeal diversity in wine-grape vineyard soils throughout Napa Valley, California. We describe how vineyard management practices influence soil resources, which in turn determine shifts in soil-borne bacterial communities. Soil bacterial communities were structured with respect to management practices, specifically cover crop presence and cover crop mix, tillage, and agricultural system designation, i.e. conventional, organic and biodynamic production systems. Distinctions with respect to management were associated with differences in pH and soil resource pools: total carbon and total nitrogen of the <53 and 53–250 μm particulate organic matter fractions, and potentially mineralizable nitrogen. Findings in this study suggest management practices in vineyard production systems directly influence soil microbial community structure, as mediated by shifts in soil resource pools. However, hierarchical effects occur, in which β -diversity is more strongly affected by specific management practices only within certain soil types, tillage or no-till soils or winegrowing region. This work allows for subsequent assessments of interrelationships of vineyard management, microbial biodiversity and their combined influence on soil quality, vine health, and berry quality.

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1. Introduction

Vineyard soil microorganisms are affected by winegrowing region, climate and topography, as mediated in part by their suite of impacts on soil properties like pH and soil organic matter pools (Burns et al., 2015). These same soil properties are directly influenced by vineyard management practices. Soil microorganisms also

influence their local environment through pathogen suppression; decomposition processes that affect soil organic matter (SOM) mineralization, contribution and preservation of SOM and aggregate stability; and availability of nitrogen and other mineral nutrients (Kögel-Knabner, 2002; Kuzyakov et al., 2002; Grandy and Neff, 2008; Plaza et al., 2013). These processes and their controls on soil structure and nutrient availability reflect the possible indirect effects of soil microorganisms on plant growth, health and fruit development (Garbeva et al., 2004; Compant et al., 2010). Vineyard management practices and production systems that alter the soil environment, and thus may contribute to shaping the microbial community, include: cover crop use, tillage, compost application, and conventional, organic, or biodynamic systems. Here, we focus on establishing a baseline understanding of the relationships

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between management practices and changes soil microorganisms within winegrowing regions. This represents the baseline from which we can subsequently delineate the ecological roles of specific taxa to elicit desired outcomes in wine grape production. In other words, altering management practices to change soil properties, which in turn shift key individual or consortia of soil microorganisms, could tune interactions among wine grapes, the soil environment, and associated microorganisms to influence wine grape production.

The soil microbial roles discussed above are intrinsically coupled to both soil quality and soil health. Soil quality refers to the fitness of soil for a particular purpose (Doran et al., 1996; Pierce and Larson, 1993), and thus, requires a specific definition for each purpose. In viticulture, soil quality is defined as “the soil’s ability to support the production of a crop while minimizing negative effects on the environment” (Riches et al., 2013). Soil health is subtly distinct from soil quality. Soil health is defined as “the continued capacity of soil to function as a vital living system, within ecosystem and land-use boundaries, to sustain biological productivity, maintain the quality of air and water environments, and promote plant, animal, and human health” (Doran et al., 1996). Soil organic matter stability is intrinsically coupled to concepts of soil quality and health. Microorganisms are intimately linked with the cycling and stability of soil organic matter, among other functions related to soil health, and are sensitive to changes in soil attributes and management (e.g. Calderón et al., 2001; Jackson et al., 2003; Giller et al., 1997; Grandy and Neff, 2008; Cotrufo et al., 2015). Therefore, measurements of soil-borne microbial communities, such as biomass, structure and functions, have been recommended as good indicators of soil quality (e.g. Jackson et al., 2003; Riches et al., 2013; Steenwerth et al., 2003; Chaparro et al., 2012).

In order to implement assessments of soil microbial community structure for soil health monitoring, additional research is needed to understand the link between soil microbial community structure and soil functions, as they relate to soil health. Studies have begun to show empirically that soil microbial community structure and function are linked (Fierer et al., 2012a, 2012b), and soil biodiversity is assumed to improve ecosystem resilience by offering functional redundancy (Giller et al., 1997). Soil biodiversity is recognized for its importance to agricultural sustainability in an economic, social, and ecological context (Brussaard et al., 2007). By describing the effect of agricultural management practices on the soil microbial community structure, we aim to form the foundation from which linkages among soil quality, agroecosystem function, and soil biodiversity can be built to better define soil health for wine grape production. Recent work has shown that climate, region, soil type, and wine grape variety can play strong roles in structuring microbial communities in vineyard soil, the vine phyllosphere, must and wine, and that soil microbial activities and wine metabolome are correlated with microbial community structure (Bokulich et al., 2014, 2016; Burns et al., 2015; Zarraonaindia et al., 2015). However, no single study examines the vineyard microbiome from soil to wine nor do they examine effects of vineyard management practice on soil microbial communities.

Numerous studies have assessed the effects of land use and agricultural management practices on soil quality, soil properties, and soil microbial communities (e.g. Castañeda et al., 2015; Drenovsky et al., 2010; Steenwerth et al., 2003). Land-use effects on soil microbial communities are thought to be mediated mostly through alteration of soil properties. Soil properties correlated with soil microbial community structure include soil texture, pH, water content, carbon (C) and nitrogen (N) content, and C:N ratio (e.g. Cookson et al., 2006; Drenovsky et al., 2004; Fierer and Jackson, 2006; Fierer et al., 2012a; Hogberg et al., 2007; Steenwerth et al., 2008; Lauber et al., 2009). Plants alter many soil properties as

well as soil aggregation and soil nutrient status, through root exudation and fine root turnover. In turn, this affects the soil microbial environment, resulting in shifts in the soil microbial community (Angers and Caron, 1998; Berg and Smalla, 2009; Garbeva et al., 2004; Haichar et al., 2014; Kowalchuk et al., 2002; Shamoot et al., 1968; Starkey, 1929). Tillage disturbance also alters the distribution of soil organic matter and soil structure, thereby causing shifts in aggregate size, composition, and stability, and changing soil nutrient availability (Calderón et al., 2001; Elliott, 1986; Giller et al., 1997; Lee et al., 2009). Compost amendments add labile carbon and nitrogen, nutrients, and active microbial communities to soil (Bossio et al., 1998; Carpenter-Boggs et al., 2000; Pérez-Piqueres et al., 2006). Consequently, these changes mediate shifts in microbial communities and microbial processes (e.g. Calderón et al., 2000, 2001; Doran, 1980; Jackson et al., 2003; Strauss et al., 2015). These practices are embedded within conventional, organic, and biodynamic agricultural management systems, which differ primarily in their methods of fertilization and control of disease, insects, and weeds. Though effects of pesticides and fertilizers on soil microbial communities are well studied with clear effects (Fierer et al., 2012a; Hussain et al., 2009; Imfeld and Vuilleumier, 2012; Jacobsen and Hjelmsø, 2014), studies based on a comparison of conventional, organic, or biodynamic systems, have not been consistent in showing the same effects on soil microbial communities (Bossio et al., 1998; Carpenter-Boggs et al., 2000; Cookson et al., 2006).

Vineyard management in Napa Valley, California, includes this array of management practices and production systems across a range of soil types, allowing us to examine how vineyard floor management practices influence soil bacterial community structure in the context of environmental and edaphic factors. We measured differences in the soil-borne bacterial and archaeal community composition and diversity by sequencing the V4 small subunit ribosomal RNA gene (16S V4 rDNA). We hypothesized that variations in soil bacterial communities, at the landscape scale, result from different agricultural management practices, as mediated through changes in soil properties. The scope is delineated in this manner to extend the observations of Burns et al. (2015), who recently examined the roles of winegrowing region, or appellation, climate and topography on soil bacterial communities across this same suite of sites.

2. Materials and methods

2.1. Overview

The methodology for soil characterization, DNA extraction, library preparation and sequencing has been described in detail in Burns et al. (2015). Distinct from this current effort, data in Burns et al. (2015) were used to examine the effect of geographic region, climate and soil type on soil microbial communities. These sequence data were deposited previously in the QITA data bank, Study ID 10082.

2.2. Soil sampling and site characterization

Soil samples were collected from 57 sites in 19 wine grape vineyards, with three sites per vineyard, throughout Napa Valley, California, and treated as a completely randomized design. See Burns et al. (2015) for a complete description of the experimental design, approach and details on specific practices at each vineyard. Details of management practices were gathered through interviews with vineyard managers. Soil samples were collected March–June 2011, at a depth of 0–5 cm, from the centers of the vineyard alleyways. Plant residues and shoots, if present, were removed prior

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