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Soil bacterial communities exhibit systematic spatial variation with landform across a commercial potato field

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ABSTRACT

Topography drives spatial variation of soil edaphic factors at the landscape scale however, it is unclear how it influences the spatial distribution of bacterial communities in distances relevant to agro-ecosystem management. This study examined the influence of soil physico-chemical properties and topographic features on bacterial communities and diversity in a commercial potato field with a rolling landform. Eighty-three soil samples were systematically collected across a transect 1100 m long. A significant negative correlation ($r = -0.73$) between soil pH (range 4.3–7.0) and slope gradient (range 1.8–11.9%) was observed. Regressions and/or a canonical correspondence analysis showed that pH, slope gradient and organic carbon were the major factors influencing bacterial α-diversity based on 16S rRNA gene sequences. Semivariogram analyses revealed that the bacterial α-diversity, the relative abundance of most phyla, pH and slope gradient showed strong to medium spatial autocorrelations with a range between 20.8 and 217.8 m. These results evidenced that soil pH and slope gradient were the major factors explaining variation in the spatial structure of the bacterial community. Our results showed that the soil bacterial communities varied in a systematic and predictable pattern in an agricultural field in response to variation in soil physico-chemical properties and topographic features.

1. Introduction

Soil physico-chemical properties are well-recognized factors influencing the soil microbial community composition and diversity in terrestrial ecosystems (Fierer and Jackson, 2006; Lauber et al., 2009). The extent to which these factors affect microbial community composition has implications on ecosystem functioning. In agricultural ecosystems, the response of microbial communities to soil physico-chemical properties and other environmental factors determines the sustainability of agriculture, where microbial communities play a pivotal role by decomposing soil organic matter and mineralizing nutrients (Gougoulias et al., 2014).

The shift in soil bacterial communities in response to soil edaphic factors is well recognized in different types of ecosystems (Lauber et al., 2008; Rousk et al., 2010). Agricultural practices alter soil physico-chemical properties, which in turn can influence bacterial community composition and diversity. Cropping systems (Bossio et al., 1998), soil type and crop management practices (Jangid et al., 2008; Cederlund et al., 2014; Ramirez et al., 2010) were shown to change soil bacterial abundance and diversity through changes in soil pH and soil organic carbon (SOC) availability (Rousk et al., 2010; Peacock et al., 2001).

Topography often drives spatial variation of soil edaphic factors at the landscape scale (Moore et al., 1993) through its effects on the distribution of various factors, such as hydrological processes and soil erosion processes (Li et al., 2008). Solar radiation and temperature are affected by slope aspect (Holland and Steyn, 1975; Dubayah and Rich, 1995). Soil moisture regimes also vary with upper slope positions usually drier and better drained whereas lower slope positions are wetter and may be poorly drained (Moore et al., 1993). The majority of eroded soil is deposited locally in the lower-slope positions or depressional areas, resulting in changes in soil texture and soil organic matter. These processes often result in the development of different soils and in the formation of a soil *catena* along the slope (Pennock et al., 1987; Li et al., 2011).

Various geostatistical techniques were used to describe the spatial variability of bacterial community diversity and their spatial relationship with other variables (Nunan et al., 2005). There is evidence of a spatial structure to soil microorganisms, with scales ranging from millimeters to hundreds of meters. Several studies have examined bacterial diversity at small (cm to < 10 m) scales (Nunan et al., 2005; Franklin and Mills, 2003; Ritz et al., 2004; O'Brien et al., 2016). Other studies have reported on spatial structure of microbial communities at spatial

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scales of km to hundreds of km (Zinger et al., 2011; Griffiths et al., 2011). In contrast, few studies have examined taxonomic variation in microbial (Osborne et al., 2011; Rosenzweig et al., 2016) or functional (Enwall et al., 2010; Philippot et al., 2013) communities at the scale at which agricultural management practices are performed (e.g., ~10 to 100 m scale) within individual fields (Cambouris et al., 2014). Therefore, the spatial structure of microbial communities within individual agricultural fields remains largely unexplored.

The aim of this study was to examine the influence of soil physico-chemical properties and topographic features on bacterial community composition and diversity using a transect in a commercial potato field with a rolling landform. We hypothesized that bacterial community diversity exhibits systematic spatial patterns, and that local soil physico-chemical properties and topographic features would directly influence the structure of the soil bacterial communities.

2. Materials and methods

2.1. Field site description

This study used samples collected from a transect in a commercial potato field located in New Brunswick, Canada in 2014. The field has grassed terrace diversions at approximately 60 m intervals to reduce water erosion. The transect was approximately 1100 m long and located between two terrace diversions near the lower portion of the field (Fig. 1A). Two grassed waterways were present at the lowest points along the transect, oriented perpendicular to the direction of the transect. Soils at the field site were generally developed in loamy glacial till and classified as podzols based on Food and Agriculture Organization of the United Nations.

The field was cropped to potatoes in 2014 using standard production practices (Atlantic Canada Potato Guide; http://publications.gc.ca/collections/collection_2015/aac-aafc/A53-1281-1967-eng.pdf). The preceding crop was spring barley (*Hordeum vulgare* L.). The field was limed in spring. Potatoes (cv. Russet Burbank) were planted in May and hilled in July 2014. Fertilizer was banded at planting at a rate of 1350 kg ha^{-1} (analysis N:P:K 17:12:17).

Standard commercial herbicides, pesticides and fungicides were applied to control diseases, insects, and weeds. All crop inputs were applied uniformly throughout the field. No irrigation was applied as is common in this region. Daily average air temperature and total precipitation during the crop growing season (25 May 2014–15 September 2014) were 17 °C and 495 mm, respectively, as measured at the nearest weather station (St Leonard CS, New Brunswick; http://climate.weather.gc.ca/).

2.2. Topographic features

Imagery was collected with an Ebee Unmanned Aerial Vehicle (UAV) equipped with a CANON 110 camera in spring of 2014, and a Digital Elevation Model (DEM) was created in Pix4D using the point cloud and the DEM routines. The original DEM was in 0.075 m resolution. The DEM was imported into ArcGIS (version 10.1), coarsened to 2 m (nearest neighbor), and then smoothed for 5 times (9 nodes average) to eliminate random errors. Topographic features including slope gradient, slope curvature, and aspect were determined using the Slope, Curvature and Aspect tool, respectively, in the Arc Toolbox of ArcGIS (version 10.4.1). The slope curvature was a single value which reflects both plan and profile curvature. The smoothed DEM was imported into LandMapR tool kit to divide the field into five landform elements (crest, upper-slope, mid-slope, lower-slope and depression) following the procedure described by Li et al. (2011). The geographic coordinates of each sampling location were recorded using a Trimble GeoXH GPS unit with Can-Net correction service (10 cm horizontal accuracy). The topographic features for each sampling point were extracted in ArcGIS based on their coordinates.

2.3. Field soil sampling procedure

The experimental transect consisted of 83 sampling locations, with the distance between adjacent sampling locations ranging from 0.9 to 86.7 m (Fig. 1B). Locations of soil sampling points were determined following a stratified random sampling method described by Pennock et al. (2008). In brief, the aforementioned landform element was used as the strata and points were randomly assigned to each landform element at a probability proportional to its area. Points were sparse after the initial allocation. To facilitate spatial analysis for short ranges, one slope was randomly selected and additional sample points were assigned, again based on the stratified random sampling method. This nested sampling allowed the coverage for the whole field as well as enough short-range point pairs with a manageable sample size. A non-uniform distance between sampling locations also facilitated the development of semi-variograms. Soil samples were collected shortly before vine desiccation on September 15, 2014.

One composite soil sample was collected from each sampling location. Each composite soil sample consisted of 10 soil cores collected from 0 to 15 cm depth in the potato hill. Soil was thoroughly mixed, and ~10 g of soil was subsampled, placed in a 15 ml falcon tube, stored under cool conditions during transport, and stored at −80 °C until used to evaluate the diversity of bacterial communities. The remainder of the soil sample was stored under cool conditions during transport, and passed through a 4.5 mm sieve. A subsample of approximately 20 g was oven dried at 105 °C to determine gravimetric water content (GWC). The remaining soil was dried at 30 °C for 72 h then stored at room temperature until further soil analyses.

2.4. Soil physico-chemical properties

Soil pH was determined in soil water suspension (1:1) (Hendershot et al., 2008). Soil texture was assessed using the pipette method following organic matter removal (Kroetsch and Wang, 2008). The soil organic carbon (SOC) and total nitrogen (TN) concentrations were measured by dry combustion (Skjemstad and Baldock, 2008) using a VarioMacro (Elementar Americas Inc., Mt. Laurel, New Jersey).

2.5. DNA extraction, library preparation and 16S rRNA gene sequencing

Total DNA was extracted from 0.5 g of each soil sample using the method described by Griffiths et al. (2000). The genomic DNA was purified using PowerClean®DNA clean up kit (MoBio Laboratories, Carlsbad, CA, USA) and quantified using Fluoroskan Ascent™ Microplate Fluorometer (ThermoFisher Scientific, MA, USA). The bacterial V3-V4 region of 16S rRNA gene was amplified using the 341F and 806R primers with Illumina adapter sequences (Klindworth et al., 2013). Library preparation and sequencing were carried out following the instruction for 16S metagenomic sequencing library preparation and sequencing protocol available at the Illumina website (http://support.illumina.com/downloads/16s_metagenomic_sequening_library_preparation.html). Briefly, amplification was carried out in a total volume of 25 µl with the following component: 12.5 ng DNA template, 12.5 µl KAPA HiFi HotStart Ready Mix, 5 µM of each primer. The PCR condition was 95 °C for 3 min and 25 cycles of 95 °C for 30 s, 55 °C for 30 s and 72 °C for 30 s and 5 min at 72 °C for elongation. The PCR product was purified using AMPure XP beads (Beckman Coulter, Pasadena, CA, USA) following the manufacturer's instruction. For each of the 83 samples, a dual indexed library was prepared using Nextera®XT Index Kit. An equal amount of DNA from each library was pooled then sequenced using the Illumina MiSeq Sequencer and the MiSeq Reagent kit v3 and following the 2 × 300 bp paired-end sequencing protocol (Illumina Inc., USA).