Soil microbial communities have distinct spatial patterns in agricultural fields

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Soil microbial communities mediate many important soil processes in agricultural fields, however their spatial distribution at distances relevant to precision agriculture is poorly understood. This study examined the soil physico-chemical properties and topographic features controlling the spatial distribution of soil microbial communities in a commercial potato field in eastern Canada using next generation sequencing. Soil was collected from a transect (1100 m) with 83 sampling points in a landscape with rolling topography. A significant negative correlation (r = -0.73) between soil pH (range 4.3-7.0) and slope gradient (range 2-12 %) was observed, a finding attributed to greater soil erosion on steep slopes resulting in exposure of low pH subsoil. Proteobacteria, Actinobacteria and Acidobacteria were the most abundant bacterial phyla, with average relative abundance of 32, 21 and 15%, respectively. Bacterial diversity at the phylum level was found to be primarily related to soil pH. Ascomycota and Basidiomycota were the most abundant fungal phyla, with average relative abundance of 69 and 15%, respectively. Fungal diversity at the phylum level was primarily related to soil organic carbon (SOC) and soil pH. Semivariogram analyses revealed that the bacterial α-diversity, the relative abundance of most bacterial and fungal phyla, pH and slope gradient showed strong to medium spatial autocorrelations with a range between 30 to 92 m. Soil microbial communities varied in a systematic and predictable pattern in response to variation in soil physico-chemical properties and topographic features. The two major factors influencing bacterial and fungal communities (soil pH and SOC) can be managed through application of lime and organic amendments, and therefore it may be possible to influence diversity of microbial communities at spatial scales relevant to precision agriculture.

Keywords. *Next generation sequencing, semivariogram, microbial diversity.*

Introduction

Precision agriculture uses knowledge of spatial variation of topographic attributes, and of soil physical and chemical properties, to optimize agricultural production practices. In contrast, limited work has been done on characterization of the spatial distribution of soil biological parameters in the context of precision agriculture (Adamchuk et al. 2017). An improved understanding of the spatial distribution of soil biological factors may provide valuable new insights into how precision agriculture can be applied within agricultural cropping systems.

Soil microbial communities play an important role in eco-system functioning. Within agricultural systems, microbial communities play a pivotal role in decomposition of soil organic matter and crop residues and in nutrient cycling (Gougoulias et al. 2014). The composition and diversity of soil microbial communities in terrestrial ecosystems are influenced by soil physico-chemical properties (Fierer and Jackson 2006; Lauber et al. 2009). Cropping systems (Bossio et al. 1998), soil type and crop management practices (Jangid et al. 2008; Cederlund et al. 2014; Ramirez et al. 2010) influence soil bacterial abundance and diversity through their effects on soil physico-chemical properties, particularly soil pH and soil organic carbon (SOC) availability (Rousk et al. 2010; Peacock et al. 2001). Topography affects the spatial variation of soil physico-chemical properties at the landscape scale (Moore et al. 1993) through its effects on factors such as hydrological processes and soil erosion processes (Li et al. 2008).

There is evidence of a spatial structure to soil organisms over a wide range of spatial scales. Studies have examined bacterial diversity at small (cm to < 10 m) scales (Franklin and Mills 2003), as well the spatial structure of microbial communities at large (km to hundreds of km) scales (Zinger et al. 2011). Few studies have examined taxonomic variation in microbial (Rosenzweig et al. 2016) or functional (Philippot et al. 2013) communities at a scale relevant to precision agriculture.

This study examined the influence of soil physico-chemical properties and topographic features on bacterial and fungal community composition and diversity using a transect in a commercial potato field in eastern Canada with a rolling landform.

Materials and Methods

Field site description

A transect was established in a commercial potato field in New Brunswick Canada in September 2014. The transect was approximately 1,100 m long, and was located between two grassed terrace diversions at approximately 60 m spacing established to reduce water erosion. Soils at the field site were generally developed in loamy glacial till and classified as podzols. The field was cropped to potatoes in 2014. The preceding crop was spring barley. The field was limed in spring of 2014.

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. The DEM was imported into ArcGIS and topographic features (elevation, slope gradient, slope curvature, and aspect) were determined. The slope curvature was a single value which reflects both plan and profile curvature.

Soil sampling and analyses

The experimental transect consisted of 83 sampling locations, with the distance between adjacent sampling locations ranging from 0.9 to 86.7 m (Fig. 1). A non-uniform distance between sampling locations was selected to facilitate development of semivariograms. Soil samples were collected shortly before vine desiccation on September 15, 2014.

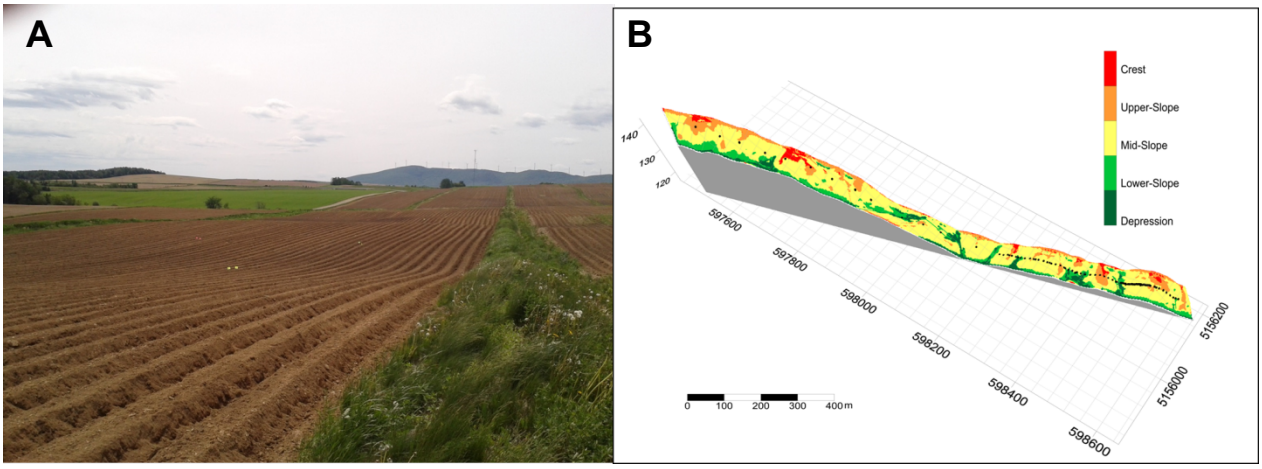

Figure 1: A) Transect was in a field located between two grassed diversions; B) Transect was established with 83 sampling locations (black dots) over a distance of approximately 1,100 m.

One composite soil sample was collected from each sampling location from 0-15 cm depth in the potato hill. Soil pH was determined in a 1:1 soil water suspension. Soil texture was assessed using the pipette method following organic matter removal. The SOC was measured by dry combustion using an Elementar VarioMacro (Elementar Americas Inc., Mt. Laurel, New Jersey).

Microbial community analyses

Diversity of soil bacterial and fungal communities was evaluated by sequencing the bacterial 16S rRNA gene and the fungal Internal Transcribed Spacer (ITS) region of ribosomal DNA using the Illumina MiSeq system. Sequence analysis was performed in Mothur and Qiime software platforms using the Ribosomal Database Project (RDP) and Unified system for the DNA based fungal species (UNITE) reference databases for bacterial and fungal communities, respectively.

Results and Discussion

Most of the landscape consisted of upper and mid-slope positions, with the lower slope positions mostly located beyond the field boundaries (Fig. 1). The slope gradient ranged from approximately 2 to 12%. The slope curvature ranged from approximately -0.93 to 0.90 where negative values indicate concave curvature and positive values indicate convex curvature.

The physico-chemical properties of soils varied along the transect. There was a wide range in sand (312 to 550 g/kg), clay (83 to 173 g/kg), SOC (14.0 to 43.4 g/kg) and soil pH (4.3 to 7.0). Slope gradient had significant negative correlations with soil pH ($r = -0.73$) and SOC ($r = 0.28$). Slope curvature was positively correlated with sand content ($r = 0.49$) and negatively correlated with SOC ($r = -0.42$) and soil water content ($r = -0.47$).

The strong relationship between soil pH and slope gradient was attributed to greater soil erosion on steep slopes resulting in exposure of low pH subsoil. As expected, convex topographic features were associated with an increase in coarse soil particles and a decrease in SOC and

water content.

Bacterial α-diversity as measured using the Shannon index was negatively correlated with slope gradient (r = -0.69), but positively with SOC (r = 0.54) (data not shown). Bacterial α-diversity increased with increasing soil pH up to about pH 6.

Proteobacteria, Actinobacteria and Acidobacteria were the most abundant bacterial phyla, with average relative abundance of 32, 21 and 15%, respectively (Fig. 2). Relative abundance of each phyla was most strongly correlated with soil pH (Table 1). The somewhat weaker correlation of Proteobacteria with soil pH was attributed to contrasting relationships between Proteobacteria at the class level with soil pH, for example, δ-Proteobacteria were strongly positively correlated (r = 0.89) with soil pH whereas γ-Proteobacteria were strongly negatively correlated (r = -0.73) with soil pH.

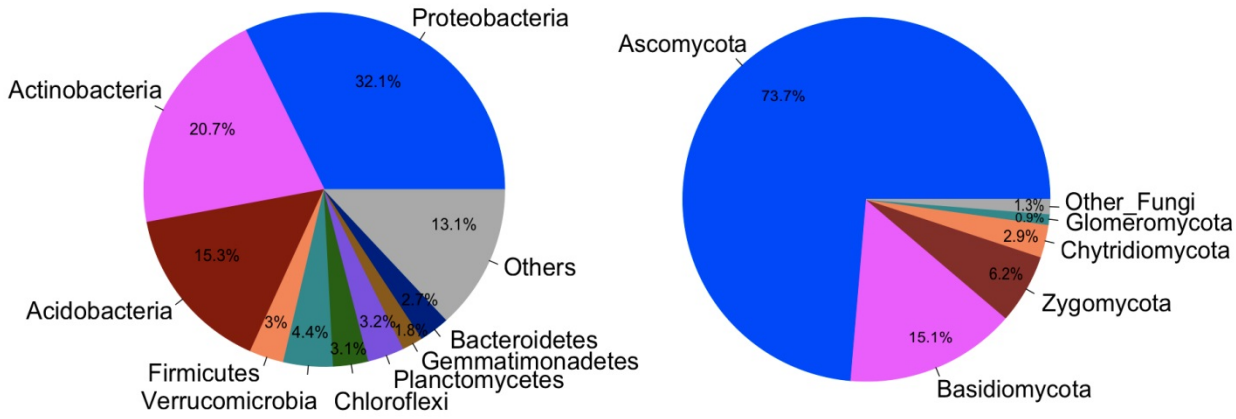

Figure 2: Relative abundance at the phylum level of A) bacterial and B) fungal communities averaged over sampling locations.

Table 1. Pearson correlation coefficients between relative abundance of bacterial phyla or class and selected physico-chemical properties.

Phylum or class	Clay	Sand	pH	TN	SOC	GWC
Proteobacteria	0.09	0.13	-0.37***	-0.22*	-0.25*	-0.17
α-Proteobacteria	-0.17	-0.07	0.37***	0.21	0.42***	0.33**
β-Proteobacteria	-0.43***	0.15	0.55***	-0.14	0.04	0.08
γ-Proteobacteria	0.34**	0.11	-0.73***	-0.26*	-0.48***	-0.37***
δ-Proteobacteria	-0.52***	-0.12	0.89***	0.17	0.5***	0.42***
Actinobacteria	0.31**	0.15	-0.58***	0.05	-0.36***	-0.25*
Acidobacteria	-0.37***	-0.19	0.81***	0.21	0.47***	0.37***

Significance levels: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$; SOC = soil organic carbon, TN = total nitrogen, GWC = gravimetric water content

Ascomycota and Basidiomycota were the most abundant fungal phyla, with average relative abundance of 69 and 15%, respectively (Fig. 2). Relative abundance of Ascomycota was significantly negatively correlated with soil pH (r = -0.48) and with SOC (r = -0.41) whereas relative abundance of Basidiomycota was significantly positively correlated with soil pH (r = 0.45) and with SOC (r = 0.33) (data not shown).

Semivariogram analyses showed that soil physico-chemical properties and topographic attributes were strongly autocorrelated in space with high R^2 values and high $C/(C_0 + C)$ values (Table 2).

Nugget values were very low, indicating that the sampling interval was short enough to capture most of the in-field variations. Sand and clay content showed short-range autocorrelations with 17.7 m and 24.8 m, respectively. Slope gradient, slope curvature and pH showed medium-range (from 44.7 m to 53.7 m) autocorrelations, whereas SOC showed long-range (> 100 m) autocorrelation. The bacterial α-diversity as measured by the Shannon index showed a strong spatial autocorrelation with R^2 of 0.92 and the semivariogram showed a medium range of 64.2 m.

Table 2. Statistics and parameters for the spherical semivariogram models of soil properties, relative abundance of bacterial phyla and bacterial diversity (Shannon index).

	C_0	C_0+C	Range (m)	R^2	C/(C_0 + C)
Soil properties and topographic attributes:					
Slope gradient	0.01	6.041	44.7	0.98	1.00
Slope curvature	0.0066	0.1662	53.7	0.84	0.96
pH	0.0001	0.2732	47.7	0.95	1.00
Sand	0.07	11.59	17.7	0.68	0.99
Clay	0.002	1.925	24.8	0.76	1.00
SOC	0.001	0.776	148.8	0.90	1.00
Relative abundance:					
Proteobacteria	3.63	19.44	3.0	0.05	0.71
α-Proteobacteria	1.95	7.478	30.4	0.80	0.74
β-Proteobacteria	0.001	1.493	3.3	0.04	1.00
γ-Proteobacteria	0.7	31.67	3.4	0.04	1.00
δ-Proteobacteria	0.3	1.116	82.3	0.85	0.73
Actinobacteria	7.98	30.01	42.5	0.93	0.74
Acidobacteria	3.2	13.47	49.6	0.94	0.76
Diversity:					
Shannon index	0.0517	0.2184	64.2	0.92	0.79

C_0 = Nugget, C_0 + C = Sill, C_0/(C_0 + C) = Proportion of structured variance, SOC = soil organic carbon, TN = total nitrogen, C:N = organic C to nitrogen ratio, GWC = gravimetric water content

The relative abundance of bacterial phyla showed strong spatial autocorrelation with R^2 ranging between 0.93 and 0.94 for with the Actinobacteria and Acidobacteria (Table 2). In contrast, Proteobacteria had an R^2 of 0.05. This was due in part to variation in the Proteobacteria at the class level with strong autocorrelation for α-Proteobacteria and δ-Proteobacteria but not β-Proteobacteria and γ-Proteobacteria. The range for Actinobacteria and Acidobacteria (41.0 to 49.3 m) was similar to that of soil pH and slope gradient.

Conclusions

This study demonstrated that the soil bacterial diversity and relative abundance of bacterial and fungal phyla varied in a systematic and predictable pattern in response to variations in topography and soil physico-chemical properties in a commercial potato field with a rolling landform. These spatial patterns were present despite intensive tillage practices and uniform cropping practices. The soil pH and SOC were the two major factors influencing the spatial distribution of bacterial and fungal communities. Both soil pH and SOC are properties which can be managed in agricultural production systems, for example through the use of lime of organic amendments. As a result, it may be possible to influence the diversity and composition of microbial communities in agricultural fields at spatial scales relevant to precision agriculture.

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