Microbial Community Structure in Long-term No-till and Intensive-till Soils

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Key words: no-till, long-term, microbial community structure

Abstract

Conversion from intensive tillage (IT) to no-till (NT) management creates an altered habitat for soil microorganisms. We utilized four long-term tillage experiments in Saskatchewan and Alberta to compare NT and IT microbial communities. Microbial abundance increased at the soil surface (0- to 5-cm depth) in NT vs. IT soils. Differences were much less pronounced or negligible at the 5- to 10-cm and 10- to 15-cm depths. Despite increased biomass of fungi and bacteria in NT surface soils no significant shift in the relative proportion of individual groups of organisms within the community was observed. Similarly, analysis of bacterial DNA fingerprints indicated that while microbial community clusters in the 0- to 5-cm depth increment were different than those at greater depth, there was no significant effect of tillage. Our results demonstrate that depth was a stronger determinant of microbial community structure than tillage management.

Introduction

Changes in the soil environment under no-till (NT) management including moisture, temperature, residue and nutrient stratification near the soil surface as well as reduced physical disturbance can influence the structure and function of bacterial and fungal communities. Recently, there has been significant focus on the importance of NT management as a tool for mitigating the effects of agriculture on climate change. Specifically, carbon (C) sequestration in NT soils can be used to offset the production of other greenhouse gases from agriculture. Similarly, microbial turnover of nitrogen (N) is important for maintaining crop available N supply. Understanding the influence of tillage on soil microbial community structure is vital to understanding the long-term sustainability and management of NT systems.

Materials and Methods

Soils were collected from four long-term experiments with paired tillage comparisons of NT and IT at Swift Current, Scott, Ellerslie and Breton. Table 1 lists site characteristics at each of the sites (Randomized Complete Block Design; n=4). These experiments were not replicated among locations and each site was subject to both cropping rotation and conventional tillage operations in the IT treatment that were typical of the regional practice.

Table 1. Location and site characteristics of tillage experiments.

Site	Soil zone	Year initiated	pH	Texture	Crop rotation
Swift Current, SK	Brown	1981	6.1	Loam	*wheat-lentil-wheat-pea
Scott, SK	Dark Brown	1979	4.6	Loam	flax-wheat-wheat-canola-wheat-wheat
Ellerslie, AB	Black	1980	5.2	Clay loam	tritcale-pea-wheat-canola
Breton, AB	Gray Luvisol	1980	5.6	Loam	tritcale-pea-wheat-canola

***** Crop phase that is underlined indicates the crop grown in 2005.

Soil sampling was conducted in spring prior to seeding, and before spring tillage operations occurred in the IT treatments. Phospholipid fatty acids (PLFA) were extracted using a modified method of White et al. (1979), based on the original method of Bligh and Dyer (1959). Extraction of DNA was performed using the MoBio Ultra Soil DNA extraction kit (MoBio Laboratories Inc., Carlsbad, CA). Universal bacterial primers U341 and U758-gc (Phillips et al. 2006) were used in the polymerase chain reaction (PCR) to amplify a fragment of 16S rRNA approximately 400bp in length. PCR products were analysed using denaturing gel gradient electrophoresis (DGGE) with the Bio-Rad DCode system (Bio-Rad, Mississauga, Ont.).

Results and Discussion

Abundance of gram negative (Gram -) and gram positive (Gram +) bacteria and arbuscular mycorrhizal fungi (AMF) at Swift Current and Scott are illustrated in Figure 1. Significant increases occurred at the at the soil surface (0- to 5-cm depth) under NT in most cases. This is in agreement with other results from the same study that demonstrated increased total, bacteria and fungal biomass in NT soils (Helgason et al. 2009). The absolute vs. relative abundance of gram negative bacteria at Scott illustrated in Figure 2 demonstrates the trend observed across most microbial groups studied. Specifically, that microbial abundance in NT increased but the proportion of the community made up of various groups of organisms remained unchanged between tillage treatments and among different depth increments. Ordination of the total PLFA profile data, expressed as mol % (using non-metric multidimensional scaling) demonstrated a clear influence of depth on microbial community structure (Fig. 3a), while tillage treatment was not a significant factor (Fig. 3b).

Analysis of community structure at Swift Current and Scott using DNA fingerprinting of the bacterial 16S rRNA gene also showed a dominant influence of depth on community structure (Fig 4a, b). Tillage did not have an influence on clustering of bacterial taxonomic units in either the entire soil profile (0- to 15-cm), or within individual depth increments.

Implications

Tillage did not have a dominant effect on microbial community structure the long-term NT and IT soils studied. Rather, community structure was influenced most by depth. Despite a lack of difference in community structure in NT vs. IT, the greater microbial biomass observed (0- to 5-cm) was sustained after approximately 25 years of NT management can influence the rates of important nutrient turnover processes.

References

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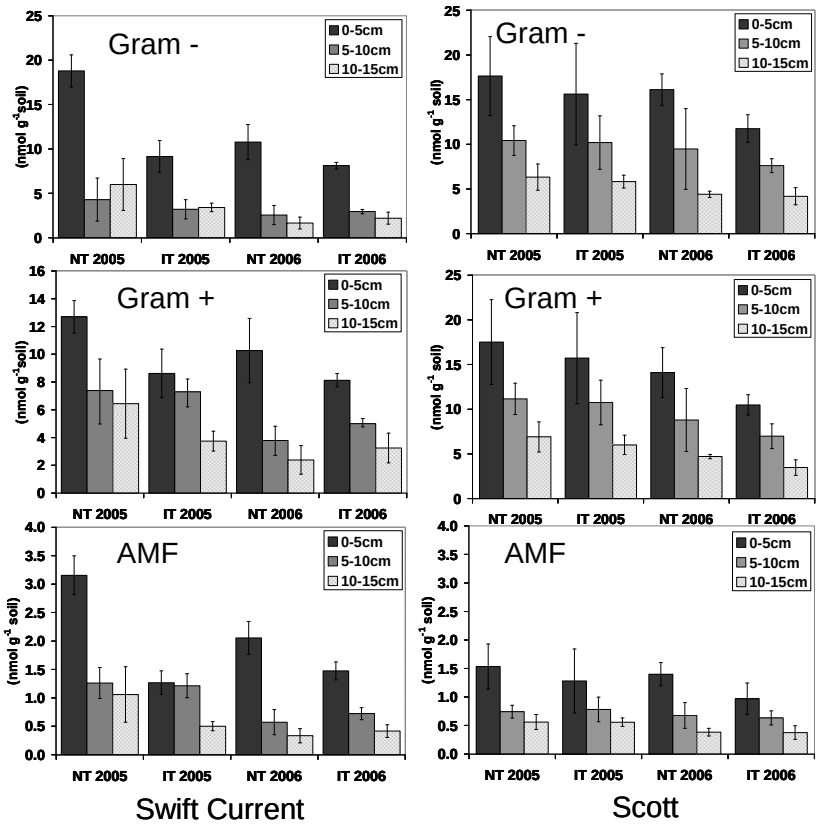

Figure 1. Phospholipid fatty acid biomarkers extracted from NT and IT soils.

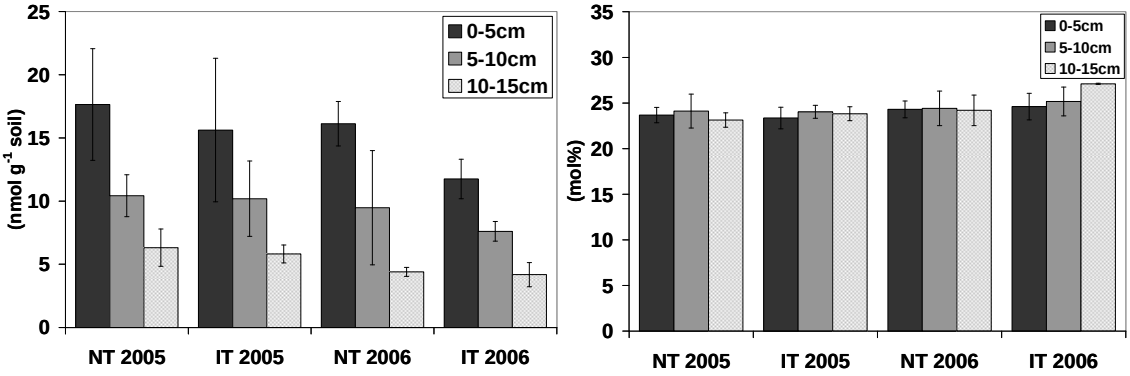

Figure 2. Absolute (nmol g^{-1} soil) vs. relative (mol%) abundance of gram negative bacteria at Scott.

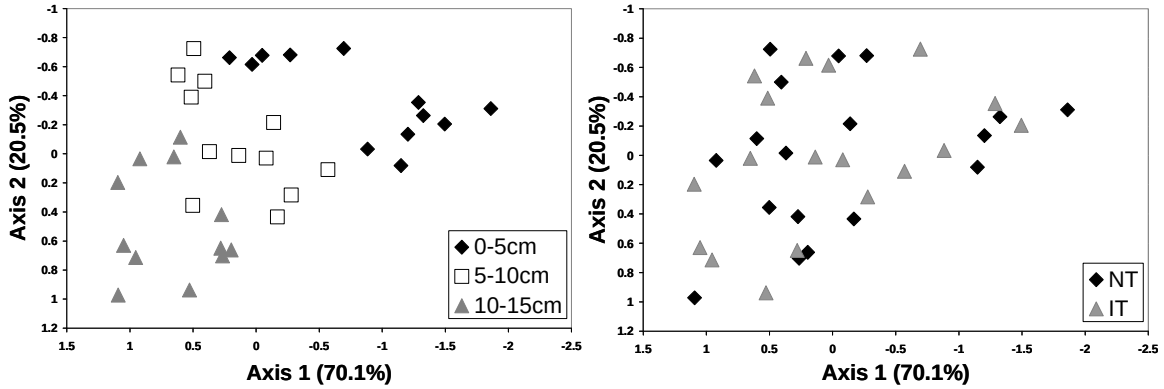

Figure 3. Ordination analysis PLFA profiles by depth (a) and tillage (b) using non-metric multidimensional scaling.

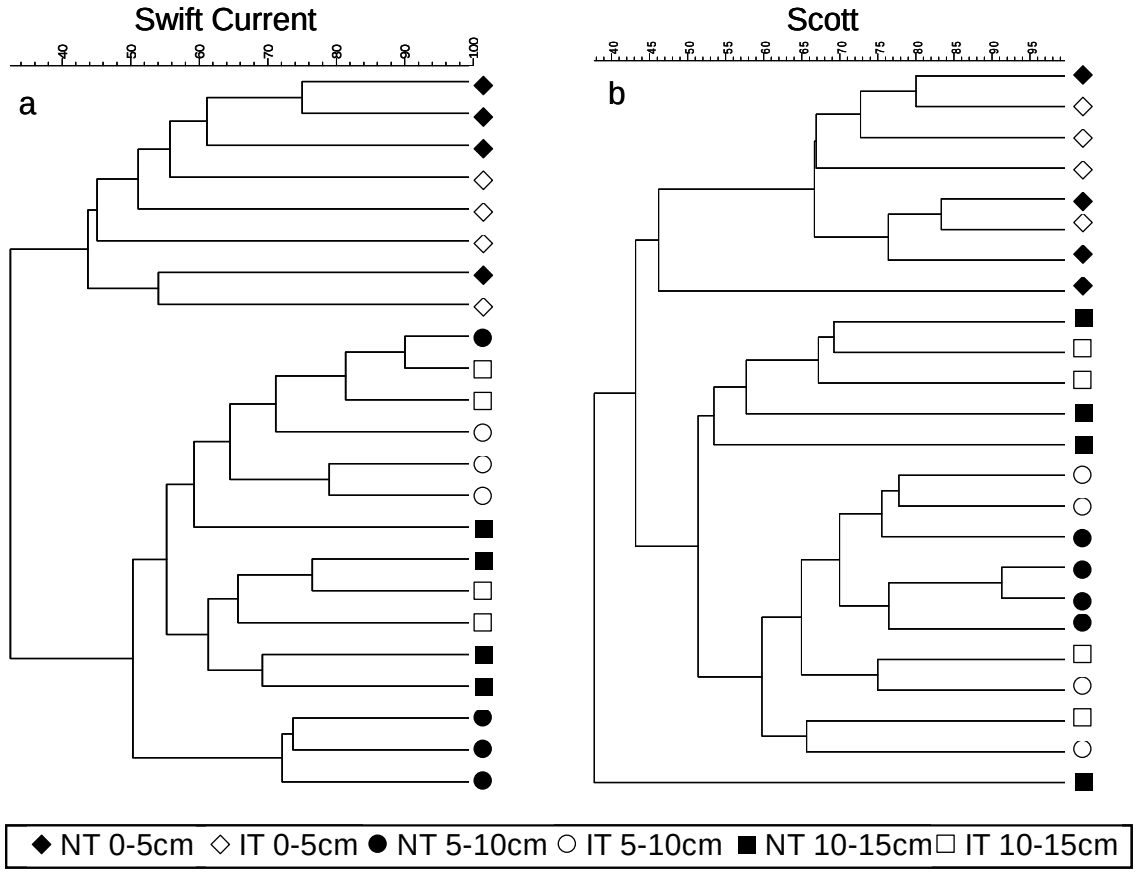

Figure 4. Dendrograms of 16S rRNA gene fingerprints at Swift Current (a) and Scott (b).