

Microbial Diversity in Long-Term Plots Using Pyrosequencing

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Introduction and Rationale

Vast number and types of microorganisms in soil are responsible for soil functions such as plant residue decomposition, maintenance of soil structure, nitrogen fixation, breakdown of toxic compounds, improvement of water quality, and emissions of greenhouse gases.

The soil bacterial community can serve as an indicator of soil health.

Genetic material, that is deoxyribonucleic acid (DNA), of bacteria can be used to study the bacterial community in a particular soil.

Knowledge about the bacterial community in soil may help farmers:

- Understand how crop production practices affect the diversity and function of bacterial species in soil.
- Better maintain high crop yields while helping to reduce the potential impacts of agriculture on climate change.

Objective

Determine the diversity of the types of bacteria in soils managed under continuous corn without rotation and under long-term (52 years) no-till (NT) and plow-till (PT) practices.

Experimental Procedure

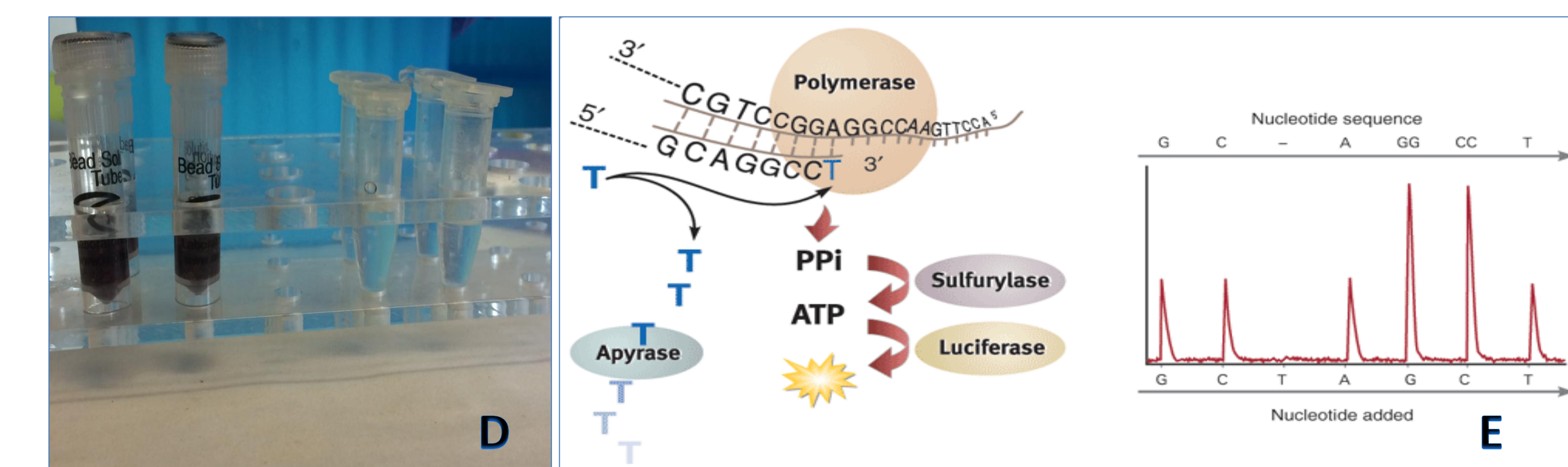


Figure 1. Pictorial representation of procedure: (A) no-till corn, (B) plow till corn, (C) collecting 10 cm deep soil samples, (D) extracting genomic DNA from bacteria in soil, and (E) pyrosequencing of bacterial DNA.

Results and Discussion

Properties	No-Till	Plow-Till
Genomic DNA concentration (ug/g)	4.72	3.17
pH	4.8	5.9
% organic matter (loss on ignition)	3.57	3.15

Table 1. NT soil had higher genomic DNA concentration than PT soil. Both soils were acidic with the NT soil needing a lime treatment. Organic matter accumulated in surface soil over 52 years to a higher level under NT than PT.

Community Parameters	No-Till	Plow-Till
Number of bacterial species	2740	1894
10 most abundant phyla and their relative abundance	<ul style="list-style-type: none"> Acidobacteria (36%) Proteobacteria (31%) Bacteroidetes (5%) Chloroflexi (5%) Actinobacteria (4%) Planctomycetes (3%) Gemmatimonadetes (3%) Nitrospirae (2%) OD1 (2%) Verrucomicrobia (1%) 	<ul style="list-style-type: none"> Proteobacteria (35%) Acidobacteria (26%) Actinobacteria (6%) Bacteroidetes (6%) Gemmatimonadetes (5%) Chloroflexi (5%) Planctomycetes (4%) Nitrospirae (2%) Verrucomicrobia (2%) WS3 (1%)

Table 2. A total of 2740 bacterial species were identified in NT soil as compared to 1894 bacterial species in PT soil. This indicates a higher species richness in NT as compared to PT soil. The ten most abundant phyla in each soil sample is shown. Each of the remaining phyla in both the soils had a relative abundance of <1%.

Above-ground activities bring about changes in the below-ground environment. The changes affect soil quality, microbial functions, plant-microbe interactions and finally soil productivity. Results in **Tables 1 and 2** and in **Figure 2** indicate that conservation tillage practices like NT not only create a soil environment that has the potential to increase organic matter content but also to affect the bacterial community richness as compared to soil mixing practices such as PT.

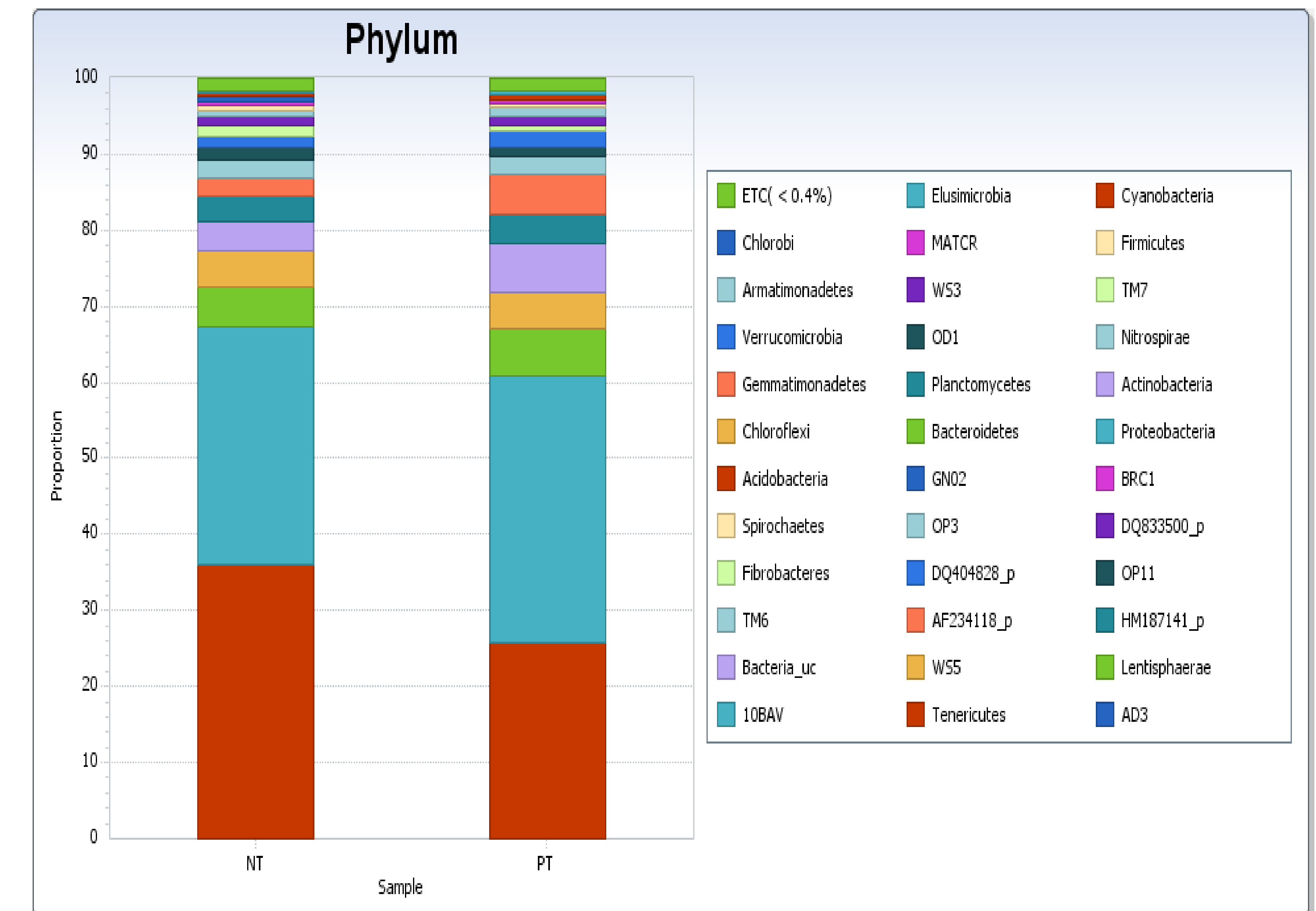


Figure 2. Relative abundance of bacterial phylogenetic groups in NT and PT soils. A total of 35 phylogenetic groups were identified in total for the NT and PT soils. NT soils had five unique groups (HM187141_p, Bacteria_uc, DQ404828_p, TM7 and, Lentisphaerae) with Acidobacteria comprising of 36% of the total population. PT soil had four unique groups (Spirochaetes, Tenericutes, 10BAV and, DQ833500_p) with Proteobacteria being the dominant (35%) phylum,

Conclusions

Long-term tillage practices affect soil chemical properties and microbial diversity. The relative abundance of the phyla Acidobacteria in NT and PT suggest the acid pH of the soils was a major factor affecting species distribution and composition. Although significant differences between types and relative abundances of phyla between the two soil samples were established, members of the phylum Acidobacteria and Proteobacteria were predominate across both samples. NT soil exhibited higher species richness than PT soil. The findings of our study can serve as a basis for conducting in-depth interaction studies between physico-chemical properties of soil and bacterial diversity. Our study also has the potential to help farmers understand climate-related challenges like greenhouse gas mitigation in terms of cropping systems, land-use management practices and the roles of microbes in soil.

Acknowledgments

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